



Full wwPDB EM Validation Report ⓘ

Nov 23, 2022 – 07:58 pm GMT

PDB ID : 7P2E
EMDB ID : EMD-13170
Title : Human mitochondrial ribosome small subunit in complex with IF3, GMPPMP and streptomycin
Authors : Itoh, Y.; Khawaja, A.; Singh, V.; Rorbach, J.; Amunts, A.
Deposited on : 2021-07-05
Resolution : 2.40 Å(reported)
Based on initial model : 6RW4

This is a Full wwPDB EM Validation 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.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

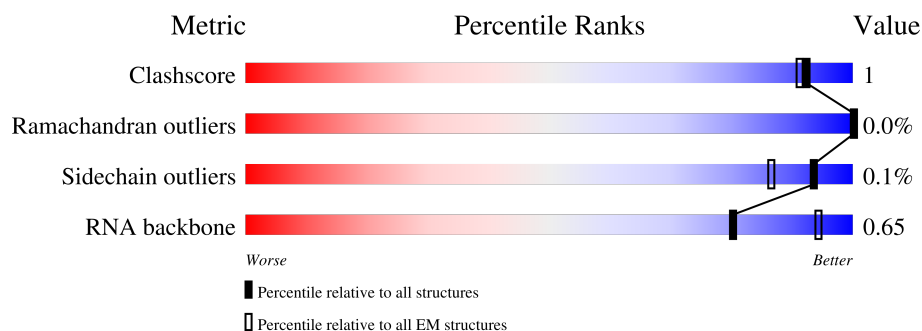
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

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









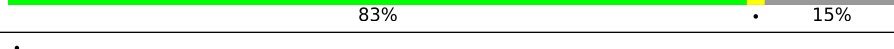
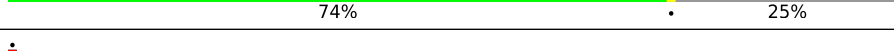
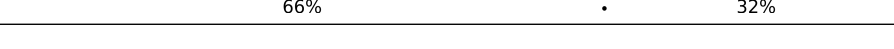
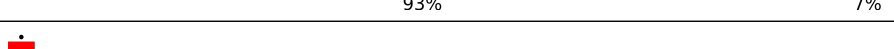
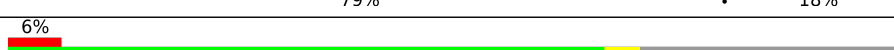

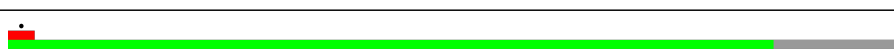

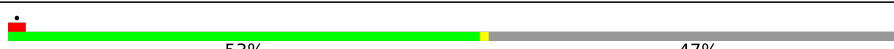


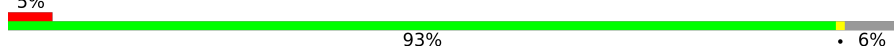
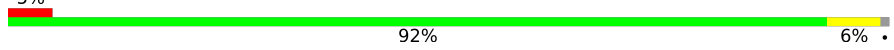

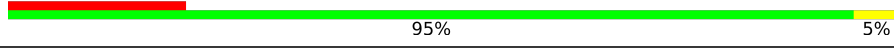




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	955	
2	B	296	
3	C	167	
4	D	430	
5	E	125	
6	F	242	
7	G	396	

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Mol	Chain	Length	Quality of chain
8	H	201	
9	I	194	
10	J	138	
11	K	128	
12	L	257	
13	M	137	
14	N	130	
15	O	258	
16	P	142	
17	Q	86	
18	R	360	
19	S	190	
20	T	173	
21	U	205	
22	V	414	
23	W	187	
24	X	398	
25	Y	395	
26	Z	106	
27	0	218	
28	1	323	
29	2	117	
30	3	199	
31	4	689	
32	8	285	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 131715 atoms, of which 59572 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 RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	955	Total	C	H	N	O	P	9	0
			30884	9183	10412	3687	6638	964		

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	225	Total	C	H	N	O	S	2	0
			3670	1173	1832	331	323	11		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	132	Total	C	H	N	O	S	0	0
			2172	699	1089	195	185	4		

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	337	Total	C	H	N	O	S	0	0
			5425	1683	2743	506	480	13		

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	122	Total	C	H	N	O	S	1	0
			1992	619	1012	180	177	4		

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	208	Total	C	H	N	O	S	0	0
			3495	1104	1770	312	298	11		

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	330	Total	C	H	N	O	S	0	0
			5433	1726	2717	485	491	14		

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	140	Total	C	H	N	O	S	0	0
			2336	745	1184	194	210	3		

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	137	Total	C	H	N	O	S	0	0
			2081	642	1061	192	182	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	184	5F0	ASN	conflict	UNP P82912

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	108	Total	C	H	N	O	S	0	0
			1727	521	888	169	143	6		

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	101	Total	C	H	N	O	S	0	0
			1748	537	886	179	141	5		

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	174	Total	C	H	N	O	S	0	0
			2994	925	1541	270	251	7		

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	119	Total	C	H	N	O	S	0	0
			1908	594	966	185	157	6		

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	110	Total	C	H	N	O	S	0	0
			1797	562	929	156	147	3		

- Molecule 15 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	193	Total	C	H	N	O	S	0	0
			3149	1014	1557	294	277	7		

- Molecule 16 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	97	Total	C	H	N	O	S	0	0
			1588	501	807	134	138	8		

- Molecule 17 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	86	Total	C	H	N	O	S	1	0
			1521	465	769	153	126	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	50	ARG	CYS	variant	UNP P82921

- Molecule 18 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	295	Total	C	H	N	O	S	0	0
			4838	1533	2429	413	455	8		

- Molecule 19 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	135	Total	C	H	N	O	S	3	0
			2255	724	1129	201	200	1		

- Molecule 20 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	T	168	Total	C	H	N	O	S	1	0
			2784	882	1405	242	244	11		

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	U	176	Total	C	H	N	O	S	0	0
			2988	916	1500	301	267	4		

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	V	362	Total	C	H	N	O	S	0	0
			5933	1904	2964	495	558	12		

- Molecule 23 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	W	100	Total	C	H	N	O	S	0	0
			1592	498	803	141	146	4		

- Molecule 24 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	X	352	Total	C	H	N	O	S	1	0
			5711	1827	2856	500	517	11		

- Molecule 25 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	149	Total	C	H	N	O	S	1	0
			2461	806	1206	209	236	4		

- Molecule 26 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	100	Total	C	H	N	O	S	0	0
			1698	534	859	153	148	4		

- Molecule 27 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	0	215	Total	C	H	N	O	S	0	0
			3584	1130	1797	339	313	5		

- Molecule 28 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	1	276	Total	C	H	N	O	S	0	0
			4507	1419	2269	381	427	11		

- Molecule 29 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	2	117	Total	C	H	N	O	S	0	0
			1904	579	969	182	166	8		

- Molecule 30 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	3	71	Total	C	H	N	O	S	0	0
			1331	403	702	135	90	1		

- Molecule 31 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	4	592	Total	C	H	N	O	S	0	0
			9593	3070	4798	812	885	28		

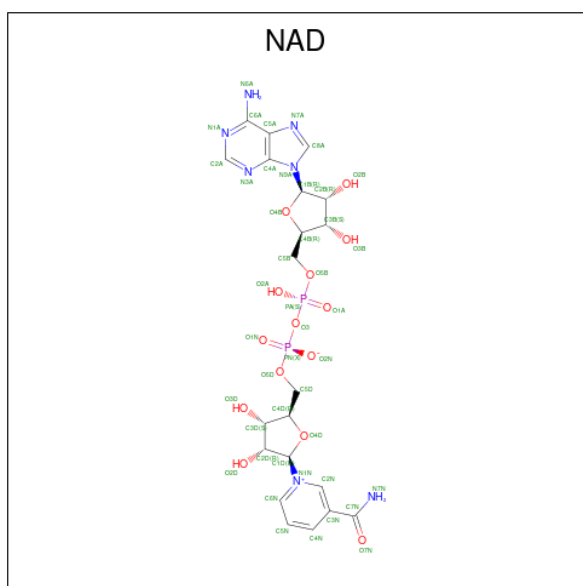
- Molecule 32 is a protein called Translation initiation factor IF-3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	8	191	Total	C	H	N	O	S	0	0
			3131	953	1588	289	293	8		

There are 9 discrepancies between the modelled and reference sequences:

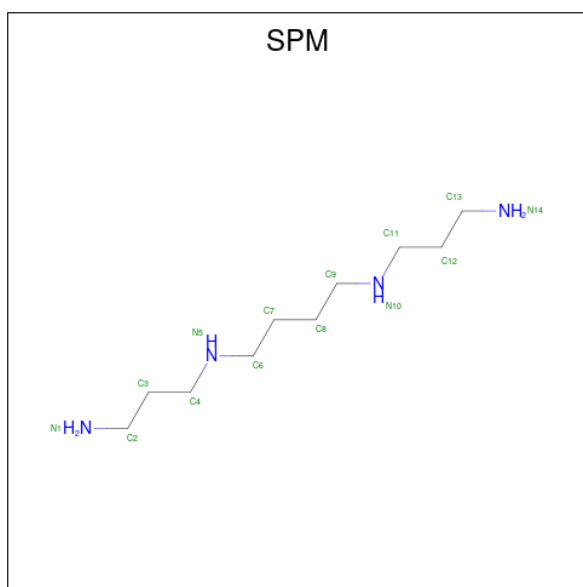
Chain	Residue	Modelled	Actual	Comment	Reference
8	68	ILE	THR	variant	UNP Q9H2K0
8	243	LEU	PHE	variant	UNP Q9H2K0
8	279	GLY	-	expression tag	UNP Q9H2K0
8	280	LEU	-	expression tag	UNP Q9H2K0
8	281	GLU	-	expression tag	UNP Q9H2K0
8	282	VAL	-	expression tag	UNP Q9H2K0
8	283	LEU	-	expression tag	UNP Q9H2K0
8	284	PHE	-	expression tag	UNP Q9H2K0
8	285	GLN	-	expression tag	UNP Q9H2K0

- Molecule 33 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



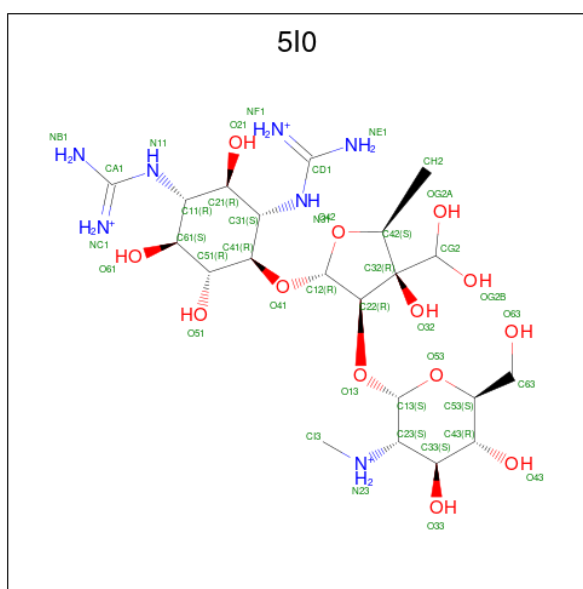
Mol	Chain	Residues	Atoms						AltConf
33	A	1	Total	C	H	N	O	P	0
			70	21	26	7	14	2	

- Molecule 34 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
34	A	1	Total	C	H	N	0
			44	10	30	4	

- Molecule 35 is [(2 {S},3 {S},4 {S},5 {R},6 {S})-2-[(2 {R},3 {R},4 {R},5 {S})-2-[(1 {R},2 {S},3 {R},4 {R},5 {S},6 {R})-2,4-bis[[azanumylidene(azanyl)methyl]amino]-3,5,6-tris(oxidanyl)cyclohexyl]oxy-4-[bis(oxidanyl)methyl]-5-methyl-4-oxidanyl-oxolan-3-yl]oxy-6-(hydroxymethyl)-4,5-bis(oxidanyl)oxan-3-yl]-methyl-azanium (three-letter code: 5I0) (formula: C₂₁H₄₄N₇O₁₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
35	A	1	Total	C	H	N	O	1
			106	27	54	7	18	

- Molecule 36 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
36	A	21	Total K 21 21	0

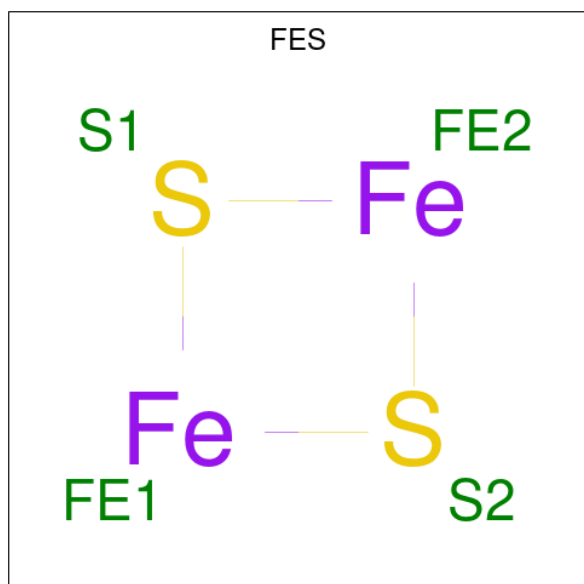
- Molecule 37 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
37	A	59	Total Mg 59 59	0
37	B	1	Total Mg 1 1	0
37	X	1	Total Mg 1 1	0
37	3	1	Total Mg 1 1	0

- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

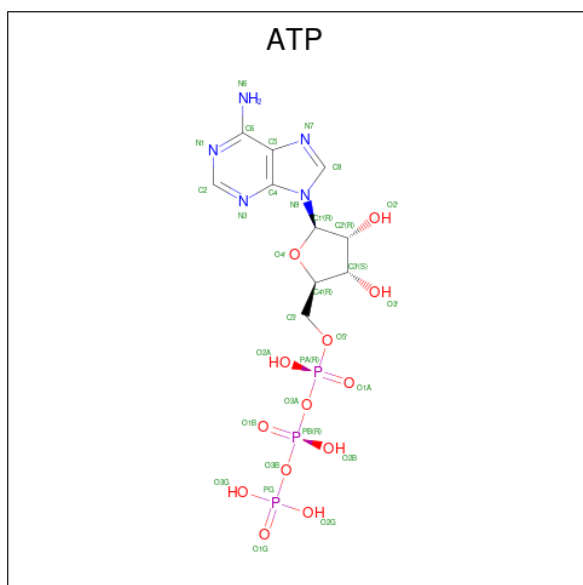
Mol	Chain	Residues	Atoms	AltConf
38	O	1	Total Zn 1 1	0

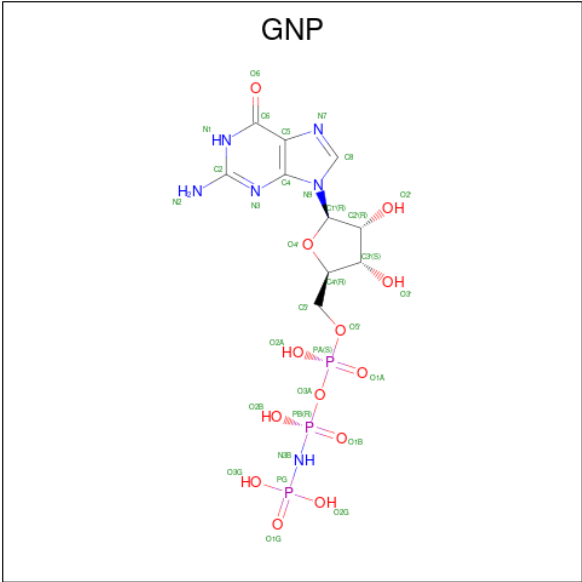
- Molecule 39 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
39	P	1	Total	Fe	S	0
			4	2	2	
39	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 40 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms						AltConf
41	X	1	Total	C	H	N	O	P	0
			45	10	13	6	13	3	

- Molecule 42 is water.

Mol	Chain	Residues	Atoms		AltConf
42	A	1857	Total	O	0
			1857	1857	
42	B	100	Total	O	0
			100	100	
42	C	65	Total	O	0
			65	65	
42	D	76	Total	O	0
			76	76	
42	E	6	Total	O	0
			6	6	
42	F	41	Total	O	0
			41	41	
42	G	99	Total	O	0
			99	99	
42	H	75	Total	O	0
			75	75	
42	I	22	Total	O	0
			22	22	
42	J	22	Total	O	0
			22	22	
42	K	60	Total	O	0
			60	60	

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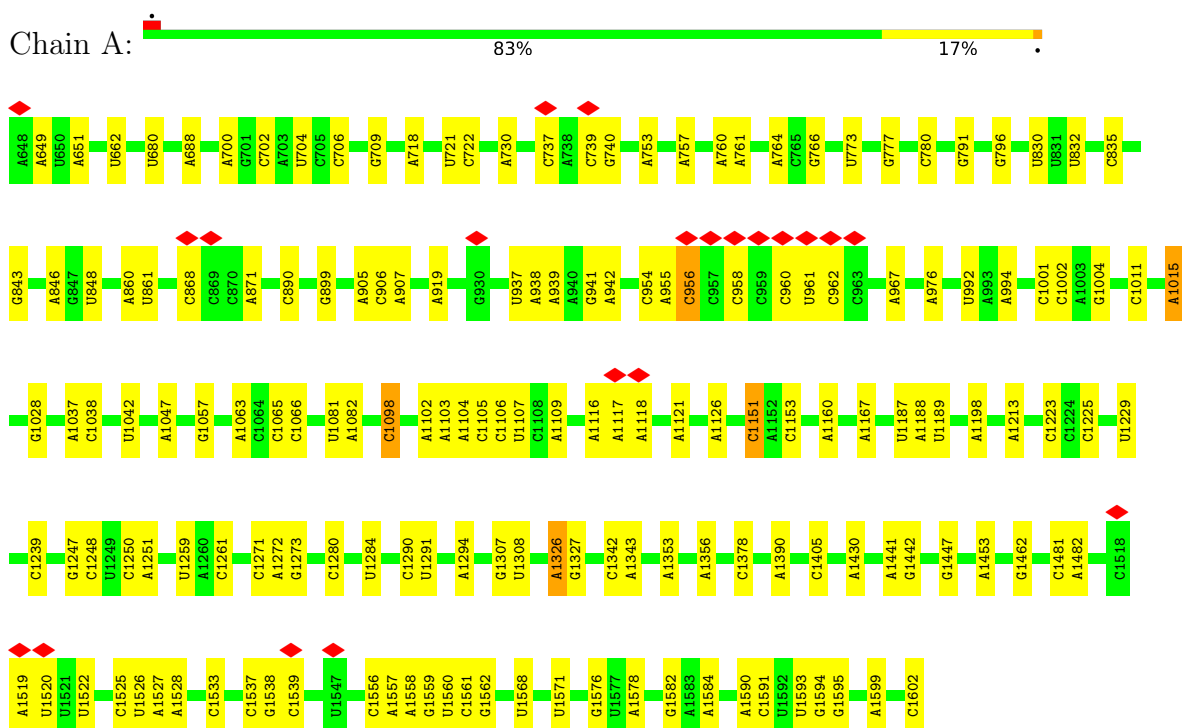
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Mol	Chain	Residues	Atoms		AltConf
42	L	28	Total 28	O 28	0
42	M	33	Total 33	O 33	0
42	N	24	Total 24	O 24	0
42	O	42	Total 42	O 42	0
42	P	20	Total 20	O 20	0
42	Q	53	Total 53	O 53	0
42	R	49	Total 49	O 49	0
42	S	25	Total 25	O 25	0
42	T	29	Total 29	O 29	0
42	U	15	Total 15	O 15	0
42	V	5	Total 5	O 5	0
42	W	27	Total 27	O 27	0
42	X	89	Total 89	O 89	0
42	Y	19	Total 19	O 19	0
42	Z	35	Total 35	O 35	0
42	0	38	Total 38	O 38	0
42	1	53	Total 53	O 53	0
42	2	26	Total 26	O 26	0
42	3	25	Total 25	O 25	0
42	4	25	Total 25	O 25	0
42	8	2	Total 2	O 2	0

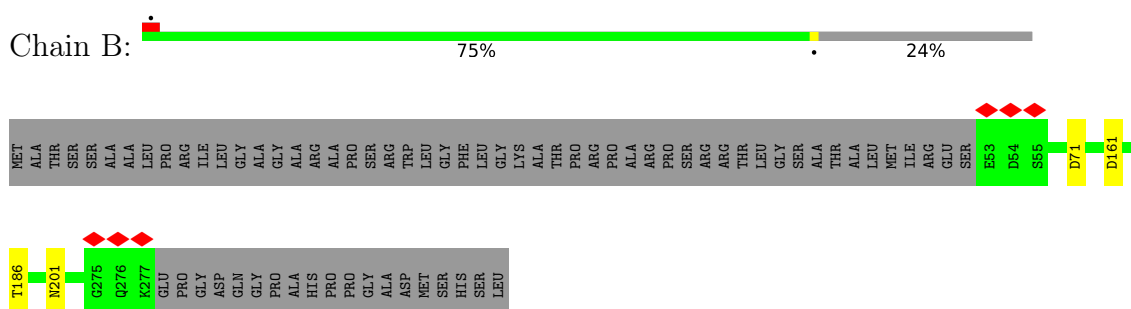
3 Residue-property plots

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: 12S mitochondrial rRNA

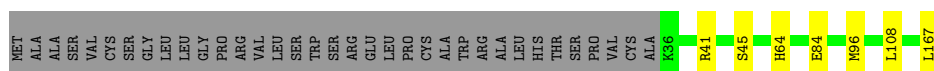


• Molecule 2: 28S ribosomal protein S2, mitochondrial



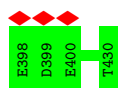
• Molecule 3: 28S ribosomal protein S24, mitochondrial





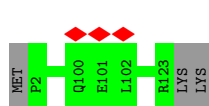
- Molecule 4: 28S ribosomal protein S5, mitochondrial

Chain D: 77% 22%



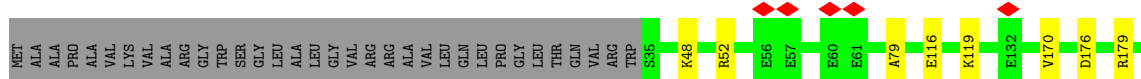
- Molecule 5: 28S ribosomal protein S6, mitochondrial

Chain E: 98%



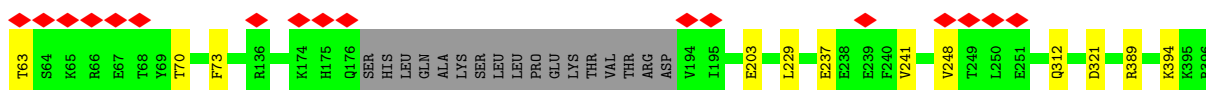
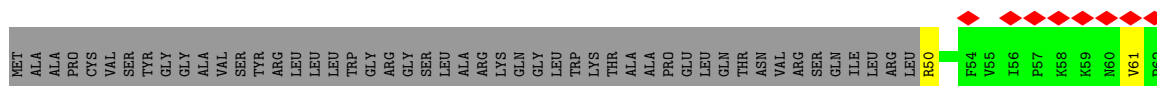
- Molecule 6: 28S ribosomal protein S7, mitochondrial

Chain F: 82% 14%



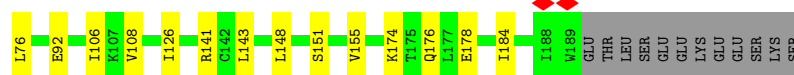
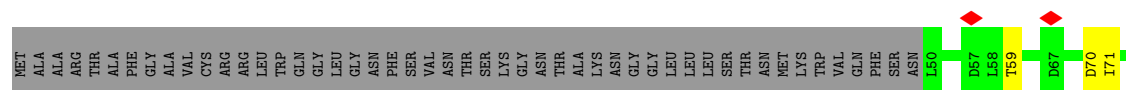
- Molecule 7: 28S ribosomal protein S9, mitochondrial

Chain G: 6% 80% 17%



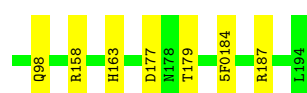
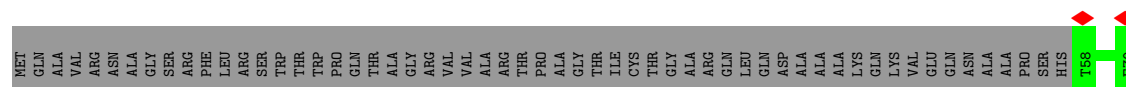
- Molecule 8: 28S ribosomal protein S10, mitochondrial

Chain H: 61% 8% 30%



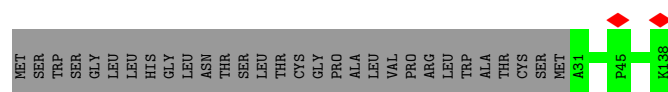
- Molecule 9: 28S ribosomal protein S11, mitochondrial

Chain I: 67% 29%



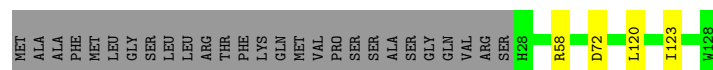
- Molecule 10: 28S ribosomal protein S12, mitochondrial

Chain J: 78% 22%



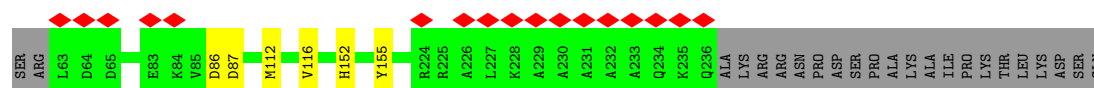
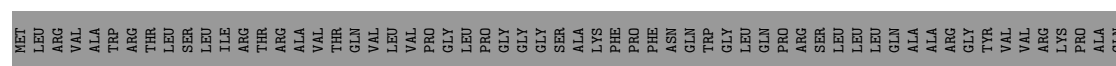
- Molecule 11: 28S ribosomal protein S14, mitochondrial

Chain K: 76% 21%



- Molecule 12: 28S ribosomal protein S15, mitochondrial

Chain L: 7% 65% 32%




- Molecule 13: 28S ribosomal protein S16, mitochondrial

Chain M: 85% 13%




- Molecule 14: 28S ribosomal protein S17, mitochondrial

Chain N:  83% 15%



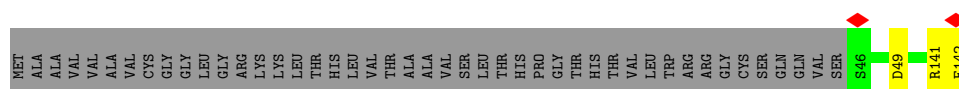
- Molecule 15: 28S ribosomal protein S18b, mitochondrial

Chain O:  74% 25%



- Molecule 16: 28S ribosomal protein S18c, mitochondrial

Chain P:  66% 32%




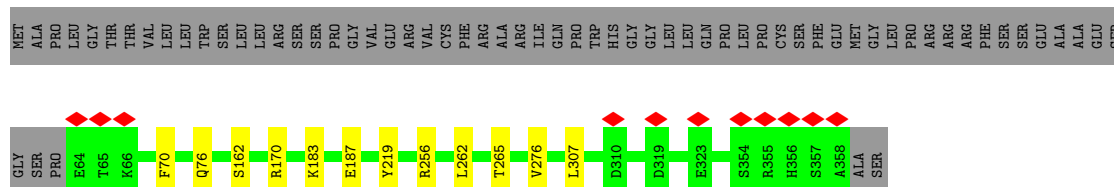
- Molecule 17: 28S ribosomal protein S21, mitochondrial

Chain Q:  93% 7%



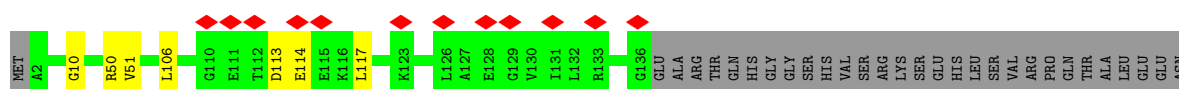
- Molecule 18: 28S ribosomal protein S22, mitochondrial

Chain R:  79% 18%



- Molecule 19: 28S ribosomal protein S23, mitochondrial

Chain S:  6% 67% 29%




GLU
THR
GLN
LYS
GLU
VAL
PRO
GLN
ASP
GLN
HIS
LEU
GLU
ALA
PRO
ALA
ALA
GLN
SER
LYS
GLY
LEU
LEU
PRO
PRO

- Molecule 20: 28S ribosomal protein S25, mitochondrial

Chain T:  97%


MET
P2
A165
A166
L167
K168
A169
ASP
ALA
GLN
ASP

- Molecule 21: 28S ribosomal protein S26, mitochondrial

Chain U:  86% 14%

MET
LEU
ARG
ARG
ALA
SER
LEU
SER
ARG
LEU
GLY
ALA
GLY
THR
PRO
CYS
ARG
PRO
ARG
ALA
LEU
VAL
PRO
LEU
LEU
ALA
ARG
GLY
R27
R86
E138
Q139
A140
R141
K142
Q201
R202
ARG
ASP
SER

- Molecule 22: 28S ribosomal protein S27, mitochondrial

Chain V:  5% 83% 13%


MET
ALA
ALA
SER
ILE
VAL
ARG
ARG
GLY
MET
LEU
LEU
ALA
ARG
VAL
VAL
GLN
PRO
GLN
SER
LEU
SER
PRO
ASP
ALA
GLY
LYS
TYR
L29
L30
V35
H38
I76
R82
D86
H87
A88
N141
D149
A172
D195
L225
Y226
L236
S269
P270
E271
D272
R277
L280
L283
L290
A293
ASP
ALA
GLY
SER
SER
GLU
GLU
GLN
SER
ASN
ASP
GLU
ASP
ASN
GLY
SER
E311
K312
V360
L364
E397
A400
K401
Q402
E403
Y404
Q405
A406
Q407
LYS
ALA
LYS
ALA
SER
ALA

- Molecule 23: 28S ribosomal protein S28, mitochondrial

Chain W:  53% 47%

MET
ALA
ALA
LEU
CYS
ARG
THR
ARG
VAL
ALA
ALA
GLU
SER
HIS
PHE
LEU
ARG
VAL
PHE
LEU
PHE
PHE
PRO
PHE
ARG
GLY
VAL
GLY
THR
GLU
SER
GLY
SER
SER
ASN
ALA
LYS
GLU
PRO
LYS
THR
ARG
ALA
GLY
PHE
ALA
SER
ALA
LEU
GLU
ARG
SER
LEU
GLN
GLY
HIS
GLU
LYS
GLU
LEU
ASP
GLY
ARG
PHE
HIS
MET
GLY
THR
GLN
ALA
ARG
GLN
SER
ILE
ALA
ALA
HIS
HIS
LEU
ASP
ASN
GLN
VAL
SER
VAL
VAL
GLU
SER
PRO
ARG
A47
I48
H81
L108
V141
L151
I152
L153
E206
L212
R213
L244
L247
K248
R249
R276
E277
E286
V307
E327
L380
H394
L398

- Molecule 24: 28S ribosomal protein S29, mitochondrial

Chain X:  84% 12%

MET
MET
LYS
GLY
ILE
THR
ARG
LEU
LEU
SER
ARG
HIS
HIS
LYS
LEU
ASP
PRO
GLY
ARG
PHE
LEU
HIS
MET
GLY
THR
GLN
ALA
ARG
GLN
SER
ILE
ALA
ALA
HIS
HIS
LEU
ASP
ASN
GLN
VAL
PRO
VAL
VAL
GLU
SER
PRO
ARG
A47
I48
H81
L108
V141
L151
I152
L153
E206
L212
R213
L244
L247
K248
R249
R276
E277
E286
V307
E327
L380
H394
L398

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|
| A2 | V33 | R36 | R37 | R38 | E39 | K40 | G41 | E42 | E48 | D64 | A65 | R79 | A80 | Q81 | E82 | A83 | A84 | R85 | M86 | R87 | S88 | R89 | Q90 | E91 | T92 | L93 | G94 | E95 | S96 | G97 | L104 | L117 | S118 |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	885199	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.563	Depositor
Minimum map value	-1.110	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	398.4, 398.4, 398.4	wwPDB
Map dimensions	720, 720, 720	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.55333334, 0.55333334, 0.55333334	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, NAD, GNP, 5MC, MG, ZN, FES, 5MU, MA6, AYA, ATP, SPM, 5F0, B8T, 5I0

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	0.25	0/22774	0.68	0/35454
2	B	0.25	0/1887	0.50	0/2552
3	C	0.25	0/1113	0.48	0/1505
4	D	0.24	0/2733	0.50	0/3659
5	E	0.24	0/1000	0.51	0/1349
6	F	0.24	0/1767	0.46	0/2373
7	G	0.24	0/2775	0.48	0/3720
8	H	0.24	0/1178	0.46	0/1598
9	I	0.24	0/1030	0.50	0/1386
10	J	0.25	0/855	0.56	0/1148
11	K	0.22	0/880	0.58	0/1182
12	L	0.23	0/1477	0.47	0/1974
13	M	0.24	0/963	0.53	0/1295
14	N	0.24	0/886	0.50	0/1199
15	O	0.24	0/1648	0.48	0/2243
16	P	0.25	0/798	0.45	0/1070
17	Q	0.24	0/759	0.57	0/1008
18	R	0.24	0/2456	0.45	0/3317
19	S	0.26	0/1153	0.50	0/1553
20	T	0.24	0/1413	0.47	0/1897
21	U	0.23	0/1510	0.53	0/2025
22	V	0.23	0/3030	0.40	0/4093
23	W	0.25	0/801	0.51	0/1079
24	X	0.24	0/2930	0.44	0/3965
25	Y	0.24	0/1289	0.40	0/1737
26	Z	0.24	0/857	0.47	0/1141
27	0	0.24	0/1834	0.54	0/2484
28	1	0.24	0/2285	0.44	0/3090
29	2	0.23	0/941	0.52	0/1257
30	3	0.23	0/640	0.56	0/844
31	4	0.24	0/4904	0.42	0/6636
32	8	0.23	0/1560	0.47	0/2089

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.24	0/72126	0.56	0/101922

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	20472	10412	10396	52	0
2	B	1838	1832	1835	4	0
3	C	1083	1089	1088	5	0
4	D	2682	2743	2741	2	0
5	E	980	1012	1013	0	0
6	F	1725	1770	1769	7	0
7	G	2716	2717	2714	11	0
8	H	1152	1184	1183	14	0
9	I	1020	1061	1052	5	0
10	J	839	888	887	0	0
11	K	862	886	885	2	0
12	L	1453	1541	1540	4	0
13	M	942	966	965	2	0
14	N	868	929	928	1	0
15	O	1592	1557	1557	2	0
16	P	781	807	806	2	0
17	Q	752	769	771	6	0
18	R	2409	2429	2428	7	0
19	S	1126	1129	1126	5	0
20	T	1379	1405	1406	0	0
21	U	1488	1500	1499	0	0
22	V	2969	2964	2961	9	0
23	W	789	803	802	1	0
24	X	2855	2856	2856	11	0
25	Y	1255	1206	1204	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	Z	839	859	858	1	0
27	0	1787	1797	1796	9	0
28	1	2238	2269	2269	5	0
29	2	935	969	971	5	0
30	3	629	702	702	1	0
31	4	4795	4798	4796	24	0
32	8	1543	1588	1587	2	0
33	A	44	26	26	0	0
34	A	14	30	26	0	0
35	A	52	54	0	0	0
36	A	21	0	0	0	0
37	3	1	0	0	0	0
37	A	59	0	0	0	0
37	B	1	0	0	0	0
37	X	1	0	0	0	0
38	O	1	0	0	0	0
39	P	4	0	0	0	0
39	T	4	0	0	0	0
40	X	31	12	12	0	0
41	X	32	13	13	0	0
42	0	38	0	0	0	0
42	1	53	0	0	0	0
42	2	26	0	0	0	0
42	3	25	0	0	0	0
42	4	25	0	0	0	0
42	8	2	0	0	0	0
42	A	1857	0	0	20	0
42	B	100	0	0	3	0
42	C	65	0	0	1	0
42	D	76	0	0	0	0
42	E	6	0	0	0	0
42	F	41	0	0	1	0
42	G	99	0	0	1	0
42	H	75	0	0	0	0
42	I	22	0	0	0	0
42	J	22	0	0	0	0
42	K	60	0	0	0	0
42	L	28	0	0	0	0
42	M	33	0	0	1	0
42	N	24	0	0	0	0
42	O	42	0	0	0	0
42	P	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Q	53	0	0	1	0
42	R	49	0	0	0	0
42	S	25	0	0	1	0
42	T	29	0	0	0	0
42	U	15	0	0	0	0
42	V	5	0	0	0	0
42	W	27	0	0	0	0
42	X	89	0	0	1	0
42	Y	19	0	0	0	0
42	Z	35	0	0	0	0
All	All	72143	59572	59468	172	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 1.

All (172) 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)
1:A:1593:U:O4	17:Q:50[B]:ARG:NH2	2.16	0.79
1:A:1353:A:N1	42:A:1805:HOH:O	2.19	0.76
19:S:10:GLY:O	42:S:201:HOH:O	2.05	0.75
24:X:327:GLU:OE1	42:X:601:HOH:O	2.08	0.70
6:F:116:GLU:OE1	42:F:301:HOH:O	2.10	0.68
1:A:937:U:OP2	42:A:1802:HOH:O	2.12	0.68
1:A:757:A:N7	42:A:1827:HOH:O	2.28	0.67
1:A:1028:G:OP1	42:A:1801:HOH:O	2.12	0.67
1:A:1047:A:OP2	42:A:1803:HOH:O	2.14	0.66
31:4:573:ALA:O	31:4:577:ASN:ND2	2.29	0.65
1:A:1453:A:N3	42:A:1831:HOH:O	2.30	0.63
28:1:254:GLU:N	28:1:254:GLU:OE1	2.32	0.63
11:K:58:ARG:NE	11:K:72:ASP:OD1	2.31	0.61
24:X:108:LEU:HD23	24:X:141:VAL:HG21	1.83	0.60
1:A:1198:A:OP2	42:A:1804:HOH:O	2.16	0.60
1:A:1294:A:OP1	2:B:201:ASN:ND2	2.35	0.60
1:A:941:G:N7	42:A:1839:HOH:O	2.32	0.60
13:M:108:GLU:OE2	42:M:201:HOH:O	2.16	0.60
24:X:276:ARG:NH2	24:X:286:GLU:OE1	2.34	0.60
15:O:54:GLU:OE1	15:O:57:LYS:NZ	2.28	0.59
2:B:161:ASP:OD2	42:B:401:HOH:O	2.16	0.59
1:A:1015:A:N7	42:A:1840:HOH:O	2.32	0.58
31:4:451:ASP:OD1	31:4:454:ARG:NH2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1560:U:O2'	32:8:171:ASP:OD2	2.11	0.57
12:L:86:ASP:OD1	12:L:87:ASP:N	2.37	0.56
27:0:41:LEU:HD13	27:0:55:TRP:CG	2.40	0.56
25:Y:322:ASP:O	25:Y:324:ASP:N	2.38	0.56
1:A:992:U:O2'	1:A:994:A:OP2	2.14	0.56
22:V:236:LEU:HD12	22:V:290:LEU:HD13	1.88	0.56
27:0:42:THR:HG22	27:0:49:ARG:HG2	1.87	0.56
31:4:631:VAL:HG21	31:4:649:VAL:HG21	1.88	0.56
7:G:248:VAL:O	7:G:248:VAL:HG13	2.05	0.55
31:4:200:ASP:OD2	31:4:243:ASN:N	2.40	0.55
27:0:215:GLY:O	27:0:216:THR:OG1	2.24	0.55
2:B:71:ASP:OD1	42:B:402:HOH:O	2.18	0.55
1:A:1038:C:HO2'	12:L:155:TYR:HH	1.54	0.54
1:A:956:C:N4	42:A:1881:HOH:O	2.39	0.54
31:4:564:ILE:O	31:4:567:THR:N	2.41	0.54
1:A:976:A:N7	42:A:1847:HOH:O	2.34	0.54
31:4:151:ASP:OD1	31:4:152:ILE:N	2.40	0.54
28:1:304:GLU:OE2	28:1:309:ILE:HD11	2.08	0.53
1:A:1098:C:OP1	1:A:1151:C:N4	2.41	0.53
31:4:274:GLN:OE1	31:4:274:GLN:N	2.40	0.53
7:G:61:VAL:O	7:G:63:THR:N	2.41	0.53
25:Y:258:ILE:HD11	31:4:317:LEU:HD22	1.89	0.53
24:X:108:LEU:HD21	24:X:307:VAL:HG11	1.89	0.53
31:4:631:VAL:CG2	31:4:649:VAL:HG21	2.38	0.53
3:C:84:GLU:N	3:C:84:GLU:OE1	2.38	0.52
13:M:19:ILE:HB	13:M:83:LEU:HD23	1.91	0.52
17:Q:86:GLY:O	42:Q:101:HOH:O	2.18	0.52
1:A:1342:C:OP2	26:Z:96:LYS:NZ	2.40	0.51
6:F:48:LYS:NZ	7:G:321:ASP:OD1	2.30	0.51
1:A:906:C:N3	7:G:50:ARG:N	2.58	0.51
31:4:618:ALA:O	31:4:622:ASN:N	2.42	0.51
1:A:1037:A:O2'	12:L:152:HIS:NE2	2.27	0.51
18:R:219:TYR:O	18:R:256:ARG:NH2	2.44	0.51
31:4:131:ASP:OD2	31:4:136:HIS:ND1	2.40	0.51
24:X:151:LEU:CD2	24:X:247:LEU:HD22	2.42	0.50
1:A:899:G:O2'	1:A:907:A:N1	2.32	0.50
16:P:49:ASP:OD2	23:W:82:SER:OG	2.23	0.50
27:0:54:ALA:O	27:0:58:VAL:HG23	2.12	0.50
1:A:1280:C:OP1	42:A:1808:HOH:O	2.19	0.50
8:H:155:VAL:HG21	28:1:129:PHE:CB	2.42	0.50
18:R:276:VAL:HG11	18:R:307:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:108:LEU:HD21	24:X:307:VAL:CG1	2.43	0.49
1:A:1063:A:N7	42:A:1851:HOH:O	2.35	0.49
22:V:82:ARG:NH1	22:V:86:ASP:OD1	2.45	0.49
24:X:153:LEU:HD21	24:X:244:LEU:HD22	1.95	0.49
1:A:1528:A:OP1	27:O:101:ARG:NH2	2.44	0.49
15:O:185:SER:O	18:R:183:LYS:NZ	2.45	0.49
7:G:229:LEU:HD21	7:G:241:VAL:HG11	1.94	0.48
12:L:112:MET:O	12:L:116:VAL:HG22	2.11	0.48
2:B:186:THR:O	42:B:403:HOH:O	2.20	0.48
1:A:1261:C:OP2	42:A:1810:HOH:O	2.20	0.48
1:A:1590:A:OP1	42:A:1809:HOH:O	2.20	0.47
18:R:162:SER:O	18:R:170:ARG:NH1	2.45	0.47
24:X:206:GLU:OE2	24:X:249:ARG:NH2	2.47	0.47
1:A:702:C:OP1	1:A:848:U:O2'	2.30	0.47
22:V:360:VAL:HG13	22:V:364:LEU:HD22	1.97	0.47
31:4:615:MET:CE	31:4:649:VAL:HG22	2.44	0.47
18:R:262:LEU:O	18:R:265:THR:OG1	2.23	0.47
19:S:106:LEU:HB2	19:S:117:LEU:HD11	1.96	0.47
31:4:615:MET:HE1	31:4:649:VAL:HG22	1.96	0.47
1:A:976:A:H5''	17:Q:2:AYA:HM3	1.97	0.47
1:A:1558[B]:A:H2'	1:A:1559[B]:G:O4'	2.14	0.47
31:4:58:VAL:HG23	31:4:58:VAL:O	2.14	0.46
31:4:372:TYR:CE2	31:4:400:LEU:HD21	2.51	0.46
22:V:141:ASN:ND2	22:V:172:ALA:O	2.47	0.46
1:A:1066:C:O2'	9:I:187:ARG:O	2.34	0.46
7:G:70:THR:HG23	7:G:73:PHE:H	1.79	0.46
24:X:151:LEU:HD23	24:X:247:LEU:HD22	1.98	0.46
6:F:119:LYS:NZ	24:X:398:LEU:O	2.46	0.46
8:H:184:ILE:HG22	8:H:184:ILE:O	2.16	0.46
4:D:103:LEU:HD11	4:D:123:ARG:HB2	1.97	0.46
32:8:91:ASP:OD1	32:8:92:GLU:N	2.48	0.46
31:4:646:THR:HG23	31:4:663:LEU:HD22	1.98	0.46
1:A:662:U:O4	42:A:1806:HOH:O	2.19	0.45
1:A:700:A:N1	1:A:709:G:O2'	2.44	0.45
7:G:237:GLU:N	7:G:237:GLU:OE1	2.46	0.45
27:O:37:ASP:O	27:O:41:LEU:N	2.48	0.45
18:R:187:GLU:OE1	18:R:187:GLU:N	2.45	0.45
31:4:577:ASN:OD1	31:4:607:ARG:N	2.47	0.45
1:A:1004:G:O2'	9:I:98:GLN:NE2	2.50	0.45
8:H:76:LEU:HD22	8:H:174:LYS:HG2	1.99	0.45
14:N:58:CYS:SG	14:N:81:LEU:HD22	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:394:LYS:NZ	42:G:408:HOH:O	2.47	0.45
8:H:176:GLN:NE2	8:H:178:GLU:OE2	2.50	0.45
9:I:163:HIS:NE2	17:Q:20:GLU:OE2	2.47	0.45
3:C:41:ARG:NH2	42:C:206:HOH:O	2.50	0.44
19:S:51:VAL:HG13	29:2:117:LEU:HD11	1.98	0.44
29:2:48:GLU:OE1	29:2:48:GLU:N	2.42	0.44
22:V:35:VAL:HG12	22:V:35:VAL:O	2.16	0.44
31:4:309:PHE:HE1	31:4:342:LEU:HD22	1.83	0.44
6:F:52:ARG:NH1	7:G:321:ASP:OD2	2.48	0.44
8:H:108:VAL:HG22	8:H:143:LEU:HD23	1.99	0.44
1:A:1229:U:O2'	1:A:1442:G:O4'	2.36	0.44
24:X:380:LEU:HD21	24:X:398:LEU:CD1	2.48	0.44
8:H:155:VAL:HG21	28:1:129:PHE:HB2	2.00	0.44
1:A:760:A:N1	1:A:780:C:O2'	2.44	0.43
3:C:96:MET:HB2	3:C:108:LEU:HD11	1.99	0.43
8:H:106:ILE:HD11	8:H:143:LEU:HD22	1.99	0.43
1:A:1057:G:H4'	1:A:1578:A:H4'	2.01	0.43
22:V:30:LEU:HD12	22:V:149:ASP:HB2	2.00	0.43
1:A:1462:G:O3'	42:A:1811:HOH:O	2.22	0.43
7:G:203:GLU:OE1	7:G:203:GLU:N	2.49	0.43
8:H:155:VAL:HG21	28:1:129:PHE:HB3	2.01	0.43
1:A:1116:A:O2'	1:A:1117:A:O4'	2.31	0.42
9:I:179:THR:HG21	17:Q:39:ILE:HD13	2.01	0.42
16:P:141:ARG:O	16:P:142:GLU:C	2.57	0.42
17:Q:72:ILE:HD13	29:2:104:LEU:HD21	2.01	0.42
1:A:1441:A:N7	42:A:1853:HOH:O	2.35	0.42
22:V:225:LEU:HD21	22:V:280:LEU:HD23	2.01	0.42
8:H:59:THR:HG23	8:H:59:THR:O	2.19	0.42
8:H:148:LEU:N	8:H:148:LEU:HD23	2.34	0.42
27:0:119:THR:OG1	27:0:124:THR:HG22	2.20	0.42
1:A:1584:MA6:OP1	30:3:145:LYS:NZ	2.50	0.42
4:D:245:VAL:HG22	4:D:271:ALA:HB1	2.01	0.42
8:H:151:SER:O	8:H:155:VAL:HG23	2.20	0.42
9:I:158:ARG:NH2	9:I:177:ASP:OD2	2.47	0.42
19:S:113:ASP:OD1	19:S:114:GLU:N	2.52	0.42
31:4:501:ASP:OD2	31:4:537:ARG:NH1	2.50	0.42
27:0:110:ASP:OD1	27:0:110:ASP:N	2.51	0.41
1:A:843:G:N2	1:A:846:A:OP2	2.50	0.41
1:A:1102:A:H5'	1:A:1576:G:H4'	2.02	0.41
31:4:236:VAL:HG12	31:4:238:TRP:H	1.85	0.41
1:A:1556:C:H2'	1:A:1557:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1259:U:H6	1:A:1326:A:HO2'	1.65	0.41
8:H:70:ASP:OD1	8:H:71:ILE:N	2.53	0.41
8:H:92:GLU:OE1	8:H:141:ARG:NH1	2.47	0.41
29:2:33:VAL:HG21	29:2:104:LEU:HD23	2.03	0.41
1:A:1308:U:O2'	3:C:64:HIS:ND1	2.49	0.41
3:C:45:SER:OG	3:C:167:LEU:OXT	2.39	0.41
6:F:176:ASP:OD2	6:F:179:ARG:NH2	2.54	0.41
8:H:76:LEU:HD12	8:H:148:LEU:HD11	2.02	0.41
1:A:1104:A:OP1	1:A:1591:C:O2'	2.34	0.41
31:4:166:VAL:HG23	31:4:167:LYS:N	2.36	0.41
31:4:615:MET:HG3	31:4:645:LEU:HD11	2.02	0.41
1:A:1213:A:N3	1:A:1239:C:O2'	2.43	0.41
22:V:76:ILE:HD13	22:V:88:ALA:HB1	2.03	0.41
6:F:170:VAL:HG13	6:F:236:LEU:O	2.21	0.41
18:R:70:PHE:O	18:R:76:GLN:NE2	2.49	0.41
31:4:508:VAL:O	31:4:508:VAL:HG12	2.21	0.40
1:A:706:C:OP1	27:0:43:ARG:NE	2.49	0.40
1:A:1272:A:N7	42:A:1867:HOH:O	2.37	0.40
29:2:64:ASP:OD1	29:2:65:ALA:N	2.54	0.40
1:A:764:A:N1	42:A:1866:HOH:O	2.37	0.40
1:A:1561:C:H2'	1:A:1562:G:O4'	2.21	0.40
1:A:1117:A:OP2	19:S:50:ARG:NE	2.54	0.40
6:F:79:ALA:O	7:G:312:GLN:NE2	2.55	0.40
11:K:120:LEU:HB3	11:K:123:ILE:HD12	2.03	0.40
22:V:225:LEU:HD11	22:V:283:LEU:HD22	2.03	0.40
31:4:616:ASP:O	31:4:620:VAL:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	225/296 (76%)	221 (98%)	4 (2%)	0	100	100
3	C	130/167 (78%)	127 (98%)	3 (2%)	0	100	100
4	D	333/430 (77%)	321 (96%)	12 (4%)	0	100	100
5	E	121/125 (97%)	120 (99%)	1 (1%)	0	100	100
6	F	206/242 (85%)	203 (98%)	3 (2%)	0	100	100
7	G	326/396 (82%)	315 (97%)	11 (3%)	0	100	100
8	H	138/201 (69%)	134 (97%)	3 (2%)	1 (1%)	22	32
9	I	133/194 (69%)	129 (97%)	4 (3%)	0	100	100
10	J	106/138 (77%)	103 (97%)	3 (3%)	0	100	100
11	K	99/128 (77%)	99 (100%)	0	0	100	100
12	L	172/257 (67%)	169 (98%)	3 (2%)	0	100	100
13	M	117/137 (85%)	117 (100%)	0	0	100	100
14	N	108/130 (83%)	106 (98%)	2 (2%)	0	100	100
15	O	191/258 (74%)	188 (98%)	3 (2%)	0	100	100
16	P	95/142 (67%)	93 (98%)	2 (2%)	0	100	100
17	Q	85/86 (99%)	84 (99%)	1 (1%)	0	100	100
18	R	293/360 (81%)	284 (97%)	9 (3%)	0	100	100
19	S	135/190 (71%)	131 (97%)	4 (3%)	0	100	100
20	T	167/173 (96%)	164 (98%)	3 (2%)	0	100	100
21	U	174/205 (85%)	174 (100%)	0	0	100	100
22	V	358/414 (86%)	349 (98%)	9 (2%)	0	100	100
23	W	98/187 (52%)	96 (98%)	2 (2%)	0	100	100
24	X	351/398 (88%)	345 (98%)	6 (2%)	0	100	100
25	Y	148/395 (38%)	145 (98%)	2 (1%)	1 (1%)	22	32
26	Z	98/106 (92%)	97 (99%)	1 (1%)	0	100	100
27	0	213/218 (98%)	211 (99%)	2 (1%)	0	100	100
28	1	274/323 (85%)	269 (98%)	5 (2%)	0	100	100
29	2	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
30	3	69/199 (35%)	68 (99%)	1 (1%)	0	100	100
31	4	588/689 (85%)	578 (98%)	10 (2%)	0	100	100
32	8	189/285 (66%)	184 (97%)	5 (3%)	0	100	100
All	All	5855/7586 (77%)	5738 (98%)	115 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	126	ILE
25	Y	323	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	200/249 (80%)	200 (100%)	0	100	100
3	C	115/143 (80%)	115 (100%)	0	100	100
4	D	281/357 (79%)	281 (100%)	0	100	100
5	E	105/107 (98%)	105 (100%)	0	100	100
6	F	185/209 (88%)	185 (100%)	0	100	100
7	G	288/342 (84%)	287 (100%)	1 (0%)	92	97
8	H	130/180 (72%)	130 (100%)	0	100	100
9	I	104/146 (71%)	104 (100%)	0	100	100
10	J	93/118 (79%)	93 (100%)	0	100	100
11	K	91/113 (80%)	91 (100%)	0	100	100
12	L	158/226 (70%)	158 (100%)	0	100	100
13	M	97/113 (86%)	97 (100%)	0	100	100
14	N	96/115 (84%)	96 (100%)	0	100	100
15	O	174/230 (76%)	174 (100%)	0	100	100
16	P	88/123 (72%)	88 (100%)	0	100	100
17	Q	79/78 (101%)	79 (100%)	0	100	100
18	R	264/318 (83%)	264 (100%)	0	100	100
19	S	117/164 (71%)	117 (100%)	0	100	100
20	T	154/157 (98%)	154 (100%)	0	100	100
21	U	152/174 (87%)	152 (100%)	0	100	100
22	V	325/364 (89%)	323 (99%)	2 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	87/158 (55%)	87 (100%)	0	100	100
24	X	312/351 (89%)	310 (99%)	2 (1%)	86	94
25	Y	138/357 (39%)	138 (100%)	0	100	100
26	Z	90/95 (95%)	90 (100%)	0	100	100
27	0	188/190 (99%)	188 (100%)	0	100	100
28	1	254/291 (87%)	254 (100%)	0	100	100
29	2	100/100 (100%)	100 (100%)	0	100	100
30	3	65/166 (39%)	65 (100%)	0	100	100
31	4	529/609 (87%)	528 (100%)	1 (0%)	93	97
32	8	172/253 (68%)	172 (100%)	0	100	100
All	All	5231/6596 (79%)	5225 (100%)	6 (0%)	93	98

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	389	ARG
22	V	38	HIS
22	V	226	TYR
24	X	81	HIS
24	X	394	HIS
31	4	486	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
8	H	109	HIS
9	I	98	GLN
25	Y	257	ASN
29	2	109	GLN
31	4	257	HIS
31	4	285	ASN
31	4	295	ASN
32	8	118	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	942/955 (98%)	104 (11%)	0

All (104) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	649	A
1	A	651	A
1	A	680	U
1	A	688	A
1	A	704	U
1	A	718	A
1	A	721	U
1	A	722	C
1	A	730	A
1	A	737	C
1	A	739	C
1	A	740	G
1	A	753	A
1	A	761	A
1	A	766	G
1	A	773	U
1	A	777	G
1	A	791	G
1	A	796	G
1	A	830	U
1	A	832	U
1	A	835	C
1	A	860	A
1	A	861	U
1	A	868	C
1	A	871	A
1	A	890	C
1	A	905	A
1	A	919	A
1	A	938	A
1	A	939	A
1	A	942	A
1	A	954	C
1	A	955	A
1	A	956	C
1	A	958	C
1	A	960	C
1	A	961	U

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Mol	Chain	Res	Type
1	A	962	C
1	A	967	A
1	A	1001	C
1	A	1002	C
1	A	1011	C
1	A	1015	A
1	A	1042	U
1	A	1065	C
1	A	1081	U
1	A	1082	A
1	A	1098	C
1	A	1103	A
1	A	1105	C
1	A	1106	C
1	A	1107	U
1	A	1109	A
1	A	1118	A
1	A	1121	A
1	A	1126	A
1	A	1151	C
1	A	1153	C
1	A	1160	A
1	A	1167	A
1	A	1187	U
1	A	1188	A
1	A	1189	U
1	A	1223	C
1	A	1225	C
1	A	1247	G
1	A	1248	C
1	A	1250	C
1	A	1251	A
1	A	1271	C
1	A	1273	G
1	A	1284	U
1	A	1290	C
1	A	1291	U
1	A	1307	G
1	A	1326	A
1	A	1327	G
1	A	1343	A
1	A	1356	A

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Mol	Chain	Res	Type
1	A	1378	C
1	A	1390	A
1	A	1405	C
1	A	1430	A
1	A	1447	G
1	A	1481	C
1	A	1482	A
1	A	1519	A
1	A	1520	U
1	A	1522	U
1	A	1525	C
1	A	1526	U
1	A	1527	A
1	A	1533	C
1	A	1537	C
1	A	1538	G
1	A	1539	C
1	A	1568	U
1	A	1571	U
1	A	1582	G
1	A	1594	G
1	A	1595	G
1	A	1599	A
1	A	1602	C

There are no RNA pucker outliers to report.

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

8 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MA6	A	1584	1	19,26,27	0.78	0	18,38,41	0.58	0
9	5F0	I	184	9	8,8,9	0.58	0	7,9,11	1.09	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	AYA	Q	2	17	6,7,8	0.75	0	5,8,10	0.49	0
1	B8T	A	1486	1	19,22,23	0.32	0	26,31,34	0.33	0
1	MA6	A	1583	1	19,26,27	0.77	0	18,38,41	0.60	0
1	5MC	A	1488	1	18,22,23	0.31	0	26,32,35	0.43	0
1	5MU	A	1076	1	19,22,23	0.30	0	28,32,35	0.33	0
29	AYA	2	2	29	6,7,8	0.80	0	5,8,10	0.51	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	A	1584	1	-	2/7/29/30	0/3/3/3
9	5F0	I	184	9	-	0/9/9/10	-
17	AYA	Q	2	17	-	0/4/6/8	-
1	B8T	A	1486	1	-	0/7/27/28	0/2/2/2
1	MA6	A	1583	1	-	0/7/29/30	0/3/3/3
1	5MC	A	1488	1	-	0/7/25/26	0/2/2/2
1	5MU	A	1076	1	-	0/7/25/26	0/2/2/2
29	AYA	2	2	29	-	0/4/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	184	5F0	OD1-C1-CB	-2.39	118.46	125.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1584	MA6	C5-C6-N6-C9
1	A	1584	MA6	C4'-C5'-O5'-P

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1584	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	Q	2	AYA	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 92 ligands modelled in this entry, 84 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	SPM	A	1702	-	13,13,13	0.28	0	12,12,12	0.96	0
39	FES	P	201	16,5	0,4,4	-	-	-	-	-
41	GNP	X	502	-	29,34,34	1.22	4 (13%)	33,54,54	1.99	5 (15%)
35	5I0	A	1703[B]	-	41,43,43	0.54	1 (2%)	54,65,65	0.93	4 (7%)
40	ATP	X	501	37	26,33,33	0.76	0	31,52,52	0.65	0
35	5I0	A	1703[A]	-	41,43,43	0.49	1 (2%)	54,65,65	0.94	4 (7%)
33	NAD	A	1701	37	42,48,48	0.57	0	50,73,73	0.56	1 (2%)
39	FES	T	201	20,13	0,4,4	-	-	-	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	SPM	A	1702	-	-	0/11/11/11	-
39	FES	P	201	16,5	-	-	0/1/1/1
41	GNP	X	502	-	-	1/14/38/38	0/3/3/3
35	5I0	A	1703[B]	-	-	0/24/90/90	0/3/3/3
40	ATP	X	501	37	-	0/18/38/38	0/3/3/3
35	5I0	A	1703[A]	-	-	1/24/90/90	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	NAD	A	1701	37	-	5/26/62/62	0/5/5/5
39	FES	T	201	20,13	-	-	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	X	502	GNP	PB-O2B	-3.18	1.48	1.56
41	X	502	GNP	PG-O1G	3.18	1.51	1.46
35	A	1703[B]	5IO	C23-N23	2.49	1.51	1.47
35	A	1703[A]	5IO	C23-N23	2.15	1.51	1.47
41	X	502	GNP	PG-O2G	-2.13	1.51	1.56
41	X	502	GNP	PG-O3G	-2.04	1.51	1.56

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	X	502	GNP	C5-C6-N1	-7.42	113.28	123.43
41	X	502	GNP	C2-N1-C6	5.87	125.26	115.93
35	A	1703[A]	5IO	C12-O42-C42	-3.26	103.25	108.38
35	A	1703[B]	5IO	C12-O42-C42	-3.26	103.25	108.38
35	A	1703[A]	5IO	C43-C33-C23	-3.14	105.74	110.34
41	X	502	GNP	C4-C5-C6	-3.13	117.81	120.80
35	A	1703[A]	5IO	N11-CA1-NC1	-3.10	115.18	120.59
35	A	1703[B]	5IO	N11-CA1-NC1	-3.10	115.18	120.59
35	A	1703[B]	5IO	C43-C33-C23	-2.94	106.04	110.34
41	X	502	GNP	N3-C2-N1	-2.85	123.42	127.22
41	X	502	GNP	C2-N3-C4	-2.69	112.28	115.36
33	A	1701	NAD	C5A-C6A-N6A	2.30	123.85	120.35
35	A	1703[A]	5IO	NB1-CA1-N11	2.11	124.25	119.55
35	A	1703[B]	5IO	NB1-CA1-N11	2.11	124.25	119.55

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
41	X	502	GNP	PB-N3B-PG-O1G
33	A	1701	NAD	C2N-C3N-C7N-O7N
33	A	1701	NAD	C2N-C3N-C7N-N7N
33	A	1701	NAD	C4N-C3N-C7N-O7N
33	A	1701	NAD	C4N-C3N-C7N-N7N
35	A	1703[A]	5IO	C13-C23-N23-CI3

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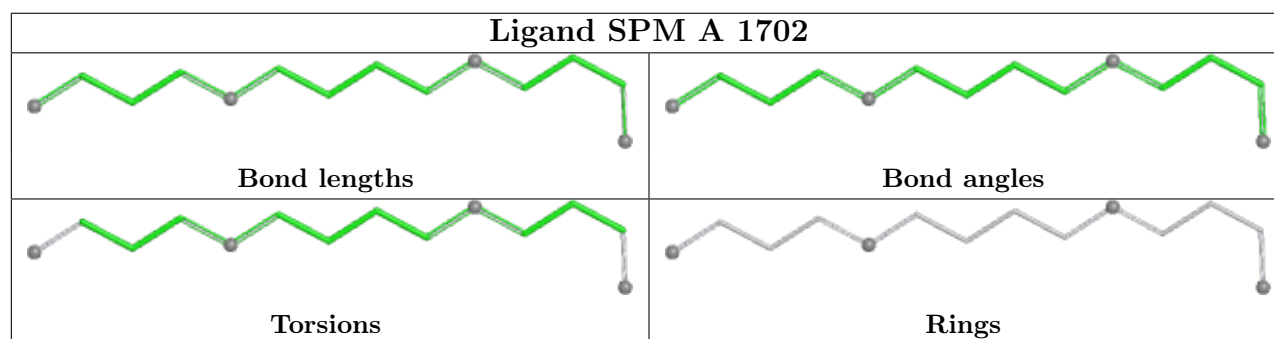
Continued from previous page...

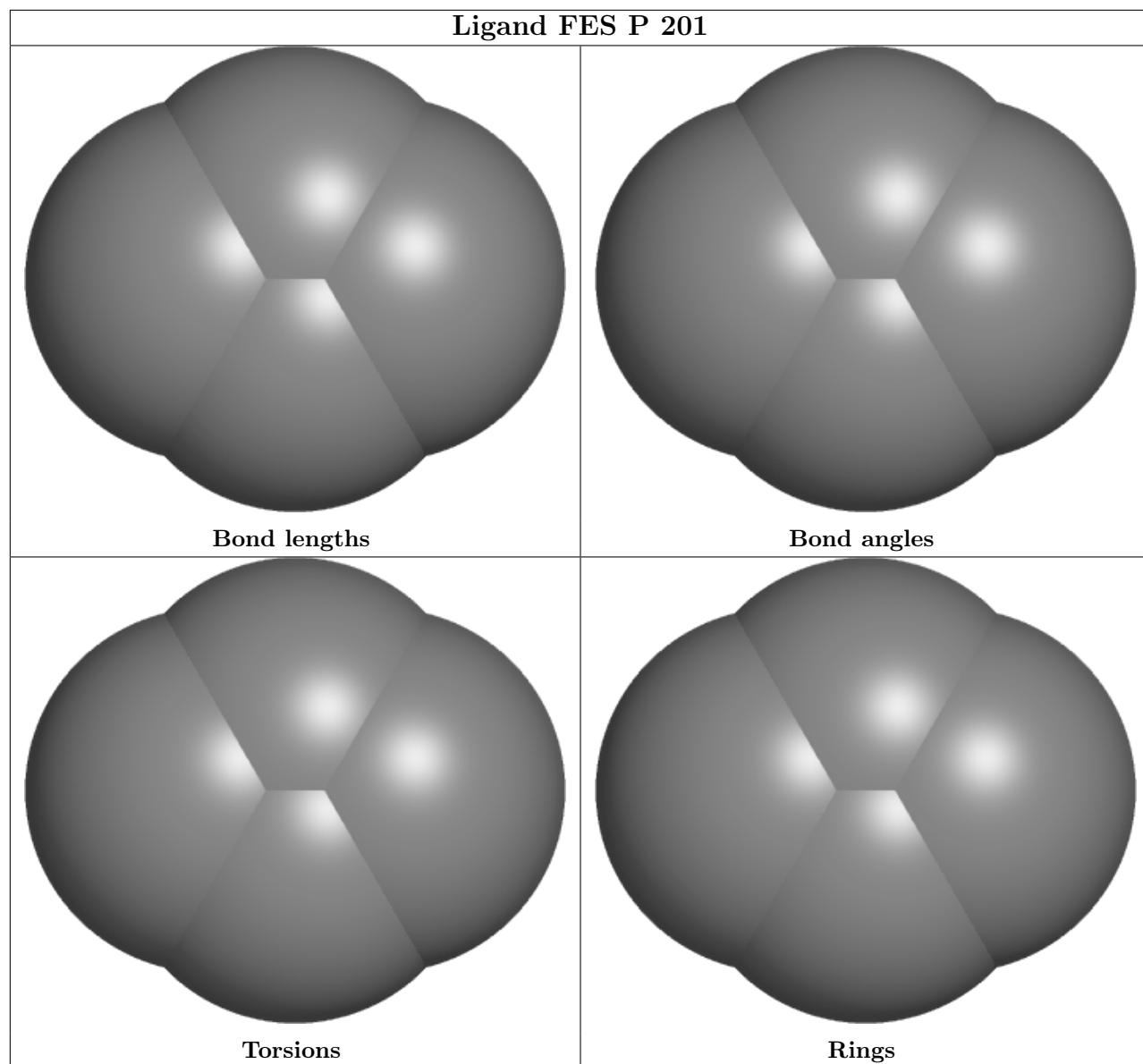
Mol	Chain	Res	Type	Atoms
33	A	1701	NAD	PN-O3-PA-O1A

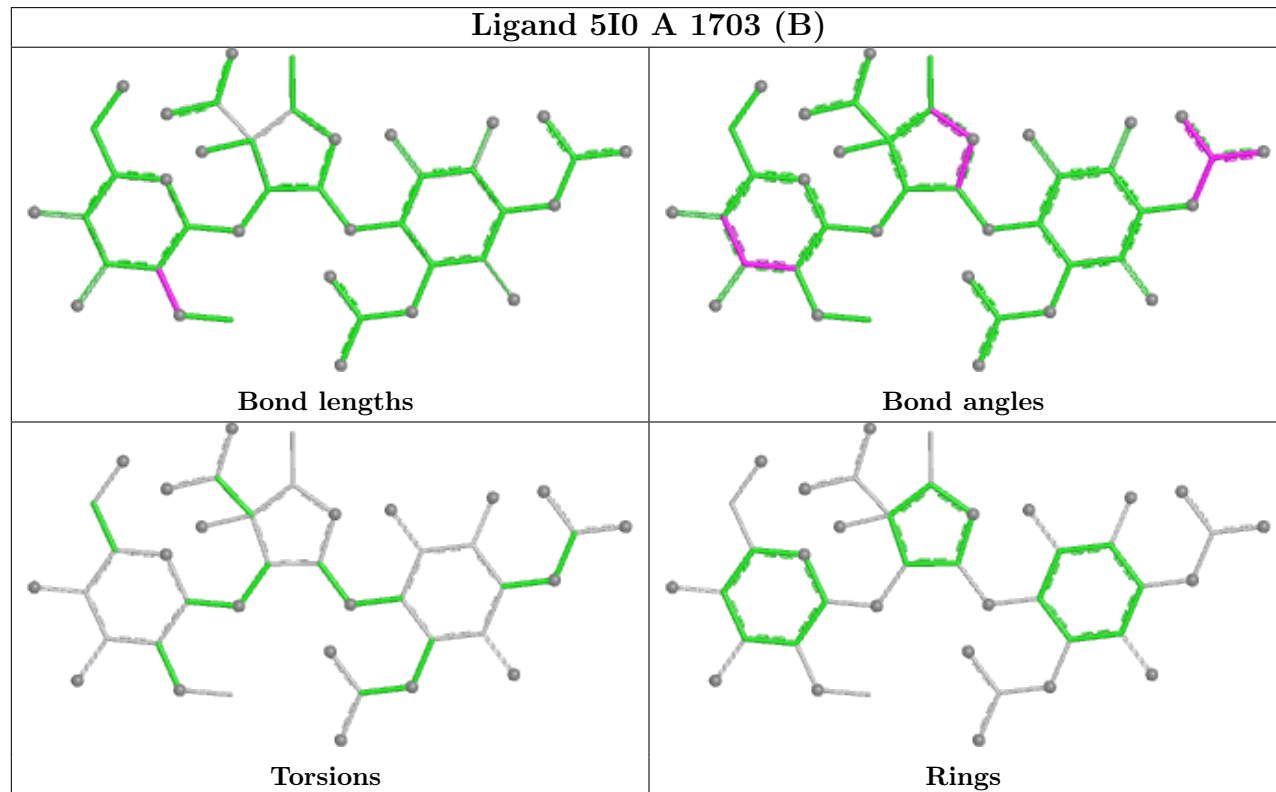
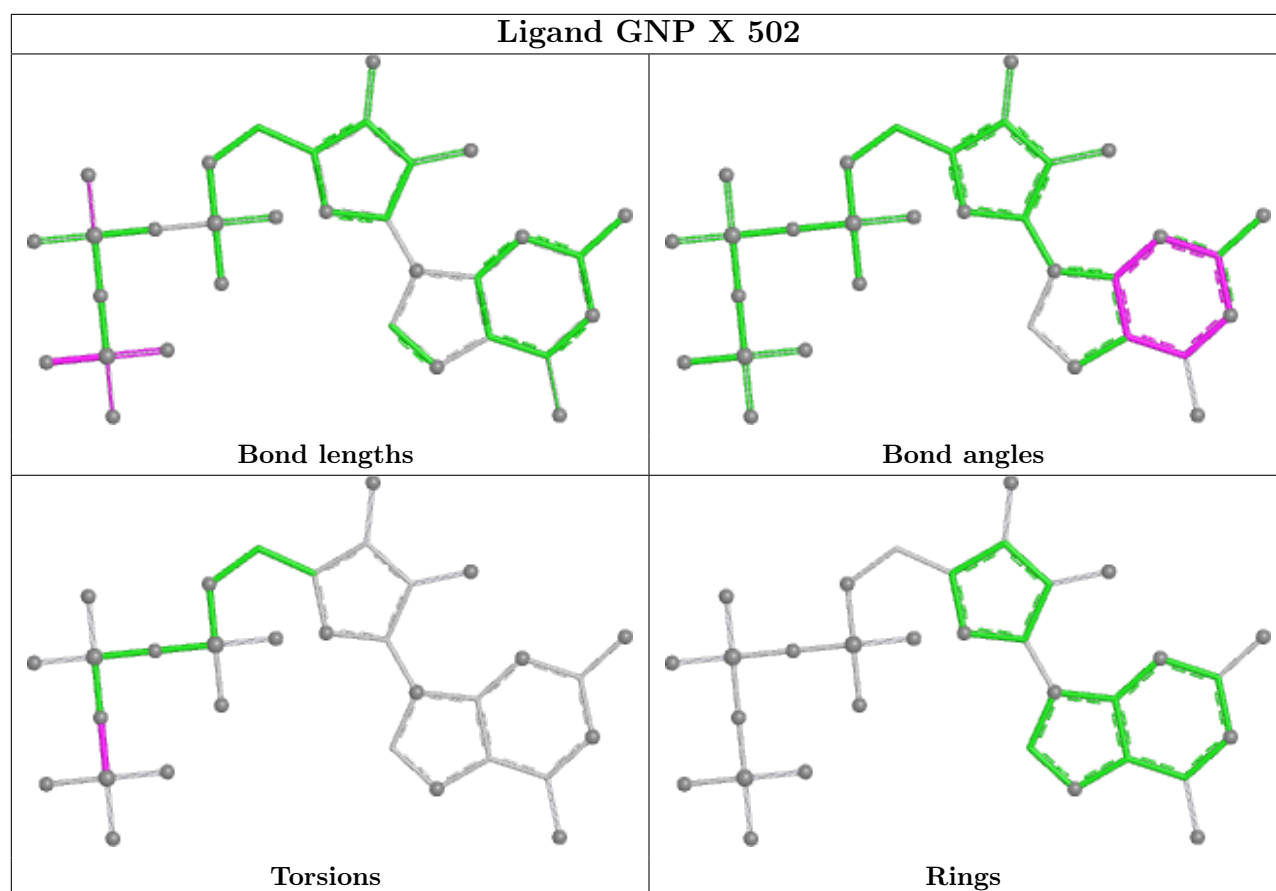
There are no ring outliers.

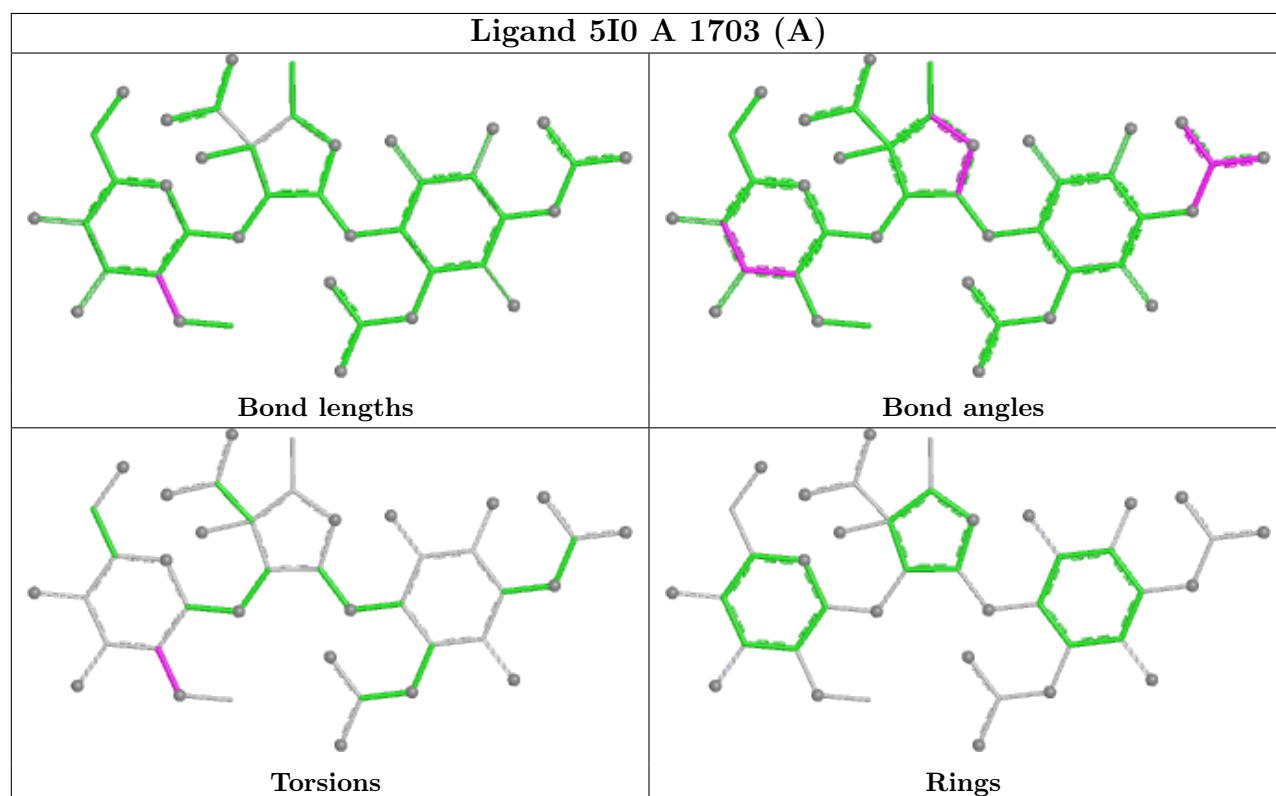
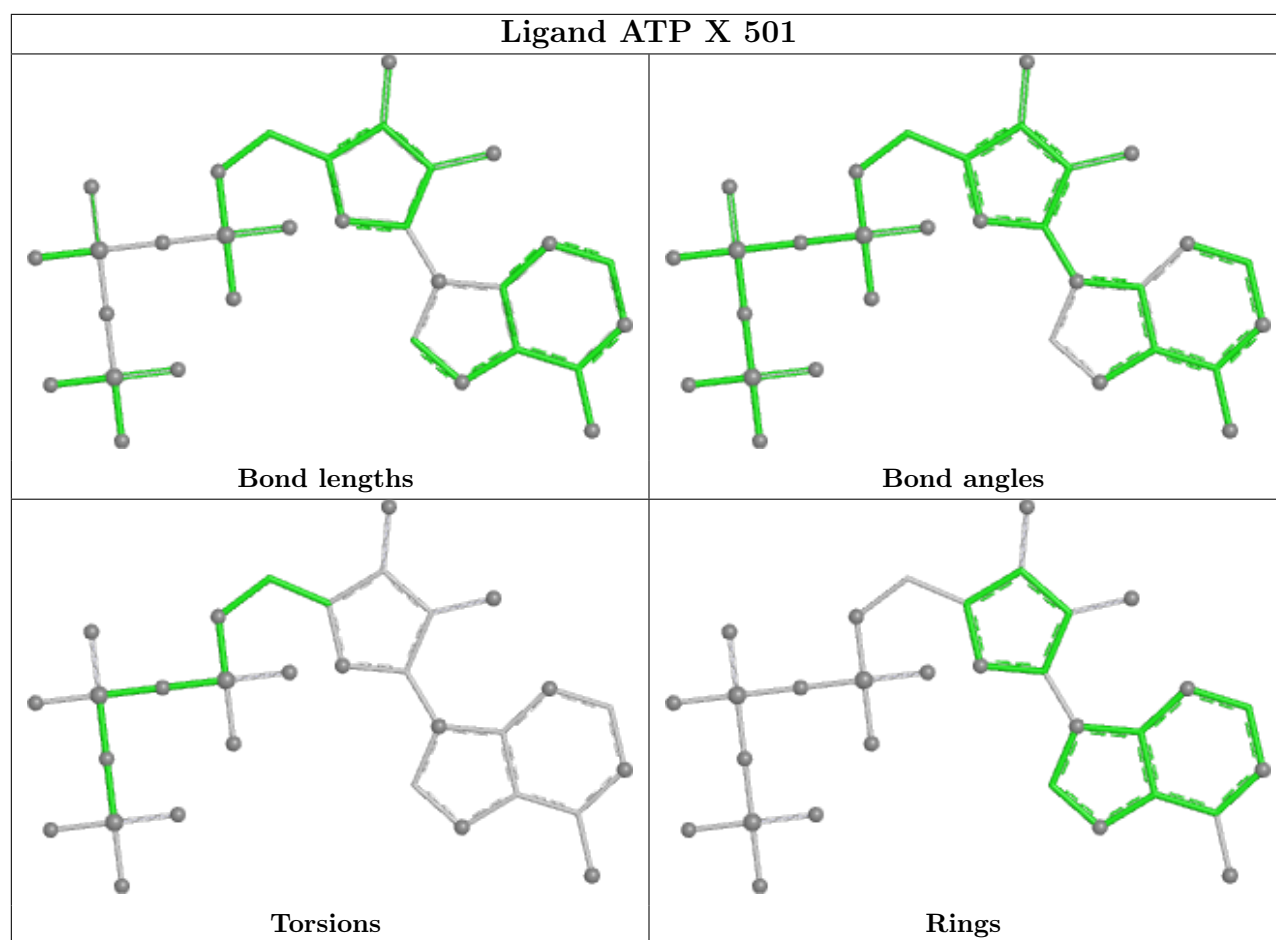
No monomer is involved in short contacts.

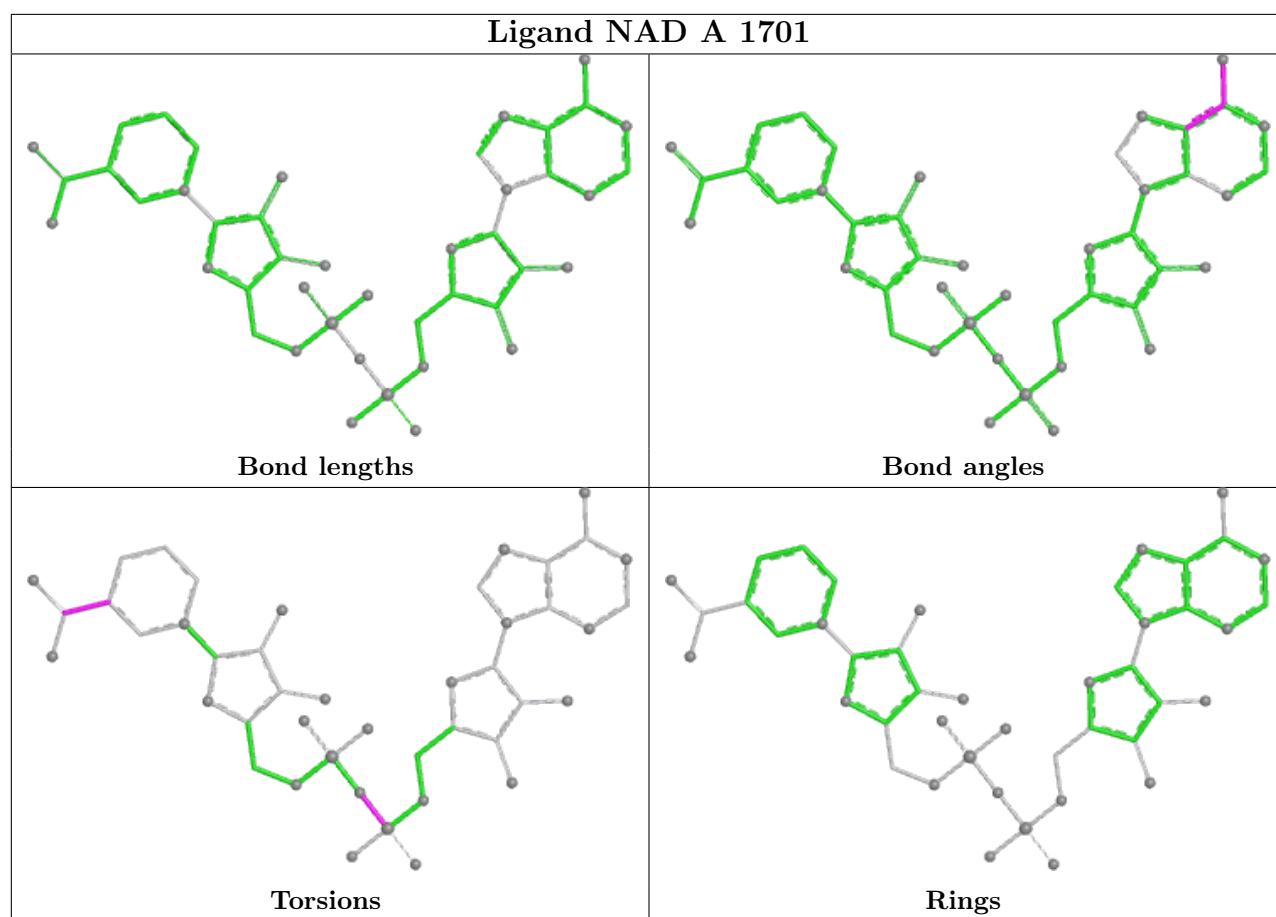
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

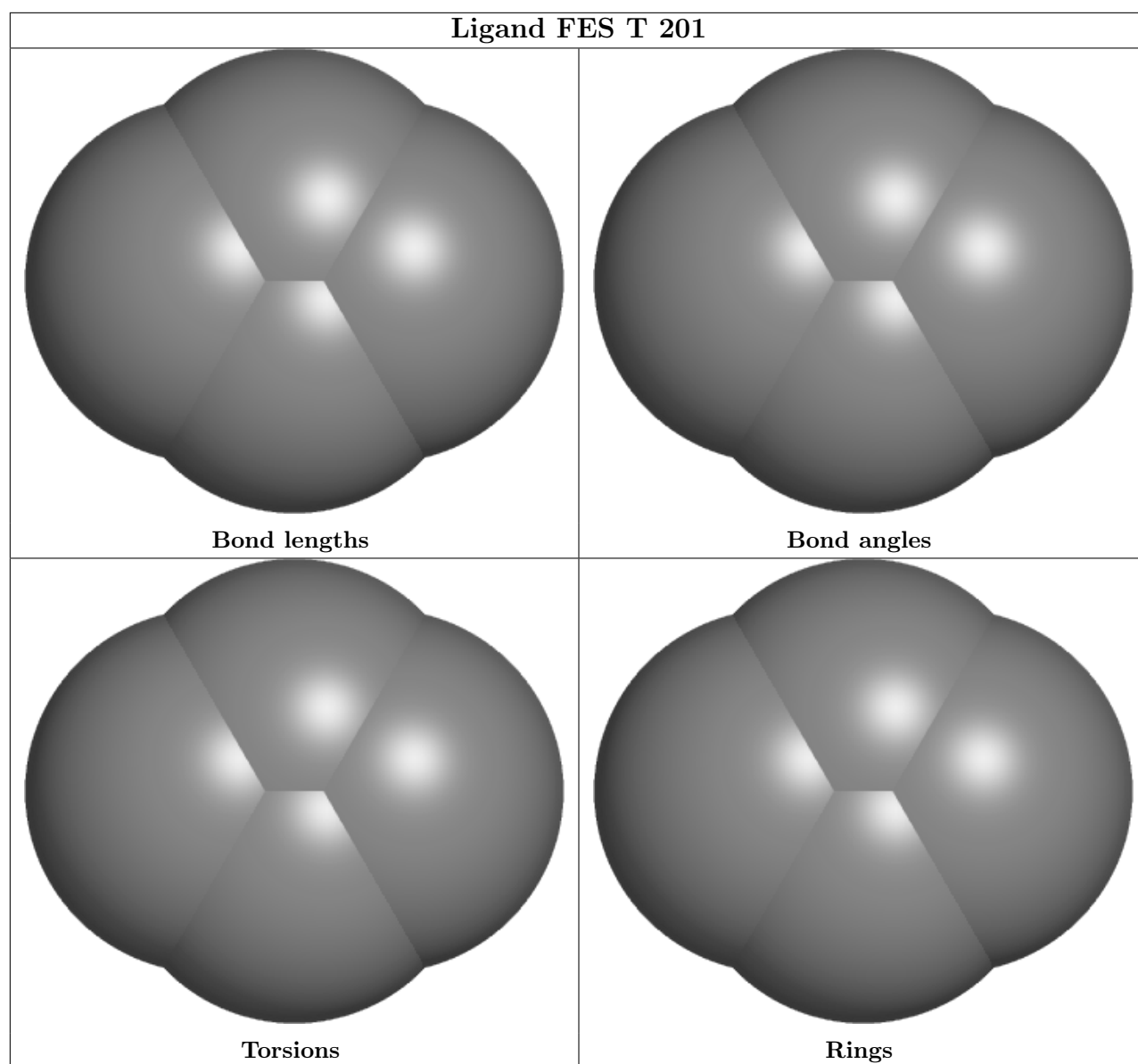












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

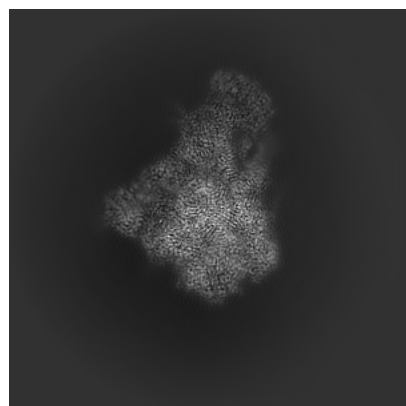
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13170. These allow visual inspection of the internal detail of the map and identification of artifacts.

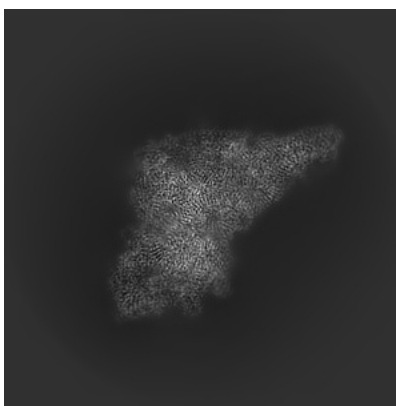
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

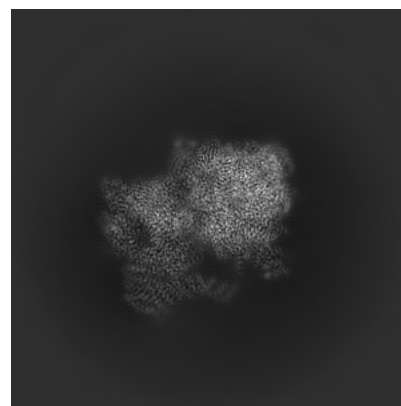
6.1.1 Primary map



X

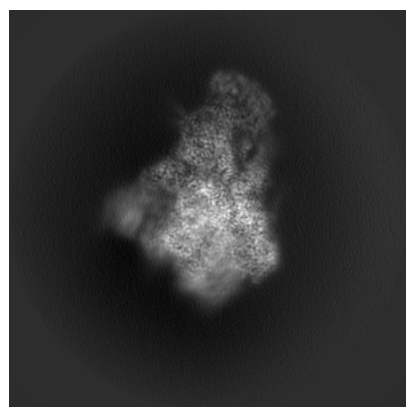


Y

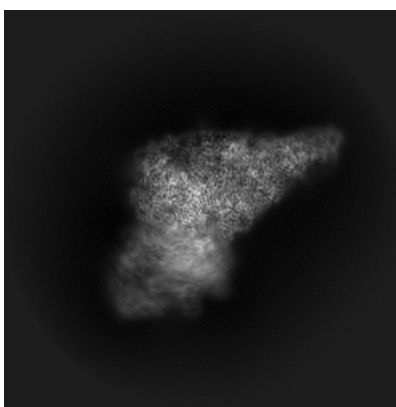


Z

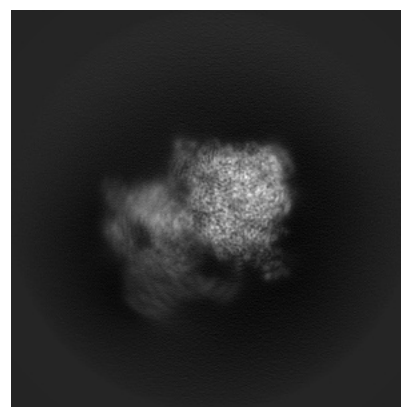
6.1.2 Raw map



X



Y

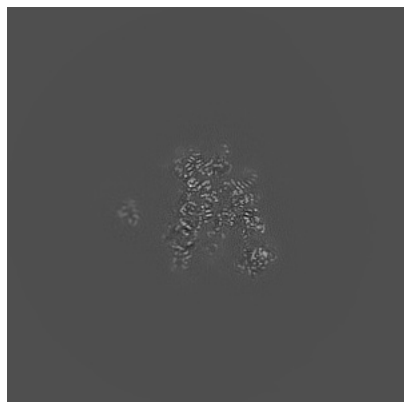


Z

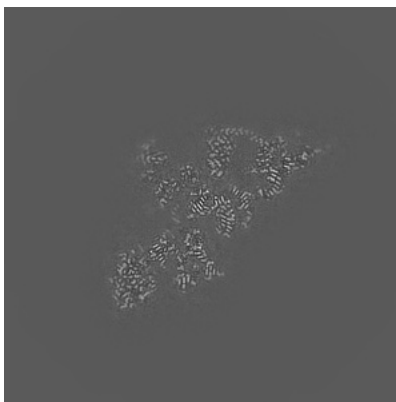
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

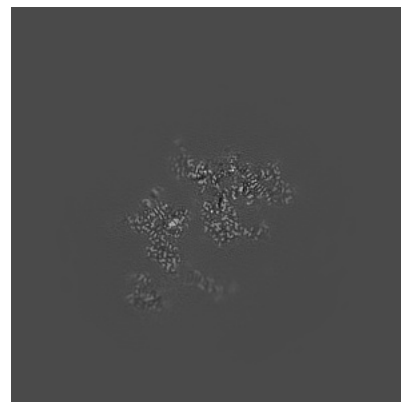
6.2.1 Primary map



X Index: 360

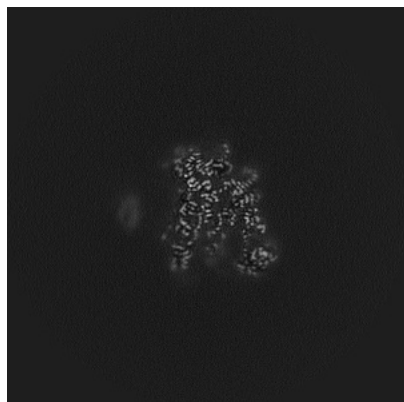


Y Index: 360

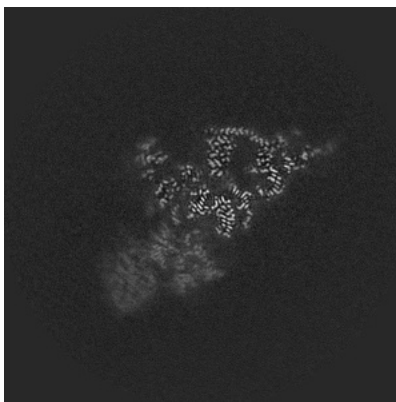


Z Index: 360

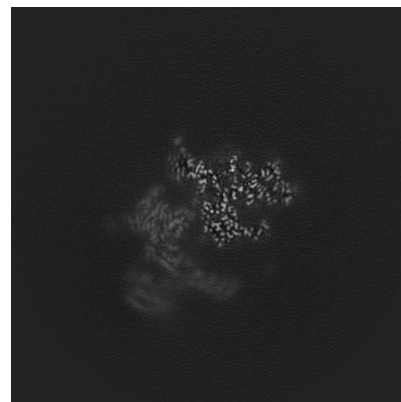
6.2.2 Raw map



X Index: 240



Y Index: 240

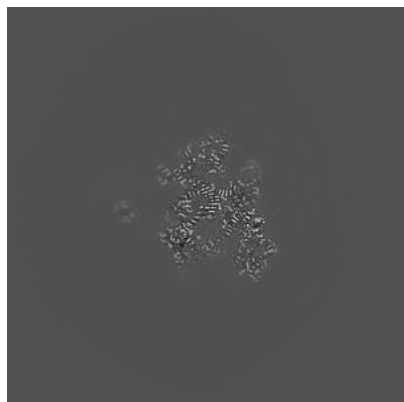


Z Index: 240

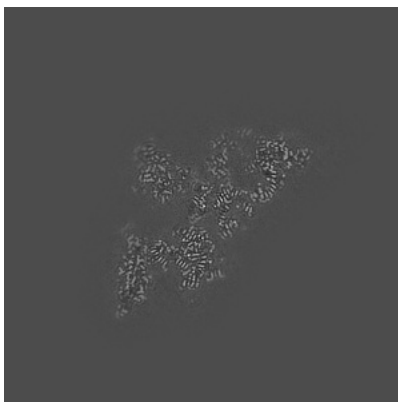
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

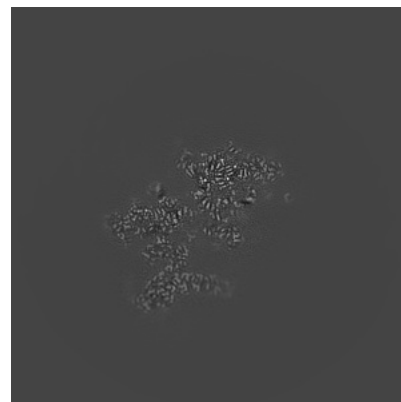
6.3.1 Primary map



X Index: 372

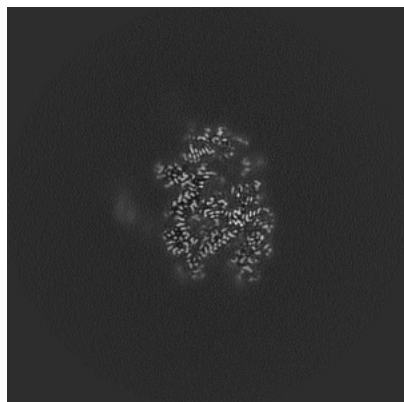


Y Index: 352

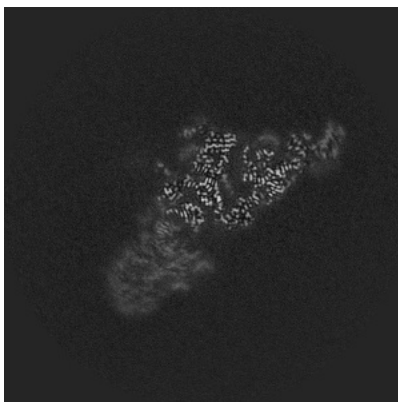


Z Index: 341

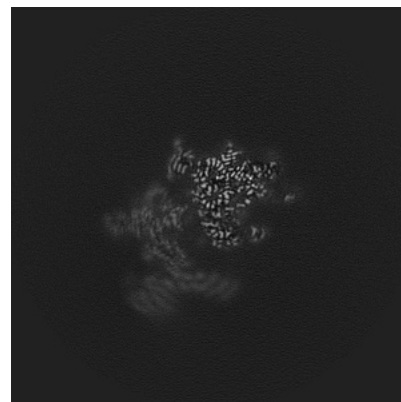
6.3.2 Raw map



X Index: 259



Y Index: 255

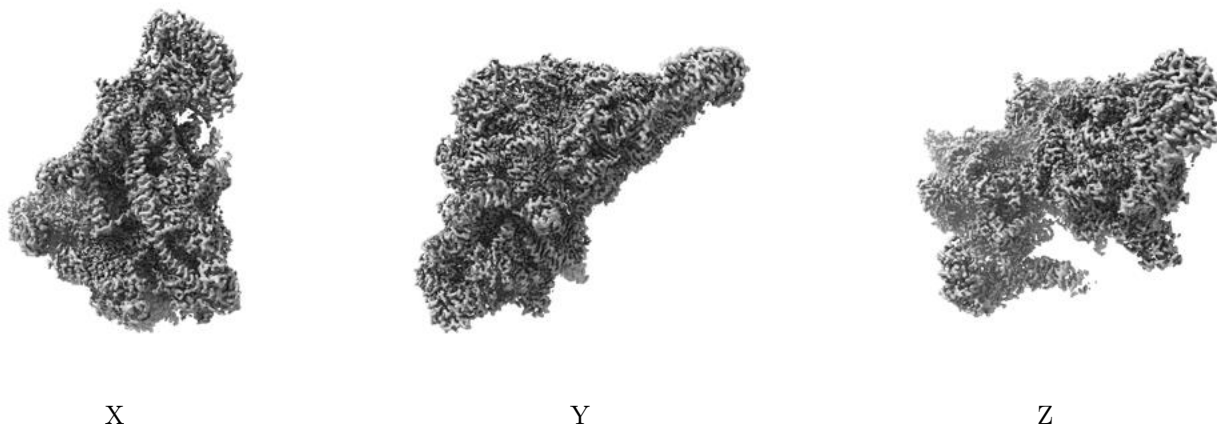


Z Index: 233

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

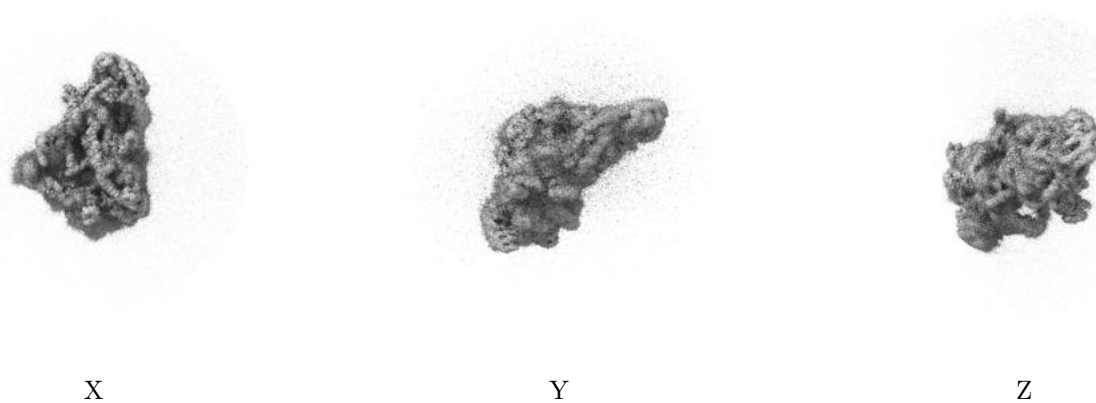
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

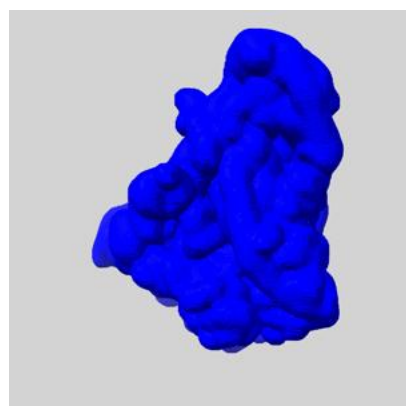
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

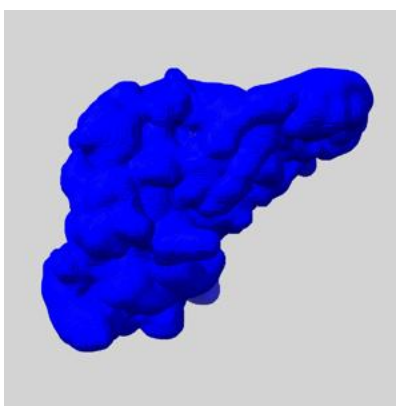
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

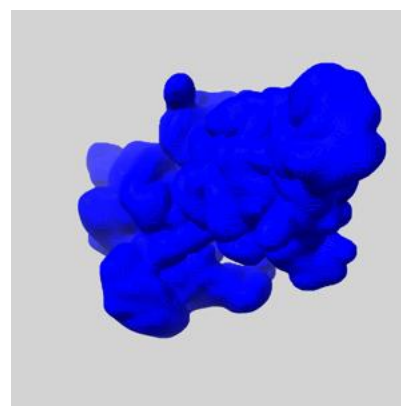
6.5.1 emd_13170_msk_1.map [i](#)



X



Y

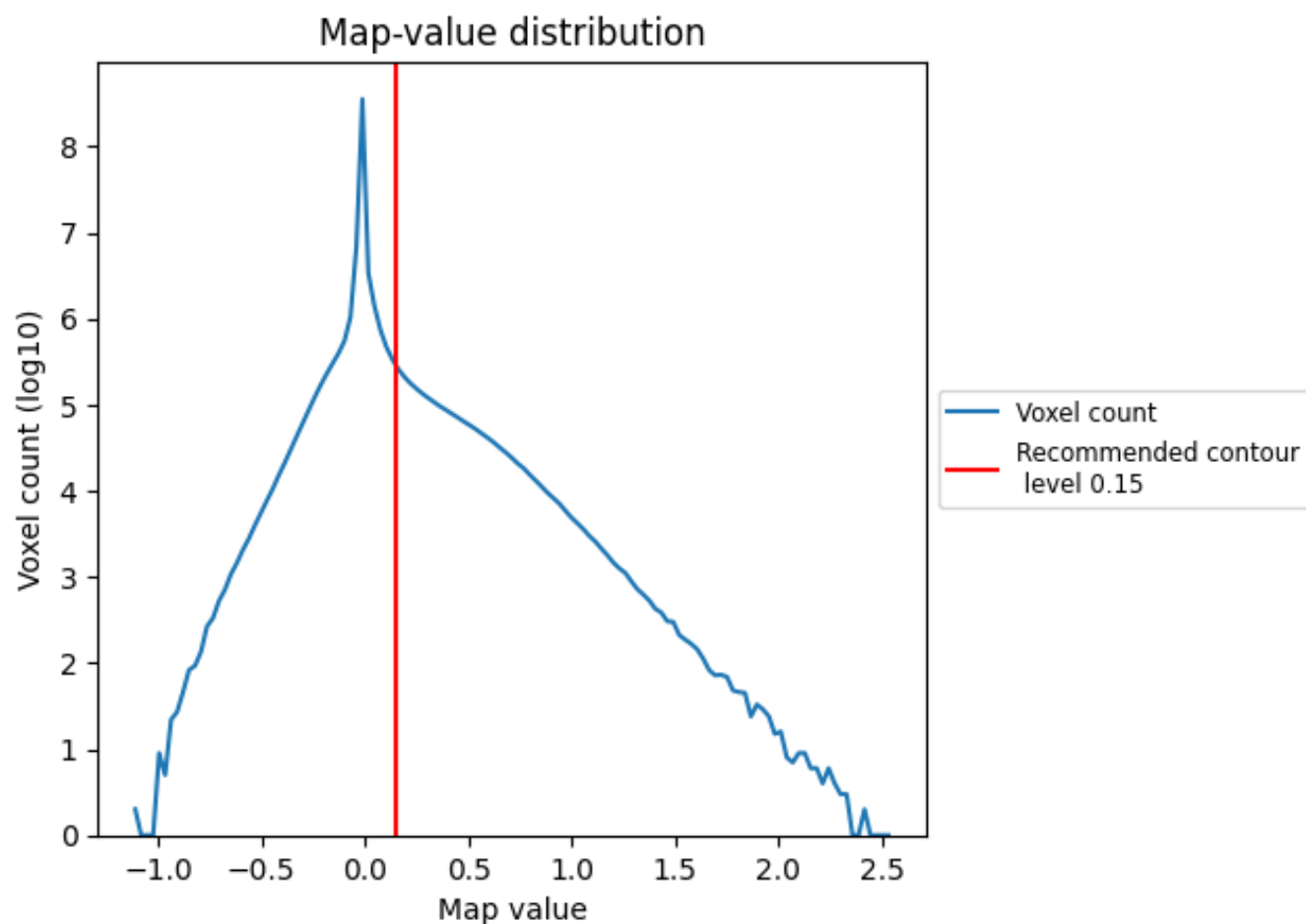


Z

7 Map analysis [i](#)

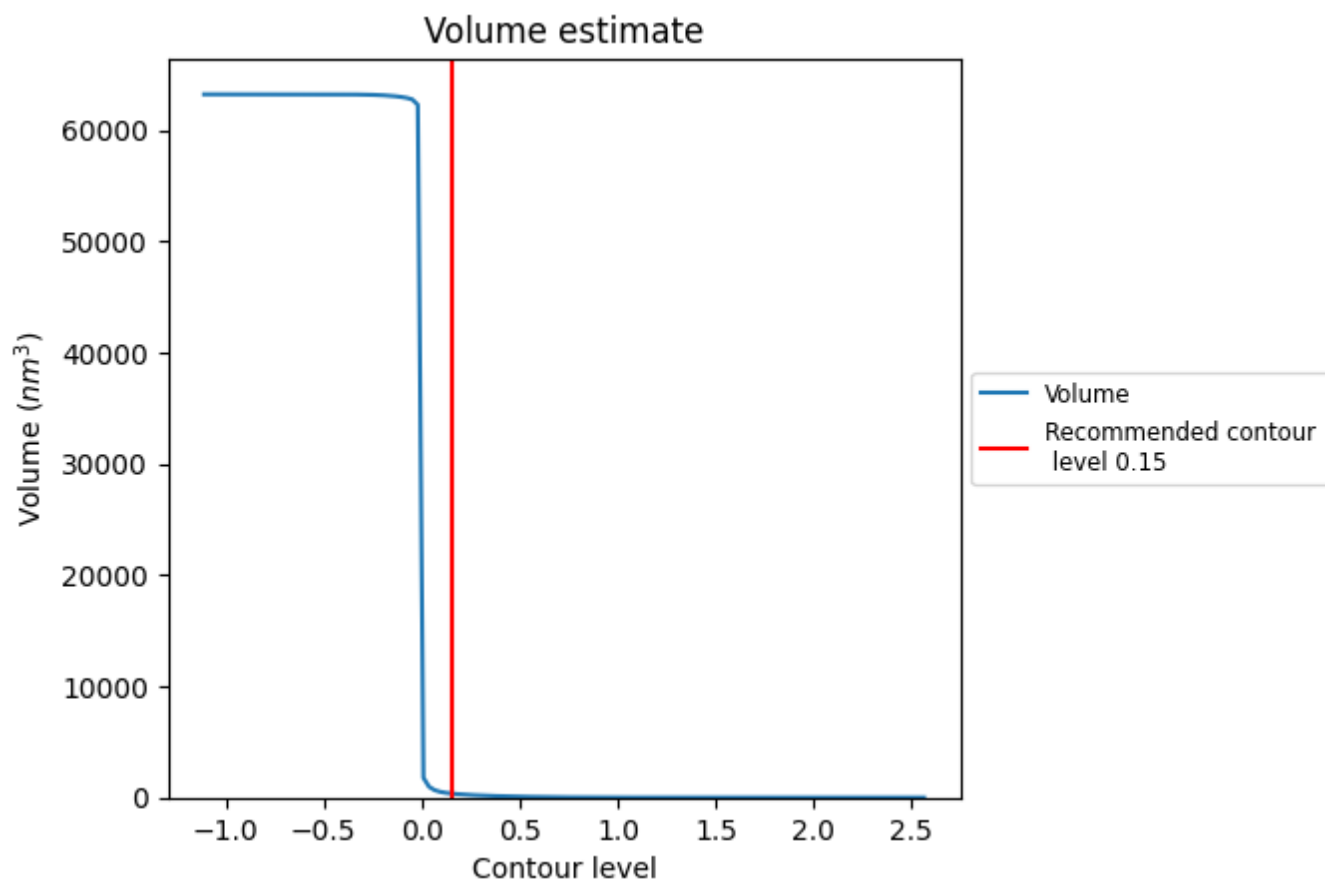
This section contains the results of statistical analysis of the map.

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.

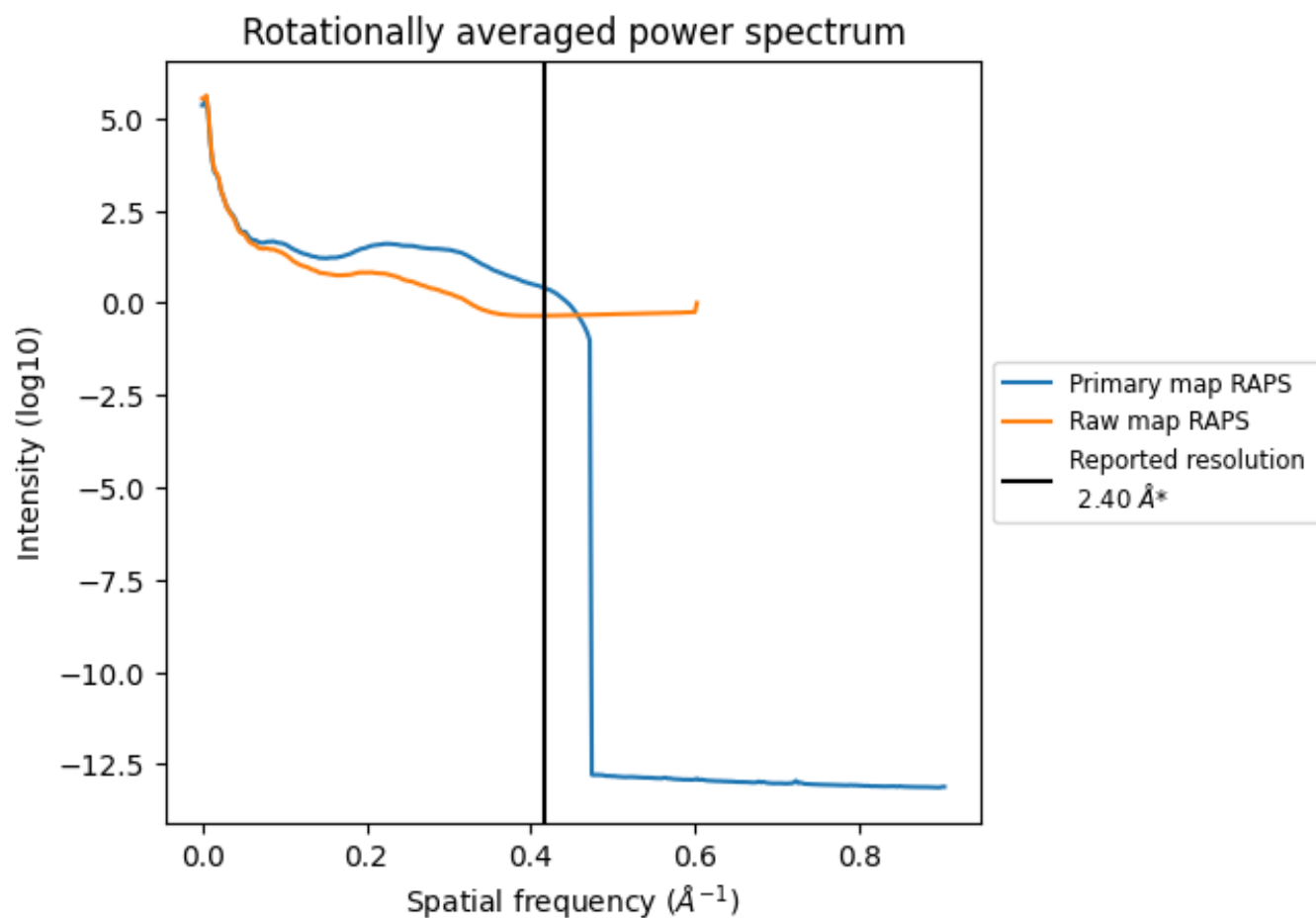
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 366 nm^3 ; this corresponds to an approximate mass of 330 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 ⓘ

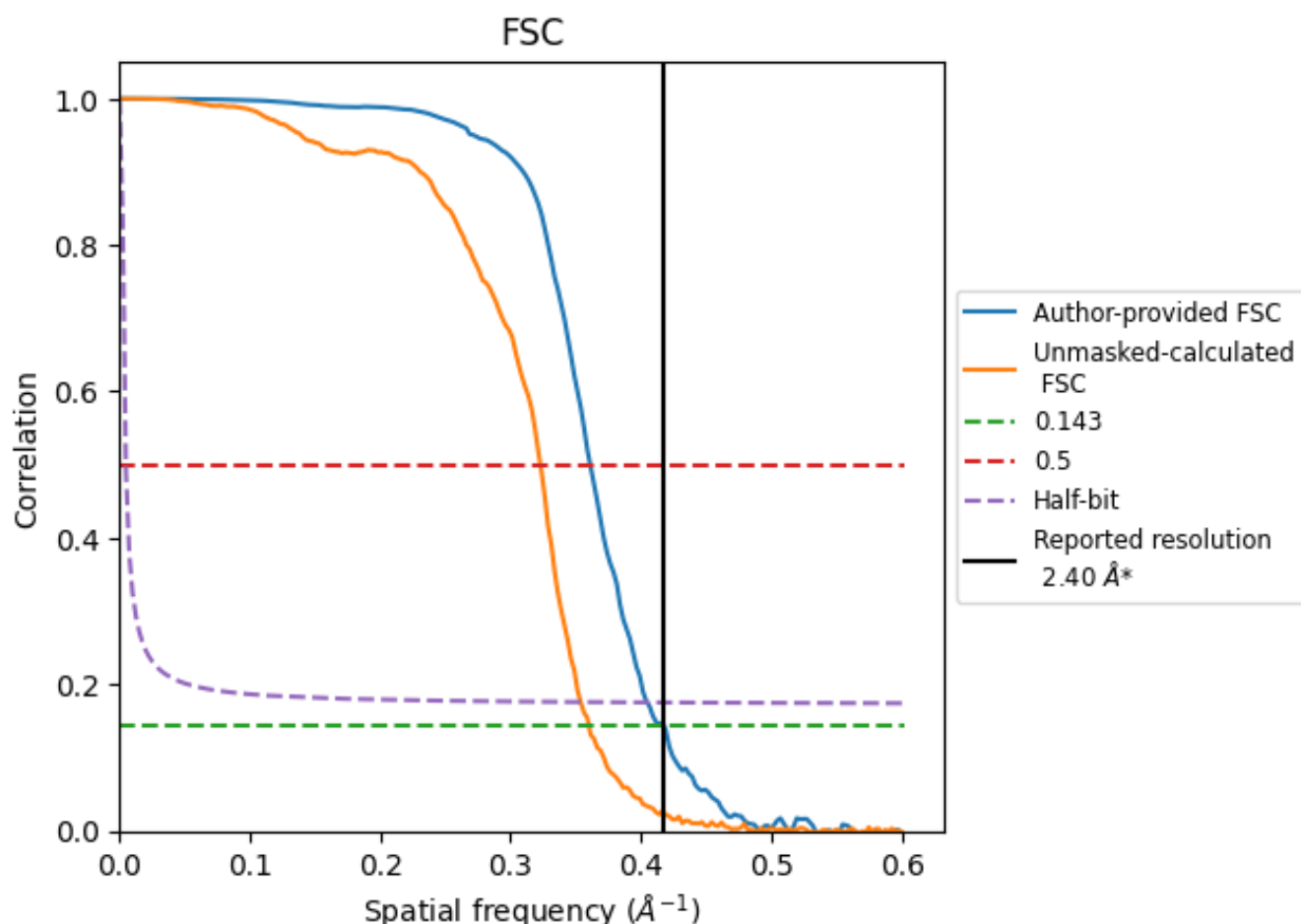


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

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 0.417 \AA^{-1}

8.2 Resolution estimates [i](#)

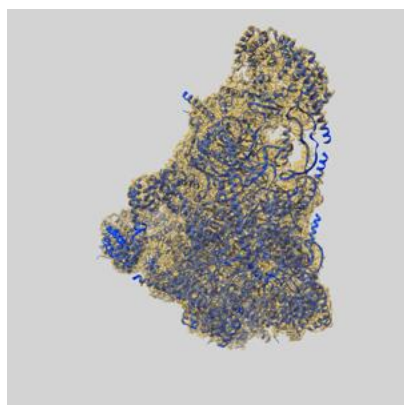
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.39	2.77	2.47
Unmasked-calculated*	2.78	3.10	2.83

*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 2.78 differs from the reported value 2.4 by more than 10 %

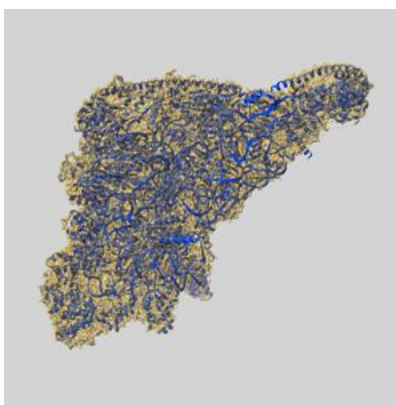
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13170 and PDB model 7P2E. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

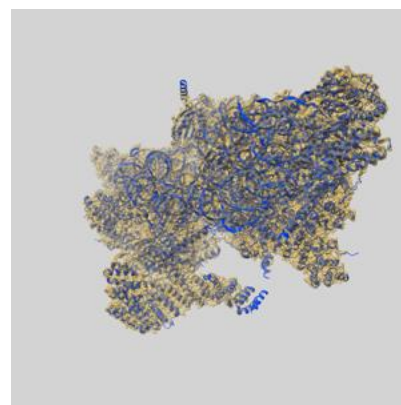
9.1 Map-model overlay [i](#)



X



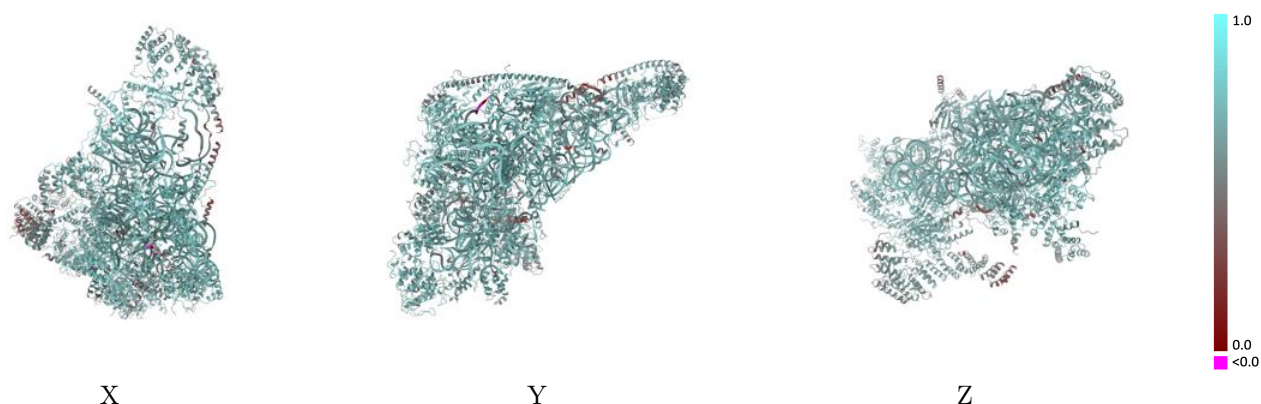
Y



Z

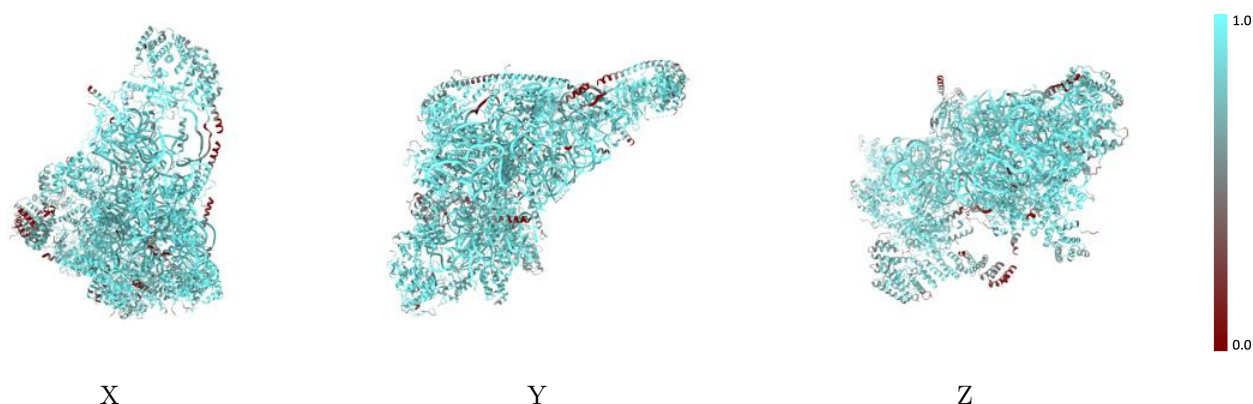
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



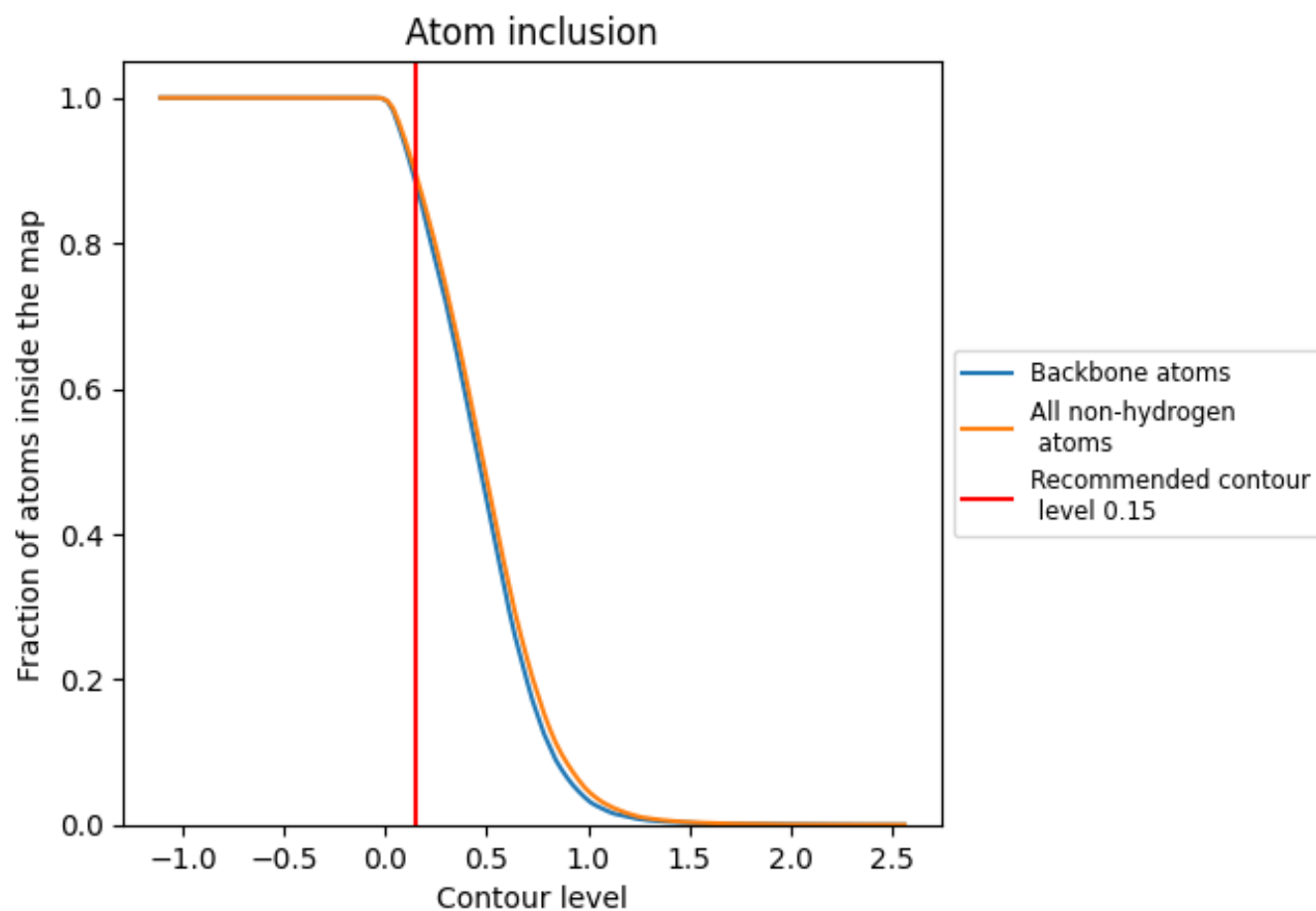
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).



































































9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 90% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8953	 0.6670
0	 0.8963	 0.6700
1	 0.8655	 0.6570
2	 0.7193	 0.6000
3	 0.9250	 0.6960
4	 0.7315	 0.5660
8	 0.6184	 0.5640
A	 0.9597	 0.6930
B	 0.9350	 0.7130
C	 0.9639	 0.7340
D	 0.8889	 0.6730
E	 0.9005	 0.6700
F	 0.8859	 0.6580
G	 0.8458	 0.6510
H	 0.8928	 0.6910
I	 0.9371	 0.6910
J	 0.9142	 0.6850
K	 0.9694	 0.7360
L	 0.8535	 0.6580
M	 0.9232	 0.7080
N	 0.9458	 0.7120
O	 0.9164	 0.6850
P	 0.9209	 0.6970
Q	 0.9746	 0.7290
R	 0.8733	 0.6530
S	 0.8428	 0.6430
T	 0.9043	 0.6930
U	 0.8179	 0.6340
V	 0.8035	 0.6150
W	 0.9248	 0.6920
X	 0.9242	 0.6770
Y	 0.7833	 0.6140
Z	 0.8834	 0.6810

