



wwPDB EM Validation Summary Report ⓘ

Dec 29, 2024 – 11:44 PM EST

PDB ID : 7Z34
EMDB ID : EMD-14471
Title : Structure of pre-60S particle bound to DRG1(AFG2).
Authors : Prattes, M.; Grishkovskaya, I.; Bergler, H.; Haselbach, D.
Deposited on : 2022-03-01
Resolution : 3.80 Å(reported)
Based on initial model : 6N8K

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:

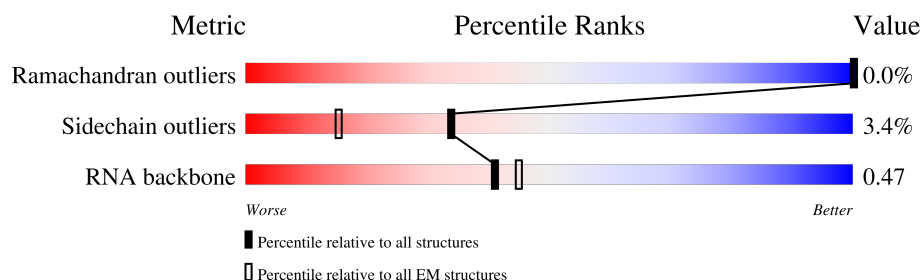
EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 3.80 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.






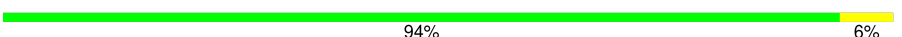
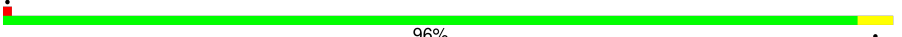





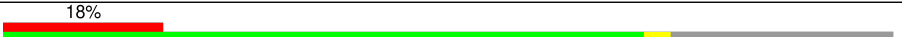


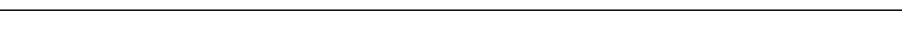
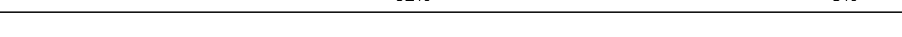
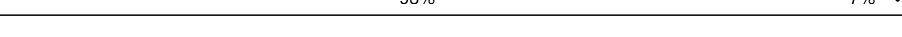
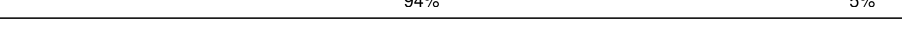
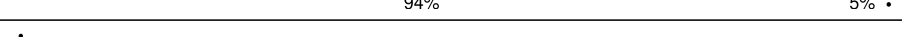
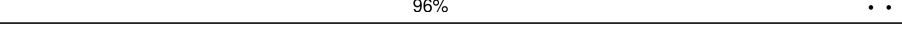
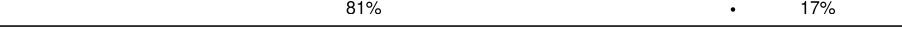

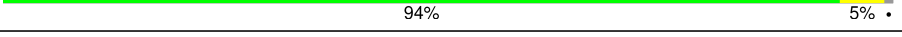
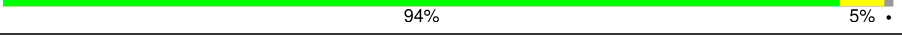

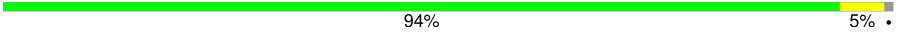
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	Aa	780	<div> <div>74%</div> <div>93%</div> <div>7%</div> </div>
1	m	780	<div> <div>69%</div> <div>93%</div> <div>6%</div> </div>
1	n	780	<div> <div>65%</div> <div>93%</div> <div>6%</div> </div>
1	t	780	<div> <div>60%</div> <div>94%</div> <div>6%</div> </div>
1	w	780	<div> <div>54%</div> <div>93%</div> <div>6%</div> </div>
1	x	780	<div> <div>66%</div> <div>94%</div> <div>6%</div> </div>
2	1	3396	<div> <div>72%</div> <div>26%</div> <div></div> </div>
3	2	121	<div> <div>83%</div> <div>17%</div> <div></div> </div>

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Mol	Chain	Length	Quality of chain
4	3	158	
5	4	593	
6	A	254	
7	B	387	
8	C	362	
9	D	297	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	I	166	
15	J	174	
16	K	149	
17	L	199	
18	M	138	
19	N	204	
20	O	199	
21	P	184	
22	Q	186	
23	R	189	
24	S	172	
25	T	160	
26	U	121	
27	V	137	
28	W	236	

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Mol	Chain	Length	Quality of chain
29	X	142	
30	Y	127	
31	Z	136	
32	a	165	
33	b	647	
34	c	105	
35	d	113	
36	e	130	
37	f	107	
38	g	121	
39	h	120	
40	i	100	
41	j	88	
42	k	78	
43	l	51	
44	o	59	
45	p	92	
46	q	106	
47	r	261	
48	u	199	
49	v	518	
50	y	245	
51	z	106	
52	0	19	
53	oC	170	

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 177847 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 ATPase family gene 2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	728	Total	C	N	O	S	0	0
			5590	3536	954	1078	22		
1	m	730	Total	C	N	O	S	0	0
			5594	3533	958	1081	22		
1	n	730	Total	C	N	O	S	0	0
			5602	3541	958	1081	22		
1	t	731	Total	C	N	O	S	0	0
			5611	3547	960	1082	22		
1	w	734	Total	C	N	O	S	0	0
			5630	3556	963	1089	22		
1	x	734	Total	C	N	O	S	0	0
			5630	3556	963	1089	22		

- Molecule 2 is a RNA chain called 35S pre-ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	3347	Total	C	N	O	P	0	0
			71573	31964	12868	23394	3347		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	157	Total	C	N	O	P	0	0
			3333	1491	584	1101	157		

- Molecule 5 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	560	Total	C	N	O	S	0	0
			4331	2732	747	837	15		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	245	Total	C	N	O	S	0	0
			1863	1162	376	324	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	273	Total	C	N	O	S	0	0
			2204	1391	382	429	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	175	Total	C	N	O	S	0	0
			1401	902	251	247	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 14 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	124	Total	C	N	O	S	0	0
			1003	628	186	185	4		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	164	Total	C	N	O	S	0	0
			1312	822	245	242	3		

- Molecule 16 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	L	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	137	Total	C	N	O	S	0	0
			1060	678	200	180	2		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	183	Total	C	N	O	0	0
			1443	896	287	260		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	154	Total	C	N	O	S	0	0
			1191	753	231	205	2		

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	154	Total	C	N	O	0	0
			1241	772	262	207		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	170	Total	C	N	O	S	0	0
			1425	916	265	241	3		

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	104	Total	C	N	O	0	0
			826	535	136	155		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	V	136	Total	C	N	O	S	0
			1004	628	189	180	7	0

- Molecule 28 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	225	Total	C	N	O	S	0
			1810	1148	306	351	5	0

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	X	120	Total	C	N	O	S	0
			960	617	168	173	2	0

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Y	126	Total	C	N	O	0	0
			994	625	192	177		

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Z	135	Total	C	N	O	0	0
			1093	710	202	181		

- Molecule 32 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	158	Total	C	N	O	S	0
			1196	750	216	228	2	0

- Molecule 33 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	630	Total	C	N	O	S	0	0
			5087	3185	914	962	26		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	128	Total	C	N	O	S	0	0
			1029	652	206	170	1		

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	77	Total	C	N	O	S	0	0
			613	391	115	107			

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 44 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	54	Total	C	N	O	S	0	0
			434	271	94	69			

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 46 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 47 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	55	Total	C	N	O	S	0	0
			470	291	100	78	1		

- Molecule 48 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	149	Total	C	N	O	S	0	0
			1256	788	252	207	9		

- Molecule 49 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	245	Total	C	N	O	S	0	0
			1946	1250	329	360	7		

- Molecule 50 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	228	Total	C	N	O	S	0	0
			1722	1068	299	349	6		

- Molecule 51 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	55	Total	C	N	O	0	0
			444	273	88	83		

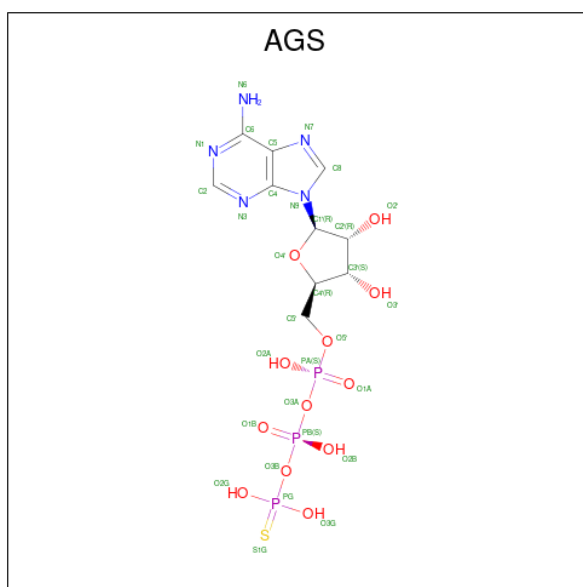
- Molecule 52 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	0	19	Total	C	N	O	0	0
			96	57	19	20		

- Molecule 53 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	oC	170	Total	C	N	O	0	0
			1021	680	170	171		

- Molecule 54 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms						AltConf
54	Aa	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	Aa	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	m	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	m	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	n	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	n	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	t	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	w	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	w	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	w	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
54	x	1	Total 31	C 10	N 5	O 12	P 3	S 1	0

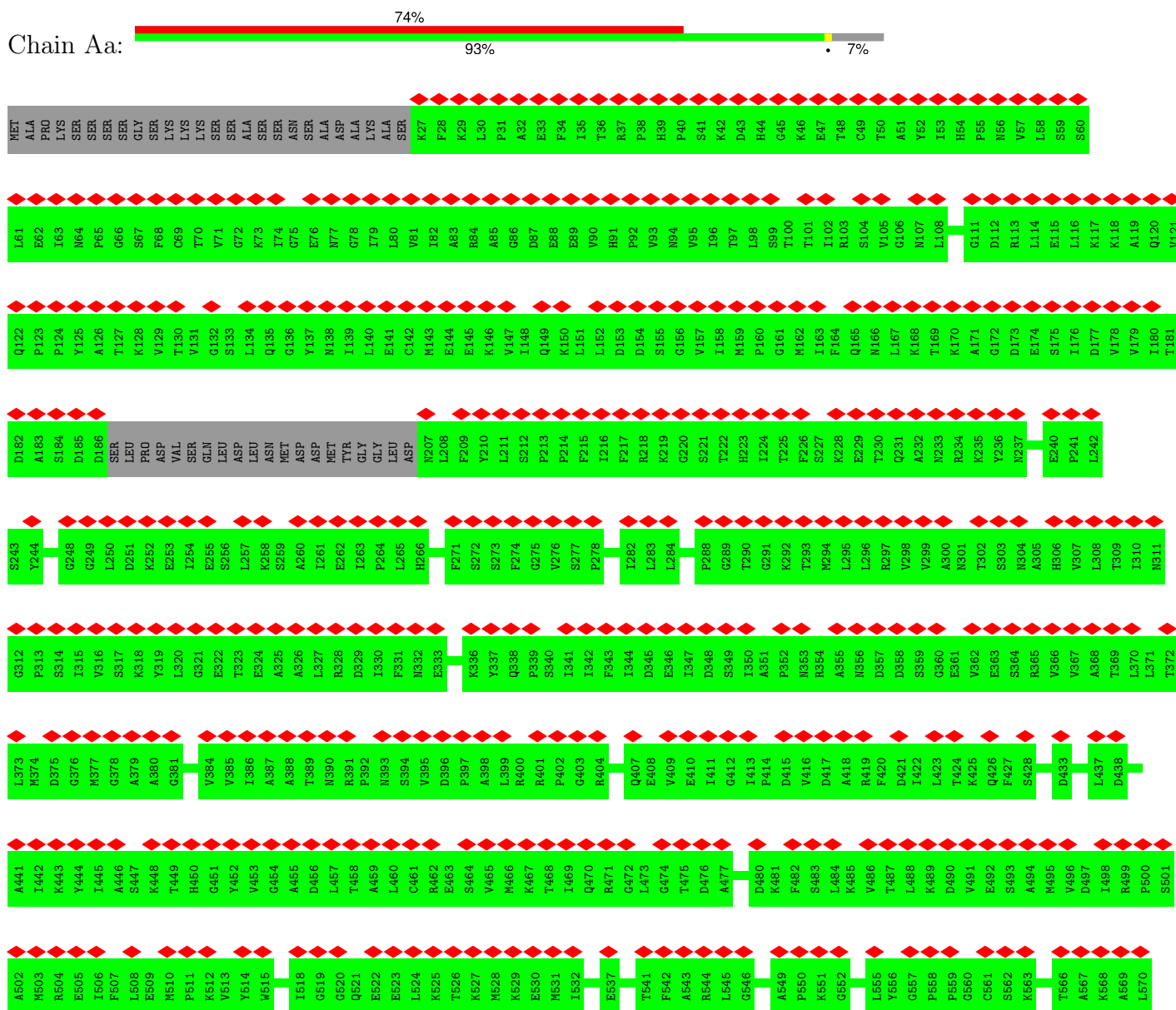
- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

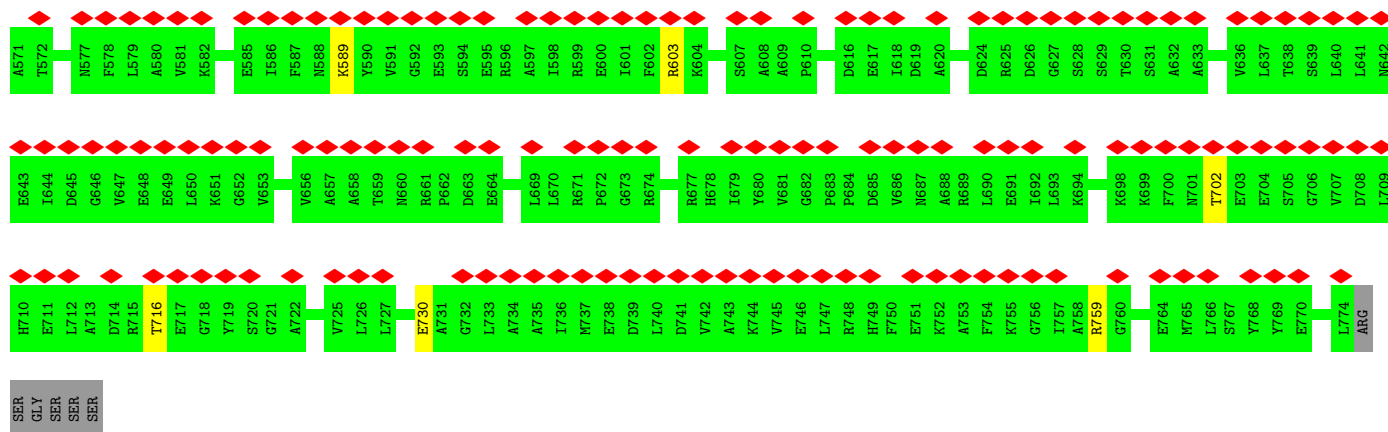
Mol	Chain	Residues	Atoms		AltConf
55	b	1	Total 1	Mg 1	0

3 Residue-property plots

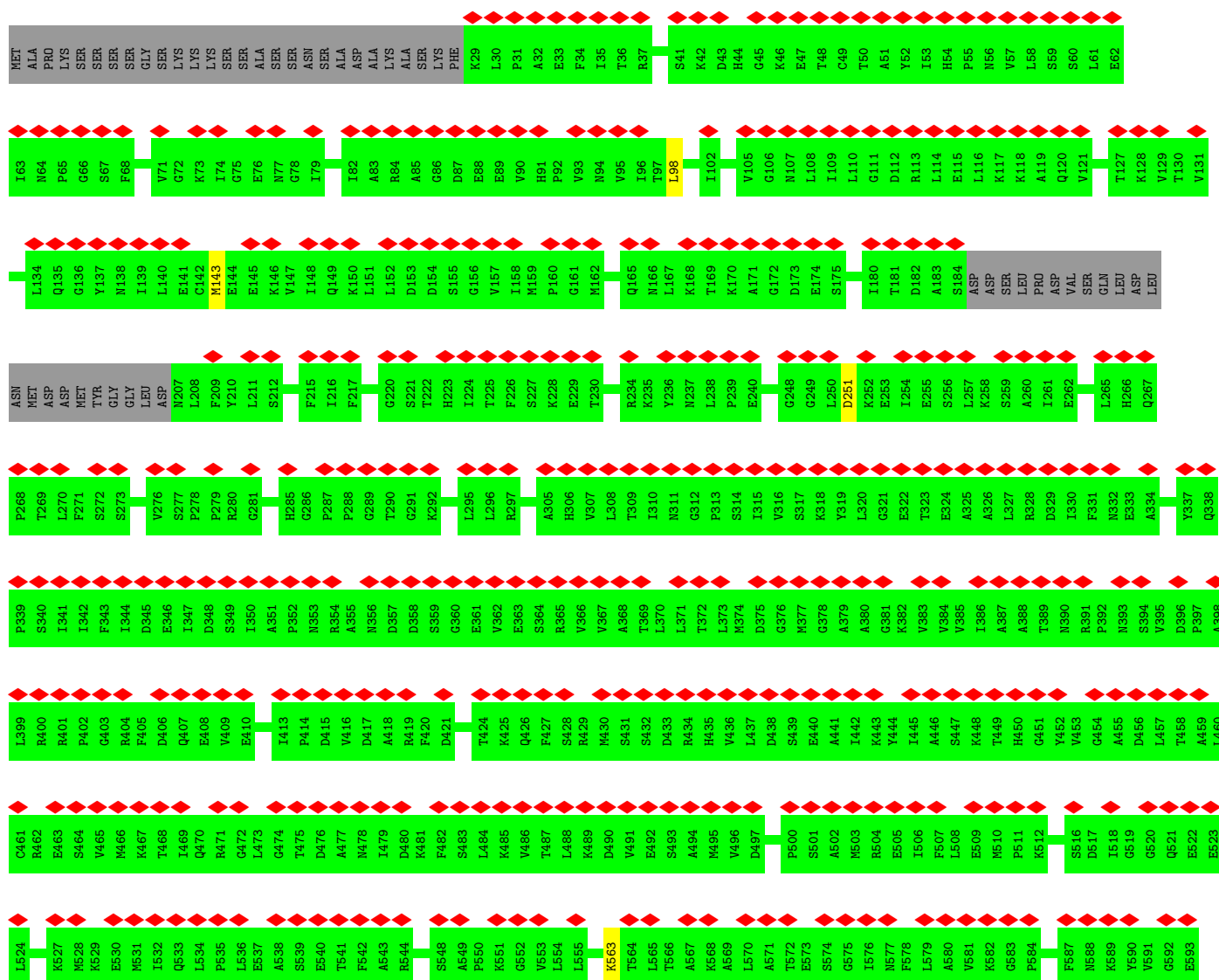
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

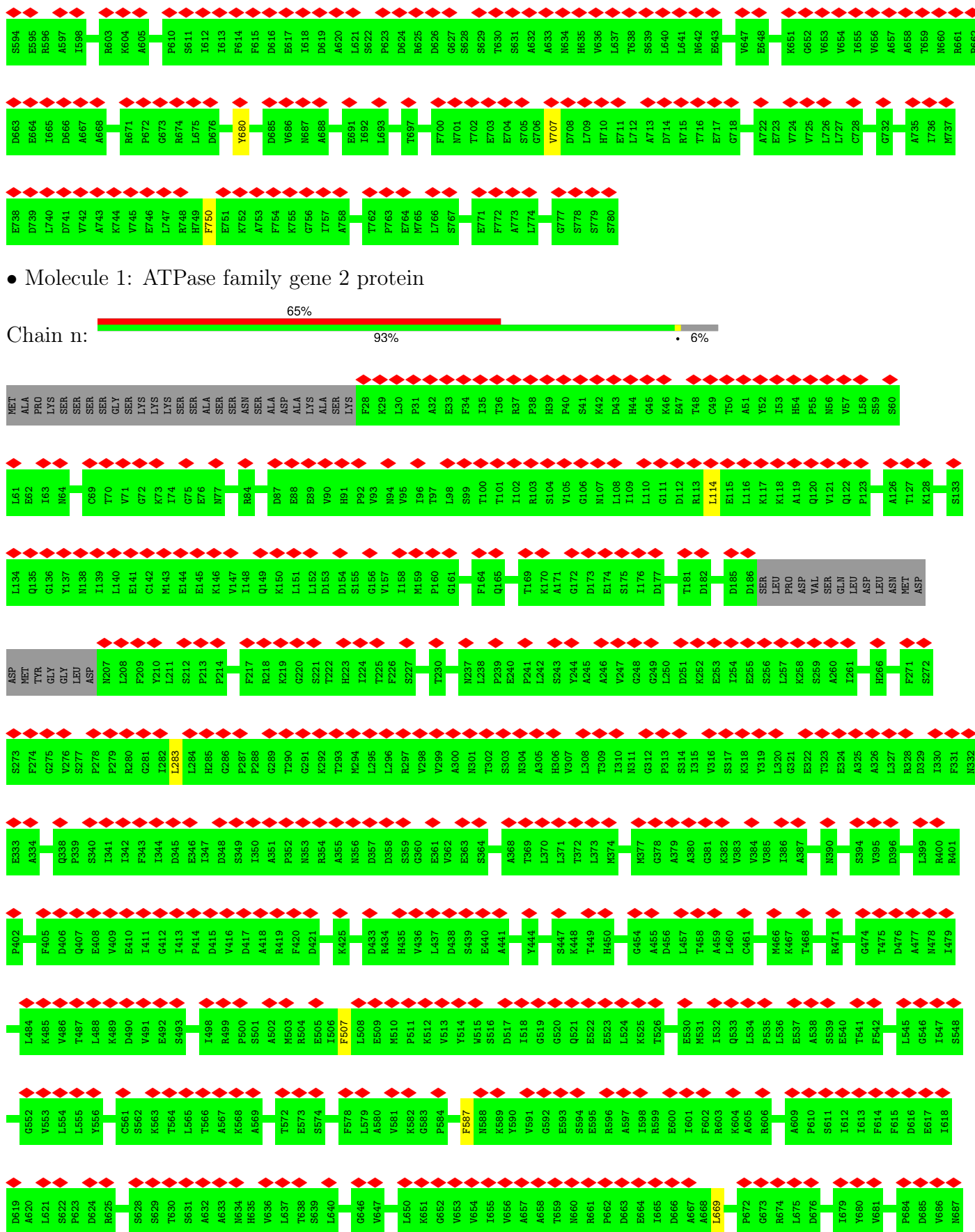
• Molecule 1: ATPase family gene 2 protein

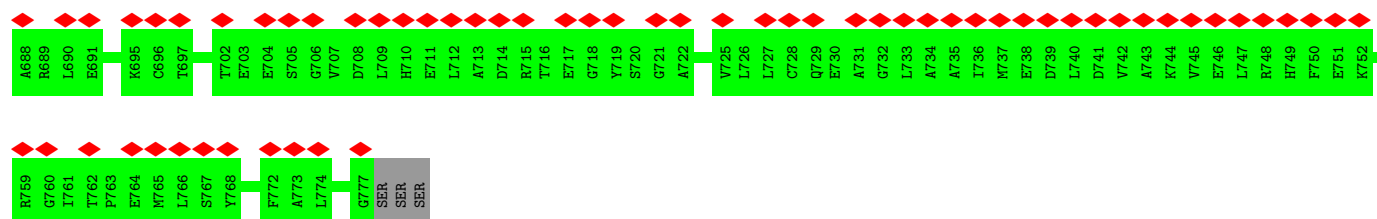




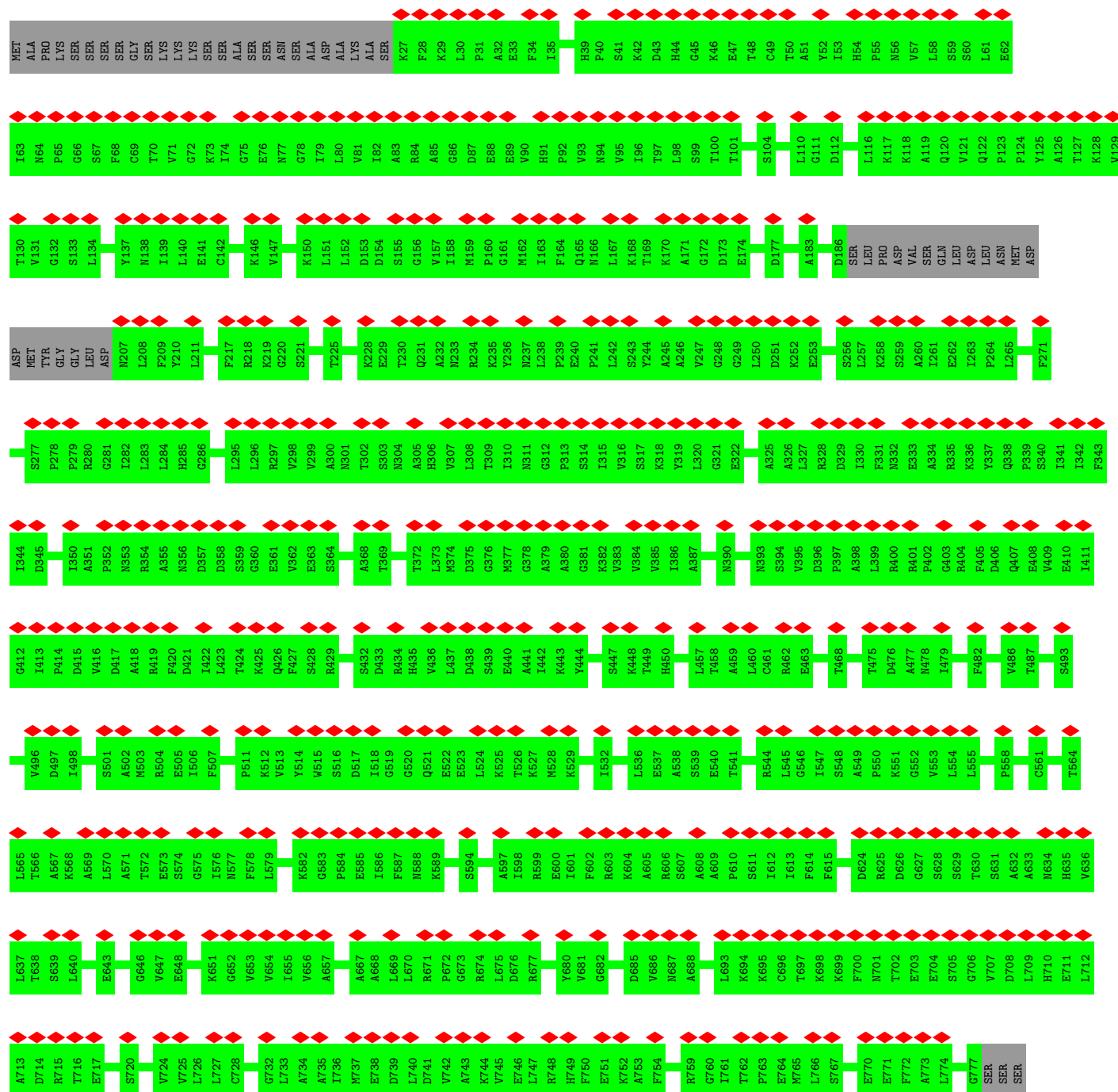
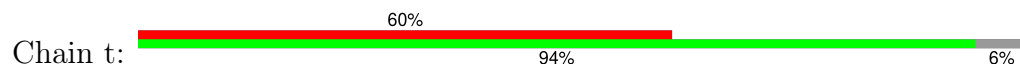
• Molecule 1: ATPase family gene 2 protein



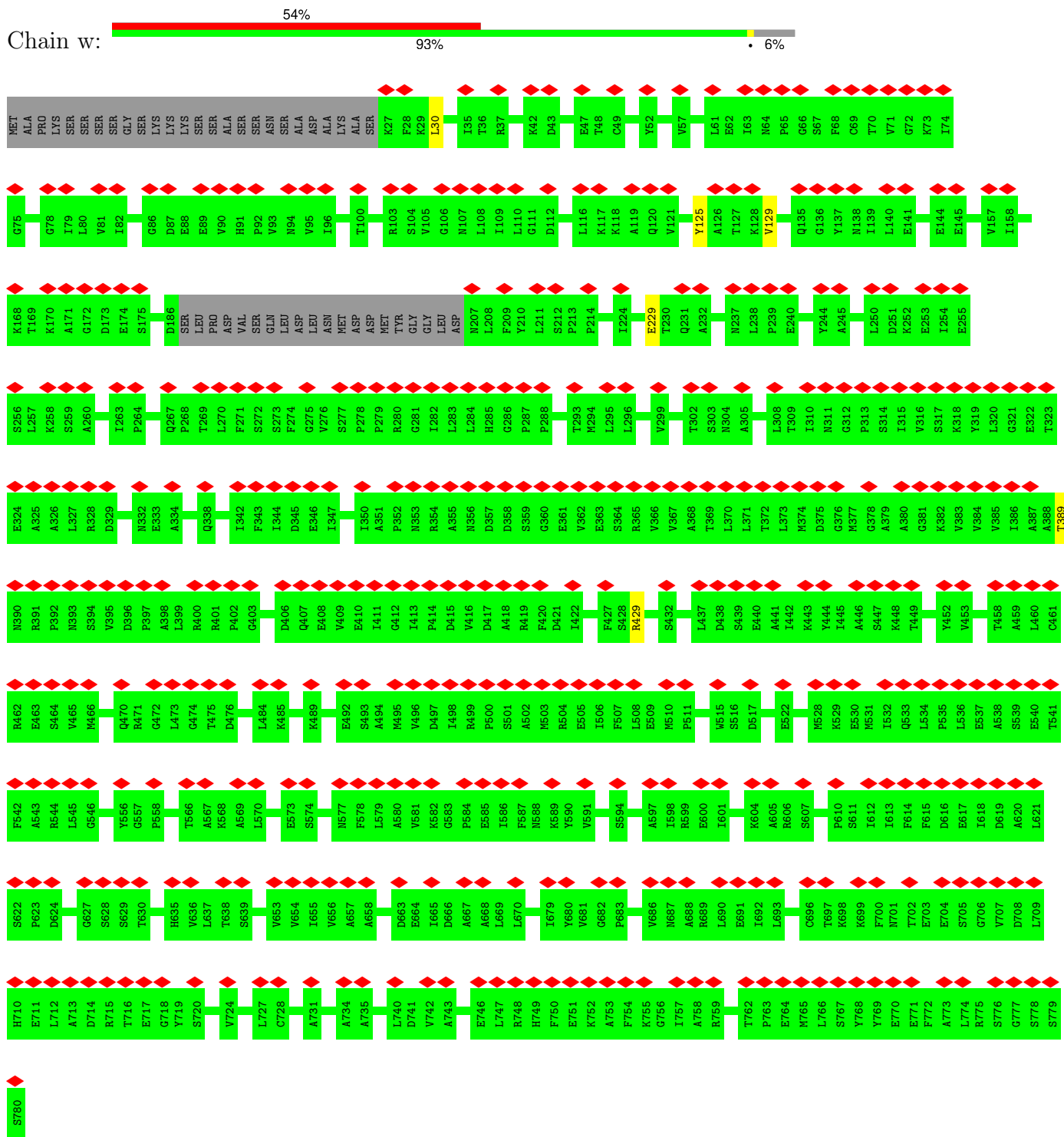




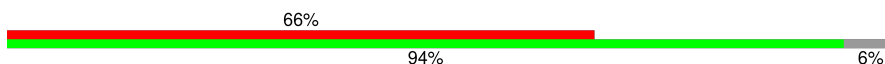
• Molecule 1: ATPase family gene 2 protein

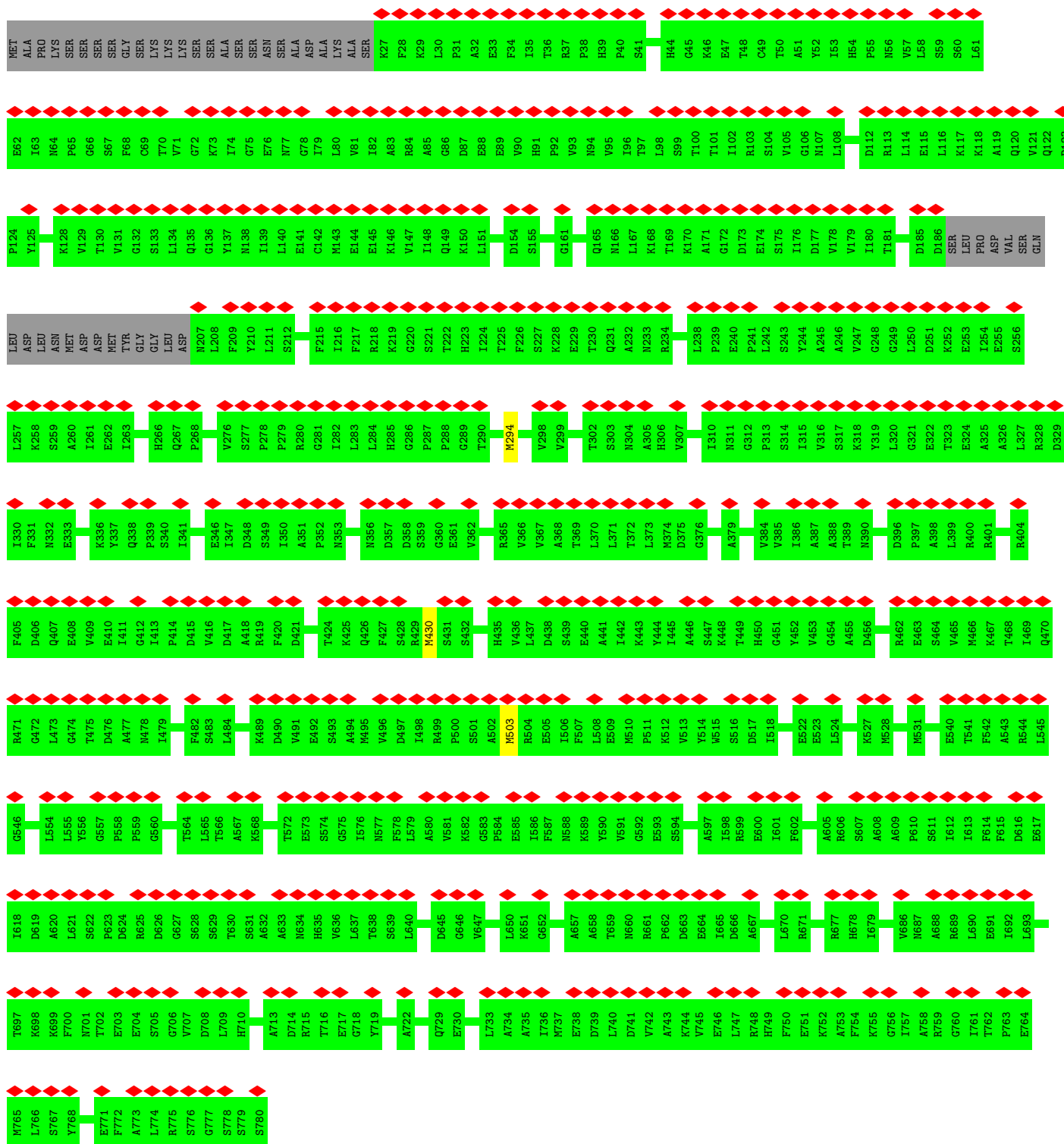


Chain w:

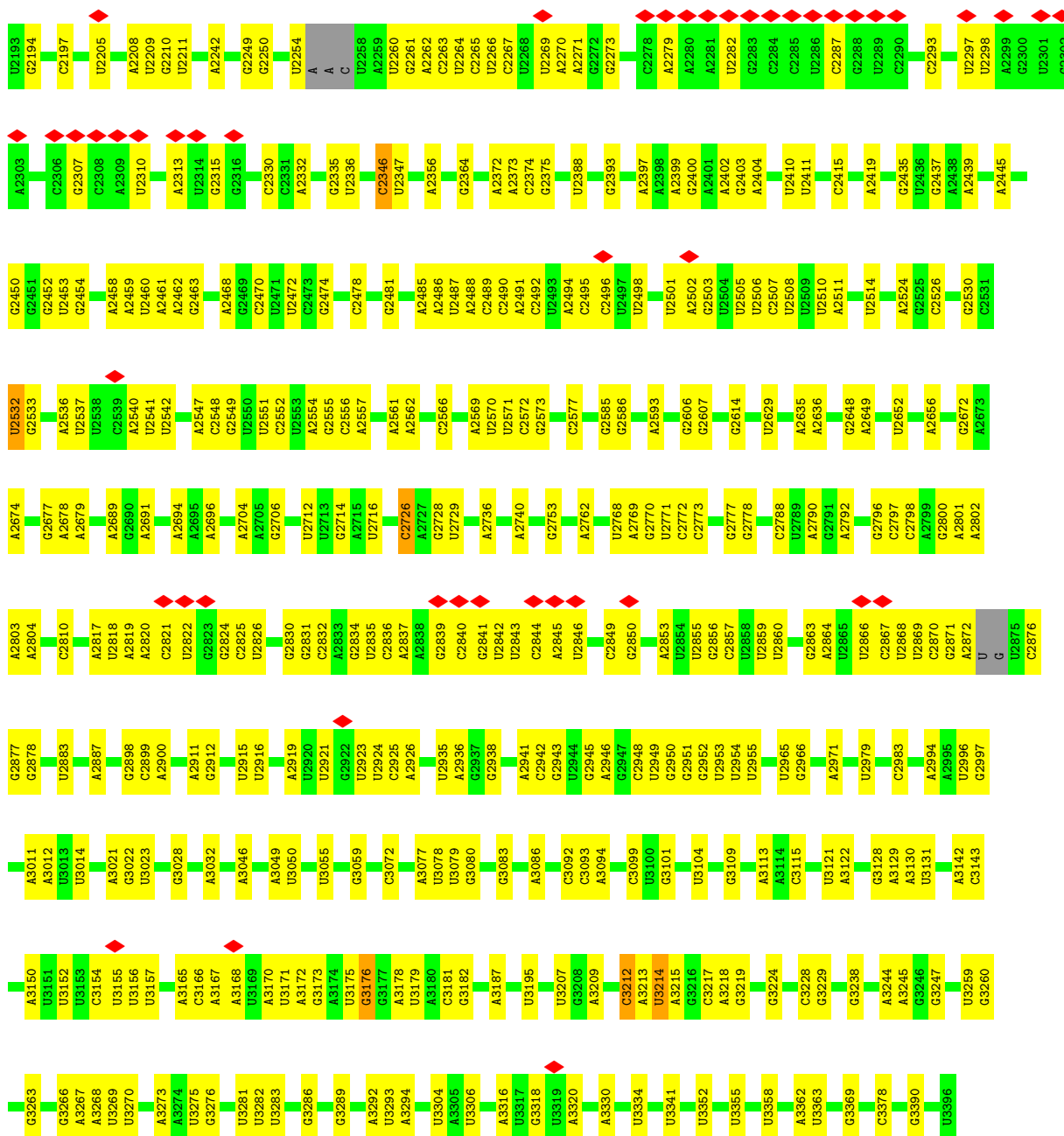


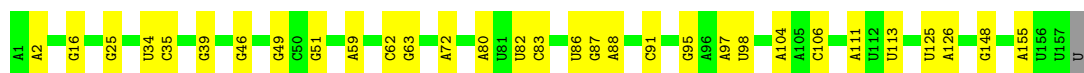
Chain x:





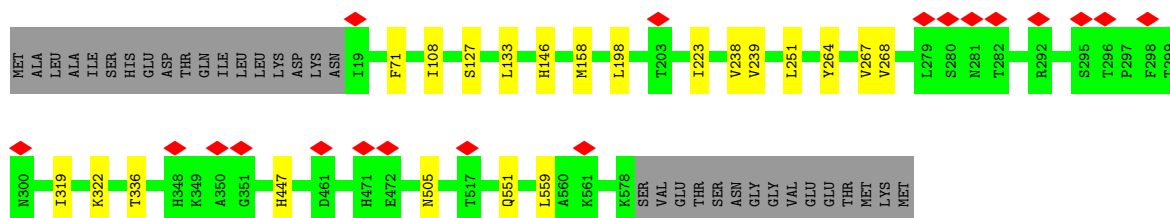






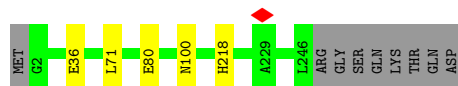
- Molecule 5: Probable metalloprotease ARX1

Chain 4: 91% 6%



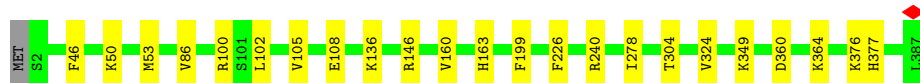
- Molecule 6: 60S ribosomal protein L2-A

Chain A: 94% 6%



- Molecule 7: 60S ribosomal protein L3

Chain B: 94% 6%



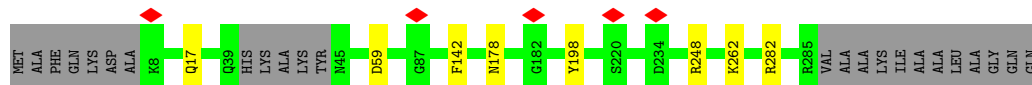
- Molecule 8: 60S ribosomal protein L4-A

Chain C: 96% 4%



- Molecule 9: 60S ribosomal protein L5

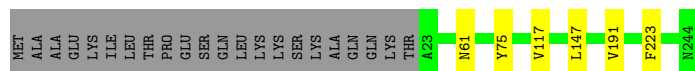
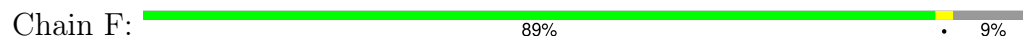
Chain D: 89% 8%



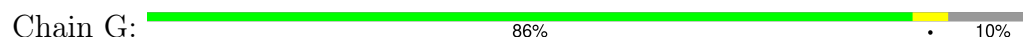
- Molecule 10: 60S ribosomal protein L6-A

Chain E: 94% 6%

- Molecule 11: 60S ribosomal protein L7-A



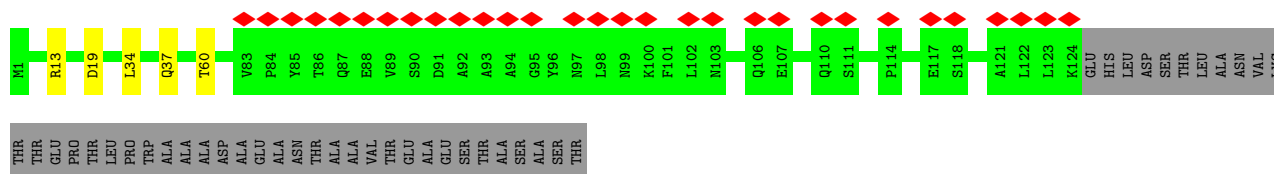
- Molecule 12: 60S ribosomal protein L8-A



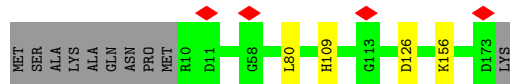
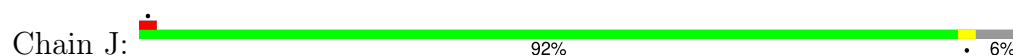
- Molecule 13: 60S ribosomal protein L9-A



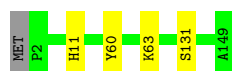
- Molecule 14: Bud site selection protein 20



- Molecule 15: 60S ribosomal protein L11-A



- Molecule 16: 60S ribosomal protein L28



- Molecule 17: 60S ribosomal protein L13-A

Chain L:  92% 5%



- Molecule 18: 60S ribosomal protein L14-A

Chain M:  93% 7%



- Molecule 19: 60S ribosomal protein L15-A

Chain N:  94% 5%



- Molecule 20: 60S ribosomal protein L16-A

Chain O:  94% 5%




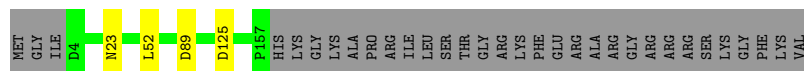
- Molecule 21: 60S ribosomal protein L17-A

Chain P:  96%




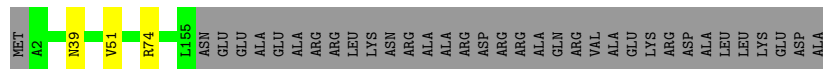
- Molecule 22: 60S ribosomal protein L18-A

Chain Q:  81% 17%



- Molecule 23: 60S ribosomal protein L19-A

Chain R:  80% 19%



- Molecule 24: 60S ribosomal protein L20-A

Chain S:  94% 5%




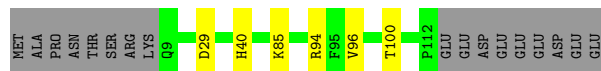
- Molecule 25: 60S ribosomal protein L21-A

Chain T:  94% 5%



- Molecule 26: 60S ribosomal protein L22-A

Chain U:  81% 5% 14%

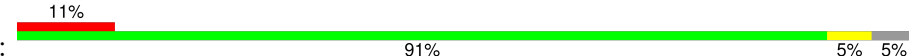


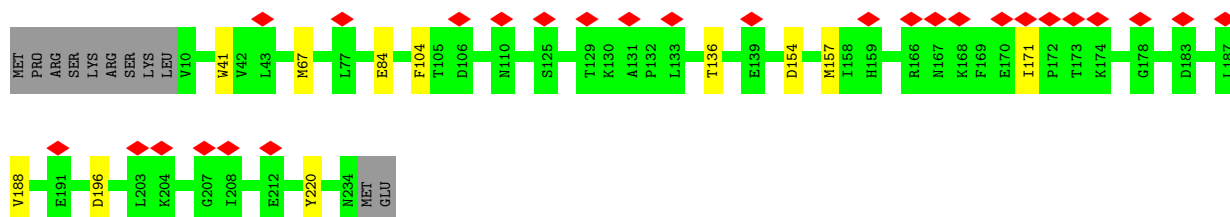
- Molecule 27: 60S ribosomal protein L23-A

Chain V:  94% 5%




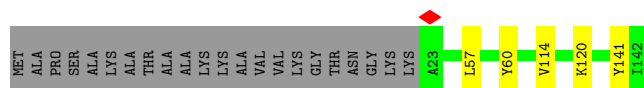
- Molecule 28: Ribosome assembly factor MRT4

Chain W:  11% 91% 5% 5%



- Molecule 29: 60S ribosomal protein L25

Chain X:  81% 15%



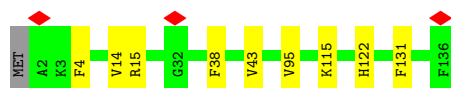
- Molecule 30: 60S ribosomal protein L26-A

Chain Y:  96%



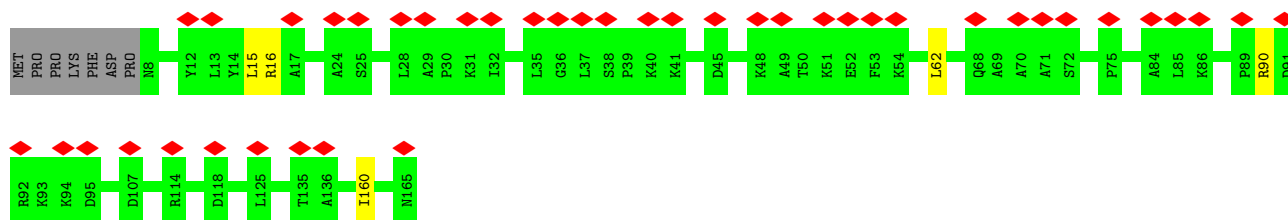
- Molecule 31: 60S ribosomal protein L27-A

Chain Z:  93%

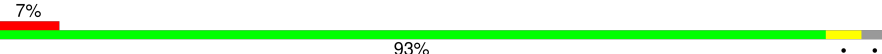


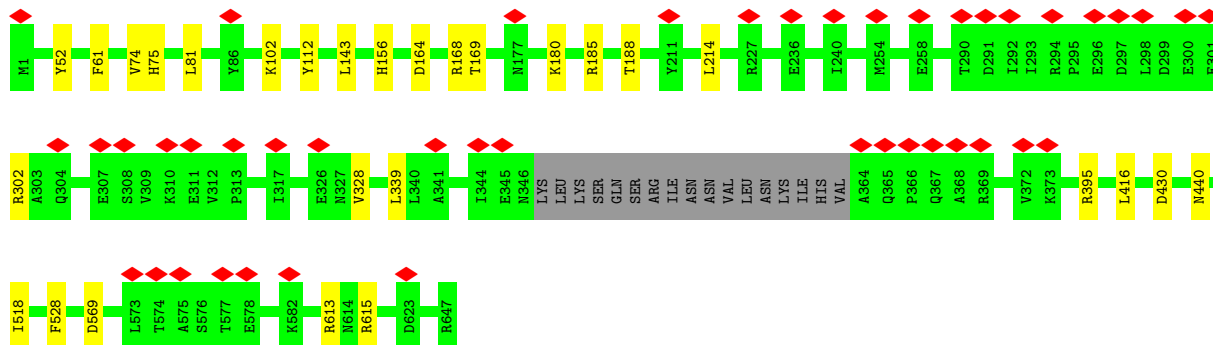
- Molecule 32: 60S ribosomal protein L12-A

Chain a:  25% 93%




- Molecule 33: Nucleolar GTP-binding protein 1

Chain b:  7% 93%



- Molecule 34: 60S ribosomal protein L30

Chain c:  90% 8%



- Molecule 35: 60S ribosomal protein L31-A

Chain d:  90% 5%



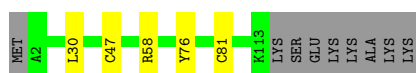
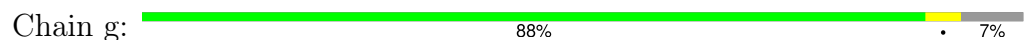
- Molecule 36: 60S ribosomal protein L32



- Molecule 37: 60S ribosomal protein L33-A



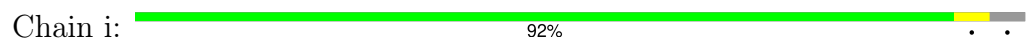
- Molecule 38: 60S ribosomal protein L34-A



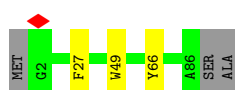
- Molecule 39: 60S ribosomal protein L35-A



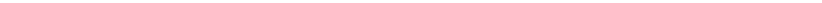
- Molecule 40: 60S ribosomal protein L36-A

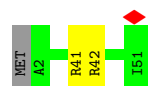


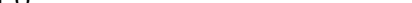
- Molecule 41: 60S ribosomal protein L37-A

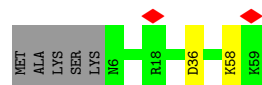


- Molecule 42: 60S ribosomal protein L38

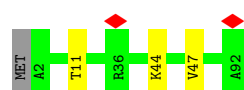
- Chain 1:  94%



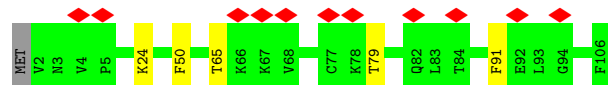
- Chain o:  88% 8%



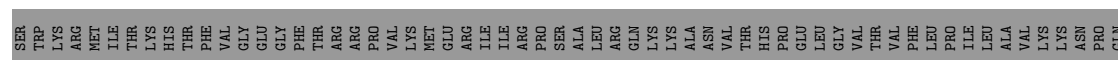
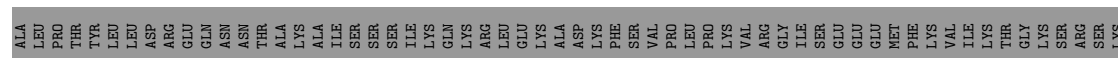
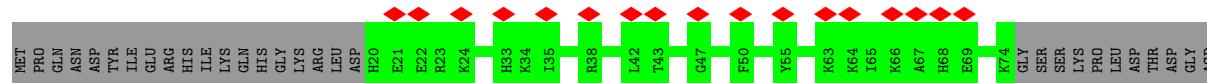
- Chain p: 96%



- Chain q:  10% 94% 5%

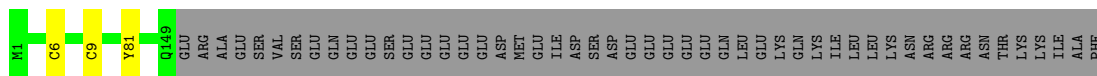


- Chain r:  7% 21% 79%



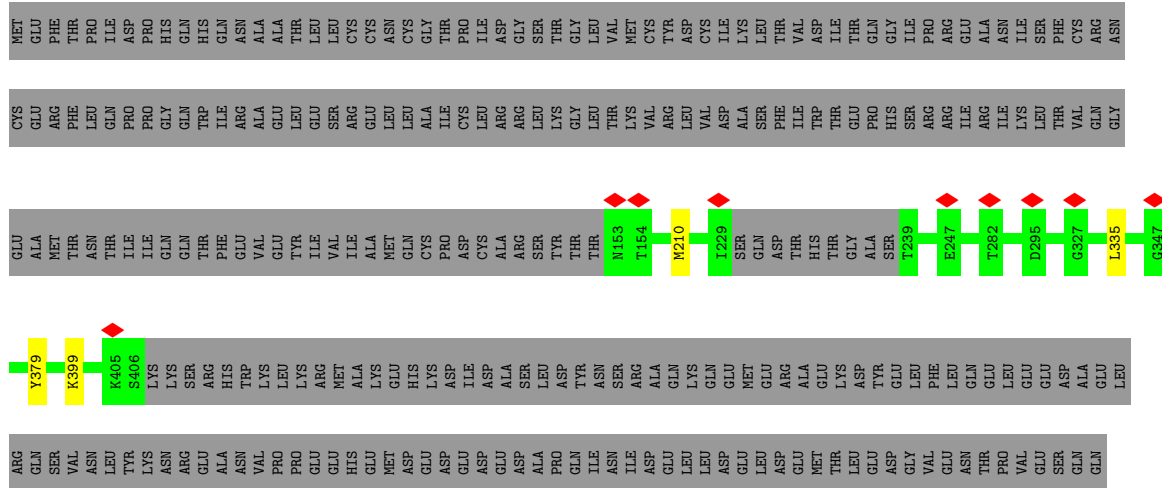
- Molecule 48: Ribosome biogenesis protein RLP24

Chain u:  73% . 25%




- Molecule 49: 60S ribosomal export protein NMD3

Chain v:  47% 53%



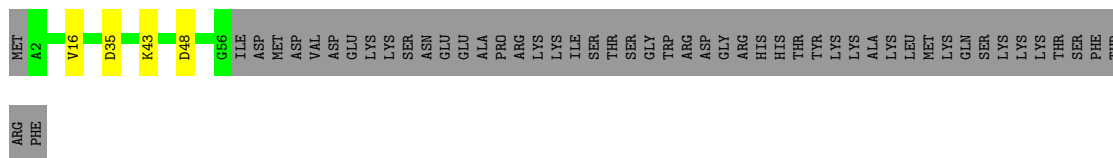
- Molecule 50: Eukaryotic translation initiation factor 6

Chain y:  87% 6% 7%



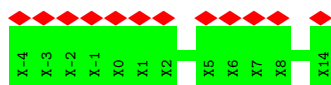
- Molecule 51: UPF0642 protein YBL028C

Chain z:  48% 0 48%



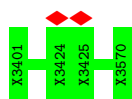
- Molecule 52: Unknown peptide

Chain 0:  63% 100%



- Molecule 53: Unknown protein

Chain oC:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1782014	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.047	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	642.0, 642.0, 642.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3375, 1.3375, 1.3375	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, AGS

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	Aa	0.24	0/5688	0.46	0/7700
1	m	0.24	0/5691	0.45	0/7702
1	n	0.24	0/5700	0.45	0/7716
1	t	0.24	0/5709	0.45	0/7727
1	w	0.24	0/5728	0.45	0/7751
1	x	0.24	0/5728	0.46	0/7751
2	1	0.29	0/80102	0.79	30/124881 (0.0%)
3	2	0.26	0/2883	0.77	0/4491
4	3	0.30	0/3724	0.76	0/5798
5	4	0.25	0/4410	0.49	0/5990
6	A	0.26	0/1897	0.55	0/2550
7	B	0.27	0/3153	0.53	0/4239
8	C	0.26	0/2802	0.51	0/3792
9	D	0.26	0/2250	0.50	0/3035
10	E	0.26	0/1425	0.49	0/1912
11	F	0.27	0/1822	0.49	0/2451
12	G	0.26	0/1830	0.48	0/2469
13	H	0.26	0/1514	0.49	0/2039
14	I	0.24	0/1018	0.47	0/1365
15	J	0.24	0/1332	0.53	0/1786
16	K	0.26	0/1204	0.50	0/1612
17	L	0.26	0/1568	0.55	0/2106
18	M	0.25	0/1075	0.50	0/1446
19	N	0.27	0/1758	0.56	0/2354
20	O	0.26	0/1586	0.49	0/2128
21	P	0.26	0/1466	0.53	0/1968
22	Q	0.25	0/1211	0.52	0/1633
23	R	0.24	0/1258	0.56	0/1679
24	S	0.27	0/1460	0.51	0/1962
25	T	0.26	0/1300	0.51	0/1743
26	U	0.26	0/843	0.46	0/1143
27	V	0.27	0/1019	0.52	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	W	0.25	0/1842	0.48	0/2487
29	X	0.27	0/975	0.49	0/1314
30	Y	0.26	0/1005	0.51	0/1341
31	Z	0.27	0/1119	0.48	0/1497
32	a	0.24	0/1210	0.46	0/1627
33	b	0.25	0/5171	0.50	0/6947
34	c	0.25	0/751	0.45	0/1008
35	d	0.26	0/887	0.51	0/1191
36	e	0.25	0/1050	0.50	0/1406
37	f	0.28	0/869	0.54	0/1168
38	g	0.26	0/891	0.55	0/1191
39	h	0.25	0/979	0.51	0/1301
40	i	0.24	0/749	0.53	0/995
41	j	0.27	0/685	0.56	0/908
42	k	0.25	0/619	0.51	0/826
43	l	0.25	0/444	0.55	0/588
44	o	0.24	0/445	0.51	0/592
45	p	0.25	0/702	0.55	0/934
46	q	0.25	0/861	0.53	0/1136
47	r	0.23	0/476	0.46	0/621
48	u	0.26	0/1278	0.55	0/1699
49	v	0.25	0/1985	0.46	0/2692
50	y	0.25	0/1744	0.51	0/2375
51	z	0.23	0/445	0.46	0/585
All	All	0.27	0/187336	0.66	30/270717 (0.0%)

There are no bond length outliers.

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	3212	C	N1-C2-O2	12.89	126.63	118.90
2	1	3212	C	N3-C2-O2	-9.12	115.52	121.90
2	1	1827	C	N3-C2-O2	-8.53	115.93	121.90
2	1	2948	C	N3-C2-O2	-7.82	116.43	121.90
2	1	27	C	N1-C2-O2	7.59	123.45	118.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	Aa	724/780 (93%)	680 (94%)	42 (6%)	2 (0%)	37	69
1	m	726/780 (93%)	707 (97%)	17 (2%)	2 (0%)	37	69
1	n	726/780 (93%)	703 (97%)	23 (3%)	0	100	100
1	t	727/780 (93%)	706 (97%)	21 (3%)	0	100	100
1	w	730/780 (94%)	702 (96%)	28 (4%)	0	100	100
1	x	730/780 (94%)	709 (97%)	21 (3%)	0	100	100
5	4	558/593 (94%)	502 (90%)	56 (10%)	0	100	100
6	A	243/254 (96%)	226 (93%)	17 (7%)	0	100	100
7	B	384/387 (99%)	345 (90%)	39 (10%)	0	100	100
8	C	359/362 (99%)	329 (92%)	30 (8%)	0	100	100
9	D	269/297 (91%)	257 (96%)	12 (4%)	0	100	100
10	E	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
11	F	220/244 (90%)	211 (96%)	9 (4%)	0	100	100
12	G	228/256 (89%)	215 (94%)	13 (6%)	0	100	100
13	H	186/191 (97%)	180 (97%)	6 (3%)	0	100	100
14	I	122/166 (74%)	114 (93%)	8 (7%)	0	100	100
15	J	162/174 (93%)	150 (93%)	12 (7%)	0	100	100
16	K	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
17	L	191/199 (96%)	176 (92%)	15 (8%)	0	100	100
18	M	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
19	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	O	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
21	P	181/184 (98%)	170 (94%)	11 (6%)	0	100	100
22	Q	152/186 (82%)	145 (95%)	7 (5%)	0	100	100
23	R	152/189 (80%)	146 (96%)	6 (4%)	0	100	100
24	S	168/172 (98%)	154 (92%)	14 (8%)	0	100	100
25	T	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
26	U	102/121 (84%)	91 (89%)	11 (11%)	0	100	100
27	V	134/137 (98%)	128 (96%)	6 (4%)	0	100	100
28	W	223/236 (94%)	209 (94%)	14 (6%)	0	100	100
29	X	118/142 (83%)	114 (97%)	4 (3%)	0	100	100
30	Y	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
31	Z	133/136 (98%)	120 (90%)	13 (10%)	0	100	100
32	a	156/165 (94%)	153 (98%)	3 (2%)	0	100	100
33	b	626/647 (97%)	569 (91%)	57 (9%)	0	100	100
34	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
35	d	105/113 (93%)	98 (93%)	7 (7%)	0	100	100
36	e	126/130 (97%)	120 (95%)	6 (5%)	0	100	100
37	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
38	g	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
39	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
40	i	94/100 (94%)	92 (98%)	2 (2%)	0	100	100
41	j	83/88 (94%)	80 (96%)	3 (4%)	0	100	100
42	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
43	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
44	o	52/59 (88%)	48 (92%)	4 (8%)	0	100	100
45	p	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
46	q	103/106 (97%)	88 (85%)	15 (15%)	0	100	100
47	r	53/261 (20%)	51 (96%)	2 (4%)	0	100	100
48	u	147/199 (74%)	140 (95%)	7 (5%)	0	100	100
49	v	241/518 (46%)	225 (93%)	16 (7%)	0	100	100
50	y	226/245 (92%)	208 (92%)	18 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	z	53/106 (50%)	53 (100%)	0	0	100	100
All	All	12482/13870 (90%)	11795 (94%)	683 (6%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	m	563	LYS
1	Aa	589	LYS
1	Aa	702	THR
1	m	707	VAL

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	Aa	614/657 (94%)	610 (99%)	4 (1%)	81	86
1	m	615/657 (94%)	610 (99%)	5 (1%)	79	84
1	n	615/657 (94%)	610 (99%)	5 (1%)	79	84
1	t	616/657 (94%)	616 (100%)	0	100	100
1	w	619/657 (94%)	613 (99%)	6 (1%)	73	80
1	x	619/657 (94%)	616 (100%)	3 (0%)	86	90
5	4	491/520 (94%)	470 (96%)	21 (4%)	25	49
6	A	188/196 (96%)	183 (97%)	5 (3%)	40	60
7	B	322/323 (100%)	299 (93%)	23 (7%)	12	36
8	C	288/289 (100%)	275 (96%)	13 (4%)	23	47
9	D	230/245 (94%)	222 (96%)	8 (4%)	31	54
10	E	152/153 (99%)	142 (93%)	10 (7%)	14	38
11	F	186/205 (91%)	180 (97%)	6 (3%)	34	56
12	G	189/208 (91%)	179 (95%)	10 (5%)	19	44
13	H	168/171 (98%)	163 (97%)	5 (3%)	36	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	I	110/141 (78%)	105 (96%)	5 (4%)	23	47
15	J	142/150 (95%)	138 (97%)	4 (3%)	38	59
16	K	118/119 (99%)	114 (97%)	4 (3%)	32	55
17	L	154/159 (97%)	145 (94%)	9 (6%)	17	42
18	M	108/109 (99%)	99 (92%)	9 (8%)	9	32
19	N	175/176 (99%)	164 (94%)	11 (6%)	15	40
20	O	160/162 (99%)	151 (94%)	9 (6%)	17	43
21	P	145/146 (99%)	139 (96%)	6 (4%)	26	50
22	Q	126/151 (83%)	122 (97%)	4 (3%)	34	56
23	R	127/154 (82%)	124 (98%)	3 (2%)	44	62
24	S	154/156 (99%)	146 (95%)	8 (5%)	19	44
25	T	136/137 (99%)	128 (94%)	8 (6%)	16	41
26	U	91/107 (85%)	85 (93%)	6 (7%)	14	38
27	V	104/105 (99%)	97 (93%)	7 (7%)	13	38
28	W	202/213 (95%)	191 (95%)	11 (5%)	18	43
29	X	104/118 (88%)	99 (95%)	5 (5%)	21	46
30	Y	109/110 (99%)	105 (96%)	4 (4%)	29	53
31	Z	115/116 (99%)	106 (92%)	9 (8%)	10	34
32	a	129/136 (95%)	124 (96%)	5 (4%)	27	51
33	b	556/573 (97%)	528 (95%)	28 (5%)	20	45
34	c	81/88 (92%)	78 (96%)	3 (4%)	29	53
35	d	94/97 (97%)	89 (95%)	5 (5%)	19	44
36	e	110/111 (99%)	104 (94%)	6 (6%)	18	43
37	f	90/91 (99%)	84 (93%)	6 (7%)	13	38
38	g	95/103 (92%)	90 (95%)	5 (5%)	19	44
39	h	104/105 (99%)	97 (93%)	7 (7%)	13	38
40	i	78/82 (95%)	74 (95%)	4 (5%)	20	45
41	j	69/71 (97%)	66 (96%)	3 (4%)	25	49
42	k	68/69 (99%)	64 (94%)	4 (6%)	16	41
43	l	45/46 (98%)	43 (96%)	2 (4%)	24	48
44	o	43/47 (92%)	41 (95%)	2 (5%)	22	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	p	71/72 (99%)	68 (96%)	3 (4%)	25	49
46	q	90/91 (99%)	85 (94%)	5 (6%)	17	43
47	r	48/229 (21%)	48 (100%)	0	100	100
48	u	132/180 (73%)	129 (98%)	3 (2%)	45	63
49	v	220/467 (47%)	216 (98%)	4 (2%)	54	71
50	y	195/211 (92%)	180 (92%)	15 (8%)	10	34
51	z	48/95 (50%)	44 (92%)	4 (8%)	9	32
All	All	10658/11745 (91%)	10298 (97%)	360 (3%)	34	55

5 of 360 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	a	160	ILE
39	h	24	LEU
33	b	112	TYR
34	c	27	TYR
42	k	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
28	W	232	ASN
1	w	588	ASN
33	b	413	ASN
1	w	311	ASN
44	o	48	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	3342/3396 (98%)	870 (26%)	38 (1%)
3	2	120/121 (99%)	20 (16%)	0
4	3	156/158 (98%)	31 (19%)	0
All	All	3618/3675 (98%)	921 (25%)	38 (1%)

5 of 921 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	4	U
2	1	14	U
2	1	16	A
2	1	22	G
2	1	23	A

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	2547	A
2	1	3228	C
2	1	2845	A
2	1	2965	U
2	1	3292	A

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 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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
54	AGS	Aa	902	-	28,33,33	0.74	1 (3%)	31,52,52	0.98	2 (6%)
54	AGS	w	903	-	28,33,33	0.73	1 (3%)	31,52,52	0.93	2 (6%)
54	AGS	n	901	-	28,33,33	0.72	1 (3%)	31,52,52	0.97	2 (6%)
54	AGS	x	901	-	28,33,33	0.73	1 (3%)	31,52,52	1.06	3 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	AGS	Aa	901	-	28,33,33	0.72	1 (3%)	31,52,52	0.95	2 (6%)
54	AGS	n	902	-	28,33,33	0.74	1 (3%)	31,52,52	0.95	2 (6%)
54	AGS	w	902	-	28,33,33	0.73	1 (3%)	31,52,52	0.97	2 (6%)
54	AGS	m	902	-	28,33,33	0.74	1 (3%)	31,52,52	0.93	2 (6%)
54	AGS	t	801	-	28,33,33	0.73	1 (3%)	31,52,52	0.95	2 (6%)
54	AGS	m	901	-	28,33,33	0.73	1 (3%)	31,52,52	0.94	2 (6%)
54	AGS	w	901	-	28,33,33	0.72	1 (3%)	31,52,52	0.95	2 (6%)

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
54	AGS	Aa	902	-	-	1/17/38/38	0/3/3/3
54	AGS	w	903	-	-	4/17/38/38	0/3/3/3
54	AGS	n	901	-	-	5/17/38/38	0/3/3/3
54	AGS	x	901	-	-	2/17/38/38	0/3/3/3
54	AGS	Aa	901	-	-	3/17/38/38	0/3/3/3
54	AGS	n	902	-	-	4/17/38/38	0/3/3/3
54	AGS	w	902	-	-	3/17/38/38	0/3/3/3
54	AGS	m	902	-	-	2/17/38/38	0/3/3/3
54	AGS	t	801	-	-	6/17/38/38	0/3/3/3
54	AGS	m	901	-	-	4/17/38/38	0/3/3/3
54	AGS	w	901	-	-	7/17/38/38	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	m	902	AGS	PG-S1G	2.17	1.95	1.90
54	w	902	AGS	PG-S1G	2.17	1.95	1.90
54	n	902	AGS	PG-S1G	2.16	1.95	1.90
54	x	901	AGS	PG-S1G	2.16	1.95	1.90
54	Aa	901	AGS	PG-S1G	2.15	1.95	1.90

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	w	902	AGS	PB-O3B-PG	-3.73	119.53	133.17
54	w	901	AGS	PB-O3B-PG	-3.63	119.90	133.17
54	n	902	AGS	PB-O3B-PG	-3.55	120.16	133.17
54	n	901	AGS	PB-O3B-PG	-3.55	120.19	133.17
54	x	901	AGS	PB-O3B-PG	-3.53	120.23	133.17

There are no chirality outliers.

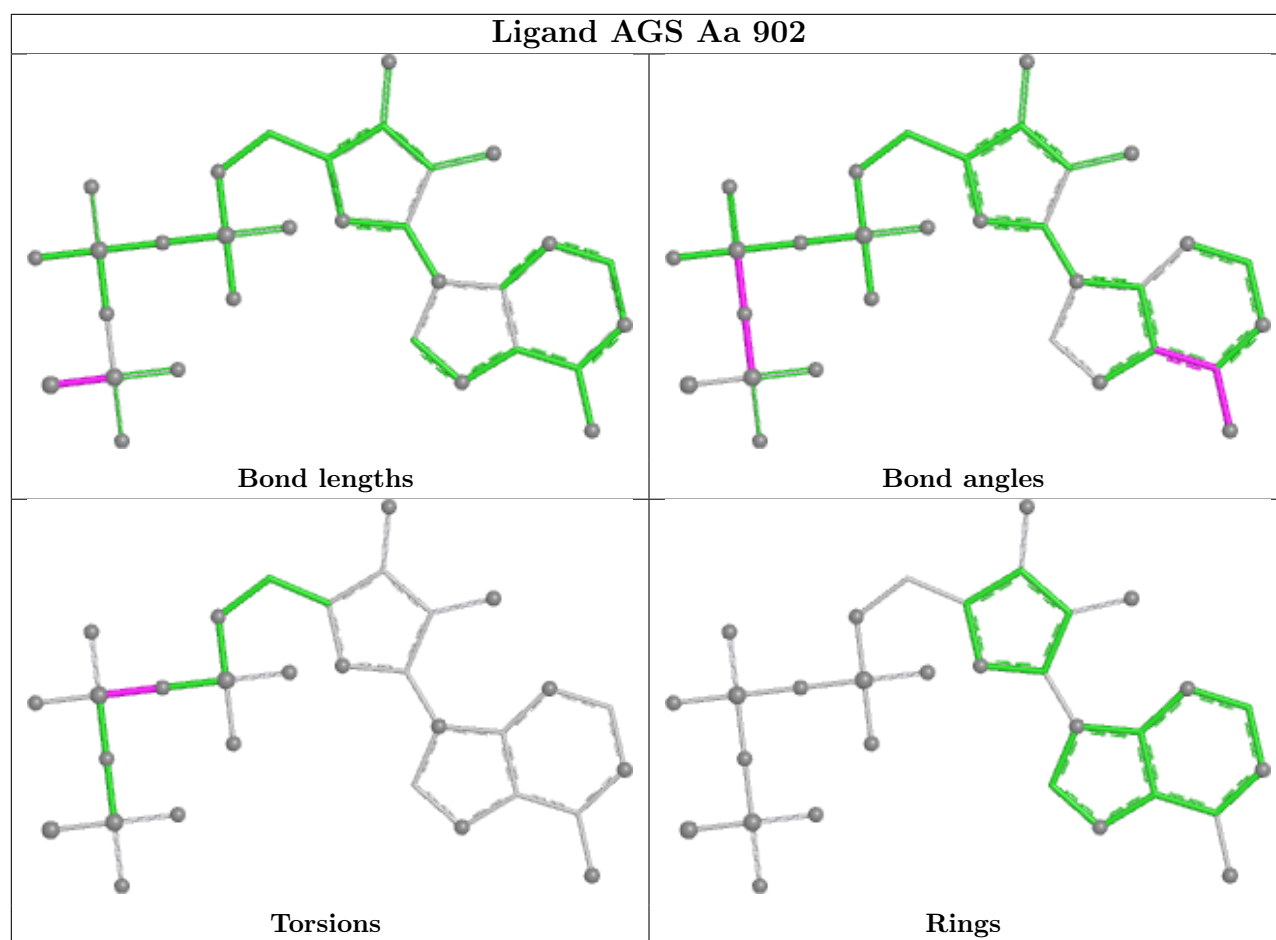
5 of 41 torsion outliers are listed below:

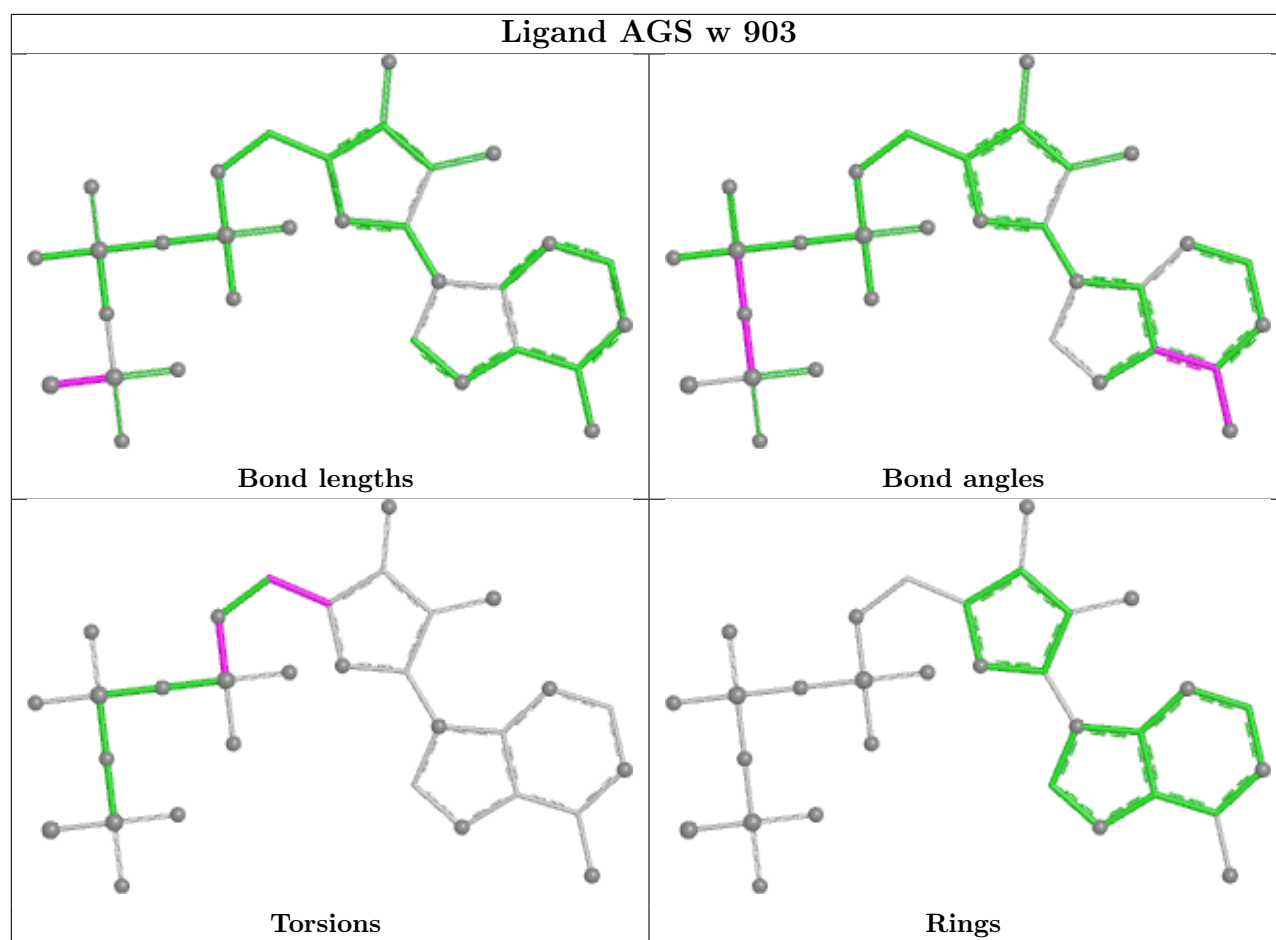
Mol	Chain	Res	Type	Atoms
54	m	902	AGS	PB-O3B-PG-O3G
54	n	901	AGS	PB-O3B-PG-O2G
54	n	901	AGS	PB-O3B-PG-O3G
54	n	902	AGS	C5'-O5'-PA-O2A
54	t	801	AGS	PB-O3B-PG-O2G

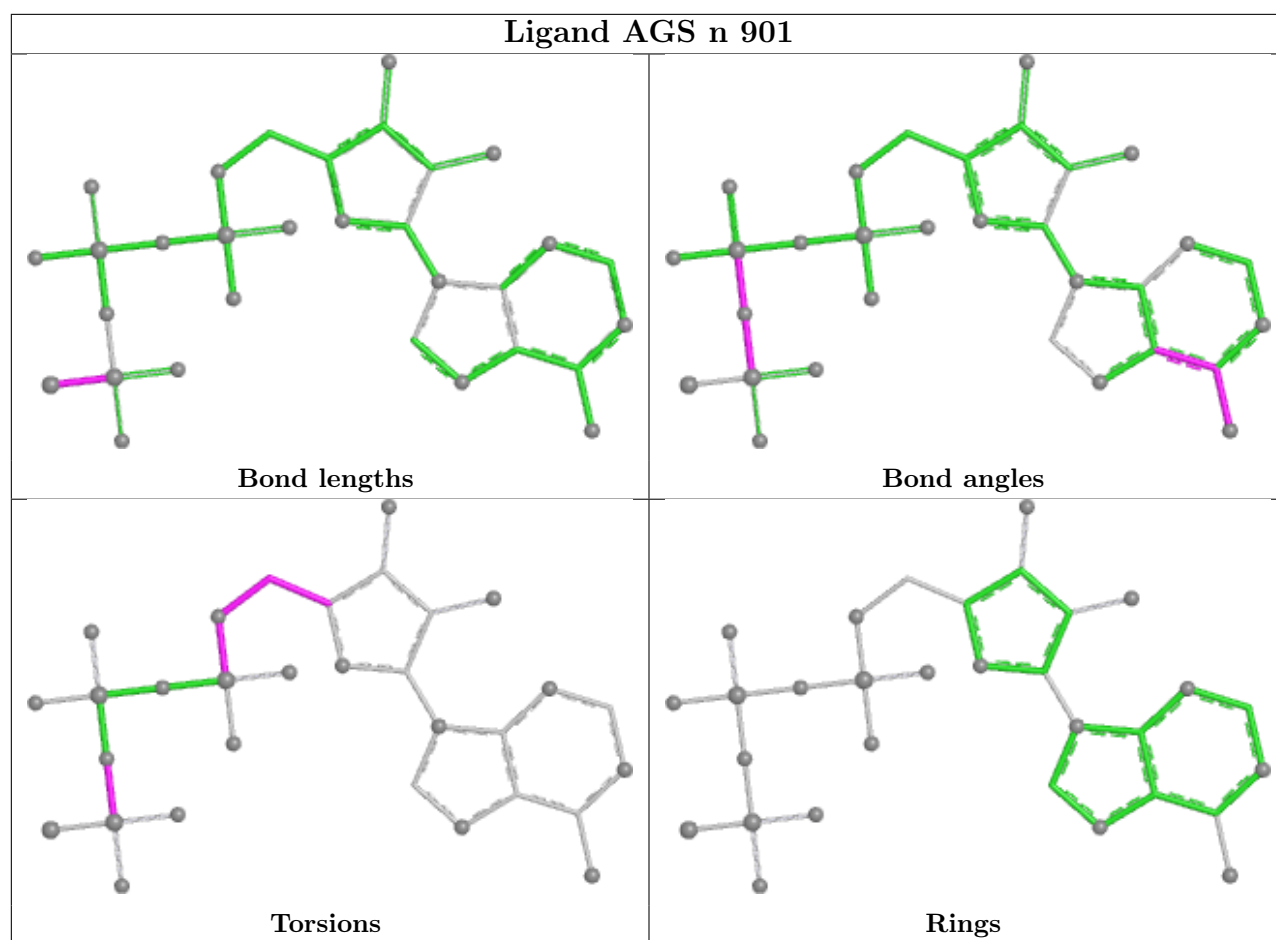
There are no ring outliers.

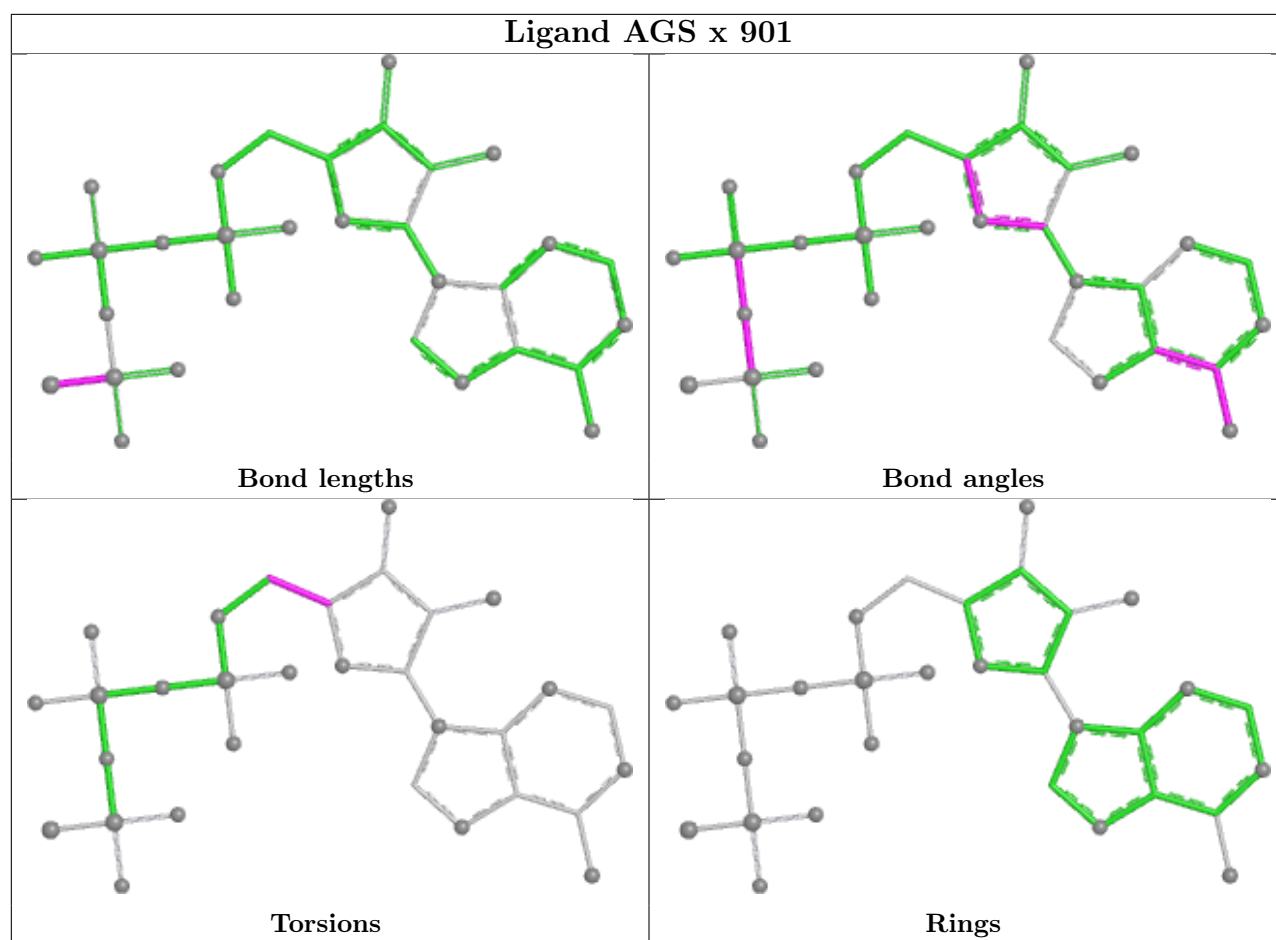
No monomer is involved in short contacts.

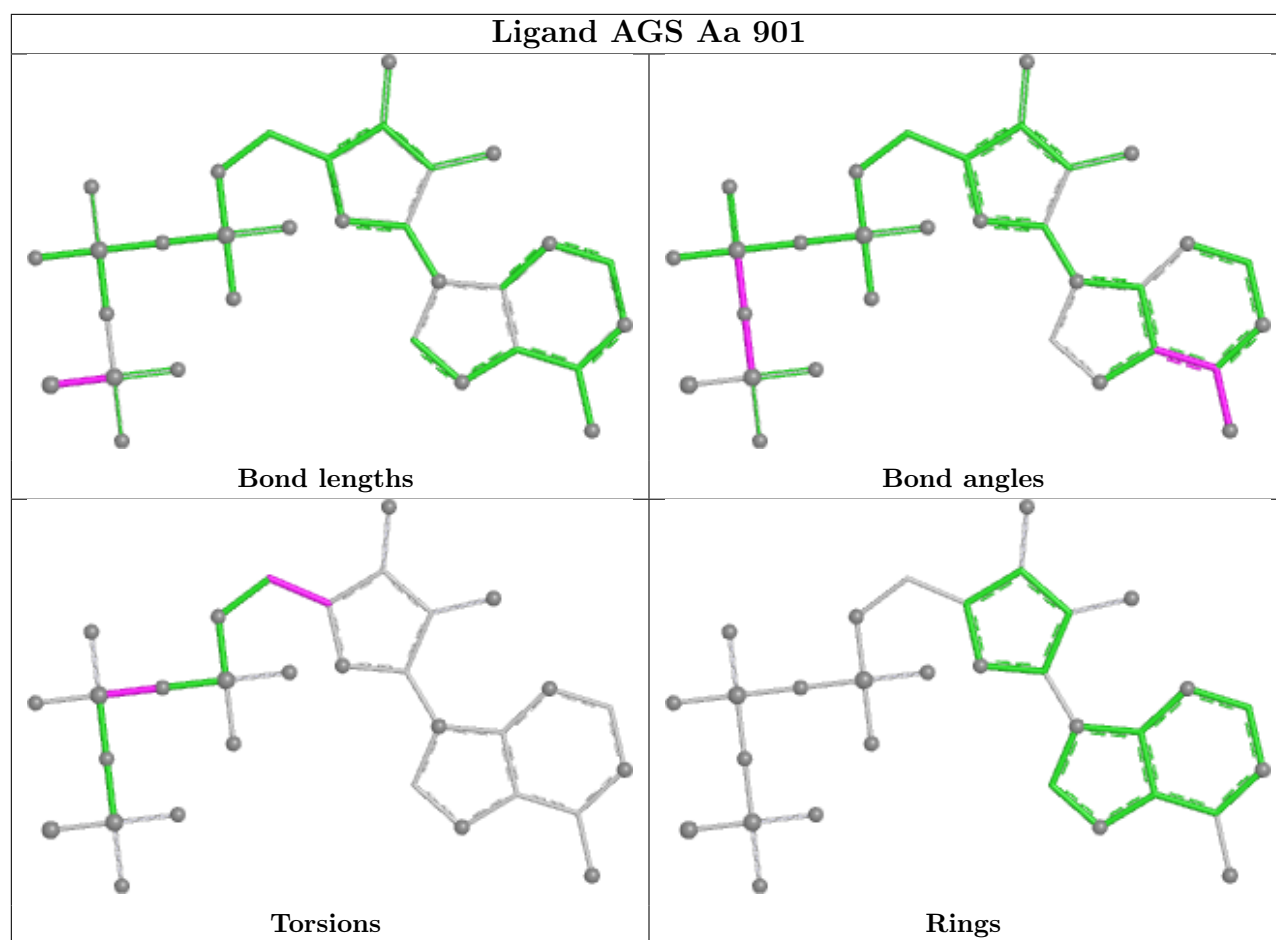
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

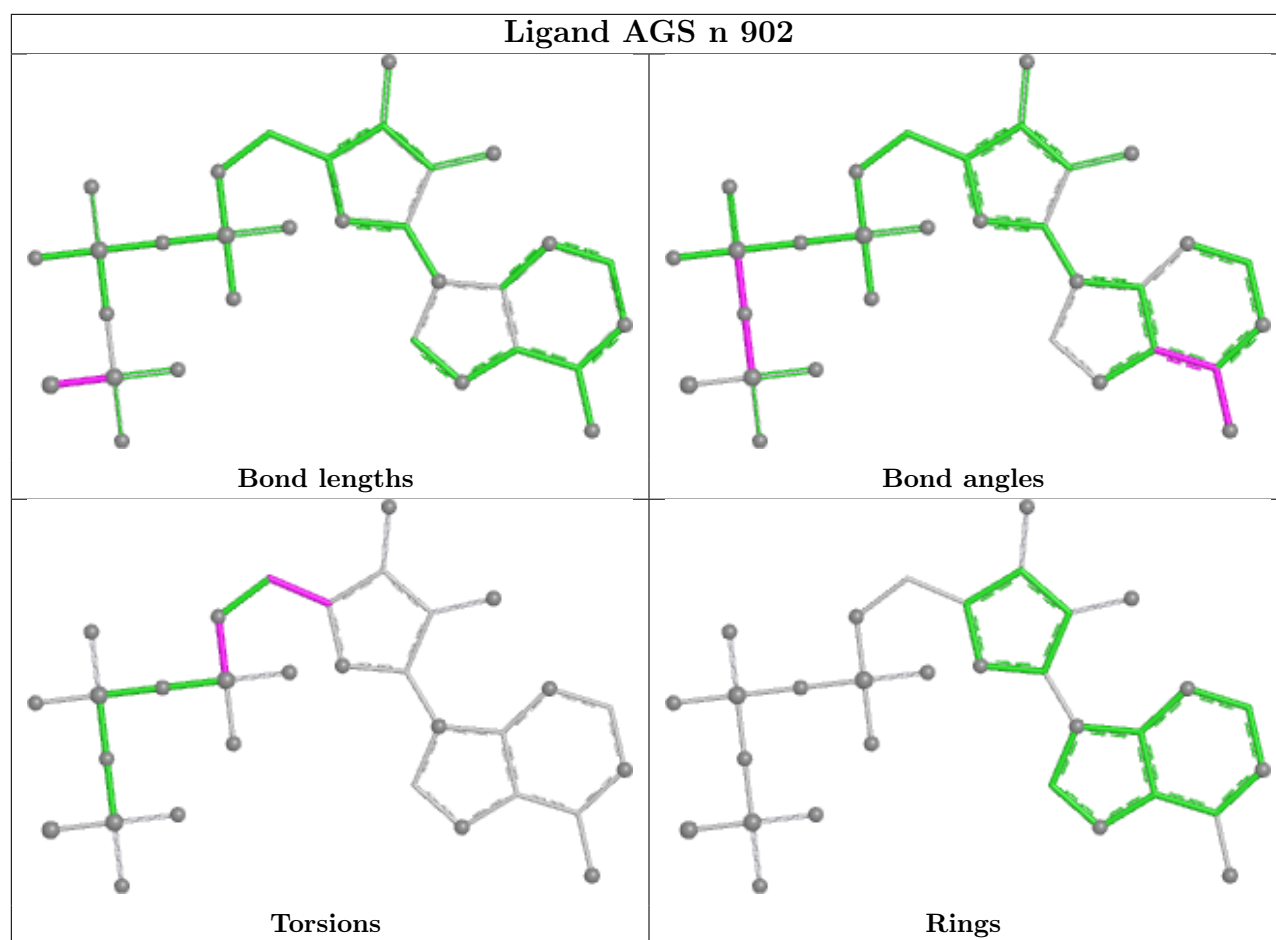


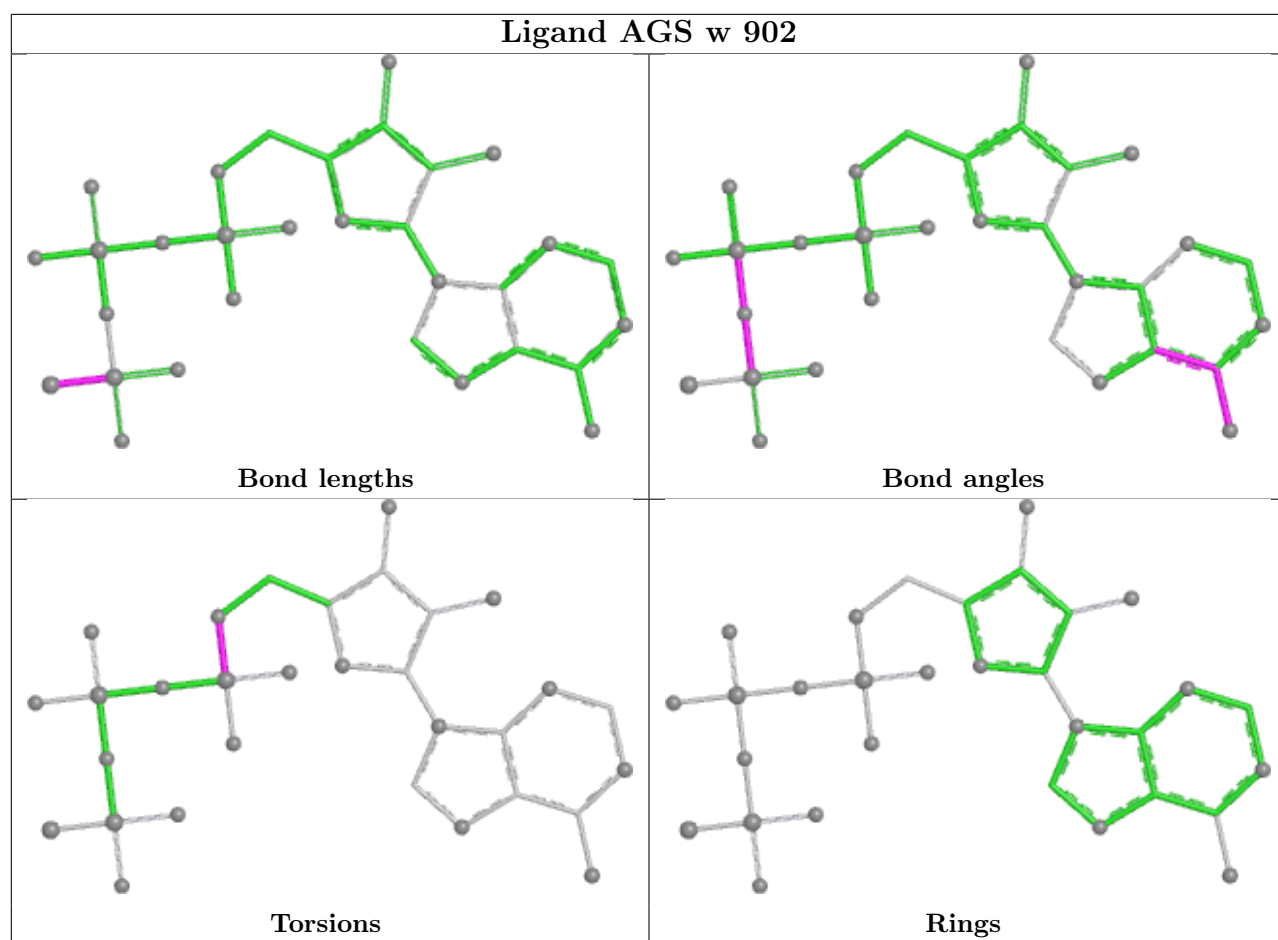


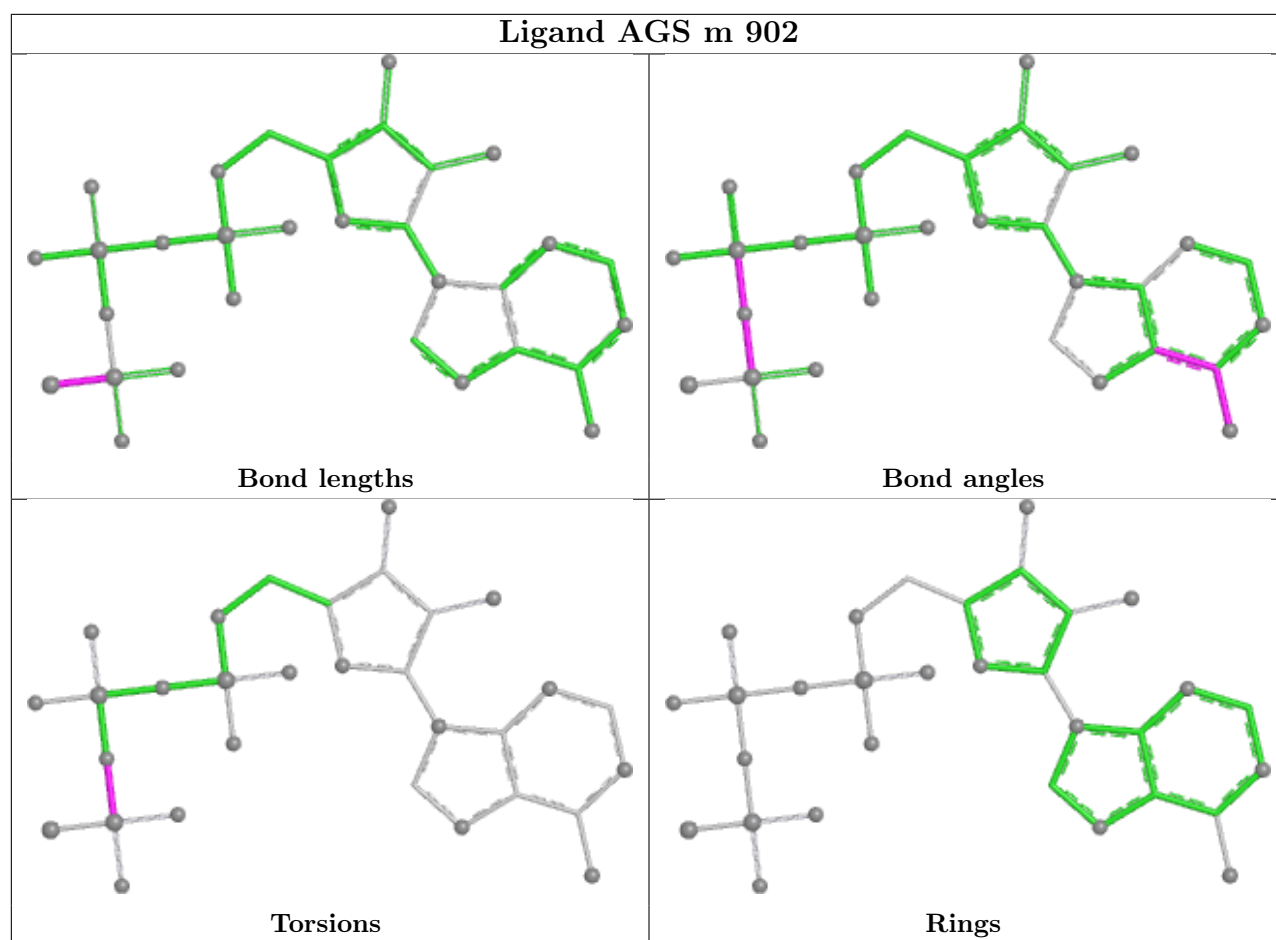


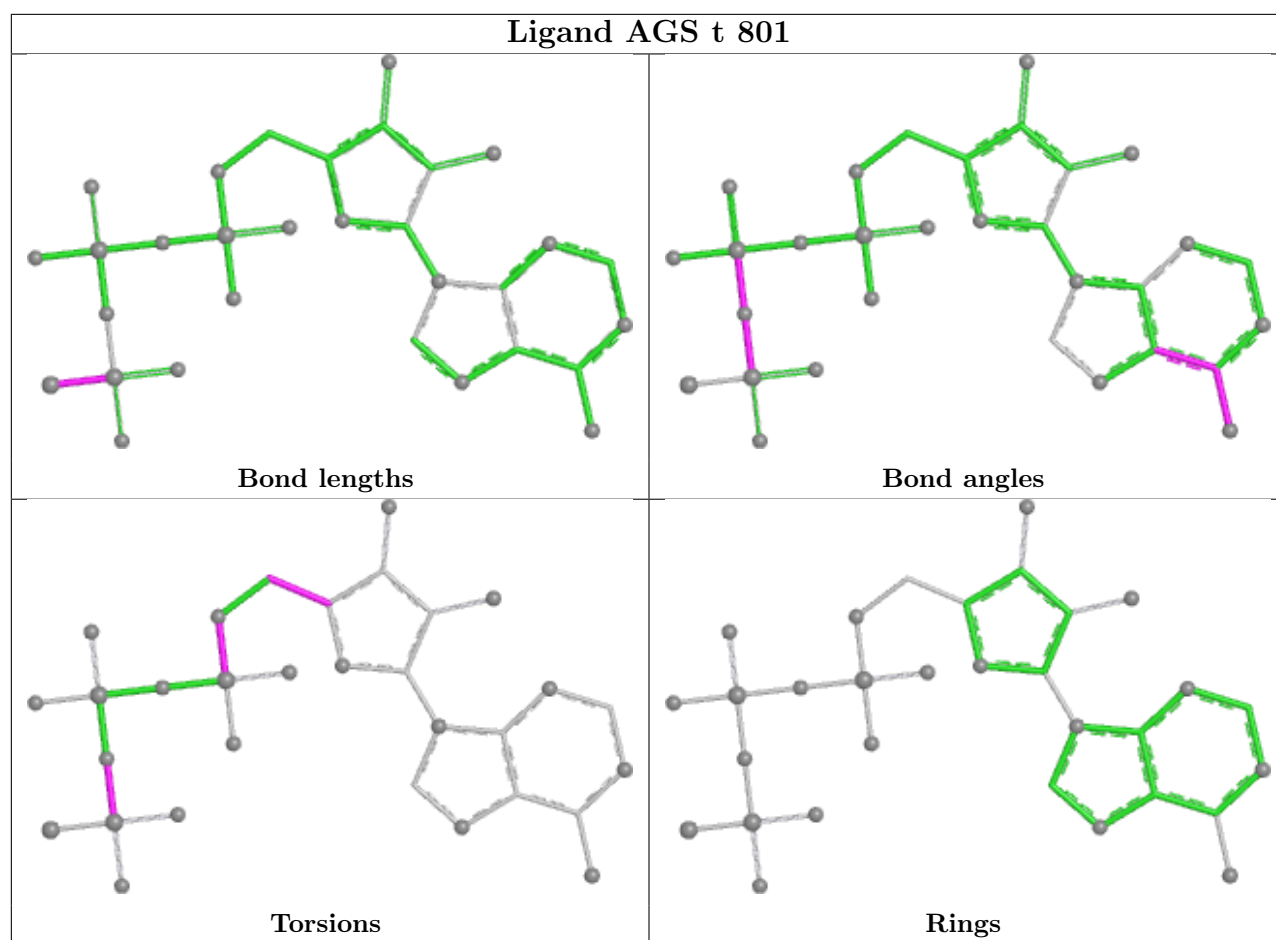


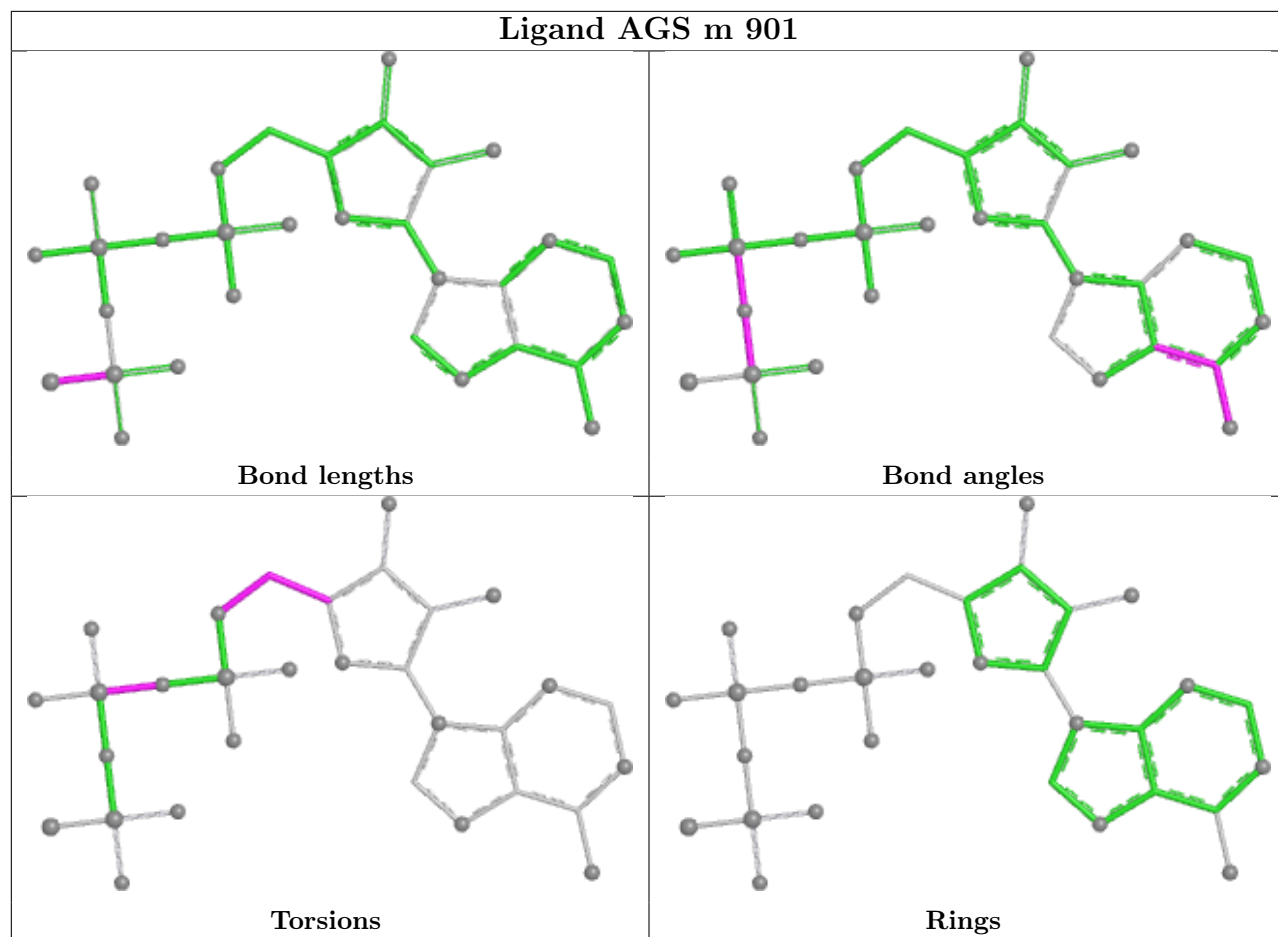


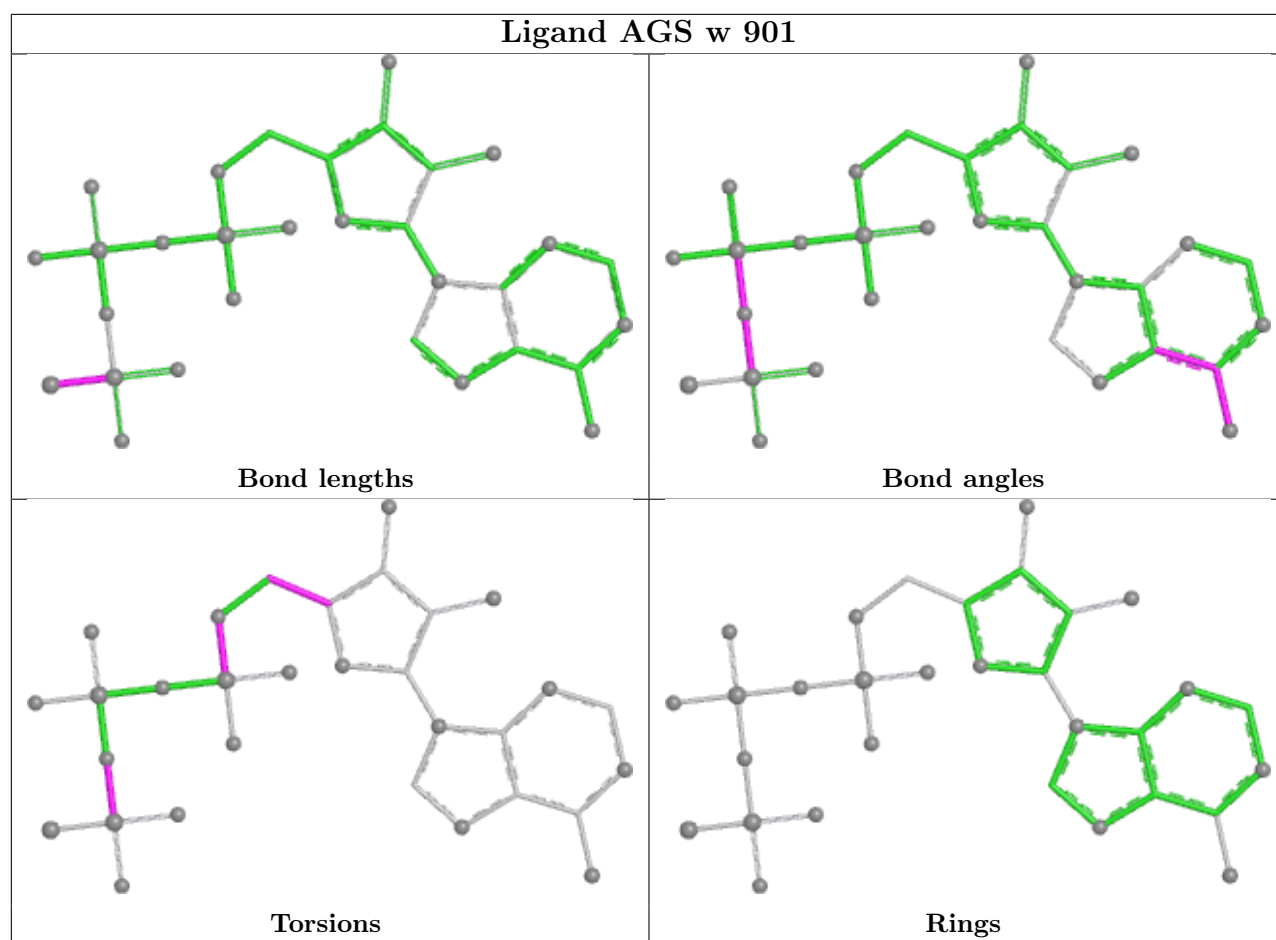












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

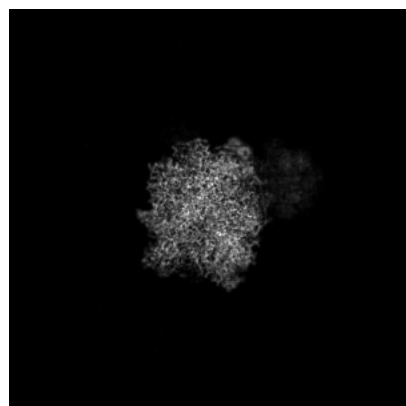
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14471. These allow visual inspection of the internal detail of the map and identification of artifacts.

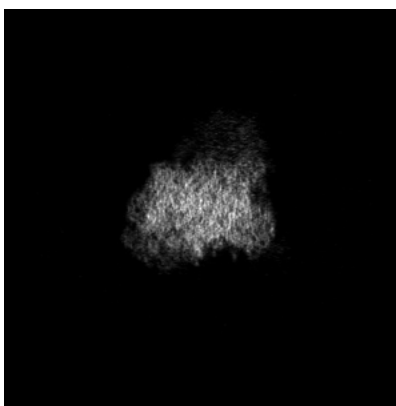
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

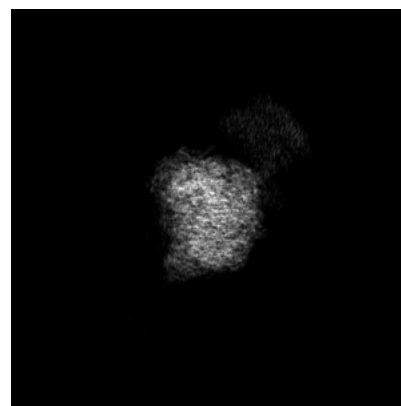
6.1.1 Primary map



X

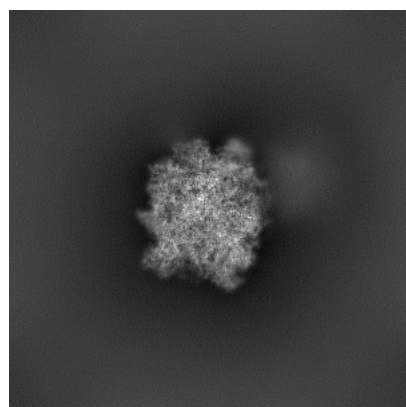


Y

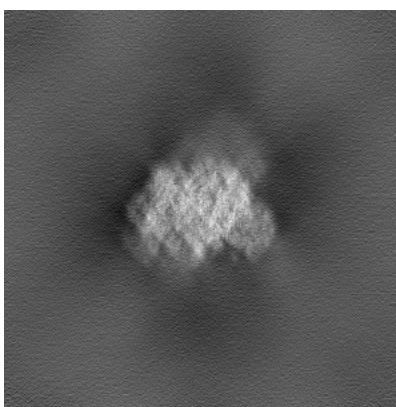


Z

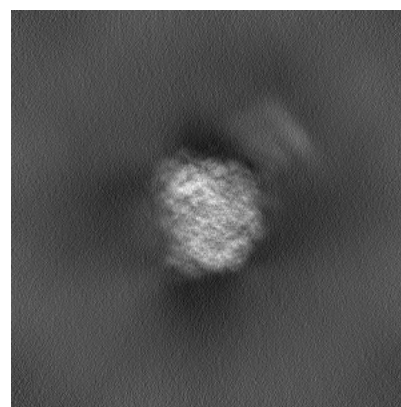
6.1.2 Raw map



X



Y



Z

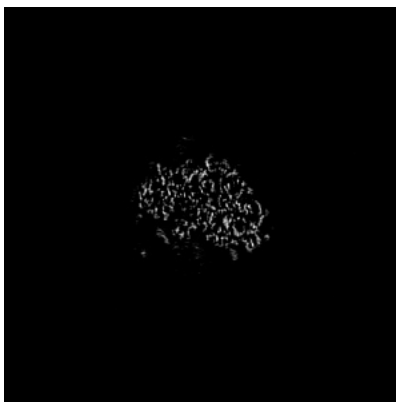
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240

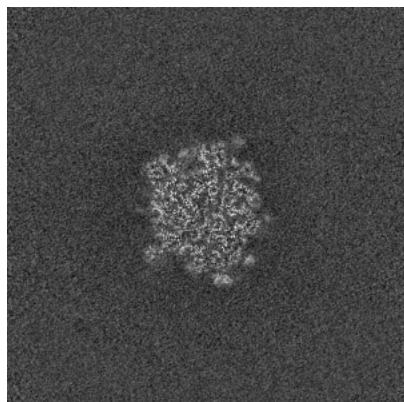


Y Index: 240

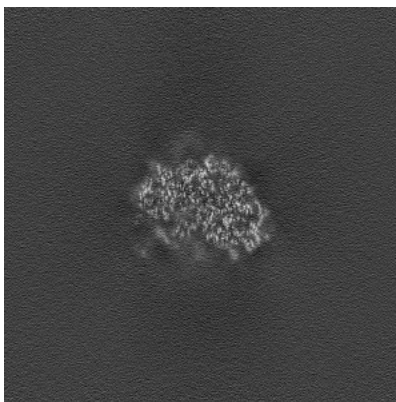


Z Index: 240

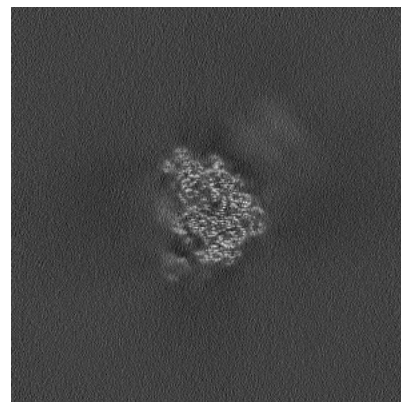
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

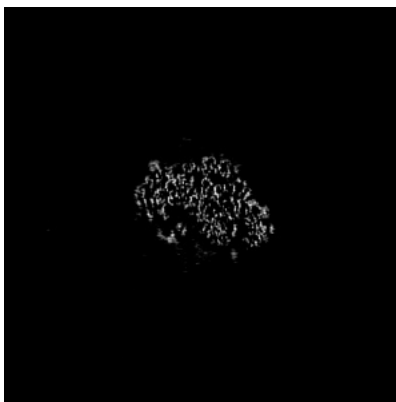
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

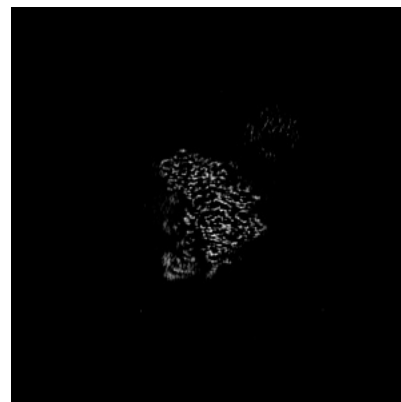
6.3.1 Primary map



X Index: 241

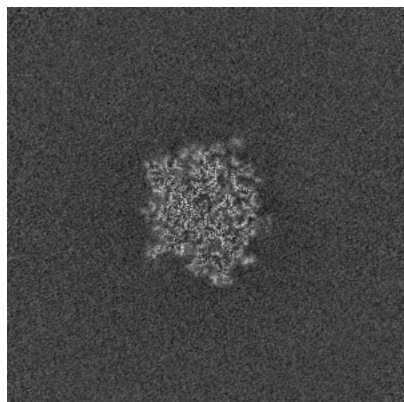


Y Index: 237

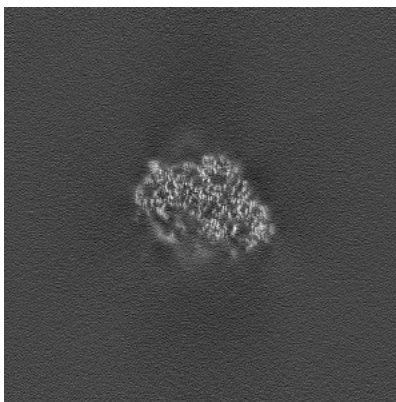


Z Index: 235

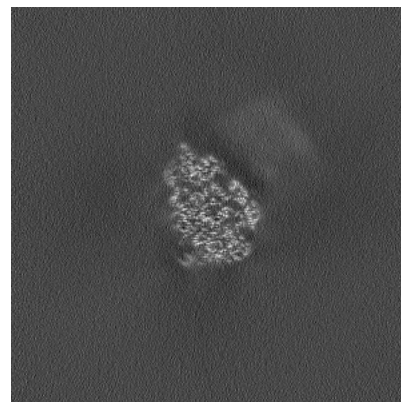
6.3.2 Raw map



X Index: 243



Y Index: 236

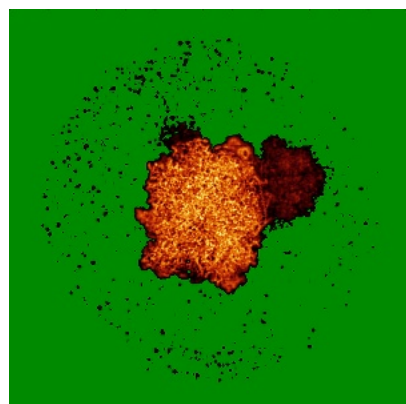


Z Index: 254

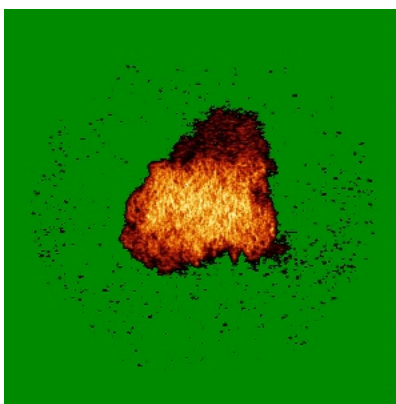
The images above show the largest variance slices of the map in three orthogonal directions.

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

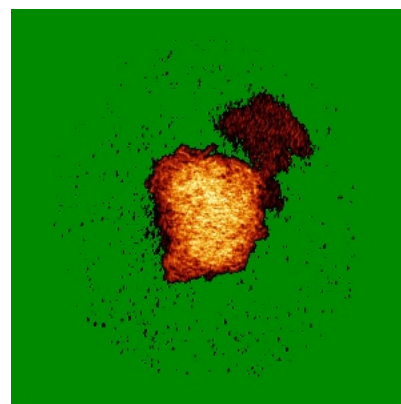
6.4.1 Primary map



X

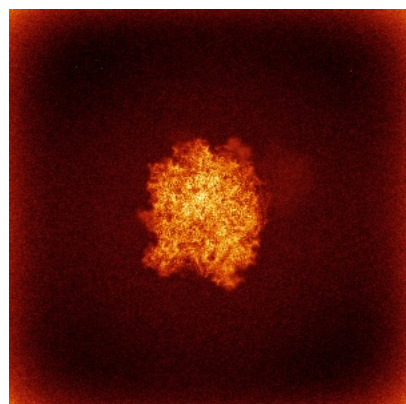


Y

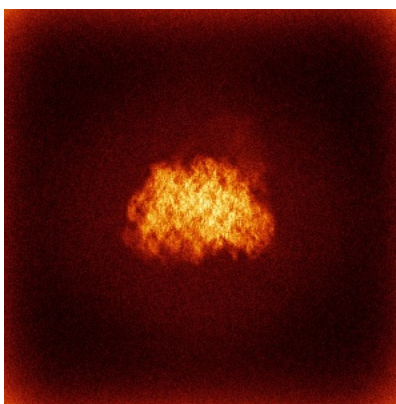


Z

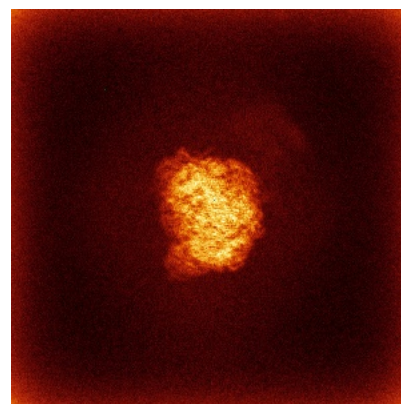
6.4.2 Raw map



X



Y

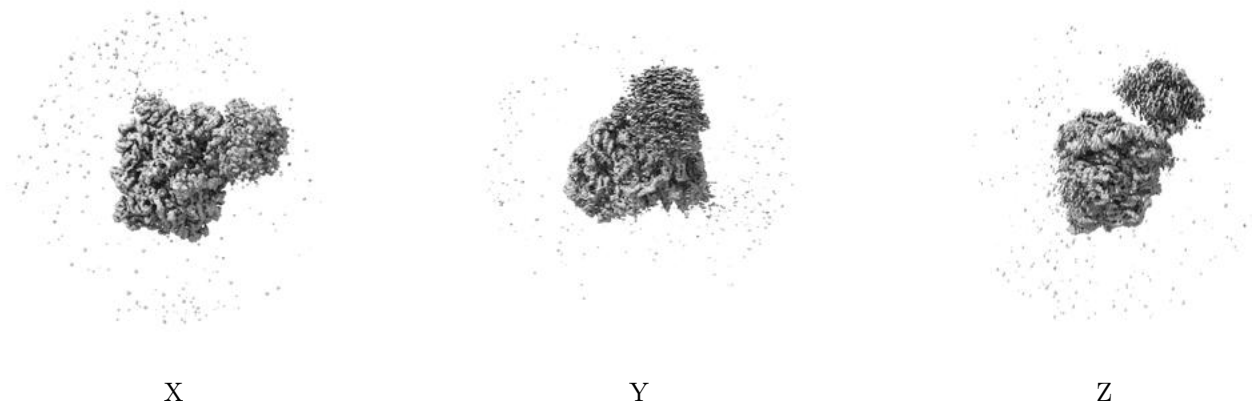


Z

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.

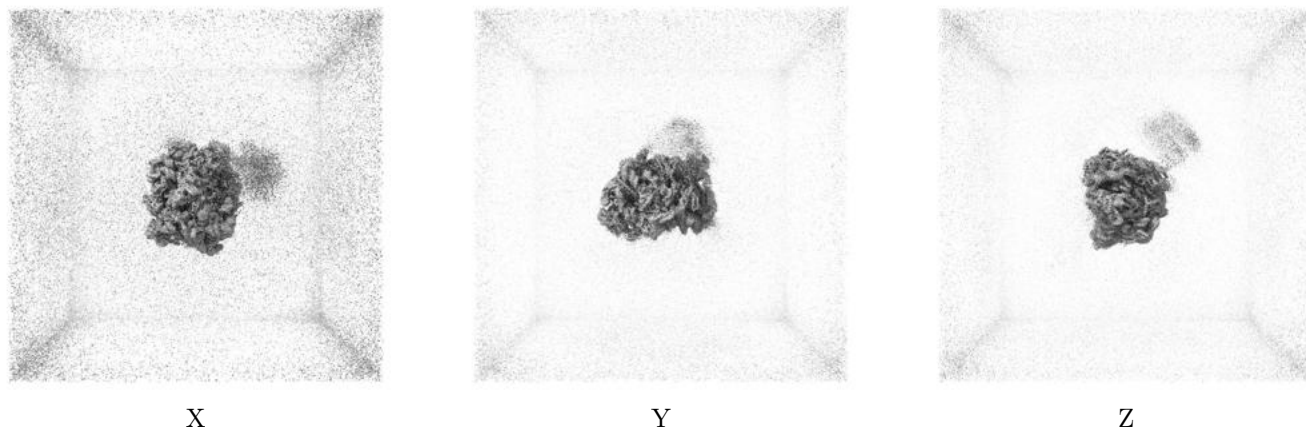
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

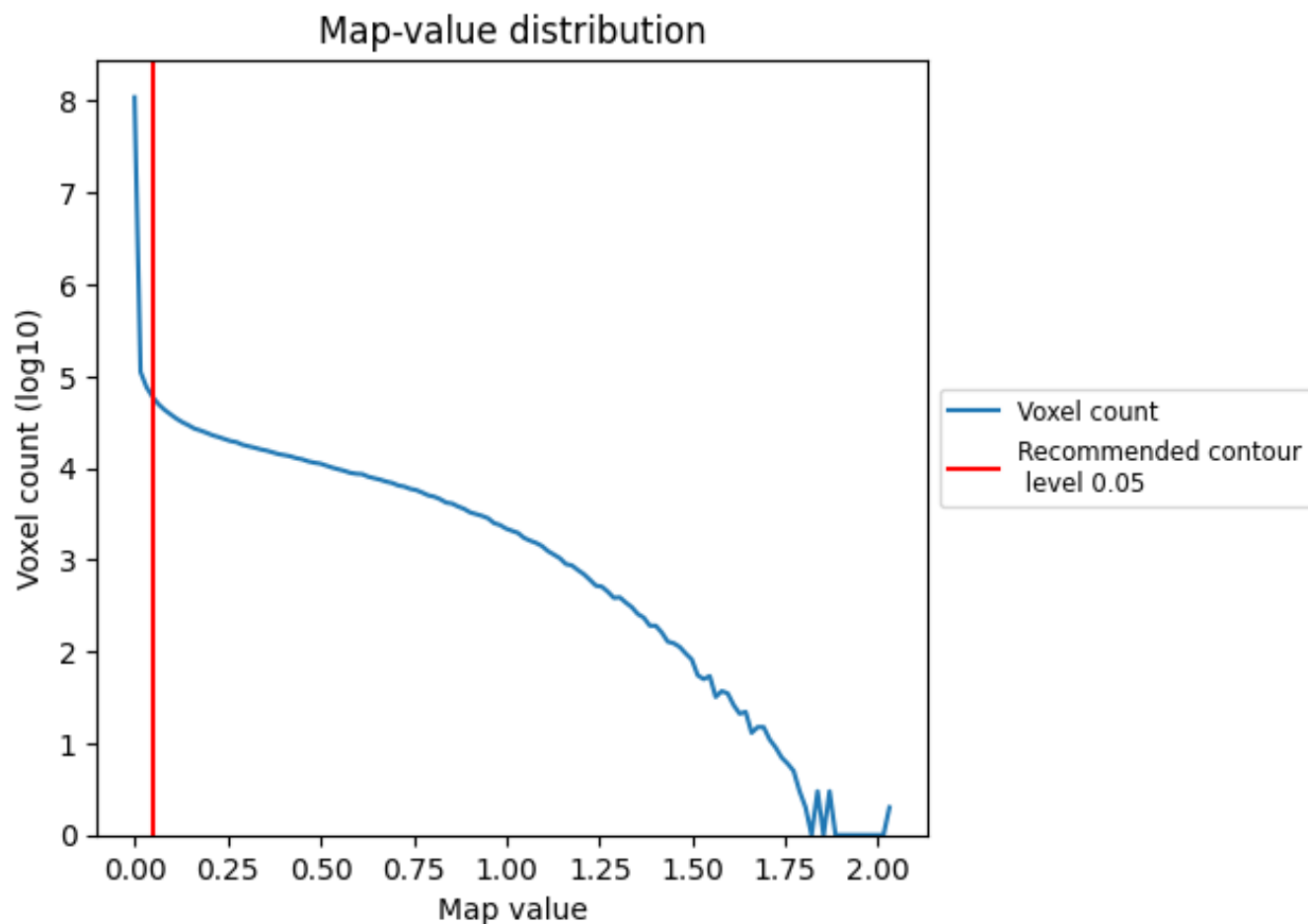
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

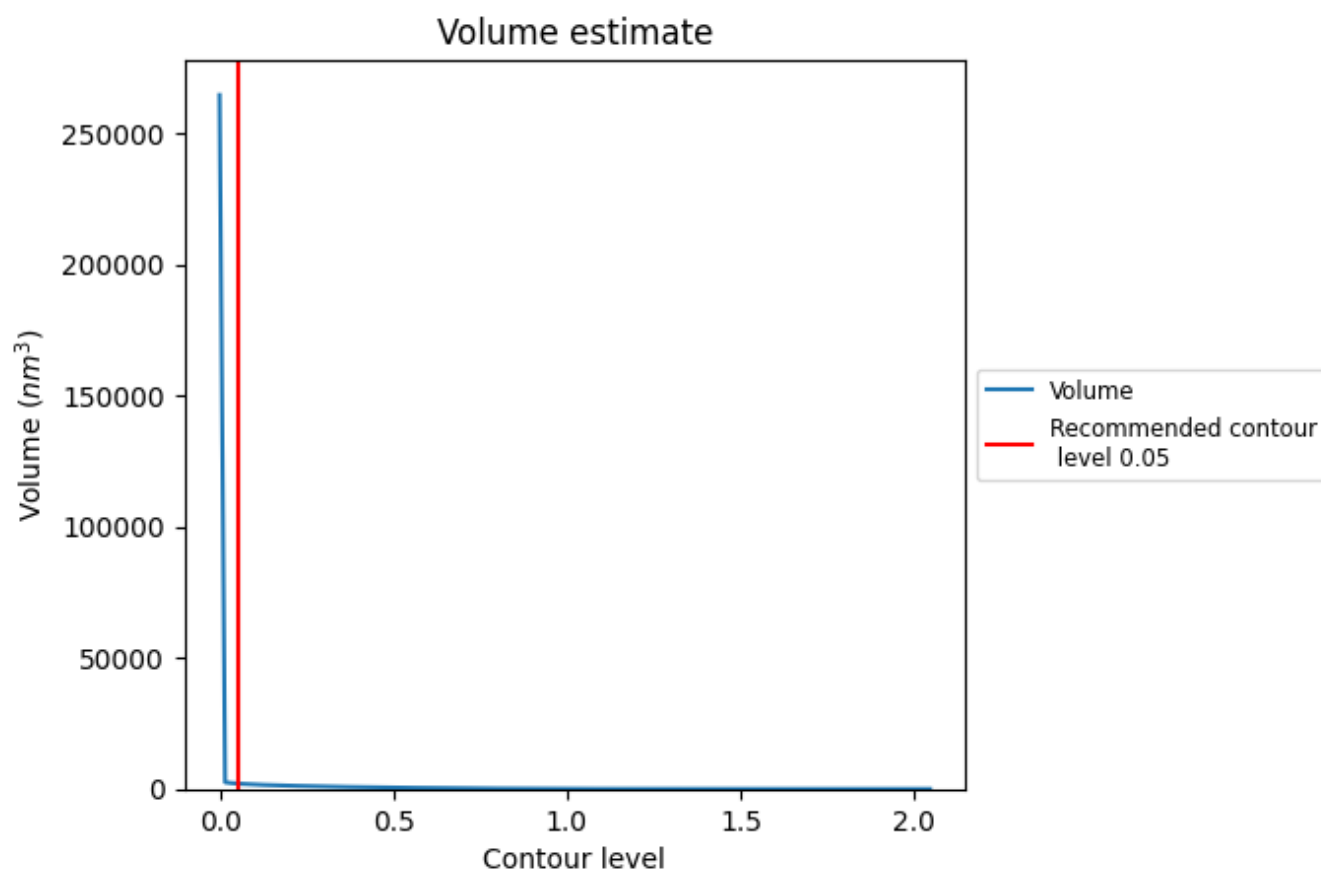
This section contains the results of statistical analysis of the map.

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.

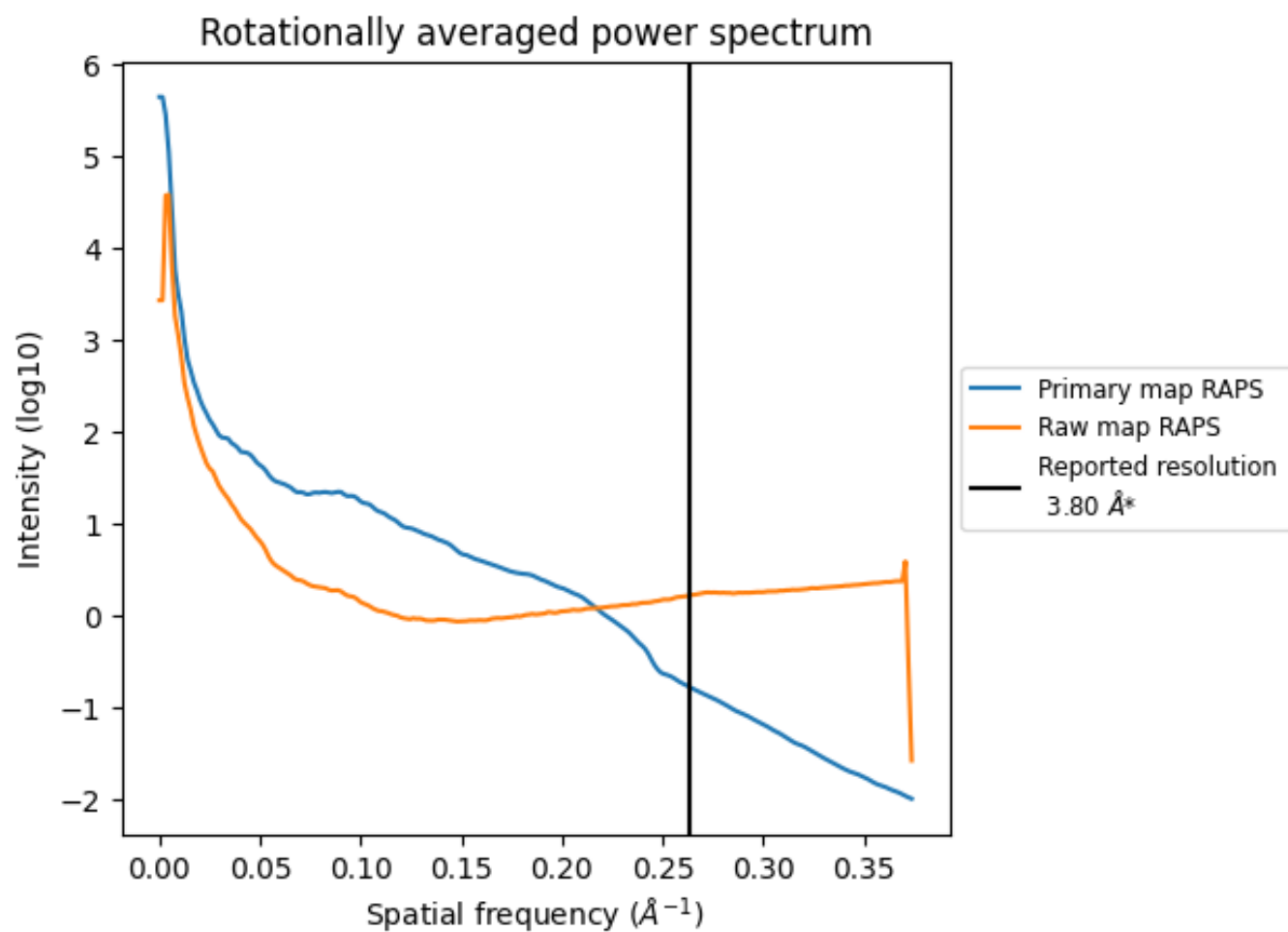
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2056 nm^3 ; this corresponds to an approximate mass of 1857 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 ⓘ

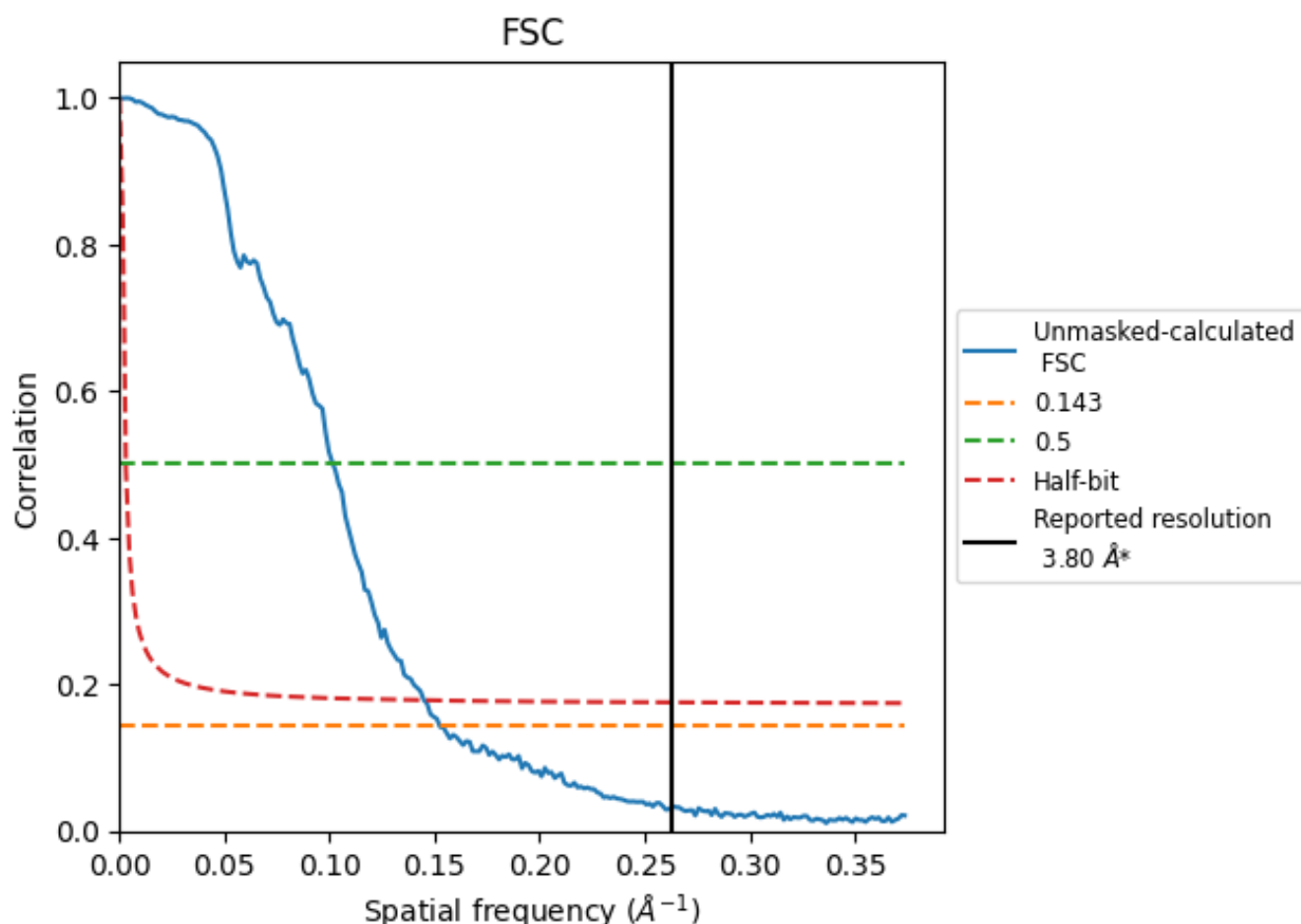


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

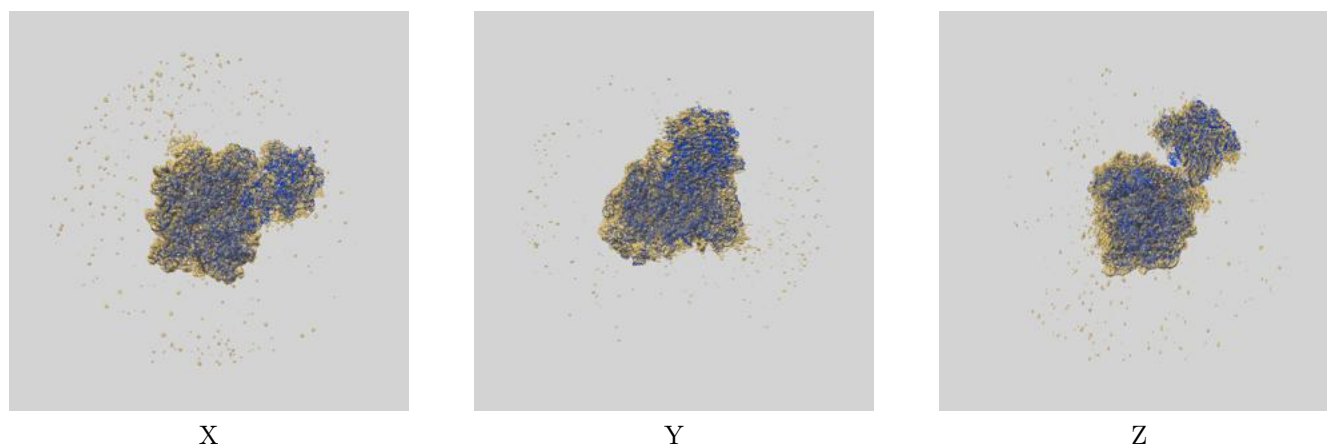
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.56	9.83	6.90

*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 6.56 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

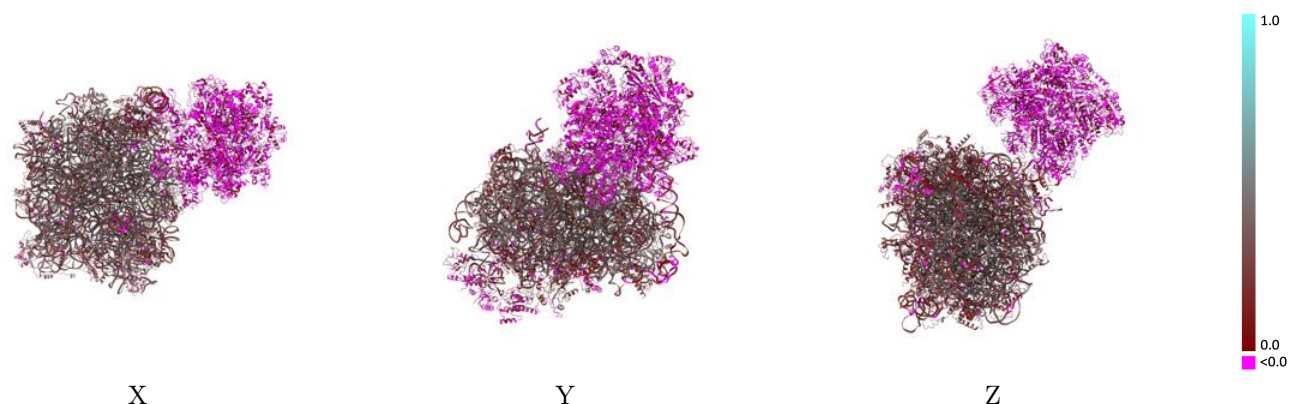
This section contains information regarding the fit between EMDB map EMD-14471 and PDB model 7Z34. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



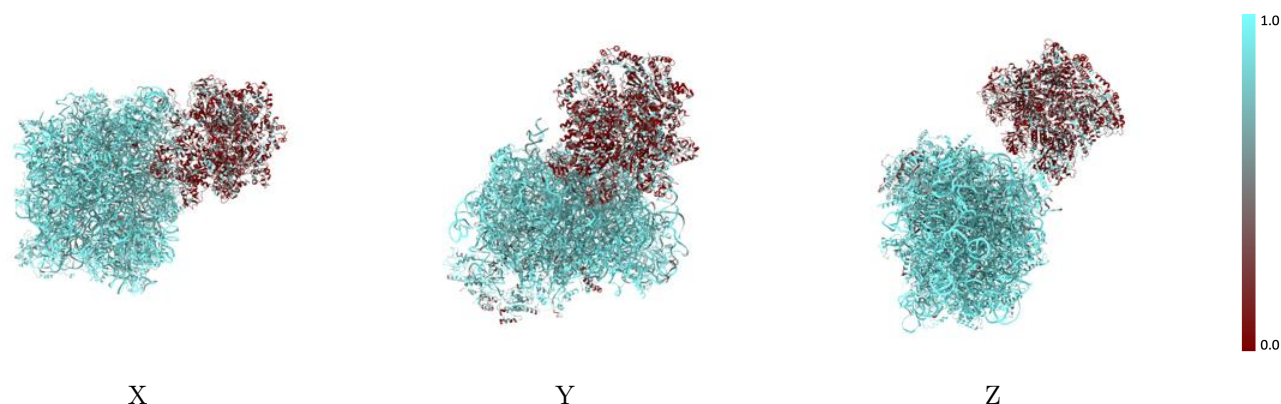
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



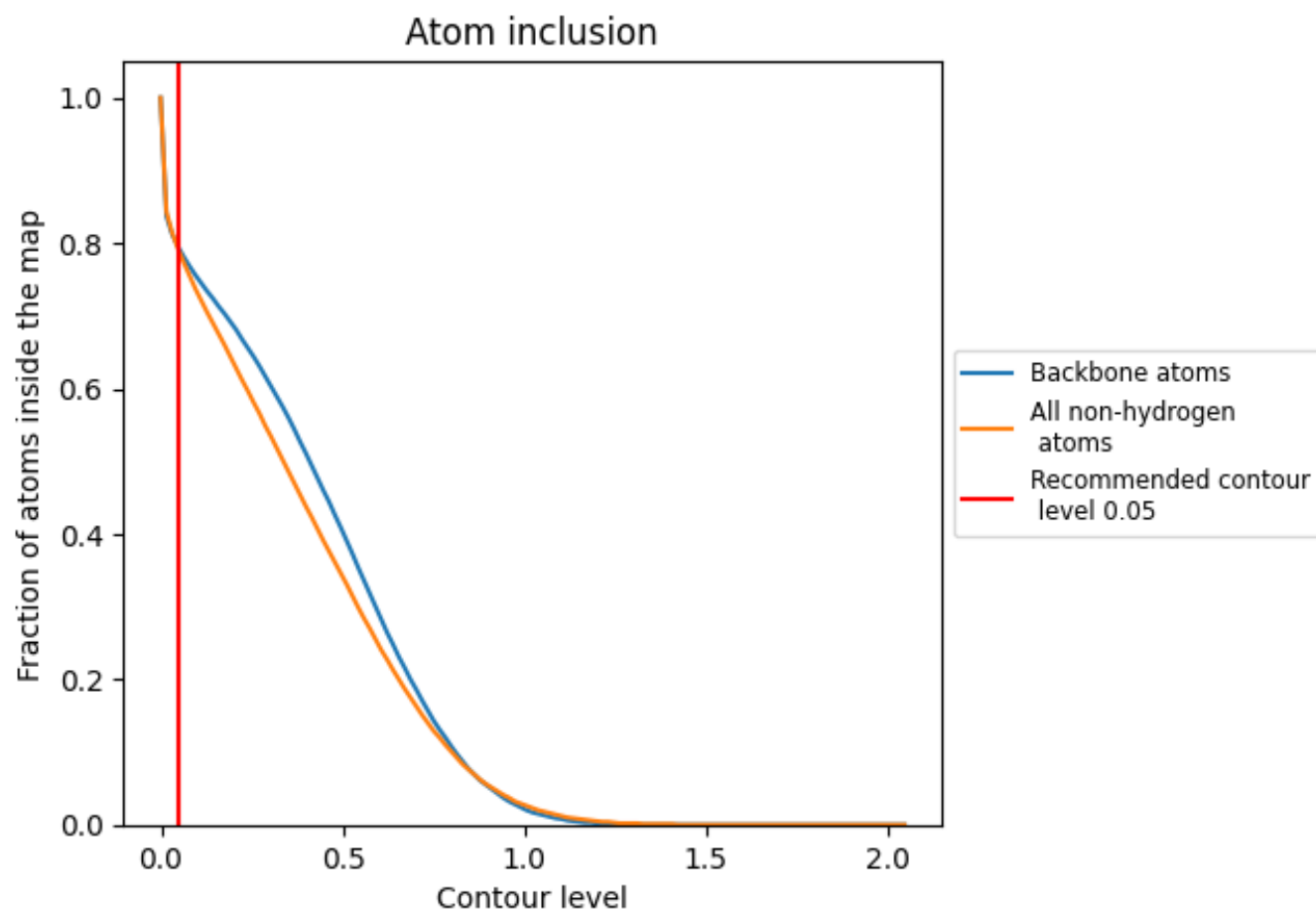
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.2270
0	 0.2810	 0.0450
1	 0.9430	 0.3120
2	 0.9590	 0.3070
3	 0.9770	 0.3520
4	 0.8610	 0.2430
A	 0.8920	 0.3020
Aa	 0.1900	 -0.0320
B	 0.9010	 0.3070
C	 0.9040	 0.3030
D	 0.8520	 0.2130
E	 0.8710	 0.2760
F	 0.9050	 0.2810
G	 0.8930	 0.2610
H	 0.8970	 0.2800
I	 0.6590	 0.1650
J	 0.8450	 0.2000
K	 0.8960	 0.3040
L	 0.9040	 0.3000
M	 0.8740	 0.2670
N	 0.8910	 0.3110
O	 0.8970	 0.2890
P	 0.8680	 0.2840
Q	 0.8870	 0.2900
R	 0.8780	 0.2610
S	 0.8840	 0.3010
T	 0.8850	 0.2880
U	 0.8990	 0.2720
V	 0.8870	 0.2950
W	 0.7970	 0.1140
X	 0.8790	 0.3020
Y	 0.8920	 0.3040
Z	 0.8760	 0.2510
a	 0.6300	 0.0470
b	 0.7880	 0.1820



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Chain	Atom inclusion	Q-score
c	 0.8840	 0.2590
d	 0.8500	 0.2850
e	 0.8980	 0.3200
f	 0.9070	 0.3350
g	 0.8620	 0.2720
h	 0.8890	 0.2880
i	 0.8690	 0.2390
j	 0.9180	 0.3350
k	 0.8630	 0.2390
l	 0.8800	 0.2800
m	 0.2600	 -0.0330
n	 0.2820	 -0.0240
o	 0.8630	 0.2480
oC	 0.9470	 0.2780
p	 0.8720	 0.2350
q	 0.7740	 0.1850
r	 0.5150	 0.0500
t	 0.3220	 -0.0230
u	 0.8770	 0.2460
v	 0.8090	 0.2320
w	 0.3860	 0.0020
x	 0.2680	 -0.0230
y	 0.8940	 0.2390
z	 0.8890	 0.2650