



Full wwPDB EM Validation Report ⓘ

Dec 10, 2022 – 09:30 am GMT

PDB ID : 5APN
EMDB ID : EMD-3152
Title : Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and N-terminally tagged Rei1
Authors : Greber, B.J.; Gerhardy, S.; Leitner, A.; Leibundgut, M.; Salem, M.; Boehringer, D.; Leulliot, N.; Aebersold, R.; Panse, V.G.; Ban, V.
Deposited on : 2015-09-17
Resolution : 3.91 Å(reported)

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
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

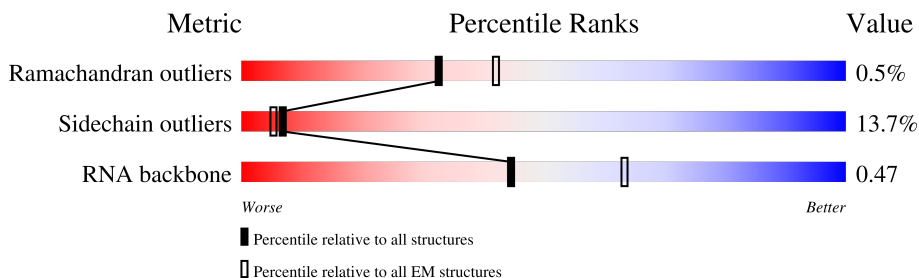
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.91 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	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	5	3396	
2	7	121	
3	8	158	
4	A	254	
5	B	387	
6	C	362	
7	D	297	
8	E	176	

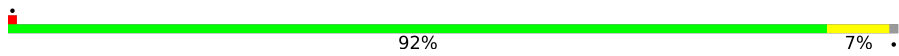

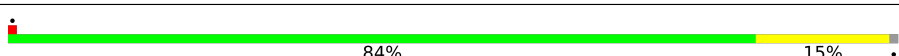
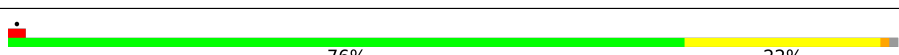
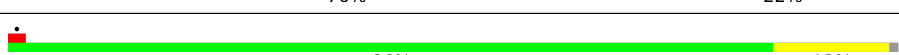

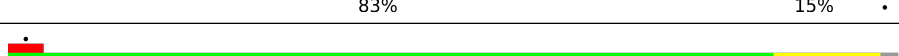
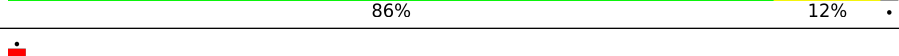


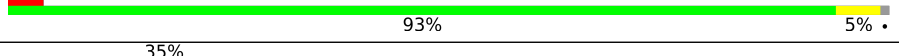

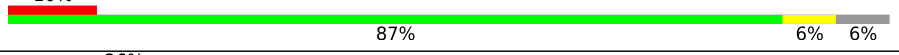

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	F	244	82% 9% 9%
10	G	256	80% 10% 10%
11	H	191	85% 15%
12	I	221	86% 10% .
13	J	174	81% 14% . .
14	L	199	87% 10% .
15	M	138	88% 11% .
16	N	204	85% 13%
17	O	199	87% 12% .
18	P	184	90% 9% .
19	Q	186	85% 15% .
20	R	189	73% 10% 17%
21	S	172	84% 15% .
22	T	160	83% 16% .
23	U	121	74% 11% 16%
24	V	137	93% 7% .
25	W	155	37% 59%
26	X	142	71% 13% 15%
27	Y	127	83% 16% .
28	Z	136	85% 12% . .
29	a	149	89% 11% .
30	b	59	85% 14%
31	c	105	83% 12% 5%
32	d	113	84% 12% .
33	e	130	88% 12% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	f	107	 92% 7%
35	g	121	 5% 79% 14% 7%
36	h	120	 84% 15%
37	i	100	 76% 22%
38	j	88	 86% 13%
39	k	78	 83% 15%
40	l	51	 86% 12%
41	m	128	 32% 9% 59%
42	o	106	 14% 88% 11%
43	p	92	 93% 5%
44	q	312	 35% 34% 62%
45	x	616	 10% 87% 6% 6%
46	y	414	 26% 48% 49%
47	z	85	 82% 100%

2 Entry composition i

There are 49 unique types of molecules in this entry. The entry contains 129324 atoms, of which 3 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	5	3112	66537	29736	11996	21694	3111	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	7	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	8	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	212	1630	1021	325	283	1	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	386	3075	1950	584	533	8	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	361	2748	1729	522	494	3	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D	294	2359	1489	412	456	2	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E	175	1355	877	242	235	1	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F	223	1791	1155	325	310	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	231	1763	1130	316	314	3	0	0

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	191	1518	963	274	277	4	0	0

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	I	213	1722	1094	325	297	6	0	0

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	169	1353	847	253	249	4	0	0

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	183	Total	C	N	O	0	0
			1442	896	287	259		

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	102	Total	C	N	O	0	0
			808	524	132	152		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	Z	135	1092	710	202	180	0	0

- Molecule 29 is a protein called 60S ribosomal protein L28.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	b	58	462	289	100	73	0	0

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	c	100	767	492	128	146	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	d	109	883	559	167	156	1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	e	129	1034	655	207	171	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	f	106	850	540	165	144	1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	k	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 43 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 44 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	120	Total	C	N	O	S	0	0
			962	618	169	172	3		

- Molecule 45 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	579	Total	C	N	O	S	0	0
			4477	2823	772	867	15		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-22	MET	-	initiating methionine	UNP Q03862
x	-21	GLY	-	expression tag	UNP Q03862
x	-20	SER	-	expression tag	UNP Q03862
x	-19	SER	-	expression tag	UNP Q03862
x	-18	HIS	-	expression tag	UNP Q03862
x	-17	HIS	-	expression tag	UNP Q03862
x	-16	HIS	-	expression tag	UNP Q03862
x	-15	HIS	-	expression tag	UNP Q03862
x	-14	HIS	-	expression tag	UNP Q03862
x	-13	HIS	-	expression tag	UNP Q03862
x	-12	SER	-	expression tag	UNP Q03862
x	-11	SER	-	expression tag	UNP Q03862
x	-10	GLY	-	expression tag	UNP Q03862
x	-9	LEU	-	expression tag	UNP Q03862
x	-8	VAL	-	expression tag	UNP Q03862
x	-7	PRO	-	expression tag	UNP Q03862
x	-6	ARG	-	expression tag	UNP Q03862
x	-5	GLY	-	expression tag	UNP Q03862
x	-4	SER	-	expression tag	UNP Q03862

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
x	-3	HIS	-	expression tag	UNP Q03862
x	-2	MET	-	expression tag	UNP Q03862
x	-1	LEU	-	expression tag	UNP Q03862
x	0	GLU	-	expression tag	UNP Q03862

- Molecule 46 is a protein called Cytoplasmic 60S subunit biogenesis factor REI1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
46	y	211	1727	1095	3	307	314	8	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	-20	HIS	-	expression tag	UNP P38344
y	-19	HIS	-	expression tag	UNP P38344
y	-18	HIS	-	expression tag	UNP P38344
y	-17	HIS	-	expression tag	UNP P38344
y	-16	HIS	-	expression tag	UNP P38344
y	-15	HIS	-	expression tag	UNP P38344
y	-14	ASP	-	expression tag	UNP P38344
y	-13	TYR	-	expression tag	UNP P38344
y	-12	ASP	-	expression tag	UNP P38344
y	-11	ILE	-	expression tag	UNP P38344
y	-10	PRO	-	expression tag	UNP P38344
y	-9	THR	-	expression tag	UNP P38344
y	-8	THR	-	expression tag	UNP P38344
y	-7	GLU	-	expression tag	UNP P38344
y	-6	ASN	-	expression tag	UNP P38344
y	-5	LEU	-	expression tag	UNP P38344
y	-4	TYR	-	expression tag	UNP P38344
y	-3	PHE	-	expression tag	UNP P38344
y	-2	GLN	-	expression tag	UNP P38344
y	-1	GLY	-	expression tag	UNP P38344
y	0	ALA	-	expression tag	UNP P38344

- Molecule 47 is a protein called ALB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	z	85	510	340	85	85	0	0

- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	5	259	Total 259	Mg 259	0
48	7	6	Total 6	Mg 6	0
48	8	7	Total 7	Mg 7	0
48	B	1	Total 1	Mg 1	0
48	C	2	Total 2	Mg 2	0
48	N	1	Total 1	Mg 1	0
48	P	1	Total 1	Mg 1	0
48	V	1	Total 1	Mg 1	0
48	a	2	Total 2	Mg 2	0

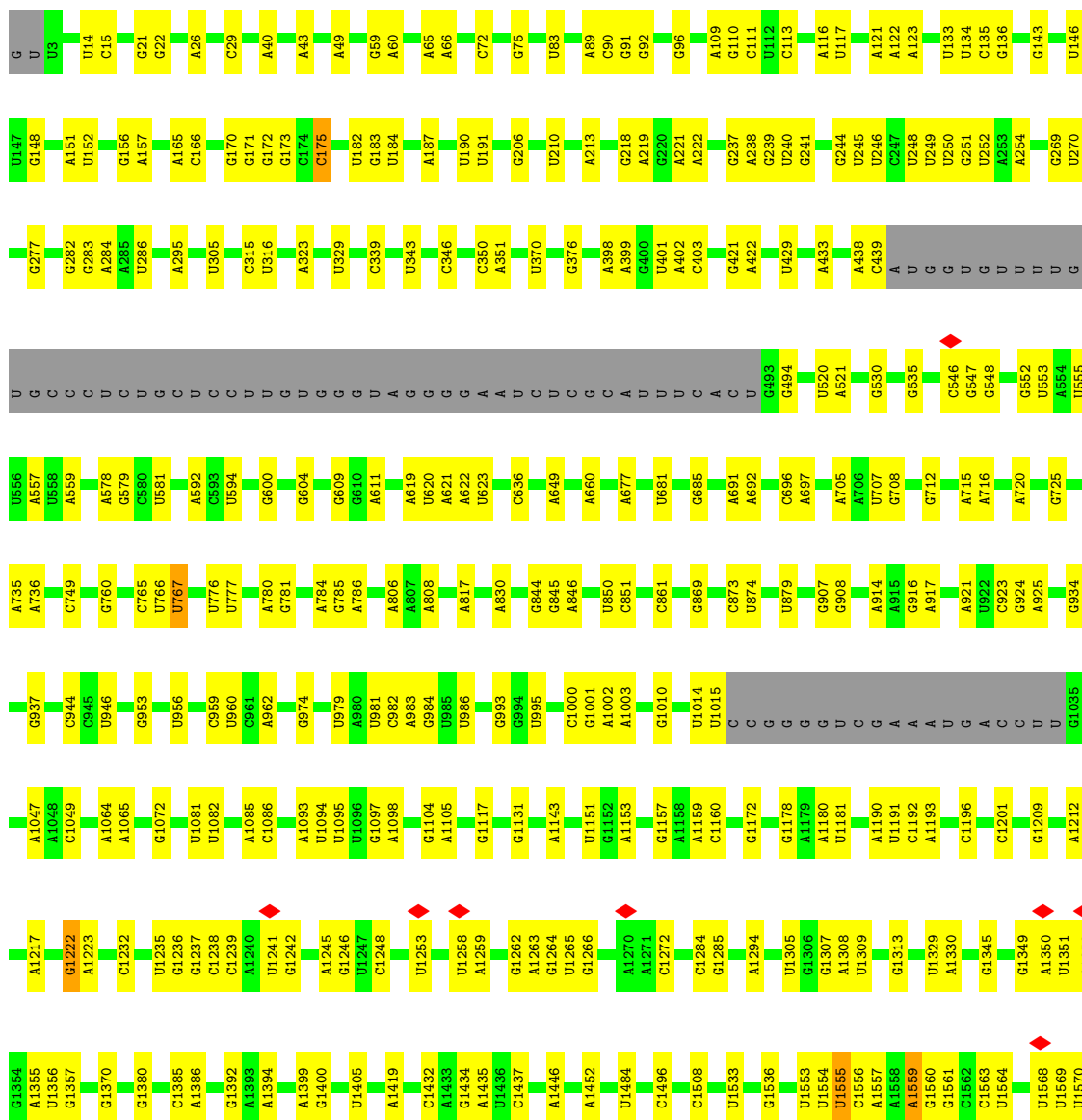
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

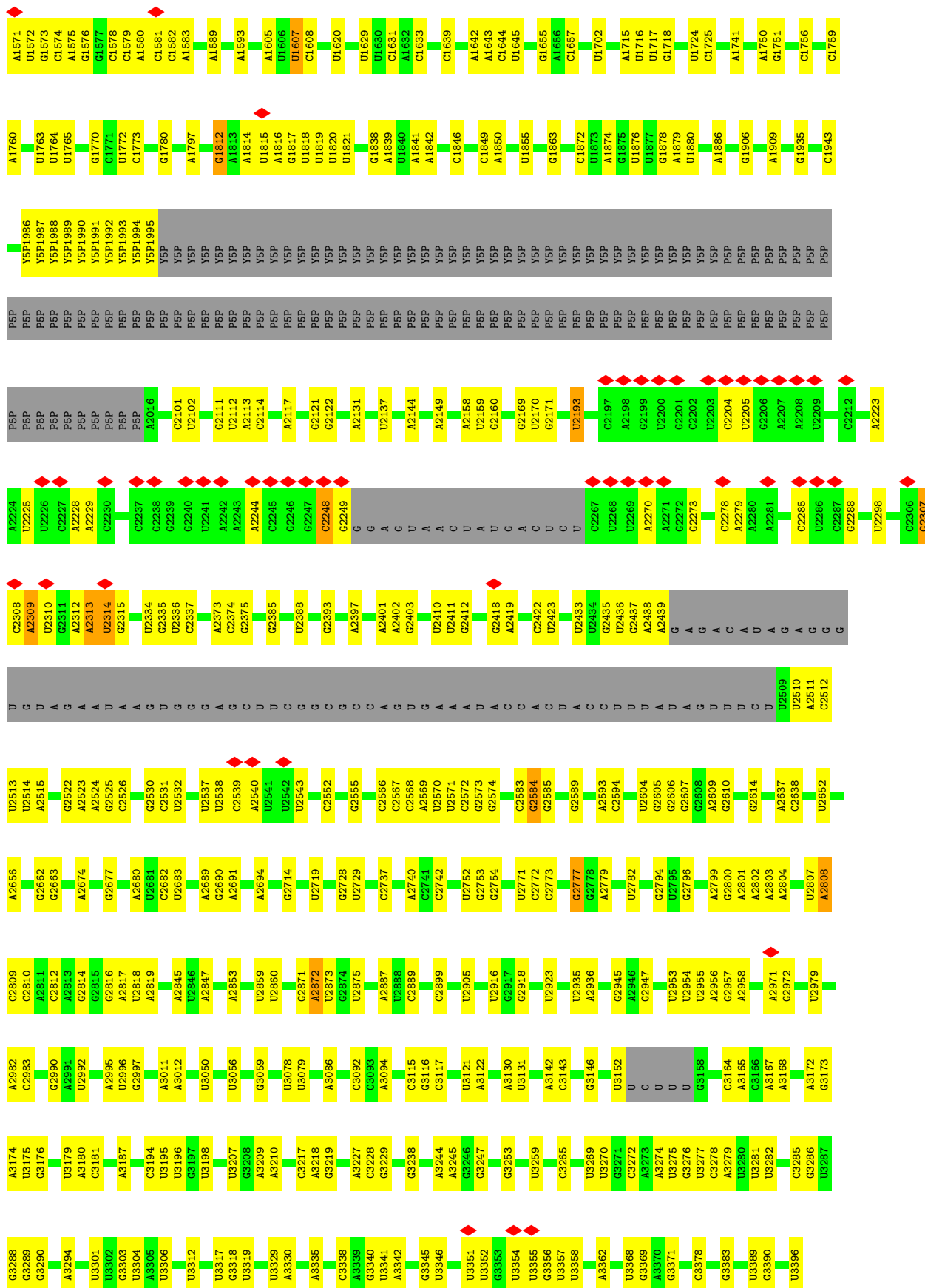
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	o	1	Total 1	Zn 1	0
49	p	1	Total 1	Zn 1	0
49	y	2	Total 2	Zn 2	0

3 Residue-property plots [i](#)

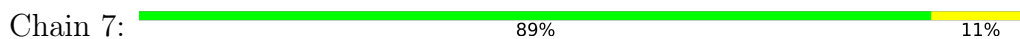
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA

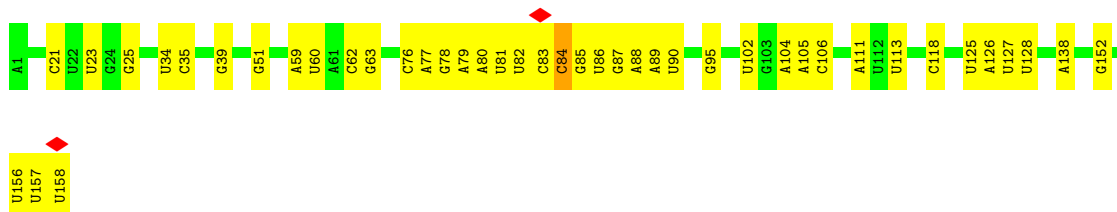




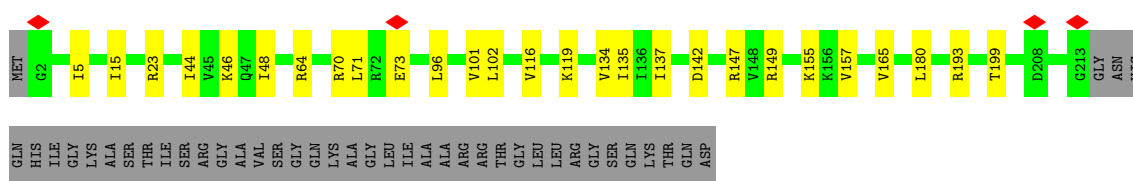
• Molecule 2: 5S rRNA



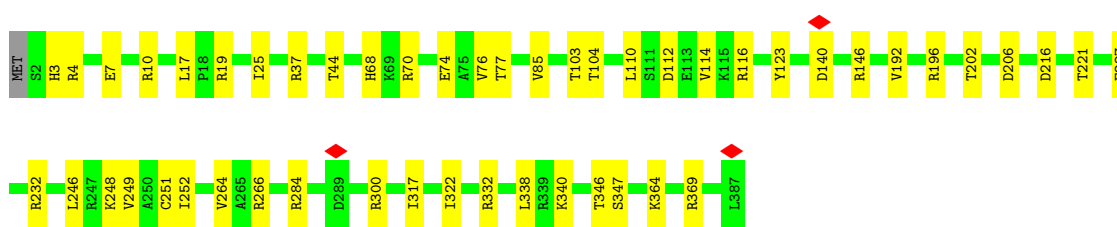
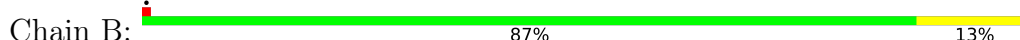
• Molecule 3: 5.8S rRNA



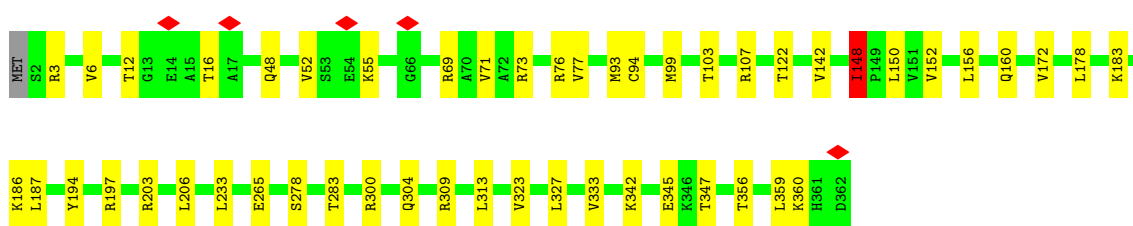
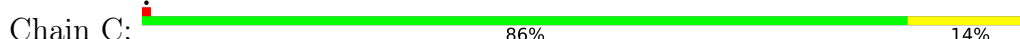
• Molecule 4: 60S ribosomal protein L2-A



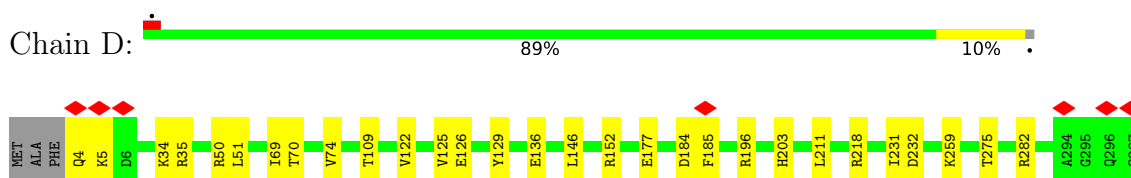
• Molecule 5: 60S ribosomal protein L3



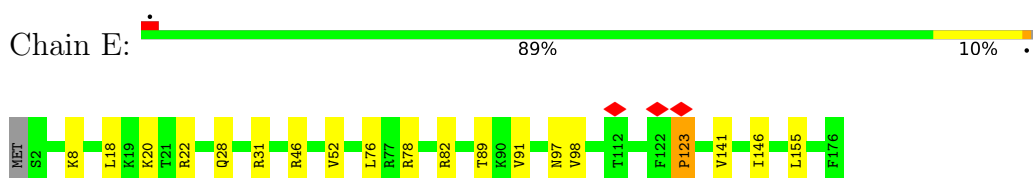
• Molecule 6: 60S ribosomal protein L4-A



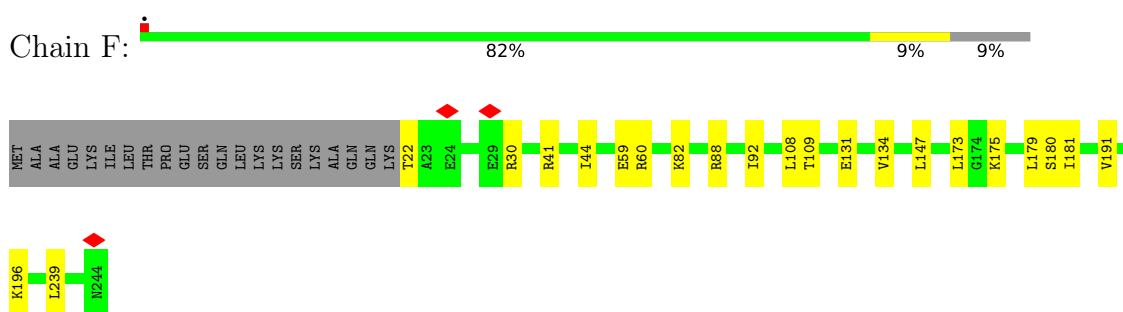
- Molecule 7: 60S ribosomal protein L5



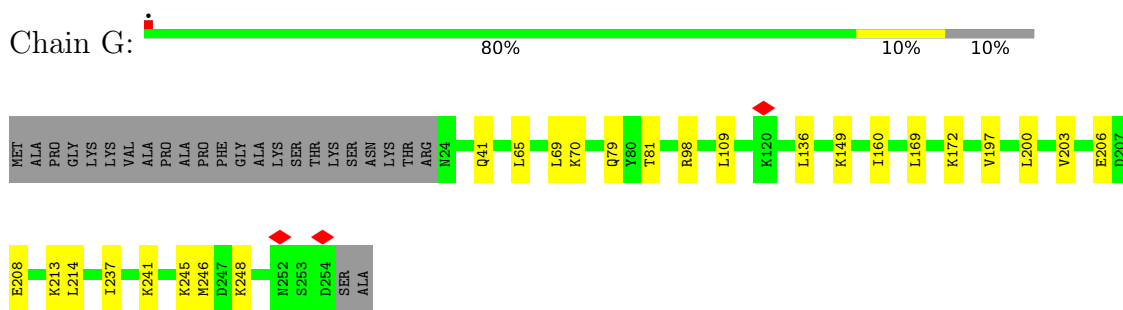
- Molecule 8: 60S ribosomal protein L6-A



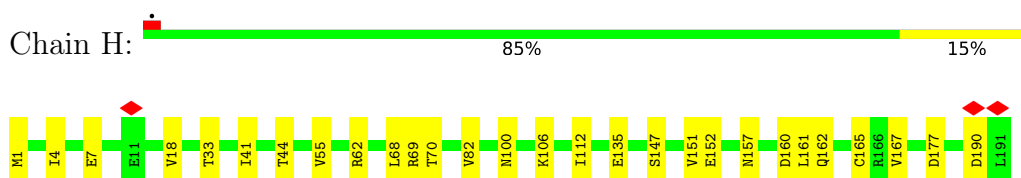
- Molecule 9: 60S ribosomal protein L7-A



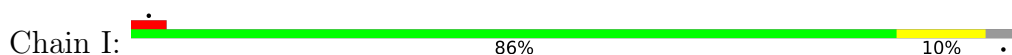
- Molecule 10: 60S ribosomal protein L8-A

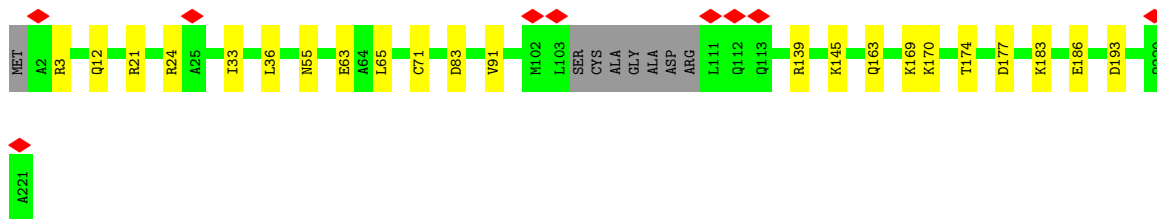


- Molecule 11: 60S ribosomal protein L9-A

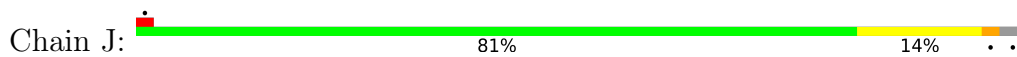


- Molecule 12: 60S ribosomal protein L10

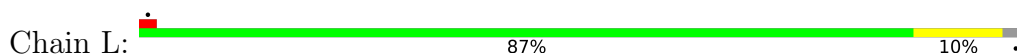




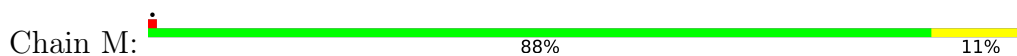
- Molecule 13: 60S ribosomal protein L11-A



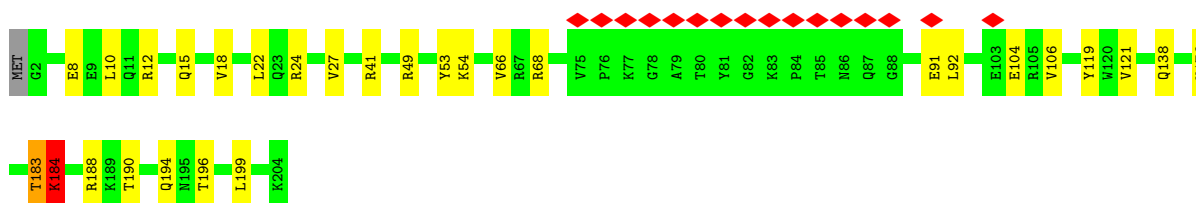
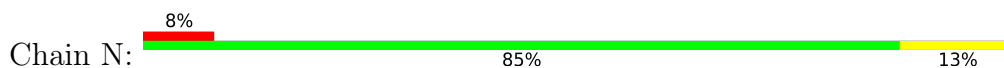
- Molecule 14: 60S ribosomal protein L13-A



- Molecule 15: 60S ribosomal protein L14-A



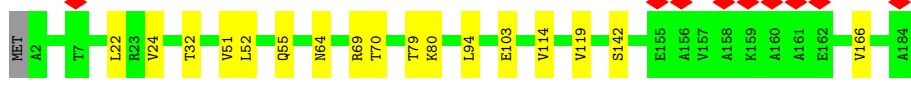
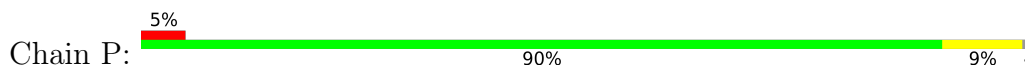
- Molecule 16: 60S ribosomal protein L15-A



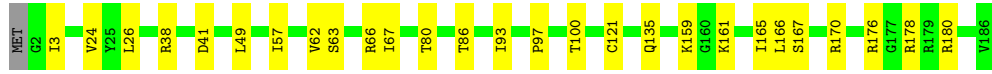
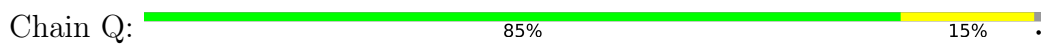
- Molecule 17: 60S ribosomal protein L16-A



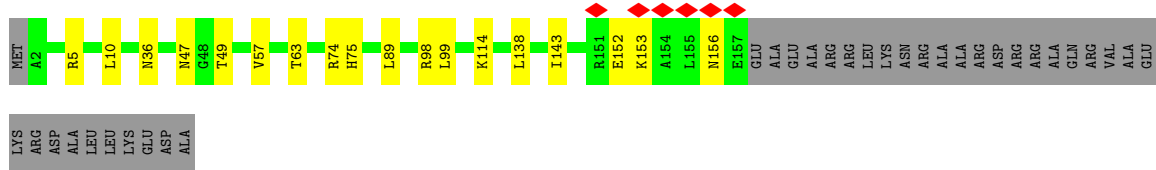
- Molecule 18: 60S ribosomal protein L17-A



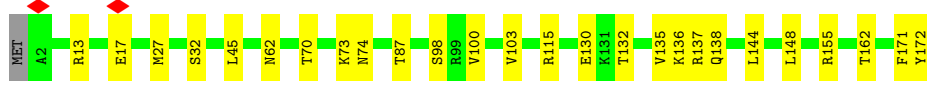
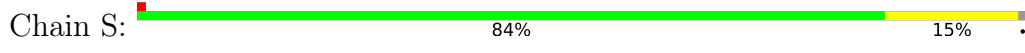
• Molecule 19: 60S ribosomal protein L18-A



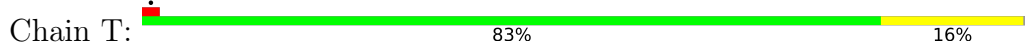
• Molecule 20: 60S ribosomal protein L19-A



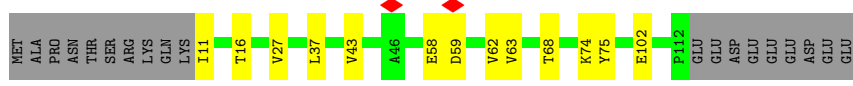
• Molecule 21: 60S ribosomal protein L20-A



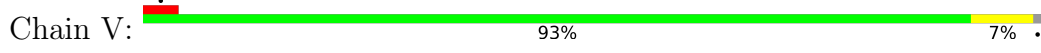
• Molecule 22: 60S ribosomal protein L21-A



• Molecule 23: 60S ribosomal protein L22-A

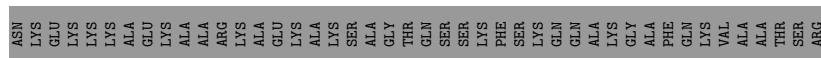
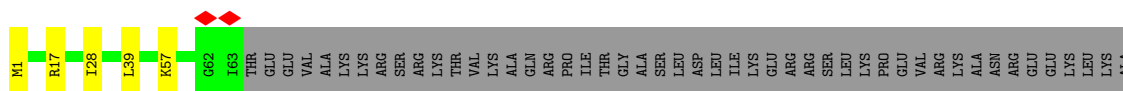


• Molecule 24: 60S ribosomal protein L23-A

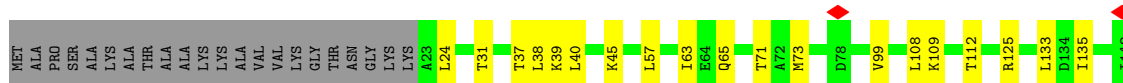




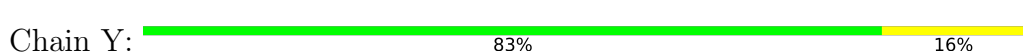
- Molecule 25: 60S ribosomal protein L24-A



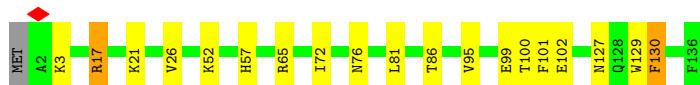
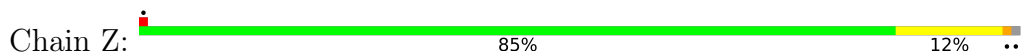
- Molecule 26: 60S ribosomal protein L25



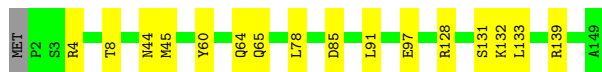
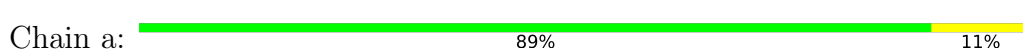
- Molecule 27: 60S ribosomal protein L26-A



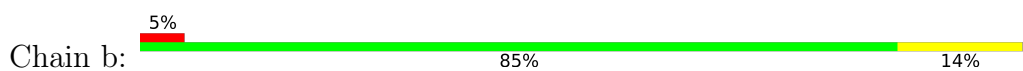
- Molecule 28: 60S ribosomal protein L27-A



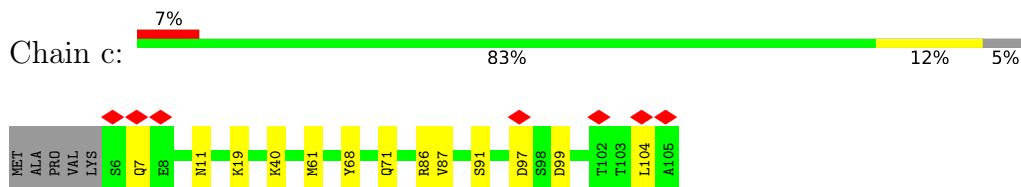
- Molecule 29: 60S ribosomal protein L28



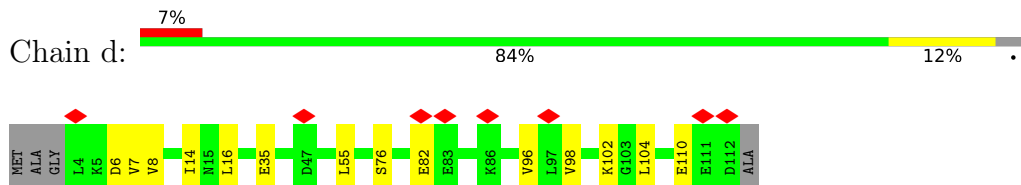
- Molecule 30: 60S ribosomal protein L29



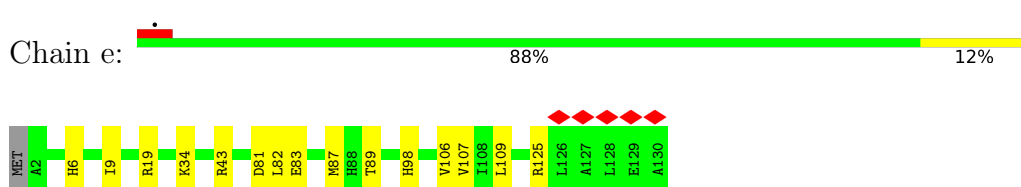
- Molecule 31: 60S ribosomal protein L30



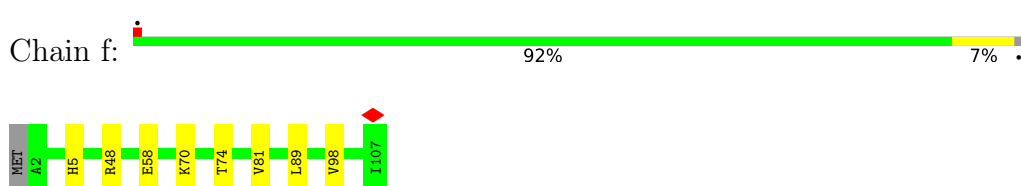
- Molecule 32: 60S ribosomal protein L31-A



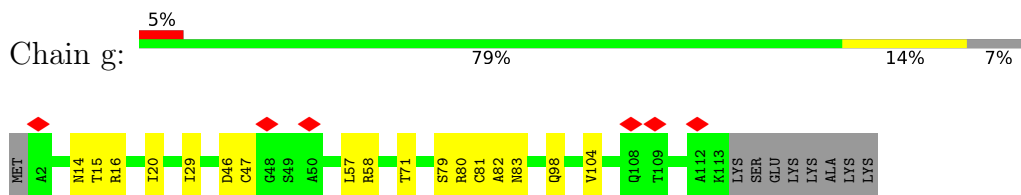
- Molecule 33: 60S ribosomal protein L32



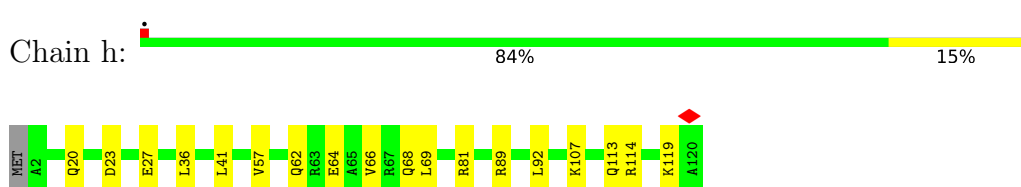
- Molecule 34: 60S ribosomal protein L33-A



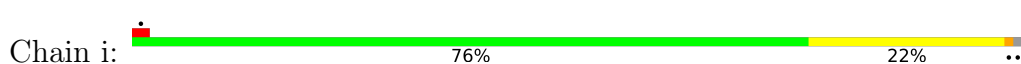
- Molecule 35: 60S ribosomal protein L34-A

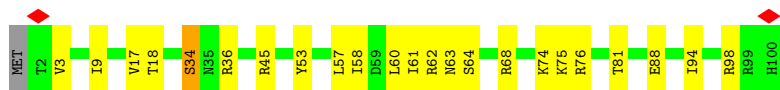


- Molecule 36: 60S ribosomal protein L35-A

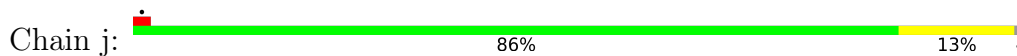


- Molecule 37: 60S ribosomal protein L36-A

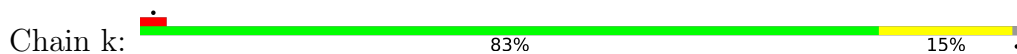




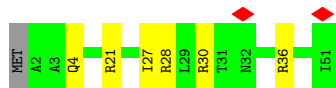
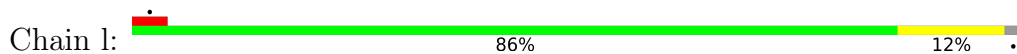
- Molecule 38: 60S ribosomal protein L37-A



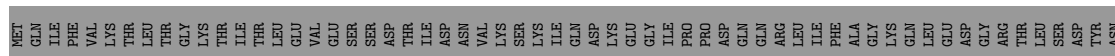
- Molecule 39: 60S ribosomal protein L38



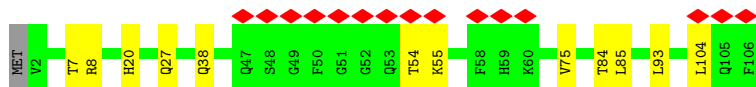
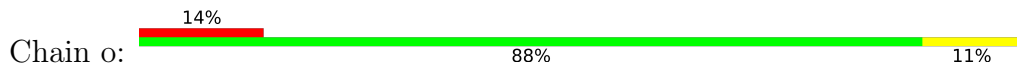
- Molecule 40: 60S ribosomal protein L39



- Molecule 41: Ubiquitin-60S ribosomal protein L40

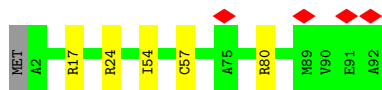


- Molecule 42: 60S ribosomal protein L42-A

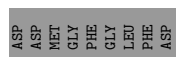
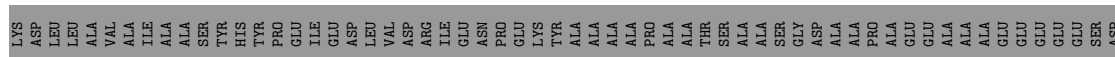
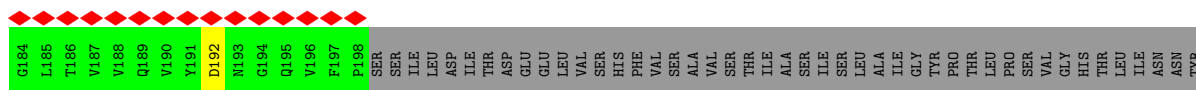
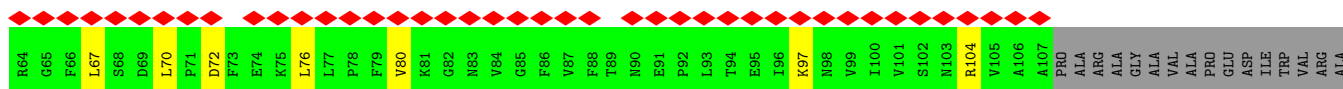
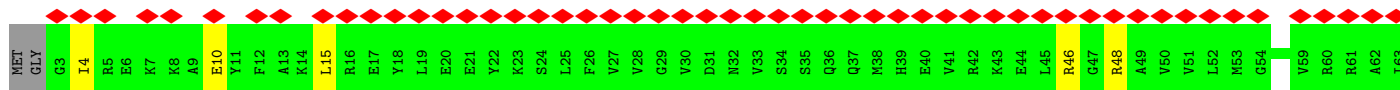


- Molecule 43: 60S ribosomal protein L43-A

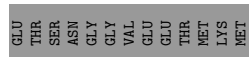
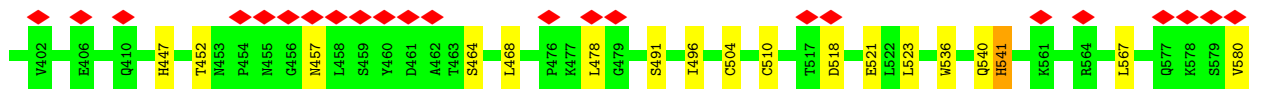
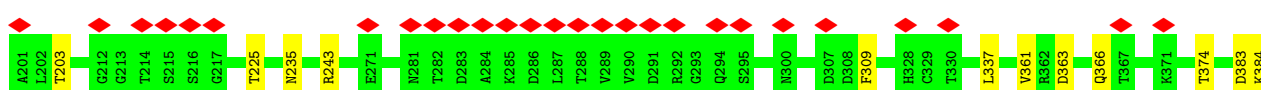
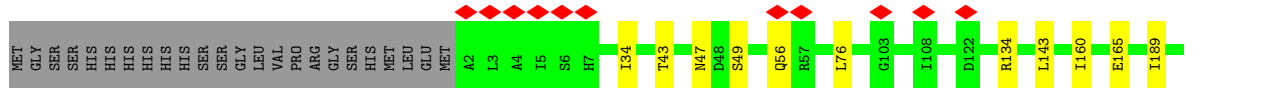
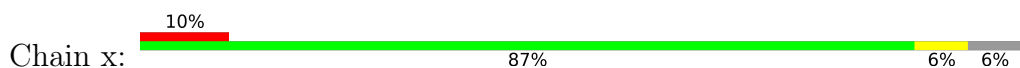




• Molecule 44: 60S acidic ribosomal protein P0

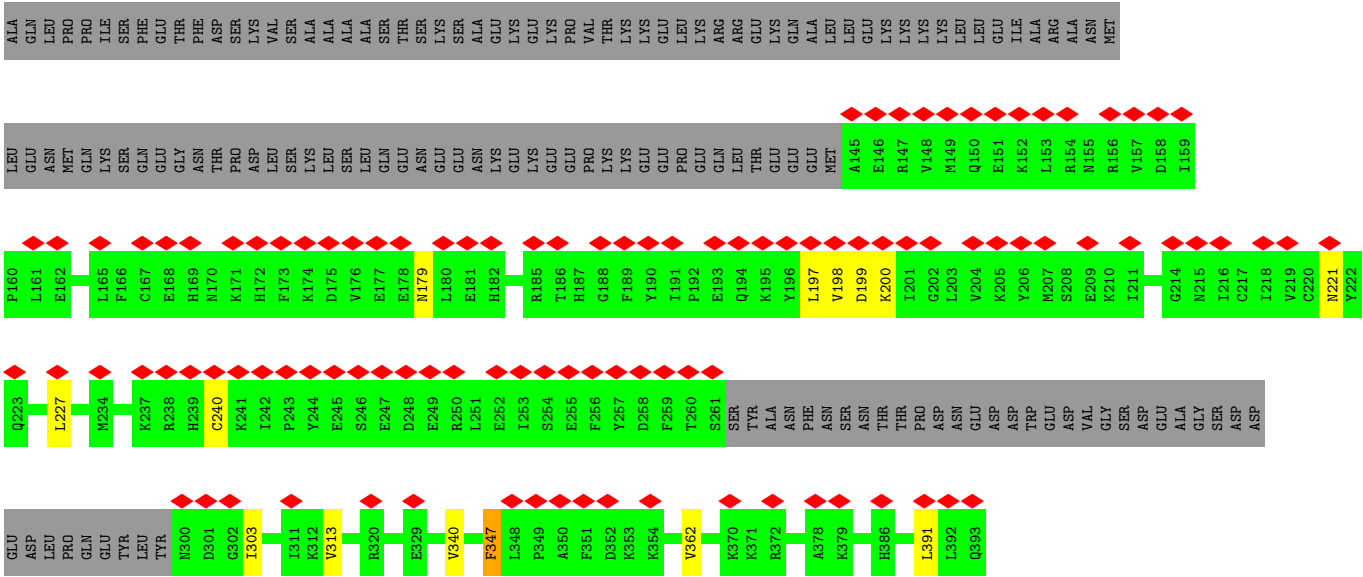


• Molecule 45: Probable metalloprotease ARX1

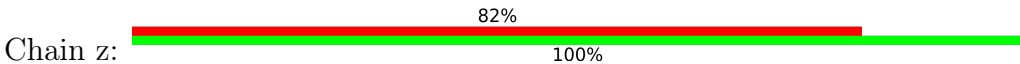


• Molecule 46: Cytoplasmic 60S subunit biogenesis factor REI1





● Molecule 47: ALB1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22040	Depositor
Resolution determination method	Not provided	
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100720	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.352	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	Depositor
Map size (\AA)	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.39, 1.39, 1.39	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: ZN, P5P, MG, Y5P

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	5	0.45	1/74039 (0.0%)	0.94	44/115426 (0.0%)
2	7	0.33	0/2883	0.85	0/4491
3	8	0.47	0/3746	0.97	1/5832 (0.0%)
4	A	0.34	0/1662	0.55	0/2236
5	B	0.36	0/3146	0.55	0/4228
6	C	0.37	0/2800	0.58	0/3790
7	D	0.34	0/2408	0.51	0/3248
8	E	0.34	0/1377	0.58	0/1851
9	F	0.36	0/1828	0.54	0/2461
10	G	0.34	0/1795	0.55	0/2429
11	H	0.34	0/1539	0.50	0/2073
12	I	0.34	0/1758	0.57	0/2358
13	J	0.33	0/1374	0.54	0/1842
14	L	0.35	0/1573	0.59	0/2113
15	M	0.34	0/1074	0.54	0/1446
16	N	0.43	0/1757	0.57	0/2354
17	O	0.37	0/1585	0.52	0/2128
18	P	0.39	0/1465	0.55	0/1968
19	Q	0.35	0/1465	0.56	0/1965
20	R	0.34	0/1275	0.48	0/1702
21	S	0.37	0/1473	0.54	0/1980
22	T	0.36	0/1300	0.51	0/1743
23	U	0.34	0/825	0.54	0/1120
24	V	0.33	0/1018	0.52	0/1369
25	W	0.36	0/533	0.47	0/707
26	X	0.35	0/974	0.60	0/1314
27	Y	0.33	0/1004	0.52	0/1341
28	Z	0.36	0/1118	0.59	0/1497
29	a	0.38	0/1204	0.57	0/1612
30	b	0.33	0/473	0.53	0/629
31	c	0.35	0/775	0.53	0/1040
32	d	0.38	0/897	0.58	0/1205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.37	0/1055	0.54	0/1413
34	f	0.39	0/868	0.55	0/1168
35	g	0.35	0/890	0.57	0/1189
36	h	0.37	0/974	0.55	0/1297
37	i	0.33	0/777	0.53	0/1033
38	j	0.39	0/696	0.58	0/923
39	k	0.35	0/614	0.58	0/822
40	l	0.37	0/443	0.53	0/588
41	m	0.33	0/423	0.53	0/562
42	o	0.38	0/860	0.59	0/1136
43	p	0.34	0/701	0.53	0/934
44	q	0.55	0/977	0.63	0/1313
45	x	0.37	0/4557	0.57	0/6189
46	y	0.41	0/1759	0.55	0/2363
All	All	0.41	1/137737 (0.0%)	0.82	45/202428 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	C	0	2
13	J	0	1
16	N	0	2
28	Z	0	1
32	d	0	2
35	g	0	1
45	x	0	2
46	y	0	1
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1394	A	N9-C4	-5.33	1.34	1.37

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	2307	G	C4-N9-C1'	-8.80	115.06	126.50
1	5	2307	G	C8-N9-C1'	8.09	137.51	127.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1555	U	N3-C2-O2	-8.00	116.60	122.20
1	5	1812	G	N3-C4-N9	-7.42	121.55	126.00
1	5	2309	A	C8-N9-C4	-6.81	103.08	105.80
3	8	84	C	C6-N1-C2	6.80	123.02	120.30
1	5	2307	G	N3-C4-N9	-6.52	122.09	126.00
1	5	1232	C	O4'-C1'-N1	6.47	113.38	108.20
1	5	1607	U	P-O3'-C3'	6.47	127.46	119.70
1	5	1555	U	P-O3'-C3'	6.36	127.34	119.70
1	5	2193	U	N1-C2-N3	6.29	118.67	114.90
1	5	2313	A	C8-N9-C4	-6.17	103.33	105.80
1	5	2872	A	P-O3'-C3'	6.16	127.09	119.70
1	5	2307	G	C6-C5-N7	6.08	134.04	130.40
1	5	2808	A	O4'-C1'-N9	6.06	113.05	108.20
1	5	175	C	C2-N1-C1'	5.98	125.38	118.80
1	5	2777	G	N3-C4-C5	5.77	131.49	128.60
1	5	2312	A	N1-C6-N6	5.77	122.06	118.60
1	5	1555	U	C6-N1-C2	-5.75	117.55	121.00
1	5	2313	A	N7-C8-N9	5.73	116.66	113.80
1	5	1559	A	P-O3'-C3'	5.66	126.49	119.70
1	5	29	C	C6-N1-C2	5.62	122.55	120.30
1	5	2584	G	C4-N9-C1'	5.60	133.78	126.50
1	5	767	U	O4'-C1'-N1	5.50	112.60	108.20
1	5	1812	G	N3-C4-C5	5.46	131.33	128.60
1	5	1574	C	C2-N1-C1'	5.45	124.80	118.80
1	5	2314	U	O5'-P-OP2	5.45	117.24	110.70
1	5	1631	C	C6-N1-C1'	5.44	127.33	120.80
1	5	2584	G	C8-N9-C1'	-5.43	119.94	127.00
1	5	2278	C	N1-C2-O2	-5.41	115.66	118.90
1	5	760	G	O4'-C1'-N9	5.38	112.50	108.20
1	5	72	C	C6-N1-C2	5.35	122.44	120.30
1	5	2248	C	C6-N1-C2	-5.34	118.17	120.30
1	5	1555	U	N1-C2-O2	5.27	126.49	122.80
1	5	2137	U	C2-N1-C1'	5.26	124.02	117.70
1	5	2584	G	N3-C4-N9	5.19	129.12	126.00
1	5	2307	G	N3-C4-C5	5.17	131.19	128.60
1	5	1496	C	C6-N1-C2	-5.14	118.24	120.30
1	5	2777	G	N3-C4-N9	-5.13	122.92	126.00
1	5	1172	G	N3-C4-C5	-5.10	126.05	128.60
1	5	1872	C	C6-N1-C2	-5.08	118.27	120.30
1	5	175	C	C6-N1-C1'	-5.04	114.75	120.80
1	5	90	C	C6-N1-C2	-5.04	118.28	120.30
1	5	1222	G	O4'-C1'-N9	5.04	112.23	108.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	2193	U	N1-C2-O2	-5.03	119.28	122.80

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	148	ILE	Peptide
6	C	197	ARG	Peptide
13	J	9	MET	Peptide
16	N	183	THR	Peptide
16	N	184	LYS	Peptide
28	Z	101	PHE	Peptide
32	d	6	ASP	Peptide
32	d	82	GLU	Peptide
35	g	80	ARG	Peptide
45	x	518	ASP	Peptide
45	x	541	HIS	Peptide
46	y	347	PHE	Peptide

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	
4	A	210/254 (83%)	193 (92%)	17 (8%)	0	100	100
5	B	384/387 (99%)	359 (94%)	25 (6%)	0	100	100
6	C	359/362 (99%)	330 (92%)	27 (8%)	2 (1%)	25	63
7	D	292/297 (98%)	283 (97%)	7 (2%)	2 (1%)	22	60

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	E	173/176 (98%)	160 (92%)	10 (6%)	3 (2%)	9	43
9	F	221/244 (91%)	211 (96%)	9 (4%)	1 (0%)	29	67
10	G	229/256 (90%)	201 (88%)	26 (11%)	2 (1%)	17	54
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	29	67
12	I	209/221 (95%)	193 (92%)	16 (8%)	0	100	100
13	J	167/174 (96%)	143 (86%)	19 (11%)	5 (3%)	4	32
14	L	192/199 (96%)	169 (88%)	21 (11%)	2 (1%)	15	52
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	15	52
17	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
18	P	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
19	Q	183/186 (98%)	173 (94%)	9 (5%)	1 (0%)	29	67
20	R	154/189 (82%)	148 (96%)	6 (4%)	0	100	100
21	S	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
22	T	157/160 (98%)	153 (98%)	2 (1%)	2 (1%)	12	48
23	U	100/121 (83%)	95 (95%)	5 (5%)	0	100	100
24	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
25	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
26	X	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
27	Y	124/127 (98%)	118 (95%)	5 (4%)	1 (1%)	19	57
28	Z	133/136 (98%)	114 (86%)	16 (12%)	3 (2%)	6	37
29	a	146/149 (98%)	131 (90%)	14 (10%)	1 (1%)	22	60
30	b	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
31	c	98/105 (93%)	91 (93%)	7 (7%)	0	100	100
32	d	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	17	54
33	e	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	19	57
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	100 (91%)	8 (7%)	2 (2%)	8	41
36	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
37	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	4	32
38	j	85/88 (97%)	78 (92%)	7 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	k	75/78 (96%)	68 (91%)	6 (8%)	1 (1%)	12	48
40	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	m	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
42	o	103/106 (97%)	96 (93%)	7 (7%)	0	100	100
43	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
44	q	116/312 (37%)	109 (94%)	7 (6%)	0	100	100
45	x	577/616 (94%)	540 (94%)	37 (6%)	0	100	100
46	y	207/414 (50%)	192 (93%)	15 (7%)	0	100	100
All	All	6982/7900 (88%)	6509 (93%)	437 (6%)	36 (0%)	32	67

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
13	J	10	ARG
13	J	95	ASN
16	N	184	LYS
13	J	115	LYS
14	L	18	TRP
28	Z	17	ARG
28	Z	130	PHE
37	i	63	ASN
8	E	123	PRO
27	Y	125	LYS
28	Z	129	TRP
35	g	83	ASN
37	i	34	SER
8	E	97	ASN
9	F	191	VAL
16	N	183	THR
22	T	69	LYS
22	T	136	ARG
29	a	78	LEU
39	k	17	ARG
6	C	71	VAL
6	C	148	ILE
13	J	12	LEU
32	d	7	VAL
35	g	82	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	i	64	SER
14	L	47	ALA
7	D	125	VAL
10	G	203	VAL
13	J	114	ILE
7	D	122	VAL
10	G	237	ILE
11	H	167	VAL
19	Q	97	PRO
33	e	6	HIS

5.3.2 Protein sidechains [i](#)

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
4	A	166/196 (85%)	139 (84%)	27 (16%)	2 16
5	B	319/323 (99%)	269 (84%)	50 (16%)	2 17
6	C	288/289 (100%)	240 (83%)	48 (17%)	2 15
7	D	243/245 (99%)	216 (89%)	27 (11%)	6 27
8	E	136/153 (89%)	119 (88%)	17 (12%)	4 23
9	F	187/205 (91%)	166 (89%)	21 (11%)	6 27
10	G	177/208 (85%)	154 (87%)	23 (13%)	4 22
11	H	171/171 (100%)	144 (84%)	27 (16%)	2 17
12	I	179/187 (96%)	157 (88%)	22 (12%)	4 24
13	J	147/150 (98%)	122 (83%)	25 (17%)	2 14
14	L	154/159 (97%)	136 (88%)	18 (12%)	5 25
15	M	108/109 (99%)	93 (86%)	15 (14%)	3 21
16	N	175/176 (99%)	147 (84%)	28 (16%)	2 16
17	O	160/162 (99%)	136 (85%)	24 (15%)	3 18
18	P	145/146 (99%)	128 (88%)	17 (12%)	5 25
19	Q	150/151 (99%)	124 (83%)	26 (17%)	2 13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	R	129/154 (84%)	111 (86%)	18 (14%)	3	21
21	S	155/156 (99%)	129 (83%)	26 (17%)	2	15
22	T	136/137 (99%)	112 (82%)	24 (18%)	2	13
23	U	89/107 (83%)	76 (85%)	13 (15%)	3	19
24	V	104/105 (99%)	95 (91%)	9 (9%)	10	37
25	W	55/129 (43%)	50 (91%)	5 (9%)	9	35
26	X	104/118 (88%)	85 (82%)	19 (18%)	1	11
27	Y	109/110 (99%)	90 (83%)	19 (17%)	2	13
28	Z	115/116 (99%)	98 (85%)	17 (15%)	3	18
29	a	118/119 (99%)	103 (87%)	15 (13%)	4	23
30	b	46/47 (98%)	38 (83%)	8 (17%)	2	13
31	c	84/88 (96%)	71 (84%)	13 (16%)	2	17
32	d	94/97 (97%)	83 (88%)	11 (12%)	5	25
33	e	110/111 (99%)	96 (87%)	14 (13%)	4	23
34	f	90/91 (99%)	82 (91%)	8 (9%)	9	36
35	g	95/103 (92%)	81 (85%)	14 (15%)	3	19
36	h	103/105 (98%)	85 (82%)	18 (18%)	2	13
37	i	80/82 (98%)	59 (74%)	21 (26%)	0	4
38	j	70/71 (99%)	59 (84%)	11 (16%)	2	17
39	k	67/69 (97%)	56 (84%)	11 (16%)	2	15
40	l	45/46 (98%)	39 (87%)	6 (13%)	4	22
41	m	47/116 (40%)	36 (77%)	11 (23%)	1	5
42	o	90/91 (99%)	78 (87%)	12 (13%)	4	22
43	p	71/72 (99%)	66 (93%)	5 (7%)	15	44
44	q	105/254 (41%)	92 (88%)	13 (12%)	4	24
45	x	508/540 (94%)	468 (92%)	40 (8%)	12	41
46	y	182/378 (48%)	168 (92%)	14 (8%)	13	41
All	All	5906/6642 (89%)	5096 (86%)	810 (14%)	7	21

All (810) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	5	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	A	15	ILE
4	A	23	ARG
4	A	44	ILE
4	A	46	LYS
4	A	48	ILE
4	A	64	ARG
4	A	70	ARG
4	A	71	LEU
4	A	73	GLU
4	A	96	LEU
4	A	101	VAL
4	A	102	LEU
4	A	116	VAL
4	A	119	LYS
4	A	134	VAL
4	A	135	ILE
4	A	137	ILE
4	A	142	ASP
4	A	147	ARG
4	A	149	ARG
4	A	155	LYS
4	A	157	VAL
4	A	165	VAL
4	A	180	LEU
4	A	193	ARG
4	A	199	THR
5	B	3	HIS
5	B	4	ARG
5	B	7	GLU
5	B	10	ARG
5	B	17	LEU
5	B	19	ARG
5	B	25	ILE
5	B	37	ARG
5	B	44	THR
5	B	68	HIS
5	B	70	ARG
5	B	74	GLU
5	B	76	VAL
5	B	77	THR
5	B	85	VAL
5	B	103	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	B	104	THR
5	B	110	LEU
5	B	112	ASP
5	B	114	VAL
5	B	116	ARG
5	B	123	TYR
5	B	140	ASP
5	B	146	ARG
5	B	192	VAL
5	B	196	ARG
5	B	202	THR
5	B	206	ASP
5	B	216	ASP
5	B	221	THR
5	B	227	GLU
5	B	232	ARG
5	B	246	LEU
5	B	248	LYS
5	B	249	VAL
5	B	251	CYS
5	B	252	ILE
5	B	264	VAL
5	B	266	ARG
5	B	284	ARG
5	B	300	ARG
5	B	317	ILE
5	B	322	ILE
5	B	332	ARG
5	B	338	LEU
5	B	340	LYS
5	B	346	THR
5	B	347	SER
5	B	364	LYS
5	B	369	ARG
6	C	3	ARG
6	C	6	VAL
6	C	12	THR
6	C	16	THR
6	C	48	GLN
6	C	52	VAL
6	C	55	LYS
6	C	69	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	C	73	ARG
6	C	76	ARG
6	C	77	VAL
6	C	93	MET
6	C	94	CYS
6	C	99	MET
6	C	103	THR
6	C	107	ARG
6	C	122	THR
6	C	142	VAL
6	C	148	ILE
6	C	150	LEU
6	C	152	VAL
6	C	156	LEU
6	C	160	GLN
6	C	172	VAL
6	C	178	LEU
6	C	183	LYS
6	C	186	LYS
6	C	187	LEU
6	C	194	TYR
6	C	203	ARG
6	C	206	LEU
6	C	233	LEU
6	C	265	GLU
6	C	278	SER
6	C	283	THR
6	C	300	ARG
6	C	304	GLN
6	C	309	ARG
6	C	313	LEU
6	C	323	VAL
6	C	327	LEU
6	C	333	VAL
6	C	342	LYS
6	C	345	GLU
6	C	347	THR
6	C	356	THR
6	C	359	LEU
6	C	360	LYS
7	D	4	GLN
7	D	5	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	D	34	LYS
7	D	35	ARG
7	D	50	ARG
7	D	51	LEU
7	D	69	ILE
7	D	70	THR
7	D	74	VAL
7	D	109	THR
7	D	126	GLU
7	D	129	TYR
7	D	136	GLU
7	D	146	LEU
7	D	152	ARG
7	D	177	GLU
7	D	184	ASP
7	D	185	PHE
7	D	196	ARG
7	D	203	HIS
7	D	211	LEU
7	D	218	ARG
7	D	231	ILE
7	D	232	ASP
7	D	259	LYS
7	D	275	THR
7	D	282	ARG
8	E	8	LYS
8	E	18	LEU
8	E	20	LYS
8	E	22	ARG
8	E	28	GLN
8	E	31	ARG
8	E	46	ARG
8	E	52	VAL
8	E	76	LEU
8	E	78	ARG
8	E	82	ARG
8	E	89	THR
8	E	91	VAL
8	E	123	PRO
8	E	141	VAL
8	E	146	ILE
8	E	155	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	F	22	THR
9	F	30	ARG
9	F	41	ARG
9	F	44	ILE
9	F	59	GLU
9	F	60	ARG
9	F	82	LYS
9	F	88	ARG
9	F	92	ILE
9	F	108	LEU
9	F	109	THR
9	F	131	GLU
9	F	134	VAL
9	F	147	LEU
9	F	173	LEU
9	F	175	LYS
9	F	179	LEU
9	F	180	SER
9	F	181	ILE
9	F	196	LYS
9	F	239	LEU
10	G	41	GLN
10	G	65	LEU
10	G	69	LEU
10	G	70	LYS
10	G	79	GLN
10	G	81	THR
10	G	98	ARG
10	G	109	LEU
10	G	136	LEU
10	G	149	LYS
10	G	160	ILE
10	G	169	LEU
10	G	172	LYS
10	G	197	VAL
10	G	200	LEU
10	G	206	GLU
10	G	208	GLU
10	G	213	LYS
10	G	214	LEU
10	G	241	LYS
10	G	245	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	G	246	MET
10	G	248	LYS
11	H	1	MET
11	H	4	ILE
11	H	7	GLU
11	H	18	VAL
11	H	33	THR
11	H	41	ILE
11	H	44	THR
11	H	55	VAL
11	H	62	ARG
11	H	68	LEU
11	H	69	ARG
11	H	70	THR
11	H	82	VAL
11	H	100	ASN
11	H	106	LYS
11	H	112	ILE
11	H	135	GLU
11	H	147	SER
11	H	151	VAL
11	H	152	GLU
11	H	157	ASN
11	H	160	ASP
11	H	161	LEU
11	H	162	GLN
11	H	165	CYS
11	H	177	ASP
11	H	190	ASP
12	I	3	ARG
12	I	12	GLN
12	I	21	ARG
12	I	24	ARG
12	I	33	ILE
12	I	36	LEU
12	I	55	ASN
12	I	63	GLU
12	I	65	LEU
12	I	71	CYS
12	I	83	ASP
12	I	91	VAL
12	I	139	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	I	145	LYS
12	I	163	GLN
12	I	169	LYS
12	I	170	LYS
12	I	174	THR
12	I	177	ASP
12	I	183	LYS
12	I	186	GLU
12	I	193	ASP
13	J	10	ARG
13	J	12	LEU
13	J	22	SER
13	J	31	THR
13	J	35	LYS
13	J	44	THR
13	J	46	VAL
13	J	51	ARG
13	J	54	VAL
13	J	67	VAL
13	J	80	LEU
13	J	85	LYS
13	J	92	ARG
13	J	94	ARG
13	J	95	ASN
13	J	106	ILE
13	J	107	ASP
13	J	112	LEU
13	J	119	SER
13	J	132	ASN
13	J	137	ARG
13	J	161	SER
13	J	165	GLN
13	J	166	LYS
13	J	174	LYS
14	L	27	ASP
14	L	52	ASP
14	L	63	VAL
14	L	67	ARG
14	L	76	THR
14	L	85	LEU
14	L	91	ARG
14	L	101	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	L	107	GLU
14	L	123	ILE
14	L	131	LYS
14	L	139	LEU
14	L	149	GLN
14	L	162	ASN
14	L	164	GLU
14	L	168	ARG
14	L	171	ARG
14	L	194	GLU
15	M	8	LYS
15	M	15	VAL
15	M	20	VAL
15	M	32	LEU
15	M	43	LYS
15	M	53	VAL
15	M	58	ILE
15	M	62	GLN
15	M	64	VAL
15	M	72	LEU
15	M	80	THR
15	M	92	GLU
15	M	106	ARG
15	M	130	THR
15	M	135	LEU
16	N	8	GLU
16	N	10	LEU
16	N	12	ARG
16	N	15	GLN
16	N	18	VAL
16	N	22	LEU
16	N	24	ARG
16	N	27	VAL
16	N	41	ARG
16	N	49	ARG
16	N	53	TYR
16	N	54	LYS
16	N	66	VAL
16	N	68	ARG
16	N	91	GLU
16	N	92	LEU
16	N	104	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	N	106	VAL
16	N	119	TYR
16	N	121	VAL
16	N	138	GLN
16	N	176	LYS
16	N	184	LYS
16	N	188	ARG
16	N	190	THR
16	N	194	GLN
16	N	196	THR
16	N	199	LEU
17	O	3	VAL
17	O	15	LEU
17	O	27	LEU
17	O	34	VAL
17	O	37	ARG
17	O	41	LEU
17	O	44	SER
17	O	59	ARG
17	O	67	THR
17	O	68	ARG
17	O	78	ARG
17	O	79	ILE
17	O	85	ARG
17	O	106	GLU
17	O	117	ARG
17	O	124	LEU
17	O	128	ARG
17	O	143	THR
17	O	160	ARG
17	O	162	VAL
17	O	171	LYS
17	O	175	THR
17	O	182	ASN
17	O	193	GLN
18	P	22	LEU
18	P	24	VAL
18	P	32	THR
18	P	51	VAL
18	P	52	LEU
18	P	55	GLN
18	P	64	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	P	69	ARG
18	P	70	THR
18	P	79	THR
18	P	80	LYS
18	P	94	LEU
18	P	103	GLU
18	P	114	VAL
18	P	119	VAL
18	P	142	SER
18	P	166	VAL
19	Q	3	ILE
19	Q	24	VAL
19	Q	26	LEU
19	Q	38	ARG
19	Q	41	ASP
19	Q	49	LEU
19	Q	57	ILE
19	Q	62	VAL
19	Q	63	SER
19	Q	66	ARG
19	Q	67	ILE
19	Q	80	THR
19	Q	86	THR
19	Q	93	ILE
19	Q	100	THR
19	Q	121	CYS
19	Q	135	GLN
19	Q	159	LYS
19	Q	161	LYS
19	Q	165	ILE
19	Q	166	LEU
19	Q	167	SER
19	Q	170	ARG
19	Q	176	ARG
19	Q	178	ARG
19	Q	180	ARG
20	R	5	ARG
20	R	10	LEU
20	R	36	ASN
20	R	47	ASN
20	R	49	THR
20	R	57	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	R	63	THR
20	R	74	ARG
20	R	75	HIS
20	R	89	LEU
20	R	98	ARG
20	R	99	LEU
20	R	114	LYS
20	R	138	LEU
20	R	143	ILE
20	R	152	GLU
20	R	153	LYS
20	R	156	ASN
21	S	13	ARG
21	S	17	GLU
21	S	27	MET
21	S	32	SER
21	S	45	LEU
21	S	62	ASN
21	S	70	THR
21	S	73	LYS
21	S	74	ASN
21	S	87	THR
21	S	98	SER
21	S	100	VAL
21	S	103	VAL
21	S	115	ARG
21	S	130	GLU
21	S	132	THR
21	S	135	VAL
21	S	136	LYS
21	S	137	ARG
21	S	138	GLN
21	S	144	LEU
21	S	148	LEU
21	S	155	ARG
21	S	162	THR
21	S	171	PHE
21	S	172	TYR
22	T	3	LYS
22	T	5	HIS
22	T	12	ARG
22	T	25	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
22	T	26	HIS
22	T	27	LEU
22	T	35	LYS
22	T	80	VAL
22	T	83	ARG
22	T	89	LEU
22	T	98	HIS
22	T	102	ARG
22	T	103	GLN
22	T	104	GLU
22	T	118	GLU
22	T	124	VAL
22	T	126	VAL
22	T	130	ARG
22	T	131	GLN
22	T	139	ARG
22	T	140	ILE
22	T	143	THR
22	T	154	VAL
22	T	157	GLU
23	U	11	ILE
23	U	16	THR
23	U	27	VAL
23	U	37	LEU
23	U	43	VAL
23	U	58	GLU
23	U	59	ASP
23	U	62	VAL
23	U	63	VAL
23	U	68	THR
23	U	74	LYS
23	U	75	TYR
23	U	102	GLU
24	V	12	ARG
24	V	13	ILE
24	V	19	VAL
24	V	28	ASN
24	V	45	ARG
24	V	58	VAL
24	V	74	MET
24	V	91	VAL
24	V	115	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	W	1	MET
25	W	17	ARG
25	W	28	ILE
25	W	39	LEU
25	W	57	LYS
26	X	24	LEU
26	X	31	THR
26	X	37	THR
26	X	38	LEU
26	X	39	LYS
26	X	40	LEU
26	X	45	LYS
26	X	57	LEU
26	X	63	ILE
26	X	65	GLN
26	X	71	THR
26	X	73	MET
26	X	99	VAL
26	X	108	LEU
26	X	109	LYS
26	X	112	THR
26	X	125	ARG
26	X	133	LEU
26	X	135	ILE
27	Y	12	ARG
27	Y	13	ARG
27	Y	14	LYS
27	Y	35	LEU
27	Y	37	LYS
27	Y	45	ILE
27	Y	50	ILE
27	Y	51	ARG
27	Y	52	ARG
27	Y	59	VAL
27	Y	60	ARG
27	Y	74	TYR
27	Y	76	LEU
27	Y	95	VAL
27	Y	97	ILE
27	Y	108	LYS
27	Y	111	LEU
27	Y	114	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	Y	120	GLN
28	Z	3	LYS
28	Z	17	ARG
28	Z	21	LYS
28	Z	26	VAL
28	Z	52	LYS
28	Z	57	HIS
28	Z	65	ARG
28	Z	72	ILE
28	Z	76	ASN
28	Z	81	LEU
28	Z	86	THR
28	Z	95	VAL
28	Z	99	GLU
28	Z	100	THR
28	Z	102	GLU
28	Z	127	ASN
28	Z	130	PHE
29	a	4	ARG
29	a	8	THR
29	a	44	ASN
29	a	45	MET
29	a	60	TYR
29	a	64	GLN
29	a	65	GLN
29	a	85	ASP
29	a	91	LEU
29	a	97	GLU
29	a	128	ARG
29	a	131	SER
29	a	132	LYS
29	a	133	LEU
29	a	139	ARG
30	b	3	LYS
30	b	14	ARG
30	b	32	LEU
30	b	33	LYS
30	b	50	THR
30	b	52	LYS
30	b	58	LYS
30	b	59	LYS
31	c	7	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
31	c	11	ASN
31	c	19	LYS
31	c	40	LYS
31	c	61	MET
31	c	68	TYR
31	c	71	GLN
31	c	86	ARG
31	c	87	VAL
31	c	91	SER
31	c	97	ASP
31	c	99	ASP
31	c	104	LEU
32	d	8	VAL
32	d	14	ILE
32	d	16	LEU
32	d	35	GLU
32	d	55	LEU
32	d	76	SER
32	d	96	VAL
32	d	98	VAL
32	d	102	LYS
32	d	104	LEU
32	d	110	GLU
33	e	9	ILE
33	e	19	ARG
33	e	34	LYS
33	e	43	ARG
33	e	81	ASP
33	e	82	LEU
33	e	83	GLU
33	e	87	MET
33	e	89	THR
33	e	98	HIS
33	e	106	VAL
33	e	107	VAL
33	e	109	LEU
33	e	125	ARG
34	f	5	HIS
34	f	48	ARG
34	f	58	GLU
34	f	70	LYS
34	f	74	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	f	81	VAL
34	f	89	LEU
34	f	98	VAL
35	g	14	ASN
35	g	15	THR
35	g	16	ARG
35	g	20	ILE
35	g	29	ILE
35	g	46	ASP
35	g	47	CYS
35	g	57	LEU
35	g	58	ARG
35	g	71	THR
35	g	79	SER
35	g	81	CYS
35	g	98	GLN
35	g	104	VAL
36	h	20	GLN
36	h	23	ASP
36	h	27	GLU
36	h	36	LEU
36	h	41	LEU
36	h	57	VAL
36	h	62	GLN
36	h	64	GLU
36	h	66	VAL
36	h	68	GLN
36	h	69	LEU
36	h	81	ARG
36	h	89	ARG
36	h	92	LEU
36	h	107	LYS
36	h	113	GLN
36	h	114	ARG
36	h	119	LYS
37	i	3	VAL
37	i	9	ILE
37	i	17	VAL
37	i	18	THR
37	i	34	SER
37	i	36	ARG
37	i	45	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	i	53	TYR
37	i	57	LEU
37	i	58	ILE
37	i	60	LEU
37	i	61	ILE
37	i	62	ARG
37	i	68	ARG
37	i	74	LYS
37	i	75	LYS
37	i	76	ARG
37	i	81	THR
37	i	88	GLU
37	i	94	ILE
37	i	98	ARG
38	j	12	HIS
38	j	17	THR
38	j	24	ARG
38	j	45	ARG
38	j	55	ARG
38	j	65	ARG
38	j	67	LEU
38	j	68	LYS
38	j	70	VAL
38	j	73	ARG
38	j	80	THR
39	k	6	THR
39	k	12	LEU
39	k	14	LEU
39	k	24	THR
39	k	31	LEU
39	k	40	GLN
39	k	41	THR
39	k	46	ARG
39	k	53	THR
39	k	61	LYS
39	k	64	LYS
40	l	4	GLN
40	l	21	ARG
40	l	27	ILE
40	l	28	ARG
40	l	30	ARG
40	l	36	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
41	m	79	GLU
41	m	88	LYS
41	m	90	ASN
41	m	93	LYS
41	m	97	ARG
41	m	106	ARG
41	m	108	THR
41	m	112	LYS
41	m	113	ARG
41	m	118	THR
41	m	127	LEU
42	o	7	THR
42	o	8	ARG
42	o	20	HIS
42	o	27	GLN
42	o	38	GLN
42	o	54	THR
42	o	55	LYS
42	o	75	VAL
42	o	84	THR
42	o	85	LEU
42	o	93	LEU
42	o	104	LEU
43	p	17	ARG
43	p	24	ARG
43	p	54	ILE
43	p	57	CYS
43	p	80	ARG
44	q	4	ILE
44	q	10	GLU
44	q	15	LEU
44	q	46	ARG
44	q	48	ARG
44	q	67	LEU
44	q	70	LEU
44	q	72	ASP
44	q	76	LEU
44	q	80	VAL
44	q	97	LYS
44	q	104	ARG
44	q	192	ASP
45	x	34	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
45	x	43	THR
45	x	47	ASN
45	x	49	SER
45	x	56	GLN
45	x	76	LEU
45	x	134	ARG
45	x	143	LEU
45	x	160	ILE
45	x	165	GLU
45	x	189	ILE
45	x	203	THR
45	x	225	THR
45	x	235	ASN
45	x	243	ARG
45	x	309	PHE
45	x	337	LEU
45	x	361	VAL
45	x	363	ASP
45	x	366	GLN
45	x	374	THR
45	x	383	ASP
45	x	384	LYS
45	x	447	HIS
45	x	452	THR
45	x	457	ASN
45	x	464	SER
45	x	468	LEU
45	x	478	LEU
45	x	491	SER
45	x	496	ILE
45	x	504	CYS
45	x	510	CYS
45	x	521	GLU
45	x	523	LEU
45	x	536	TRP
45	x	540	GLN
45	x	541	HIS
45	x	567	LEU
45	x	580	VAL
46	y	179	ASN
46	y	197	LEU
46	y	198	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	y	199	ASP
46	y	200	LYS
46	y	221	ASN
46	y	227	LEU
46	y	240	CYS
46	y	303	ILE
46	y	313	VAL
46	y	340	VAL
46	y	347	PHE
46	y	362	VAL
46	y	391	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	132	ASN
4	A	205	ASN
5	B	11	HIS
5	B	243	HIS
5	B	269	GLN
6	C	5	GLN
6	C	9	HIS
6	C	110	ASN
6	C	114	ASN
6	C	213	ASN
6	C	221	ASN
6	C	260	GLN
6	C	307	GLN
6	C	311	HIS
7	D	32	GLN
7	D	40	HIS
8	E	28	GLN
10	G	41	GLN
10	G	221	ASN
10	G	240	ASN
11	H	58	HIS
11	H	100	ASN
11	H	125	ASN
11	H	156	GLN
11	H	169	ASN
12	I	23	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	I	100	ASN
12	I	144	ASN
13	J	43	GLN
13	J	62	ASN
13	J	90	GLN
13	J	132	ASN
14	L	13	HIS
14	L	102	GLN
16	N	70	ASN
16	N	90	ASN
16	N	123	GLN
17	O	31	GLN
17	O	50	ASN
17	O	65	ASN
18	P	34	GLN
18	P	45	GLN
18	P	50	GLN
18	P	64	ASN
18	P	125	GLN
19	Q	5	HIS
19	Q	73	GLN
20	R	36	ASN
20	R	47	ASN
21	S	63	GLN
21	S	138	GLN
22	T	49	GLN
22	T	95	HIS
22	T	131	GLN
22	T	146	ASN
23	U	40	HIS
26	X	137	ASN
27	Y	26	GLN
27	Y	100	HIS
27	Y	120	GLN
28	Z	29	HIS
28	Z	36	HIS
28	Z	106	GLN
29	a	28	HIS
29	a	44	ASN
30	b	10	HIS
30	b	11	ASN
30	b	17	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	b	19	ASN
31	c	47	ASN
31	c	75	ASN
32	d	57	GLN
33	e	13	HIS
34	f	77	ASN
35	g	52	GLN
35	g	98	GLN
36	h	62	GLN
36	h	68	GLN
39	k	40	GLN
44	q	36	GLN
44	q	37	GLN
44	q	39	HIS
45	x	18	ASN
45	x	36	GLN
45	x	146	HIS
45	x	156	HIS
45	x	235	ASN
45	x	254	GLN
45	x	273	HIS
45	x	429	ASN
45	x	447	HIS
45	x	453	ASN
45	x	471	HIS
45	x	505	ASN
46	y	182	HIS
46	y	357	GLN
46	y	386	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3084/3396 (90%)	666 (21%)	79 (2%)
2	7	120/121 (99%)	13 (10%)	0
3	8	157/158 (99%)	42 (26%)	6 (3%)
All	All	3361/3675 (91%)	721 (21%)	85 (2%)

All (721) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	14	U
1	5	15	C
1	5	21	G
1	5	22	G
1	5	26	A
1	5	40	A
1	5	43	A
1	5	49	A
1	5	59	G
1	5	60	A
1	5	65	A
1	5	66	A
1	5	75	G
1	5	83	U
1	5	89	A
1	5	91	G
1	5	92	G
1	5	96	G
1	5	110	G
1	5	111	C
1	5	113	C
1	5	116	A
1	5	117	U
1	5	121	A
1	5	122	A
1	5	123	A
1	5	133	U
1	5	134	U
1	5	135	C
1	5	136	G
1	5	143	G
1	5	146	U
1	5	148	G
1	5	152	U
1	5	156	G
1	5	157	A
1	5	165	A
1	5	166	C
1	5	170	G
1	5	171	G
1	5	172	G
1	5	173	G
1	5	175	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	182	U
1	5	183	G
1	5	184	U
1	5	187	A
1	5	190	U
1	5	191	U
1	5	206	G
1	5	210	U
1	5	213	A
1	5	218	G
1	5	219	A
1	5	221	A
1	5	222	A
1	5	237	G
1	5	239	G
1	5	240	U
1	5	241	G
1	5	244	G
1	5	245	U
1	5	246	U
1	5	248	U
1	5	249	U
1	5	250	U
1	5	251	G
1	5	252	U
1	5	254	A
1	5	269	G
1	5	270	U
1	5	277	G
1	5	282	G
1	5	283	G
1	5	284	A
1	5	286	U
1	5	295	A
1	5	305	U
1	5	315	C
1	5	316	U
1	5	323	A
1	5	329	U
1	5	339	C
1	5	343	U
1	5	346	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	350	C
1	5	351	A
1	5	370	U
1	5	376	G
1	5	398	A
1	5	399	A
1	5	401	U
1	5	402	A
1	5	403	C
1	5	421	G
1	5	422	A
1	5	429	U
1	5	433	A
1	5	438	A
1	5	439	C
1	5	494	G
1	5	520	U
1	5	521	A
1	5	530	G
1	5	535	G
1	5	546	C
1	5	547	G
1	5	548	G
1	5	552	G
1	5	553	U
1	5	555	U
1	5	557	A
1	5	559	A
1	5	578	A
1	5	579	G
1	5	581	U
1	5	592	A
1	5	594	U
1	5	600	G
1	5	604	G
1	5	609	G
1	5	611	A
1	5	619	A
1	5	620	U
1	5	621	A
1	5	622	A
1	5	623	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	636	C
1	5	649	A
1	5	660	A
1	5	677	A
1	5	681	U
1	5	685	G
1	5	691	A
1	5	692	A
1	5	697	A
1	5	705	A
1	5	707	U
1	5	708	G
1	5	712	G
1	5	715	A
1	5	716	A
1	5	720	A
1	5	725	G
1	5	736	A
1	5	749	C
1	5	766	U
1	5	767	U
1	5	776	U
1	5	777	U
1	5	780	A
1	5	781	G
1	5	784	A
1	5	785	G
1	5	786	A
1	5	806	A
1	5	808	A
1	5	817	A
1	5	830	A
1	5	844	G
1	5	845	G
1	5	846	A
1	5	851	C
1	5	861	C
1	5	869	G
1	5	873	C
1	5	874	U
1	5	879	U
1	5	907	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	908	G
1	5	914	A
1	5	916	G
1	5	917	A
1	5	921	A
1	5	923	C
1	5	924	G
1	5	925	A
1	5	934	G
1	5	937	G
1	5	944	C
1	5	946	U
1	5	953	G
1	5	956	U
1	5	959	C
1	5	960	U
1	5	962	A
1	5	974	G
1	5	979	U
1	5	982	C
1	5	983	A
1	5	984	G
1	5	986	U
1	5	993	G
1	5	995	U
1	5	1000	C
1	5	1001	G
1	5	1002	A
1	5	1003	A
1	5	1010	G
1	5	1014	U
1	5	1015	U
1	5	1047	A
1	5	1049	C
1	5	1064	A
1	5	1065	A
1	5	1072	G
1	5	1081	U
1	5	1082	U
1	5	1085	A
1	5	1086	C
1	5	1093	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	1094	U
1	5	1095	U
1	5	1097	G
1	5	1098	A
1	5	1104	G
1	5	1105	A
1	5	1117	G
1	5	1131	G
1	5	1143	A
1	5	1151	U
1	5	1153	A
1	5	1157	G
1	5	1159	A
1	5	1160	C
1	5	1178	G
1	5	1180	A
1	5	1181	U
1	5	1190	A
1	5	1191	U
1	5	1192	C
1	5	1193	A
1	5	1196	C
1	5	1201	C
1	5	1209	G
1	5	1212	A
1	5	1217	A
1	5	1222	G
1	5	1223	A
1	5	1235	U
1	5	1236	G
1	5	1237	G
1	5	1239	C
1	5	1241	U
1	5	1242	G
1	5	1245	A
1	5	1246	G
1	5	1248	C
1	5	1253	U
1	5	1258	U
1	5	1259	A
1	5	1262	G
1	5	1263	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	1264	G
1	5	1265	U
1	5	1266	G
1	5	1272	C
1	5	1285	G
1	5	1294	A
1	5	1305	U
1	5	1307	G
1	5	1308	A
1	5	1309	U
1	5	1313	G
1	5	1330	A
1	5	1345	G
1	5	1349	G
1	5	1350	A
1	5	1351	U
1	5	1352	A
1	5	1353	U
1	5	1355	A
1	5	1356	U
1	5	1357	G
1	5	1370	G
1	5	1380	G
1	5	1385	C
1	5	1386	A
1	5	1392	G
1	5	1399	A
1	5	1400	G
1	5	1405	U
1	5	1419	A
1	5	1432	C
1	5	1434	G
1	5	1435	A
1	5	1437	C
1	5	1446	A
1	5	1452	A
1	5	1484	U
1	5	1508	C
1	5	1533	U
1	5	1536	G
1	5	1553	U
1	5	1554	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	1555	U
1	5	1556	C
1	5	1557	A
1	5	1559	A
1	5	1560	G
1	5	1561	G
1	5	1563	C
1	5	1564	U
1	5	1568	U
1	5	1569	U
1	5	1570	U
1	5	1571	A
1	5	1572	U
1	5	1573	G
1	5	1575	A
1	5	1576	G
1	5	1578	C
1	5	1579	C
1	5	1580	A
1	5	1581	C
1	5	1582	C
1	5	1583	A
1	5	1589	A
1	5	1593	A
1	5	1607	U
1	5	1608	C
1	5	1620	U
1	5	1629	U
1	5	1633	C
1	5	1639	C
1	5	1642	A
1	5	1643	A
1	5	1644	C
1	5	1645	U
1	5	1655	G
1	5	1657	C
1	5	1702	U
1	5	1715	A
1	5	1716	U
1	5	1717	U
1	5	1718	G
1	5	1725	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	1741	A
1	5	1750	A
1	5	1751	G
1	5	1756	C
1	5	1759	C
1	5	1760	A
1	5	1763	U
1	5	1764	U
1	5	1765	U
1	5	1770	G
1	5	1772	U
1	5	1773	C
1	5	1780	G
1	5	1797	A
1	5	1812	G
1	5	1814	A
1	5	1815	U
1	5	1816	A
1	5	1817	G
1	5	1818	U
1	5	1820	U
1	5	1821	U
1	5	1838	G
1	5	1839	A
1	5	1841	A
1	5	1842	A
1	5	1846	C
1	5	1849	C
1	5	1850	A
1	5	1855	U
1	5	1863	G
1	5	1874	A
1	5	1876	U
1	5	1878	G
1	5	1879	A
1	5	1880	U
1	5	1886	A
1	5	1906	G
1	5	1909	A
1	5	1935	G
1	5	1943	C
1	5	2101	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	2102	U
1	5	2111	G
1	5	2112	U
1	5	2113	A
1	5	2114	C
1	5	2117	A
1	5	2121	G
1	5	2122	G
1	5	2131	A
1	5	2144	A
1	5	2149	A
1	5	2158	A
1	5	2159	U
1	5	2160	G
1	5	2169	G
1	5	2170	U
1	5	2171	G
1	5	2193	U
1	5	2205	U
1	5	2223	A
1	5	2225	U
1	5	2228	A
1	5	2229	A
1	5	2244	A
1	5	2249	G
1	5	2270	A
1	5	2273	G
1	5	2279	A
1	5	2285	C
1	5	2288	G
1	5	2298	U
1	5	2307	G
1	5	2308	C
1	5	2309	A
1	5	2310	U
1	5	2313	A
1	5	2314	U
1	5	2315	G
1	5	2334	U
1	5	2335	G
1	5	2336	U
1	5	2337	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	2373	A
1	5	2374	C
1	5	2375	G
1	5	2385	G
1	5	2388	U
1	5	2393	G
1	5	2397	A
1	5	2401	A
1	5	2402	A
1	5	2403	G
1	5	2410	U
1	5	2411	U
1	5	2412	G
1	5	2418	G
1	5	2419	A
1	5	2422	C
1	5	2423	U
1	5	2433	U
1	5	2435	G
1	5	2436	U
1	5	2437	G
1	5	2438	A
1	5	2439	A
1	5	2510	U
1	5	2511	A
1	5	2512	C
1	5	2514	U
1	5	2515	A
1	5	2522	G
1	5	2523	A
1	5	2524	A
1	5	2525	G
1	5	2526	C
1	5	2530	G
1	5	2531	C
1	5	2532	U
1	5	2537	U
1	5	2538	U
1	5	2539	C
1	5	2540	A
1	5	2543	U
1	5	2552	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	2555	G
1	5	2566	C
1	5	2567	C
1	5	2568	C
1	5	2569	A
1	5	2570	U
1	5	2571	U
1	5	2572	C
1	5	2573	G
1	5	2574	G
1	5	2584	G
1	5	2585	G
1	5	2589	G
1	5	2593	A
1	5	2594	C
1	5	2604	U
1	5	2605	G
1	5	2606	G
1	5	2607	G
1	5	2609	A
1	5	2610	G
1	5	2614	G
1	5	2637	A
1	5	2638	C
1	5	2652	U
1	5	2656	A
1	5	2663	G
1	5	2674	A
1	5	2677	G
1	5	2680	A
1	5	2683	U
1	5	2689	A
1	5	2690	G
1	5	2691	A
1	5	2694	A
1	5	2714	G
1	5	2719	U
1	5	2728	G
1	5	2729	U
1	5	2737	C
1	5	2740	A
1	5	2742	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	2752	U
1	5	2753	G
1	5	2754	G
1	5	2771	U
1	5	2772	C
1	5	2773	C
1	5	2777	G
1	5	2779	A
1	5	2782	U
1	5	2794	G
1	5	2796	G
1	5	2799	A
1	5	2800	G
1	5	2801	A
1	5	2802	A
1	5	2803	A
1	5	2804	A
1	5	2807	U
1	5	2808	A
1	5	2809	C
1	5	2810	C
1	5	2812	C
1	5	2814	G
1	5	2816	G
1	5	2817	A
1	5	2818	U
1	5	2819	A
1	5	2845	A
1	5	2847	A
1	5	2853	A
1	5	2859	U
1	5	2860	U
1	5	2871	G
1	5	2872	A
1	5	2873	U
1	5	2875	U
1	5	2887	A
1	5	2889	C
1	5	2899	C
1	5	2905	U
1	5	2916	U
1	5	2918	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	2923	U
1	5	2935	U
1	5	2936	A
1	5	2945	G
1	5	2947	G
1	5	2953	U
1	5	2954	U
1	5	2955	U
1	5	2956	A
1	5	2957	G
1	5	2958	A
1	5	2972	G
1	5	2979	U
1	5	2982	A
1	5	2983	C
1	5	2990	G
1	5	2992	U
1	5	2995	A
1	5	2996	U
1	5	2997	G
1	5	3011	A
1	5	3012	A
1	5	3050	U
1	5	3056	U
1	5	3059	G
1	5	3078	U
1	5	3079	U
1	5	3086	A
1	5	3092	C
1	5	3094	A
1	5	3116	G
1	5	3117	C
1	5	3122	A
1	5	3130	A
1	5	3131	U
1	5	3142	A
1	5	3143	C
1	5	3146	G
1	5	3152	U
1	5	3164	C
1	5	3165	A
1	5	3168	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	3172	A
1	5	3173	G
1	5	3174	A
1	5	3175	U
1	5	3176	G
1	5	3179	U
1	5	3180	A
1	5	3181	C
1	5	3187	A
1	5	3194	C
1	5	3195	U
1	5	3196	U
1	5	3198	U
1	5	3207	U
1	5	3209	A
1	5	3210	A
1	5	3217	C
1	5	3218	A
1	5	3219	G
1	5	3227	A
1	5	3228	C
1	5	3229	G
1	5	3238	G
1	5	3244	A
1	5	3245	A
1	5	3247	G
1	5	3253	G
1	5	3259	U
1	5	3265	C
1	5	3269	U
1	5	3270	U
1	5	3272	C
1	5	3274	A
1	5	3275	U
1	5	3276	G
1	5	3277	U
1	5	3278	C
1	5	3279	A
1	5	3281	U
1	5	3282	U
1	5	3285	C
1	5	3286	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	3288	G
1	5	3289	G
1	5	3290	G
1	5	3294	A
1	5	3301	U
1	5	3304	U
1	5	3306	U
1	5	3312	U
1	5	3317	U
1	5	3318	G
1	5	3319	U
1	5	3329	U
1	5	3330	A
1	5	3335	A
1	5	3338	C
1	5	3341	U
1	5	3342	A
1	5	3345	G
1	5	3346	U
1	5	3351	U
1	5	3352	U
1	5	3354	U
1	5	3355	U
1	5	3356	G
1	5	3357	U
1	5	3358	U
1	5	3362	A
1	5	3368	U
1	5	3369	G
1	5	3371	G
1	5	3378	C
1	5	3383	G
1	5	3389	U
1	5	3390	G
1	5	3396	U
2	7	19	C
2	7	22	A
2	7	33	U
2	7	54	U
2	7	65	G
2	7	73	C
2	7	74	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	7	91	G
2	7	93	C
2	7	102	A
2	7	103	A
2	7	112	G
2	7	121	U
3	8	21	C
3	8	23	U
3	8	25	G
3	8	34	U
3	8	35	C
3	8	39	G
3	8	51	G
3	8	59	A
3	8	60	U
3	8	62	C
3	8	63	G
3	8	76	C
3	8	77	A
3	8	78	G
3	8	79	A
3	8	80	A
3	8	81	U
3	8	82	U
3	8	83	C
3	8	84	C
3	8	85	G
3	8	86	U
3	8	87	G
3	8	88	A
3	8	90	U
3	8	95	G
3	8	102	U
3	8	104	A
3	8	105	A
3	8	106	C
3	8	111	A
3	8	113	U
3	8	118	C
3	8	125	U
3	8	126	A
3	8	127	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	8	128	U
3	8	138	A
3	8	152	G
3	8	156	U
3	8	157	U
3	8	158	U

All (85) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	109	A
1	5	151	A
1	5	183	G
1	5	238	A
1	5	240	U
1	5	282	G
1	5	438	A
1	5	546	C
1	5	619	A
1	5	620	U
1	5	621	A
1	5	696	C
1	5	715	A
1	5	735	A
1	5	765	C
1	5	850	U
1	5	873	C
1	5	916	G
1	5	981	U
1	5	982	C
1	5	1064	A
1	5	1081	U
1	5	1222	G
1	5	1238	C
1	5	1241	U
1	5	1284	C
1	5	1307	G
1	5	1329	U
1	5	1352	A
1	5	1355	A
1	5	1555	U
1	5	1559	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	1568	U
1	5	1571	A
1	5	1580	A
1	5	1605	A
1	5	1607	U
1	5	1716	U
1	5	1724	U
1	5	1816	A
1	5	1819	U
1	5	1838	G
1	5	2101	C
1	5	2112	U
1	5	2204	C
1	5	2248	C
1	5	2307	G
1	5	2418	G
1	5	2422	C
1	5	2438	A
1	5	2513	U
1	5	2523	A
1	5	2539	C
1	5	2583	C
1	5	2584	G
1	5	2593	A
1	5	2604	U
1	5	2662	G
1	5	2682	C
1	5	2772	C
1	5	2807	U
1	5	2872	A
1	5	2954	U
1	5	2971	A
1	5	2995	A
1	5	3078	U
1	5	3115	C
1	5	3121	U
1	5	3167	A
1	5	3195	U
1	5	3218	A
1	5	3228	C
1	5	3269	U
1	5	3289	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	5	3303	G
1	5	3317	U
1	5	3340	G
1	5	3341	U
1	5	3357	U
3	8	79	A
3	8	80	A
3	8	89	A
3	8	111	A
3	8	126	A
3	8	156	U

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

20 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	P5P	5	2022	1	16,23,24	0.79	0	14,33,36	0.79	0
1	Y5P	5	1986	1	14,19,20	2.24	1 (7%)	18,26,29	1.02	1 (5%)
1	P5P	5	2024	1	16,23,24	0.79	0	14,33,36	0.76	0
1	Y5P	5	1993	1	14,19,20	2.36	1 (7%)	18,26,29	1.01	1 (5%)
1	P5P	5	2025	1	16,23,24	0.78	0	14,33,36	0.74	0
1	Y5P	5	1990	1	14,19,20	2.27	1 (7%)	18,26,29	1.07	1 (5%)
1	Y5P	5	1994	1	14,19,20	2.30	1 (7%)	18,26,29	1.07	1 (5%)
1	P5P	5	2019	1	16,23,24	0.80	0	14,33,36	0.80	0
1	P5P	5	2018	1	16,23,24	0.78	0	14,33,36	0.77	0
1	P5P	5	2023	1	16,23,24	0.81	0	14,33,36	0.83	0
1	P5P	5	2016	1	16,23,24	0.78	0	14,33,36	0.77	0
1	P5P	5	2020	1	16,23,24	0.78	0	14,33,36	0.78	0
1	Y5P	5	1987	1	14,19,20	2.32	1 (7%)	18,26,29	1.02	1 (5%)
1	Y5P	5	1989	1	14,19,20	2.31	1 (7%)	18,26,29	0.97	1 (5%)
1	P5P	5	2021	1	16,23,24	0.77	0	14,33,36	0.75	0
1	P5P	5	2017	1	16,23,24	0.78	0	14,33,36	0.76	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	Y5P	5	1995	1	14,19,20	2.29	1 (7%)	18,26,29	0.97	1 (5%)
1	Y5P	5	1992	1	14,19,20	2.23	1 (7%)	18,26,29	1.04	1 (5%)
1	Y5P	5	1988	1	14,19,20	2.26	1 (7%)	18,26,29	1.03	1 (5%)
1	Y5P	5	1991	1	14,19,20	2.35	1 (7%)	18,26,29	1.01	1 (5%)

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	P5P	5	2022	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1986	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2024	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1993	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2025	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1990	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1994	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2019	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2018	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2023	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2016	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2020	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1987	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1989	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2021	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2017	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1995	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1992	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1988	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1991	1	-	1/7/33/34	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1991	Y5P	C4-N3	-8.61	1.38	1.46
1	5	1993	Y5P	C4-N3	-8.61	1.38	1.46
1	5	1987	Y5P	C4-N3	-8.48	1.38	1.46
1	5	1989	Y5P	C4-N3	-8.47	1.38	1.46
1	5	1994	Y5P	C4-N3	-8.44	1.38	1.46
1	5	1995	Y5P	C4-N3	-8.39	1.38	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1990	Y5P	C4-N3	-8.33	1.38	1.46
1	5	1988	Y5P	C4-N3	-8.28	1.38	1.46
1	5	1986	Y5P	C4-N3	-8.21	1.38	1.46
1	5	1992	Y5P	C4-N3	-8.18	1.38	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1994	Y5P	N1-C2-N3	-3.75	114.34	125.33
1	5	1986	Y5P	N1-C2-N3	-3.73	114.38	125.33
1	5	1992	Y5P	N1-C2-N3	-3.70	114.47	125.33
1	5	1990	Y5P	N1-C2-N3	-3.69	114.52	125.33
1	5	1988	Y5P	N1-C2-N3	-3.64	114.67	125.33
1	5	1993	Y5P	N1-C2-N3	-3.53	114.97	125.33
1	5	1989	Y5P	N1-C2-N3	-3.51	115.04	125.33
1	5	1995	Y5P	N1-C2-N3	-3.50	115.07	125.33
1	5	1987	Y5P	N1-C2-N3	-3.49	115.09	125.33
1	5	1991	Y5P	N1-C2-N3	-3.41	115.32	125.33

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	5	1987	Y5P	O4'-C1'-N1-C2
1	5	1989	Y5P	O4'-C1'-N1-C2
1	5	1990	Y5P	O4'-C1'-N1-C2
1	5	1991	Y5P	O4'-C1'-N1-C2
1	5	1993	Y5P	O4'-C1'-N1-C2
1	5	1995	Y5P	O4'-C1'-N1-C2
1	5	1986	Y5P	O4'-C1'-N1-C2
1	5	1988	Y5P	O4'-C1'-N1-C2
1	5	1992	Y5P	O4'-C1'-N1-C2
1	5	1994	Y5P	O4'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 286 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	2
47	z	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1953:G	O3'	1986:Y5P	P	107.33
1	5	2025:P5P	O3'	2093:A	P	105.65
1	z	107:UNK	C	115:UNK	N	20.22
1	z	127:UNK	C	131:UNK	N	9.70

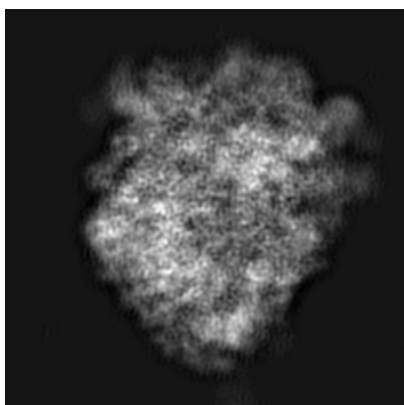
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3152. These allow visual inspection of the internal detail of the map and identification of artifacts.

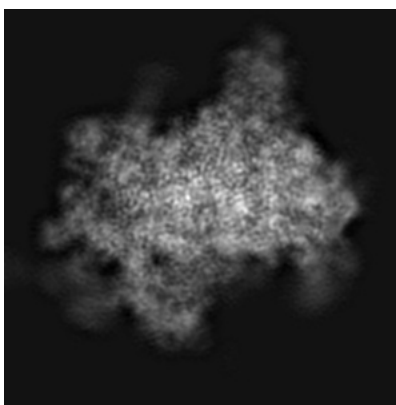
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

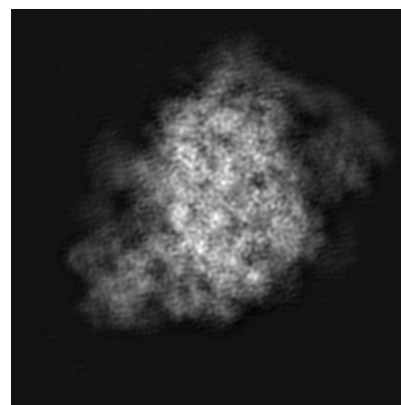
6.1.1 Primary map



X



Y

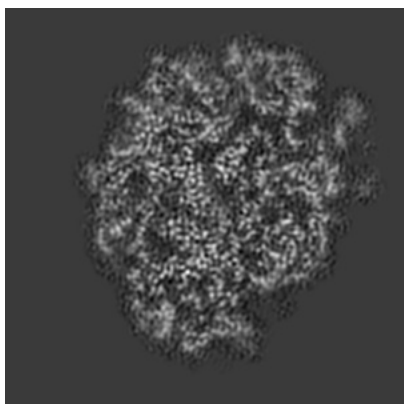


Z

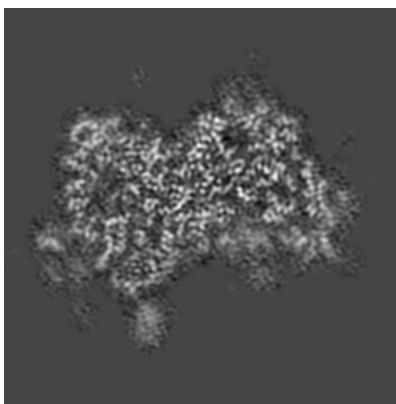
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

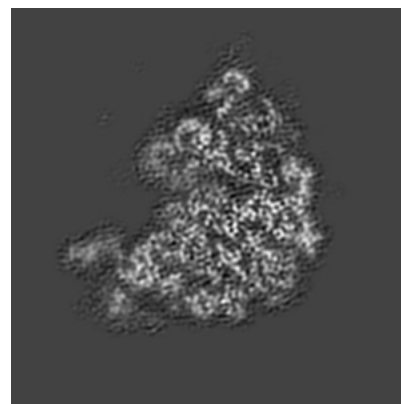
6.2.1 Primary map



X Index: 108



Y Index: 108

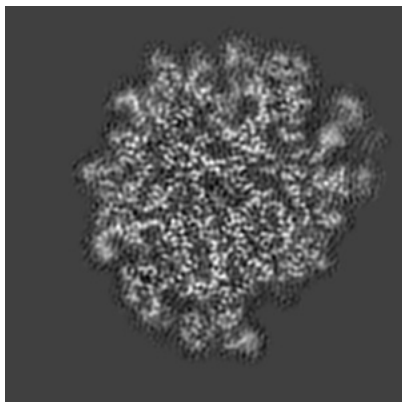


Z Index: 108

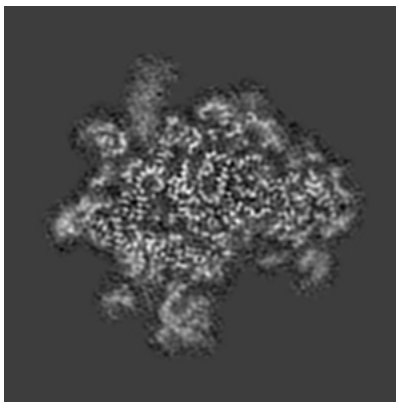
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

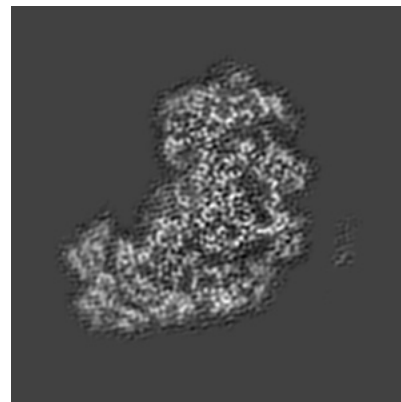
6.3.1 Primary map



X Index: 113



Y Index: 87



Z Index: 94

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

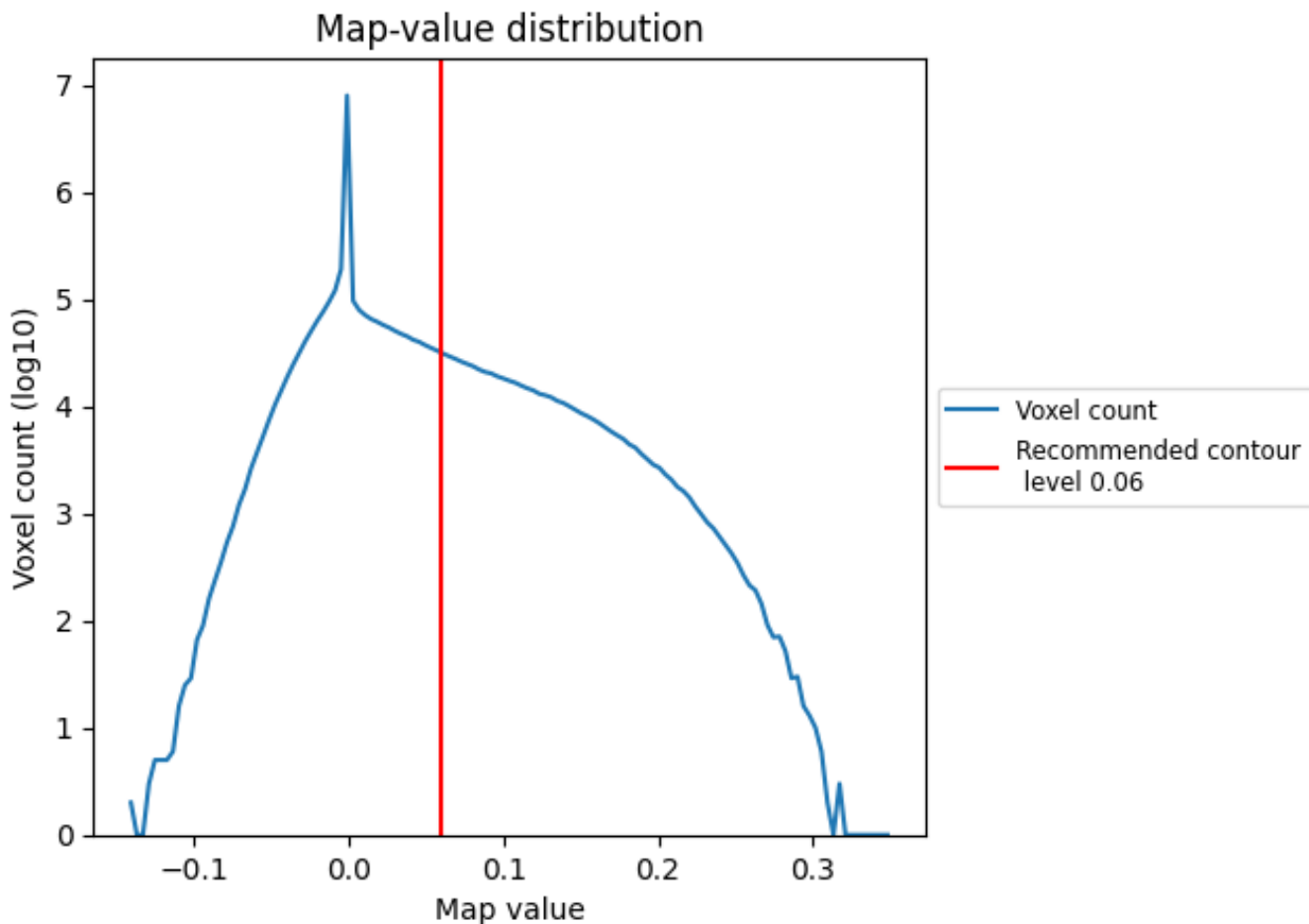
6.5 Mask visualisation

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

7 Map analysis [i](#)

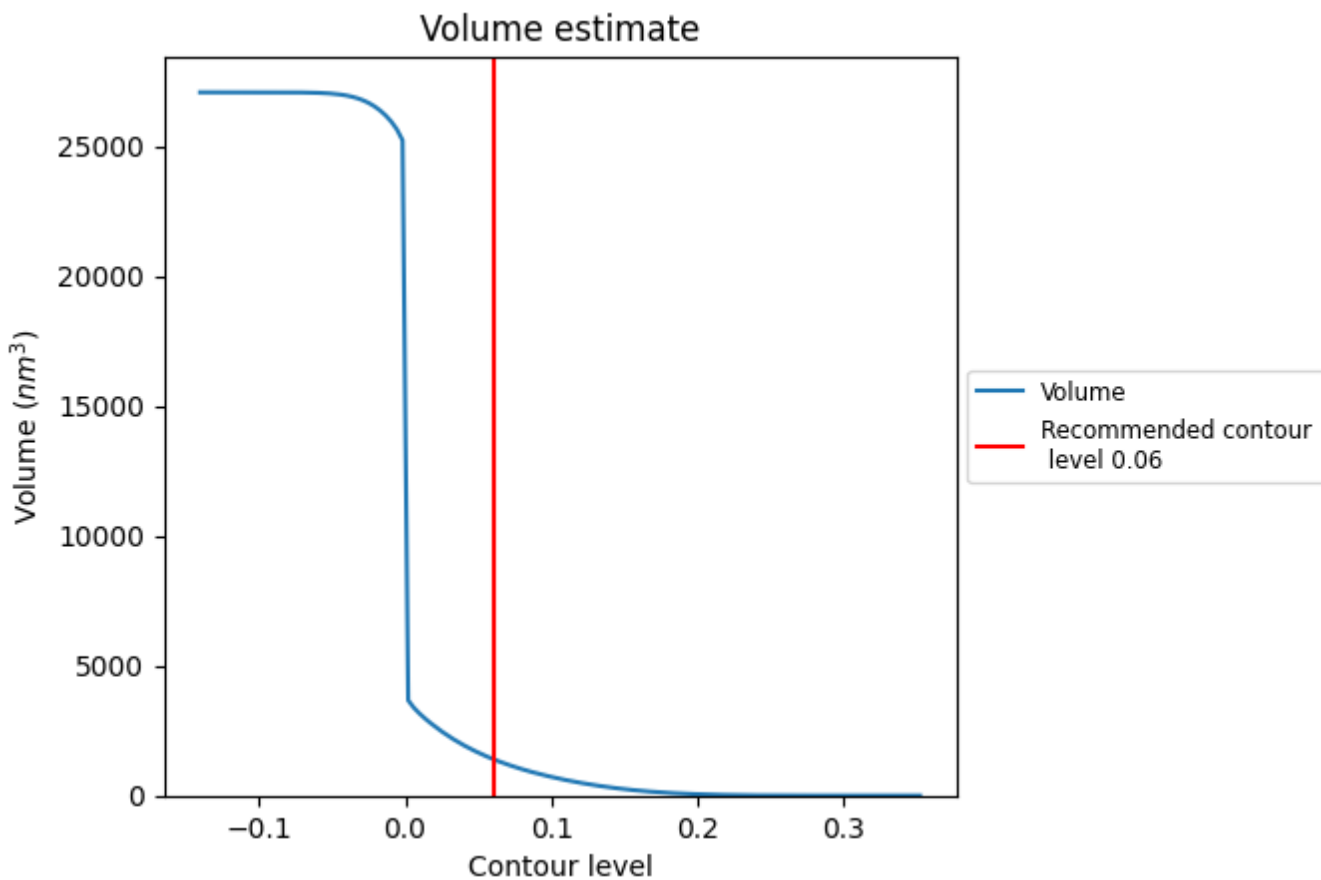
This section contains the results of statistical analysis of the map.

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.

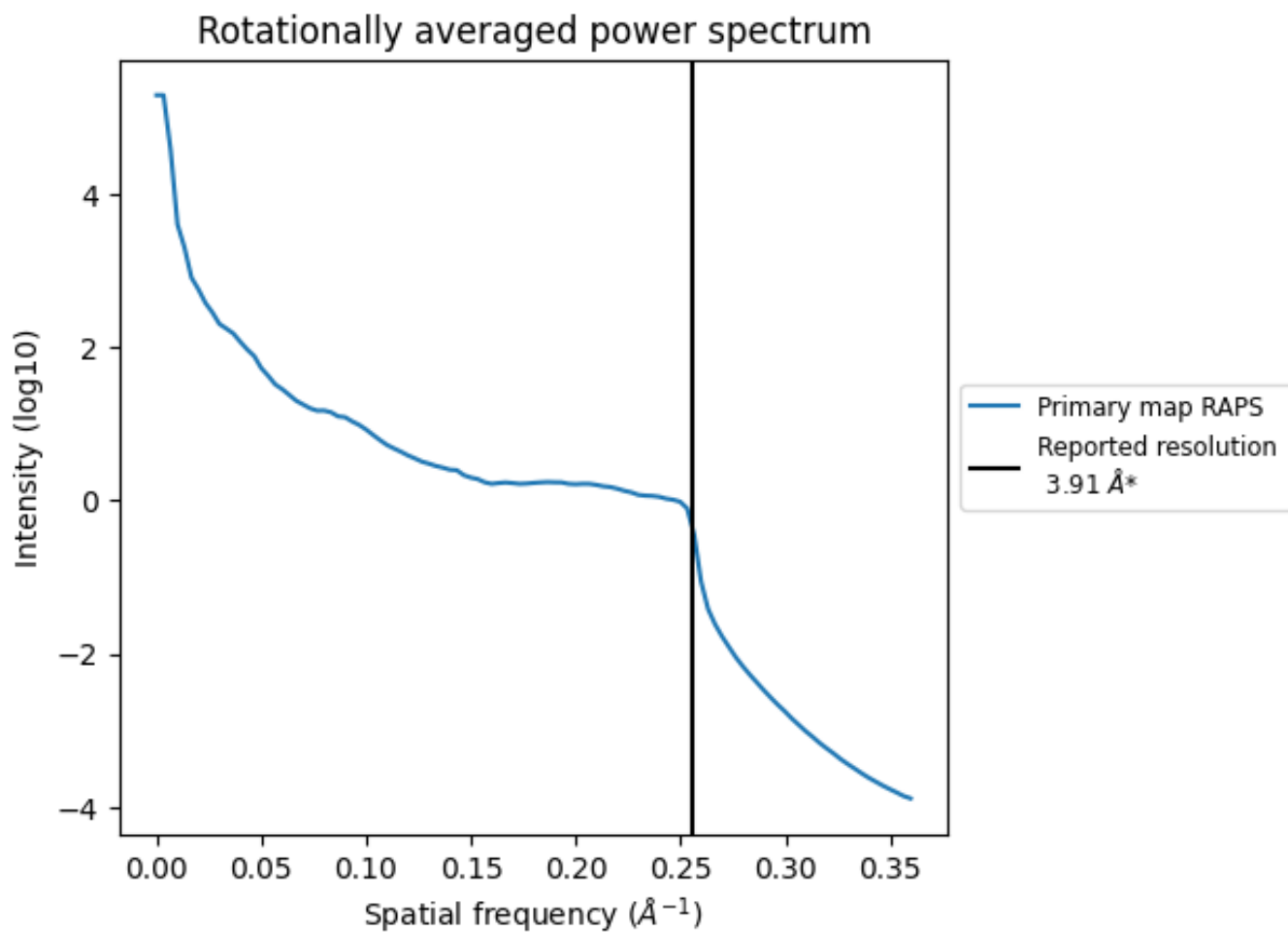
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1406 nm³; this corresponds to an approximate mass of 1270 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.256\AA^{-1}

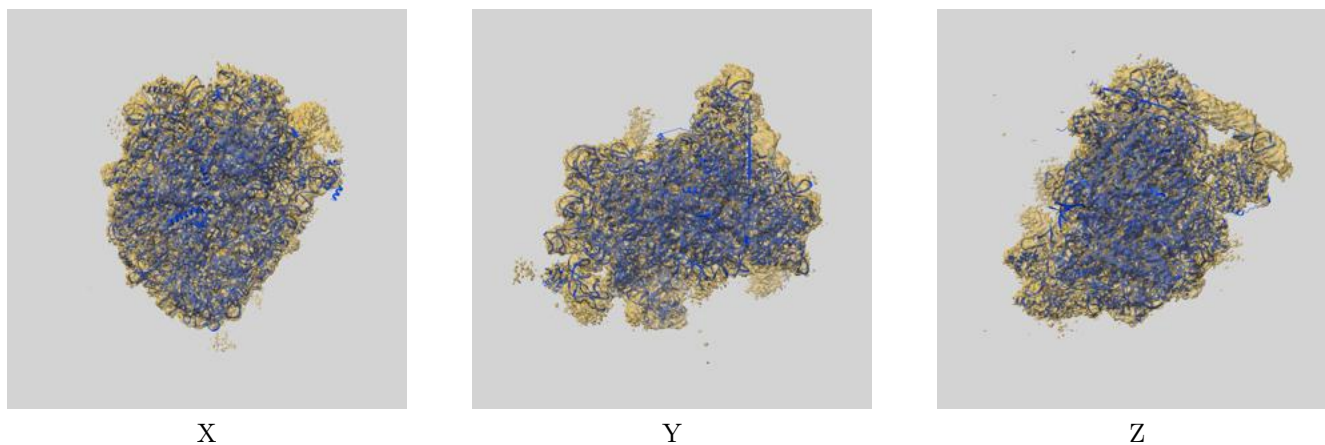
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

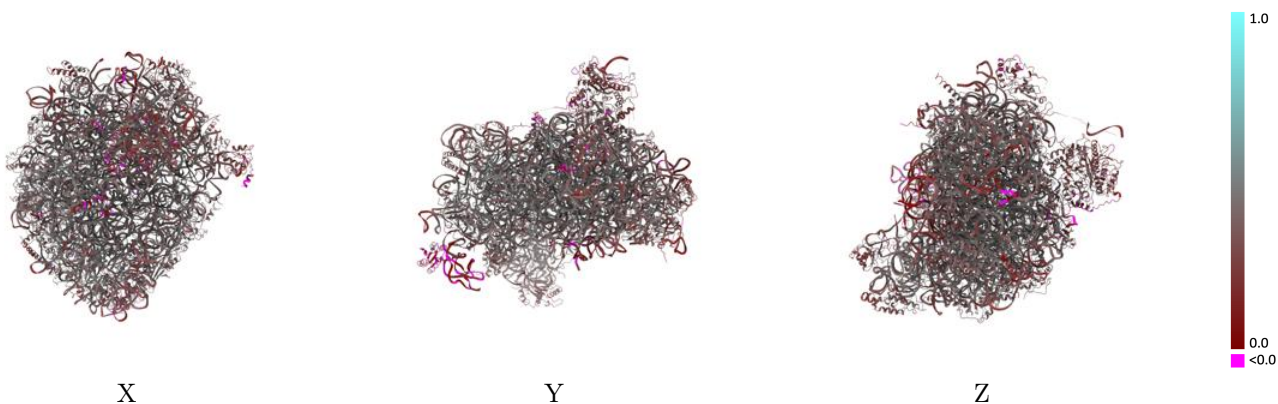
This section contains information regarding the fit between EMDB map EMD-3152 and PDB model 5APN. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



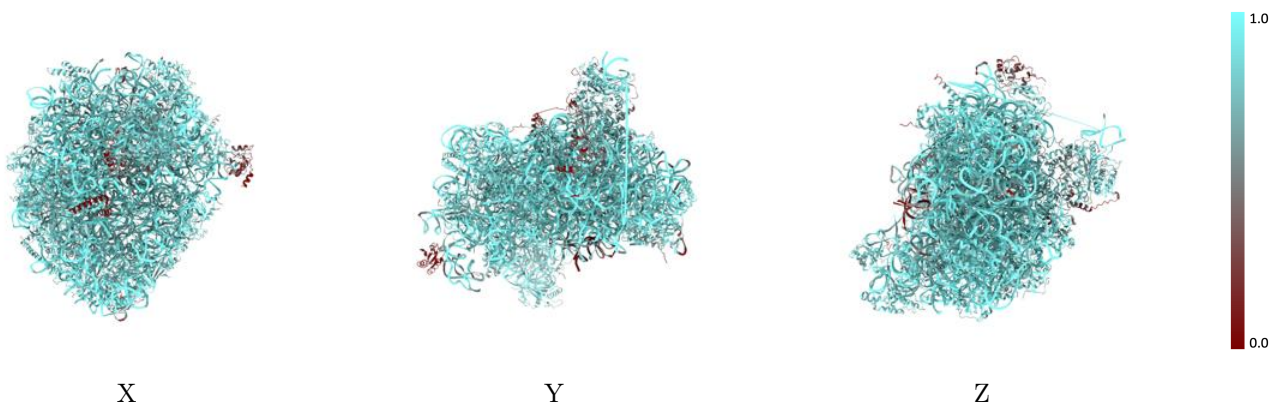
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



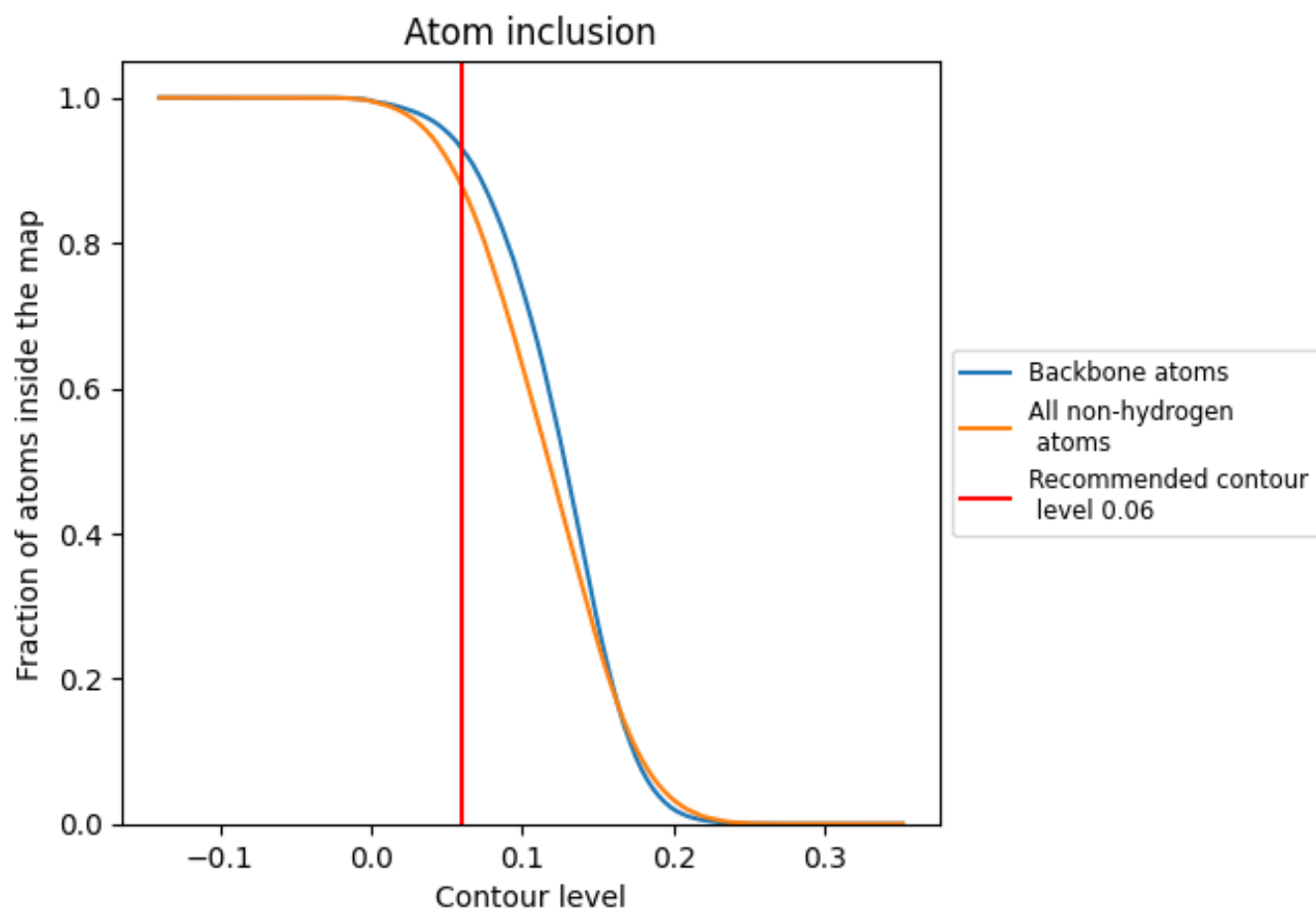
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8782	 0.3890
5	 0.9424	 0.3900
7	 0.9868	 0.3860
8	 0.9580	 0.4110
A	 0.8143	 0.4210
B	 0.8646	 0.4260
C	 0.8605	 0.4350
D	 0.8467	 0.3440
E	 0.8503	 0.3920
F	 0.8399	 0.4230
G	 0.8500	 0.3660
H	 0.8503	 0.4020
I	 0.8292	 0.4030
J	 0.8312	 0.3050
L	 0.8479	 0.4110
M	 0.8672	 0.4080
N	 0.7924	 0.4200
O	 0.8620	 0.4310
P	 0.8189	 0.4360
Q	 0.8509	 0.4350
R	 0.8300	 0.4090
S	 0.8572	 0.4310
T	 0.8347	 0.4310
U	 0.7796	 0.3730
V	 0.8173	 0.4070
W	 0.8297	 0.4050
X	 0.8068	 0.4340
Y	 0.8458	 0.4160
Z	 0.8497	 0.3590
a	 0.8689	 0.4330
b	 0.7810	 0.4000
c	 0.7616	 0.3400
d	 0.7760	 0.4280
e	 0.8145	 0.4370
f	 0.8563	 0.4520



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.7944	 0.4070
h	 0.8328	 0.3990
i	 0.7836	 0.3800
j	 0.8491	 0.4430
k	 0.7899	 0.3690
l	 0.7831	 0.4430
m	 0.8193	 0.3990
o	 0.7226	 0.3430
p	 0.8000	 0.3950
q	 0.1234	 0.0770
x	 0.7048	 0.3040
y	 0.4136	 0.2860
z	 0.1510	 0.0910