



wwPDB EM Validation Summary Report ⓘ

Dec 18, 2022 – 03:35 am GMT

PDB ID : 6ZTM
EMDB ID : EMD-11420
Title : E. coli 70S-RNAP expressome complex in collided state without NusG
Authors : Webster, M.W.; Takacs, M.; Weixlbaumer, A.
Deposited on : 2020-07-20
Resolution : 3.30 Å(reported)
Based on initial models : 6ALH, 4YBB

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

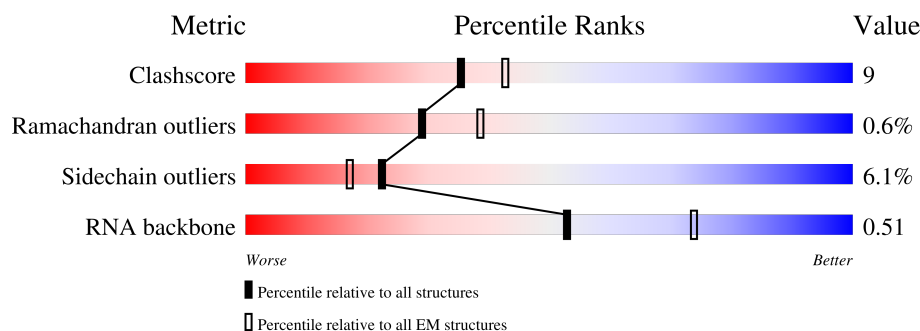
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.





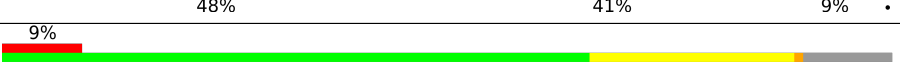
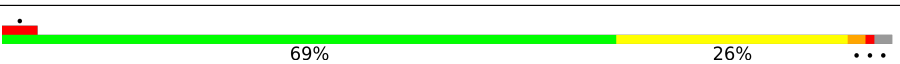


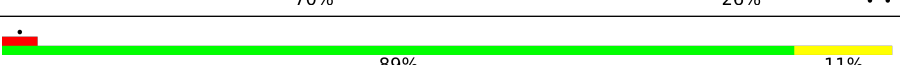



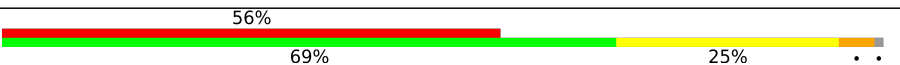
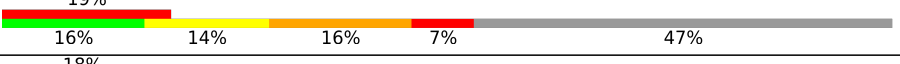

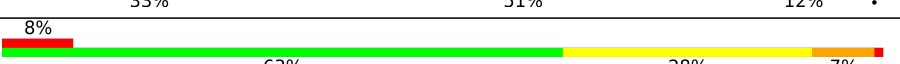

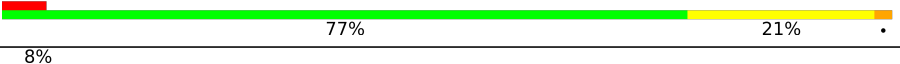


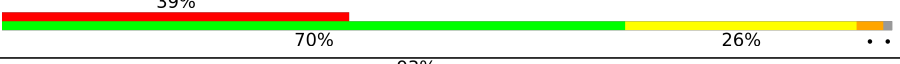
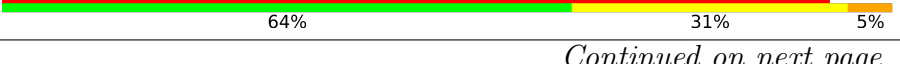



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	AA	1542	
2	AB	241	
3	AC	233	
4	AD	206	
5	AE	167	
6	AF	131	
7	AG	156	

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Mol	Chain	Length	Quality of chain
8	AH	130	
9	AI	130	
10	AJ	103	
11	AK	129	
12	AL	124	
13	AM	118	
14	AN	101	
15	AO	89	
16	AP	82	
17	AQ	84	
18	AR	75	
19	AS	92	
20	AT	87	
21	AU	71	
22	AV	57	
23	AW	77	
24	AX	76	
25	BA	2904	
26	BB	120	
27	BC	273	
28	BD	209	
29	BE	201	
30	BF	179	
31	BG	177	
32	BH	149	

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Mol	Chain	Length	Quality of chain
33	BK	142	
34	BL	123	
35	BM	144	
36	BN	136	
37	BO	127	
38	BP	117	
39	BQ	115	
40	BR	118	
41	BS	103	
42	BT	110	
43	BU	100	
44	BV	104	
45	BW	94	
46	BX	85	
47	BY	78	
48	BZ	63	
49	B1	59	
50	B2	57	
51	B3	55	
52	B4	46	
53	B5	65	
54	B6	50	
55	CN	39	
56	CT	39	
57	CA	329	

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Mol	Chain	Length	Quality of chain
57	CB	329	<div><div></div><div>50%</div><div>56%</div><div>9%</div><div>•</div><div>33%</div></div>
58	CC	1342	<div><div></div><div>28%</div><div>76%</div><div>18%</div><div>•</div><div>•</div></div>
59	CD	1407	<div><div></div><div>41%</div><div>77%</div><div>17%</div><div>•</div><div>5%</div></div>

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 171689 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1533	Total	C	N	O	P	0	0
			32907	14682	6037	10655	1533		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	226	Total	C	N	O	S	0	0
			1765	1116	317	324	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	209	Total	C	N	O	S	0	0
			1640	1038	308	291	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	156	Total	C	N	O	S	0	0
			1148	715	217	210	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	9	CYS	GLY	conflict	UNP A0A090BZW5

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	128	Total	C	N	O	S	0	0
			1031	639	207	182	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	100	Total	C	N	O	S	0	0
			800	500	153	146	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	116	Total	C	N	O	S	0	0
			866	534	170	159	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	54	Total	C	N	O	0	0
			443	281	81	81		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	30	Total	C	N	O	P	0	0
			636	285	115	206	30		

- Molecule 23 is a RNA chain called tRNA(fmet) P-site.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AW	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

- Molecule 24 is a RNA chain called Phe-NH-tRNA(Phe) A-site.

Mol	Chain	Residues	Atoms					AltConf	Trace	
24	AX	76	Total	C	N	O	P	S	0	0
			1624	724	290	533	76	1		

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	2901	Total	C	N	O	P	0	0
			62290	27795	11458	20136	2901		

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BF	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BH	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BK	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BL	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BM	144	Total	C	N	O	S	0	0
			1052	653	207	190	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BM	77	VAL	ILE	conflict	UNP P02413

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BN	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BO	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BP	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BQ	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BR	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BS	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BT	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BU	95	Total	C	N	O	S	0	0
			757	479	141	135	2		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BV	103	Total	C	N	O	0	0
			789	498	148	143		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BW	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BX	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BY	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BZ	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 50 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B2	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	B3	53	Total	C	N	O	0	0
			436	281	80	75		

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B4	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 53 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B5	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B6	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 55 is a DNA chain called Non-template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CN	30	Total	C	N	O	P	0	0
			618	294	114	180	30		

- Molecule 56 is a DNA chain called Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CT	30	Total	C	N	O	P	0	0
			606	288	105	183	30		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CA	229	Total	C	N	O	S	0	0
			1775	1106	313	350	6		
57	CB	219	Total	C	N	O	S	0	0
			1684	1051	295	332	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CC	1320	Total	C	N	O	S	0	0
			10415	6535	1815	2021	44		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CD	1333	Total	C	N	O	S	0	0
			10375	6518	1851	1956	50		

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

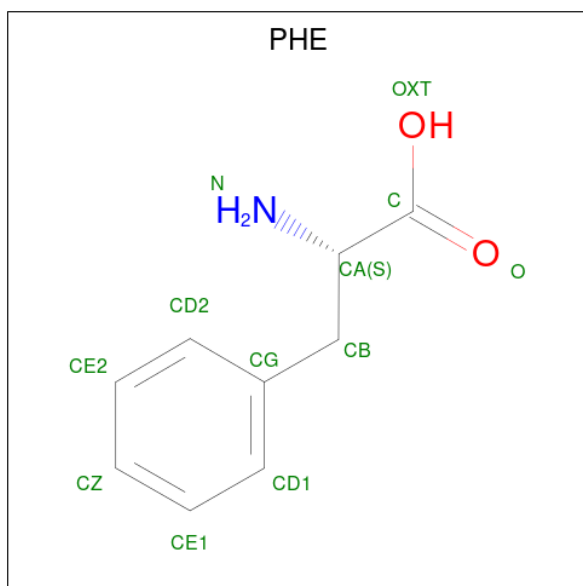
Mol	Chain	Residues	Atoms		AltConf
60	AA	119	Total	Mg	0
			119	119	
60	AW	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
60	BA	294	Total	Mg	0
			294	294	
60	BB	2	Total	Mg	0
			2	2	
60	BC	1	Total	Mg	0
			1	1	
60	BO	1	Total	Mg	0
			1	1	
60	B2	1	Total	Mg	0
			1	1	
60	CD	1	Total	Mg	0
			1	1	

- Molecule 61 is PHENYLALANINE (three-letter code: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
61	AX	1	Total	C	N	O	0
			11	9	1	1	

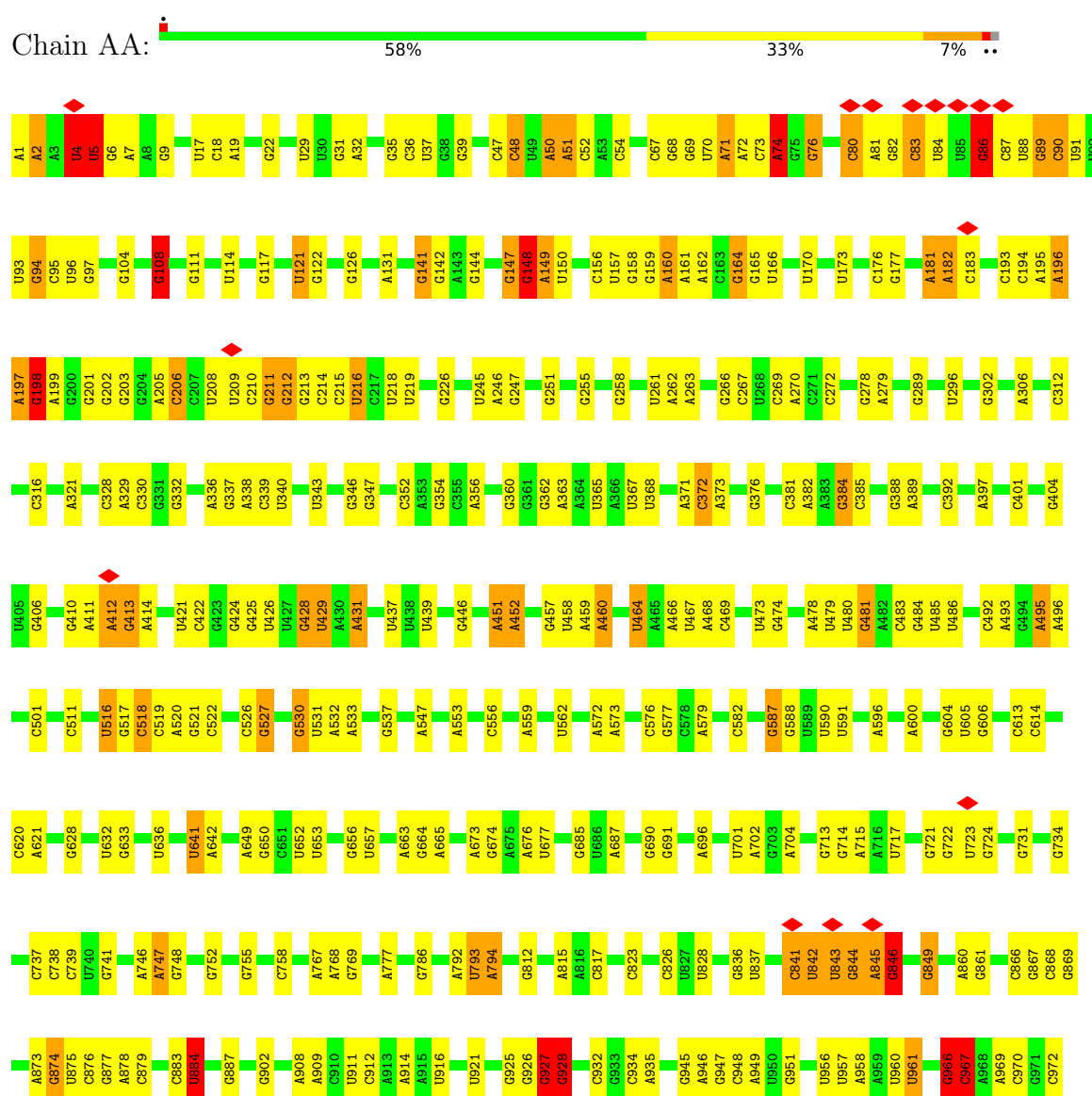
- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

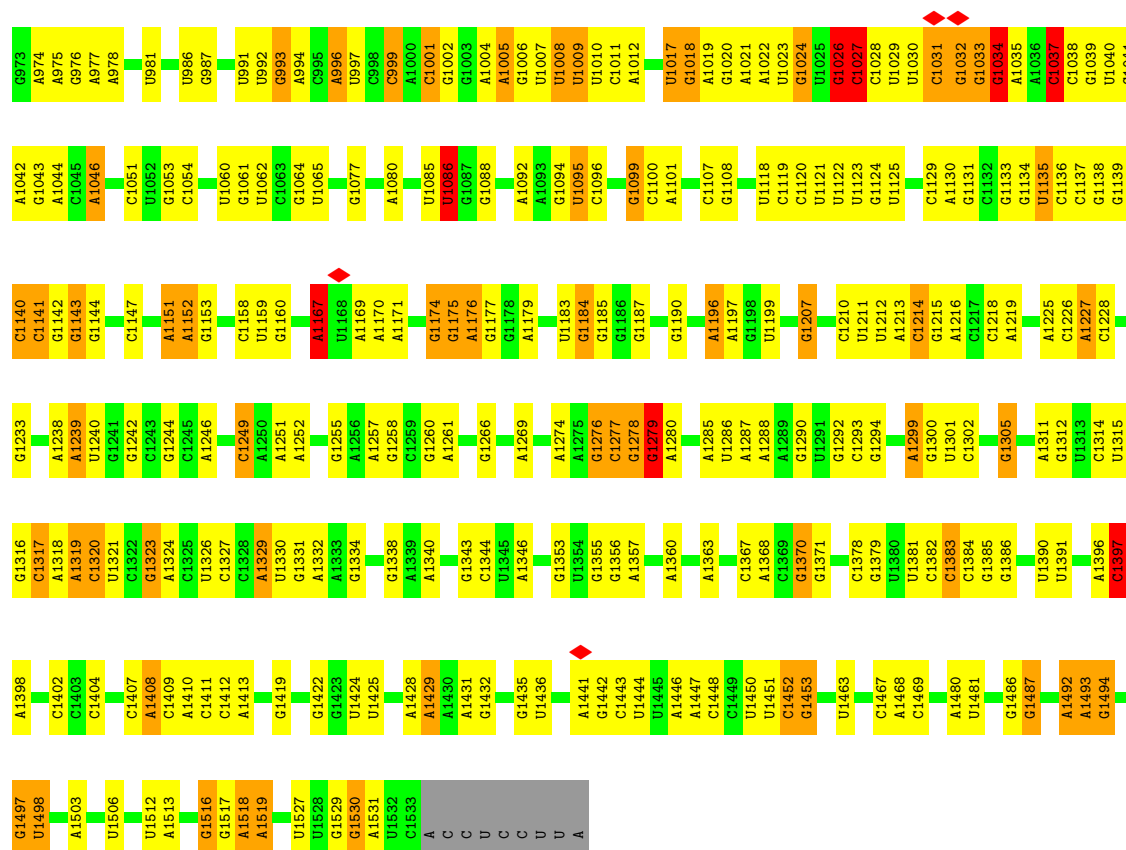
Mol	Chain	Residues	Atoms		AltConf
62	B6	1	Total	Zn	0
			1	1	
62	CD	2	Total	Zn	0
			2	2	

3 Residue-property plots

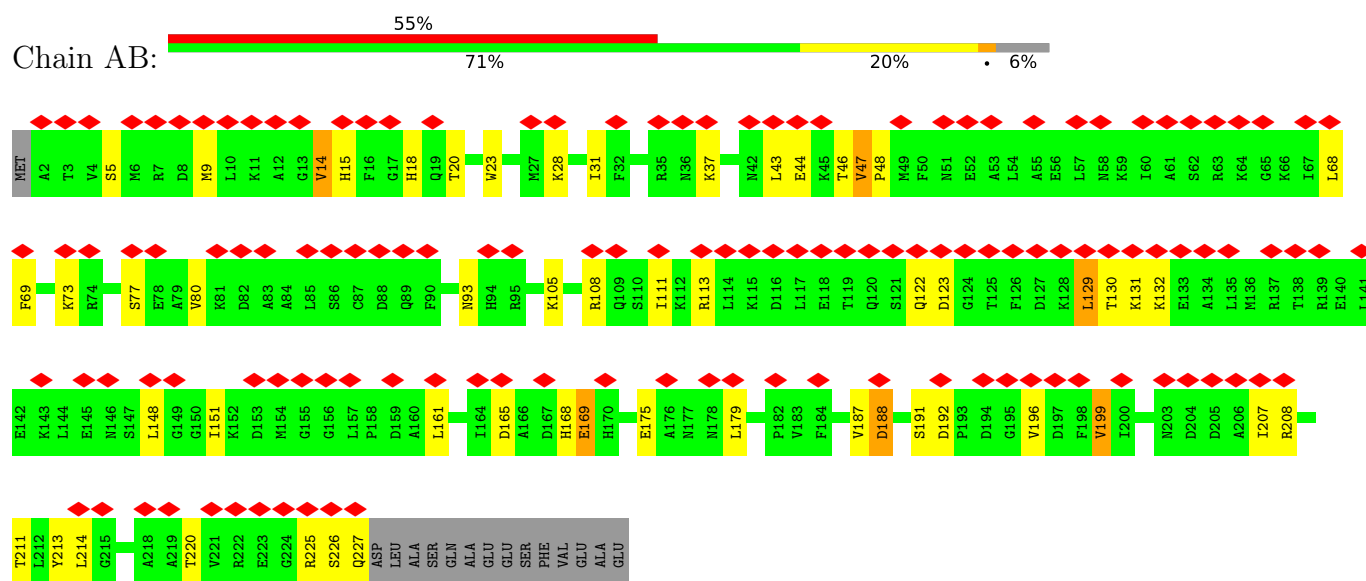
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA

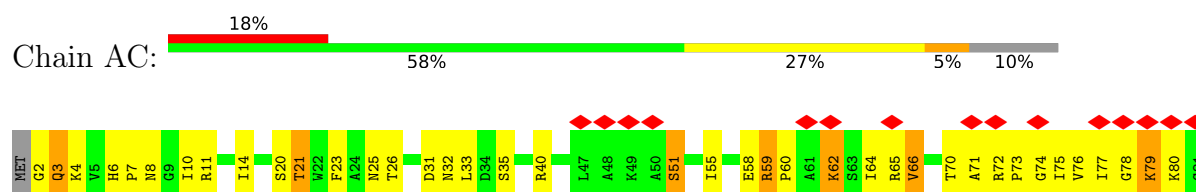


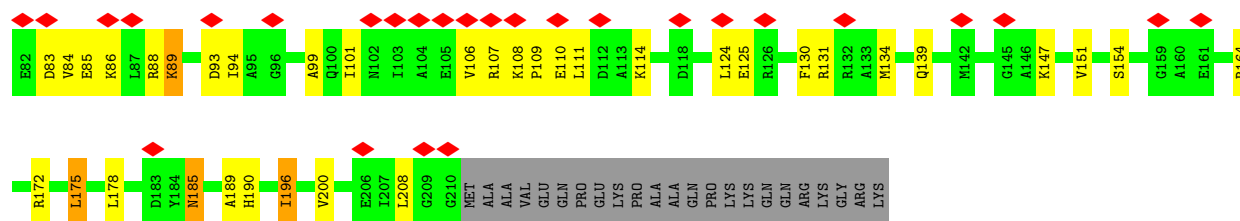


• Molecule 2: 30S ribosomal protein S2

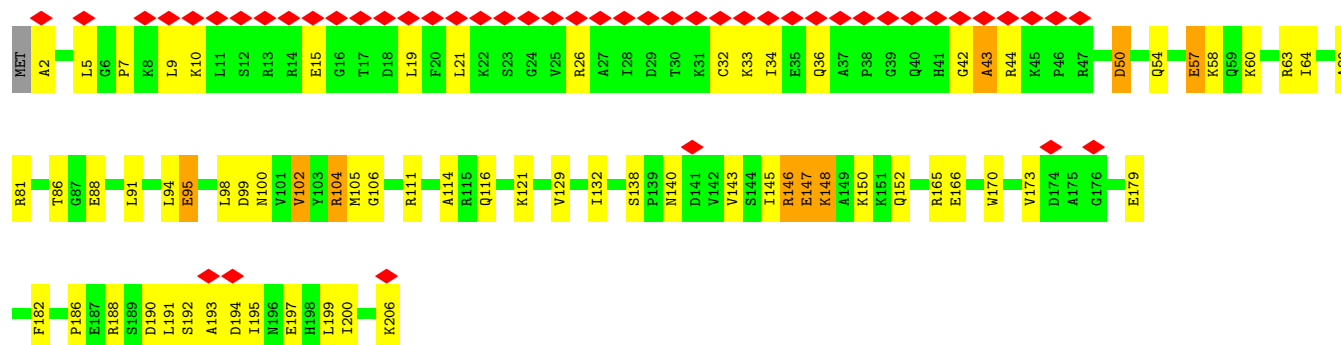


• Molecule 3: 30S ribosomal protein S3

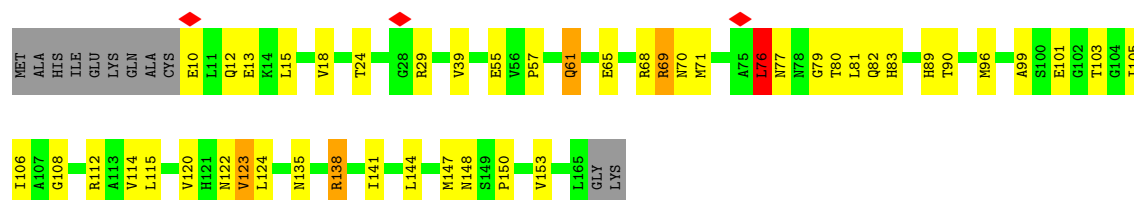




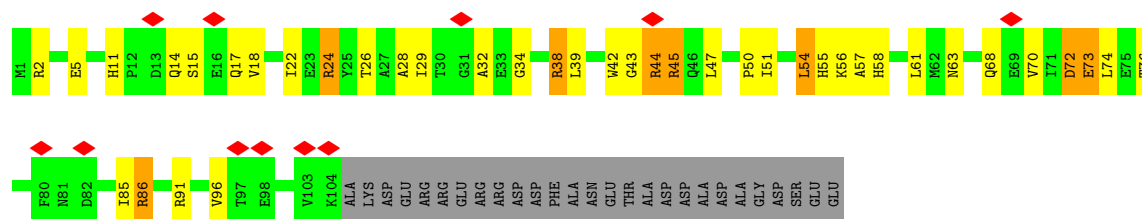
• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

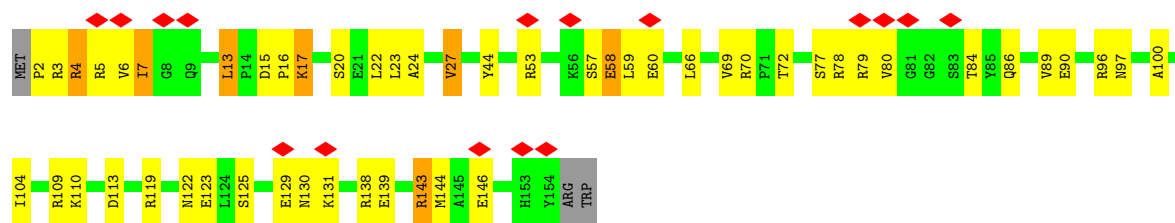


• Molecule 6: 30S ribosomal protein S6

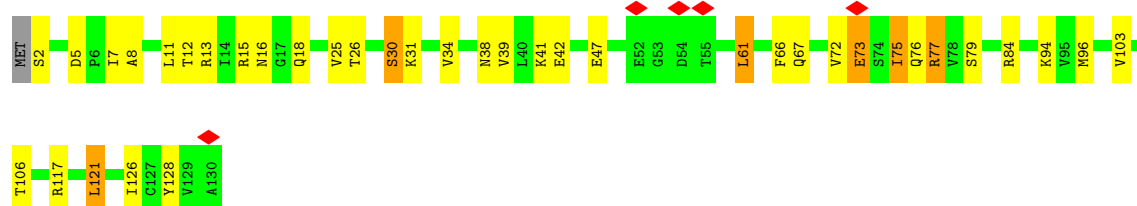


• Molecule 7: 30S ribosomal protein S7

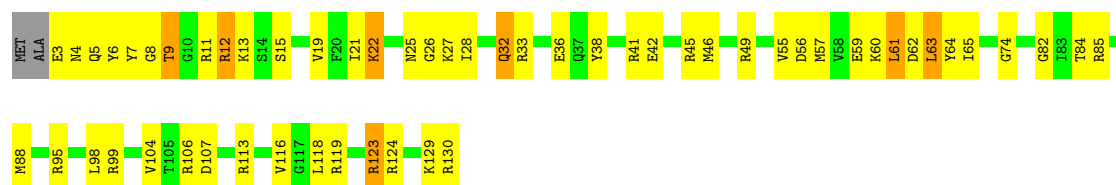




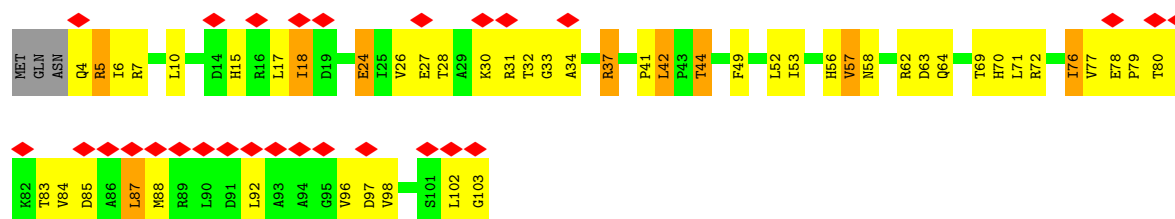
• Molecule 8: 30S ribosomal protein S8



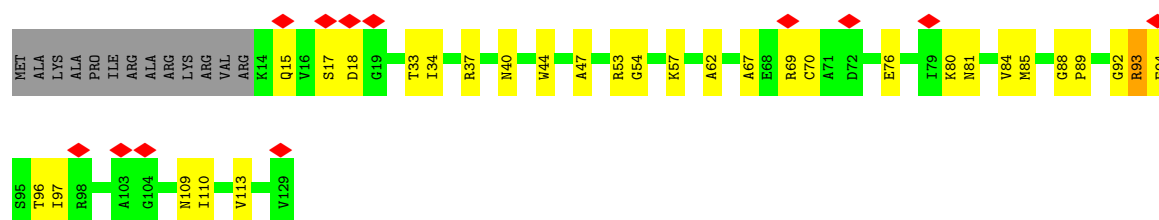
• Molecule 9: 30S ribosomal protein S9



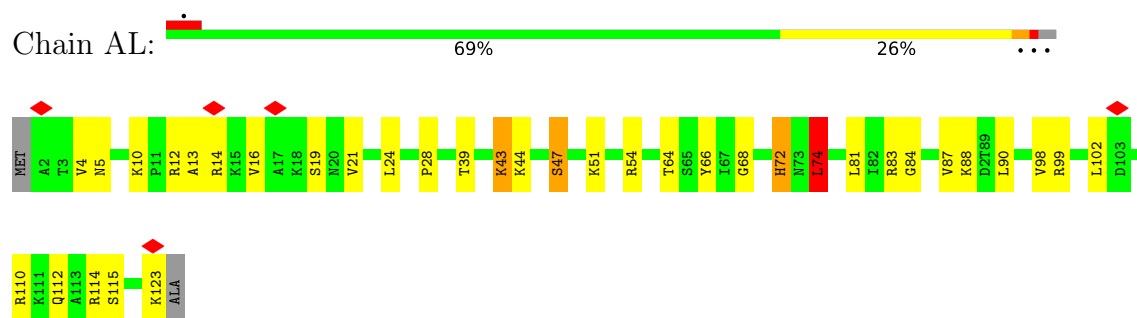
• Molecule 10: 30S ribosomal protein S10



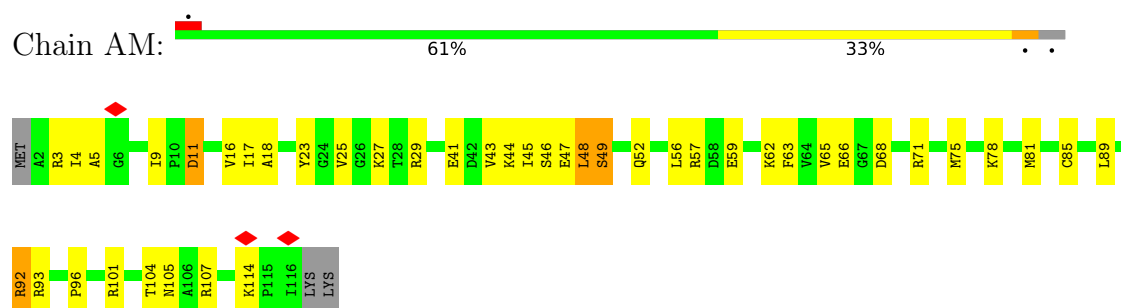
• Molecule 11: 30S ribosomal protein S11



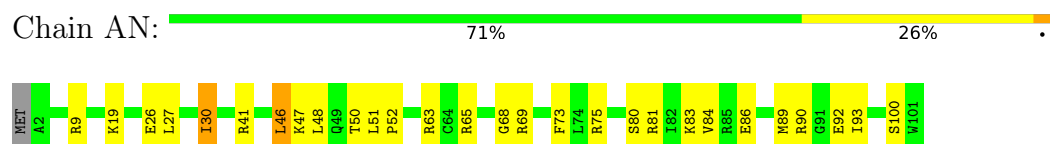
- Molecule 12: 30S ribosomal protein S12



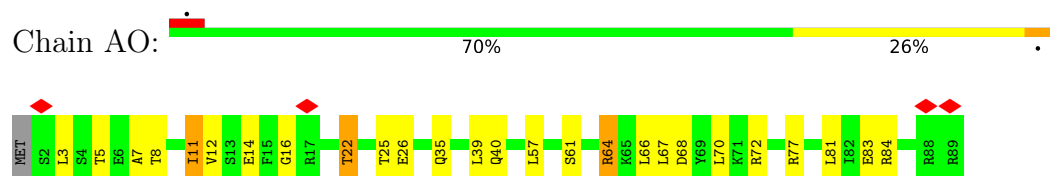
- Molecule 13: 30S ribosomal protein S13



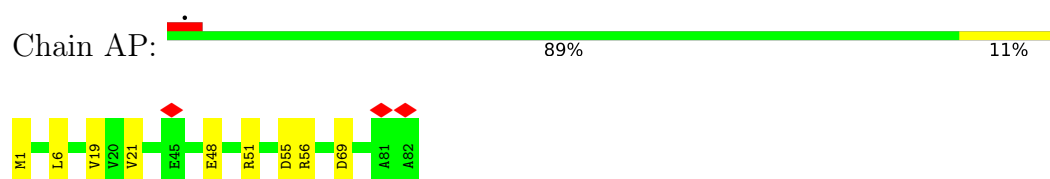
- Molecule 14: 30S ribosomal protein S14



- Molecule 15: 30S ribosomal protein S15

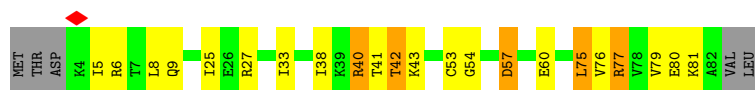


- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17





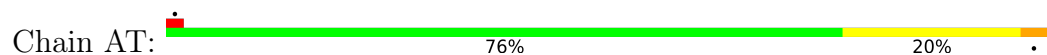
- Molecule 18: 30S ribosomal protein S18



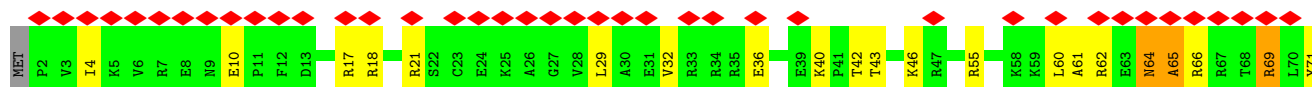
- Molecule 19: 30S ribosomal protein S19



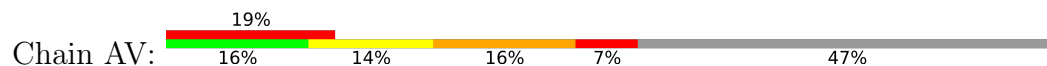
- Molecule 20: 30S ribosomal protein S20



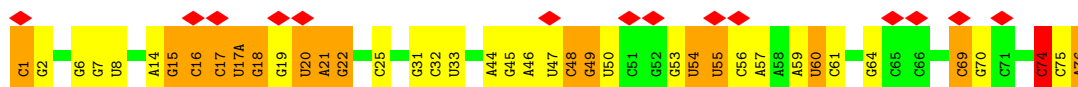
- Molecule 21: 30S ribosomal protein S21



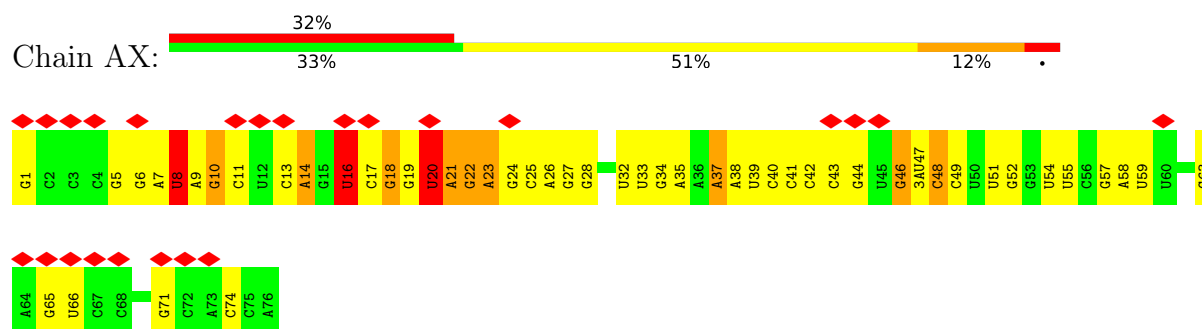
- Molecule 22: mRNA



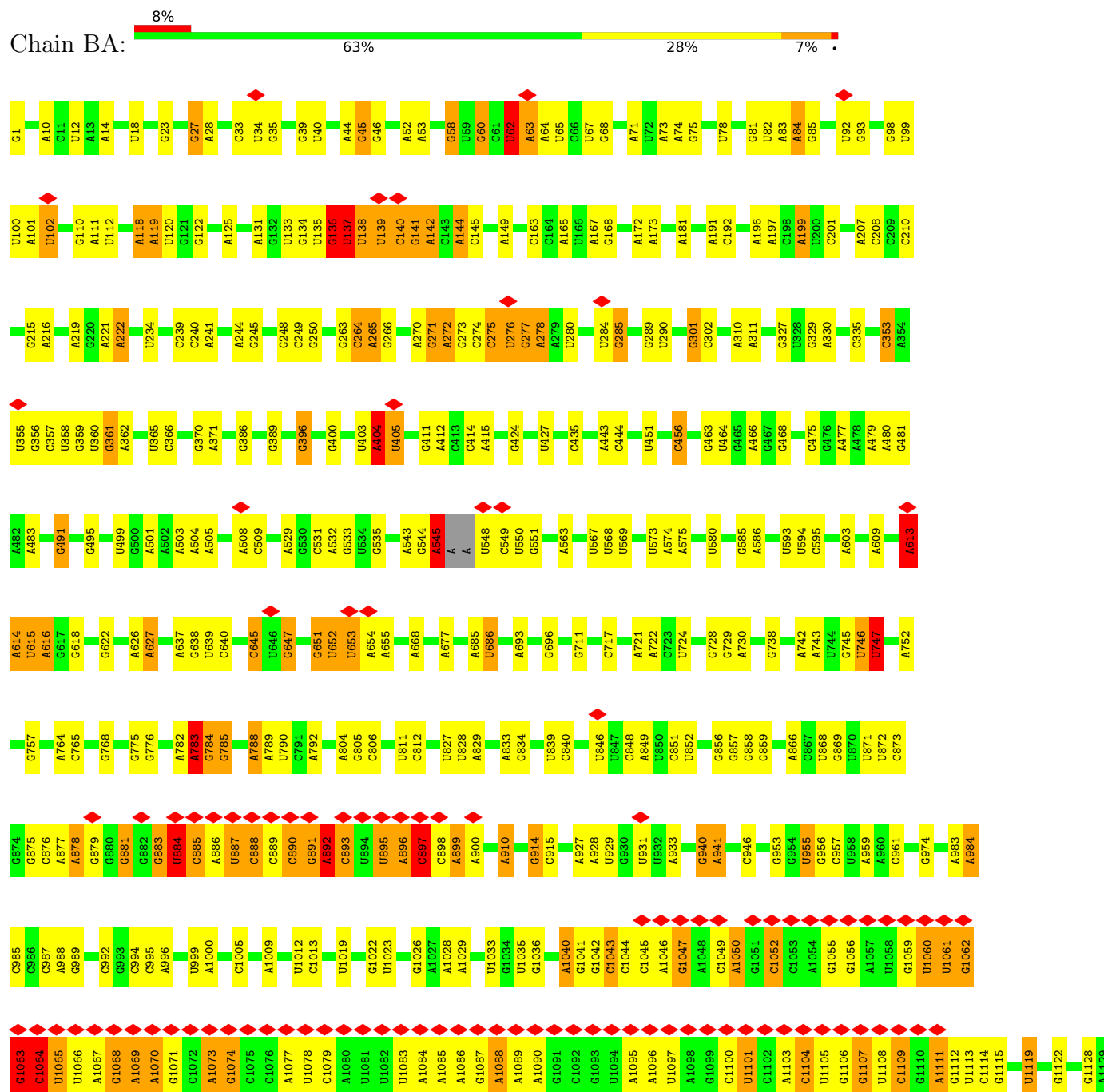
- Molecule 23: tRNA(fmet) P-site

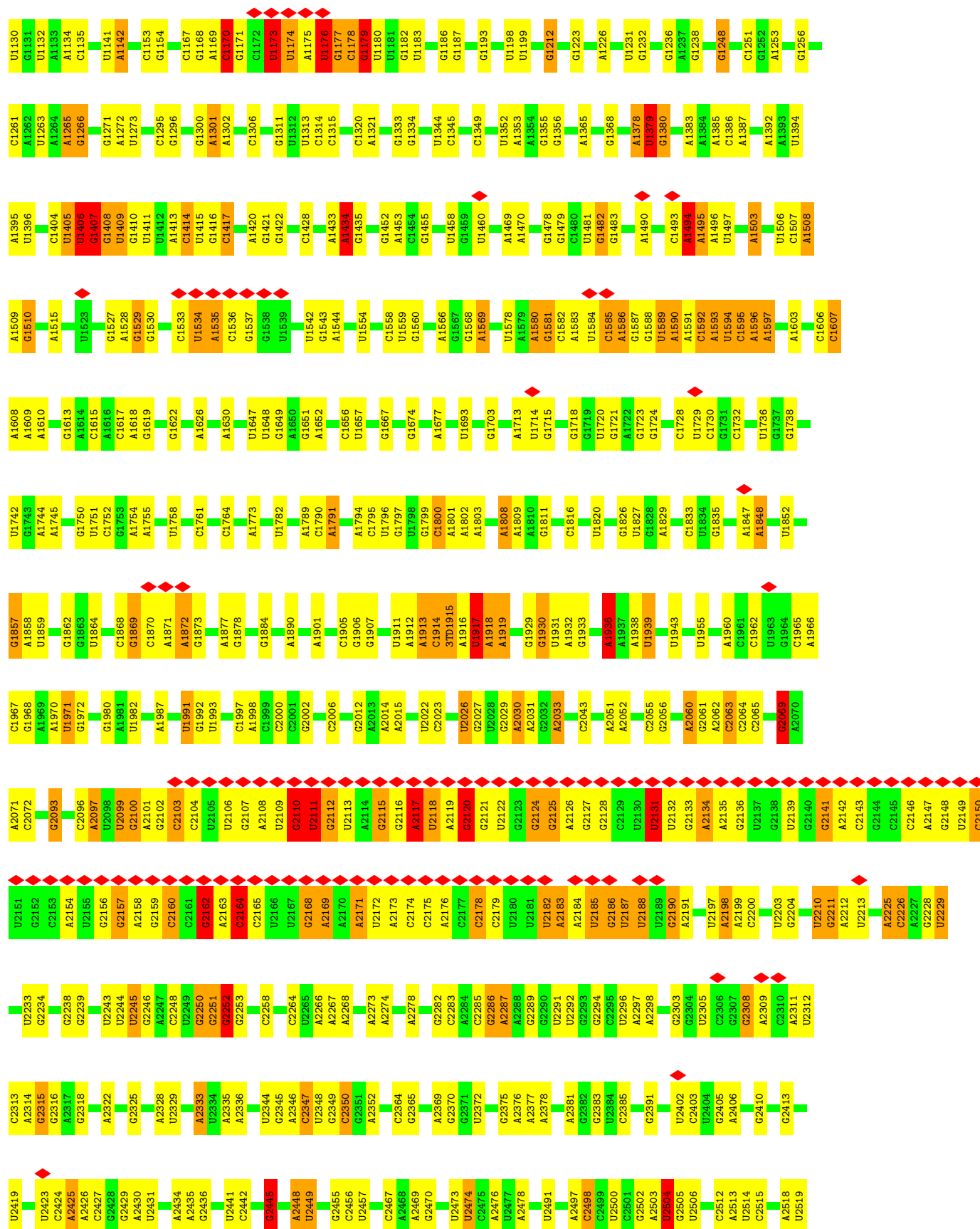


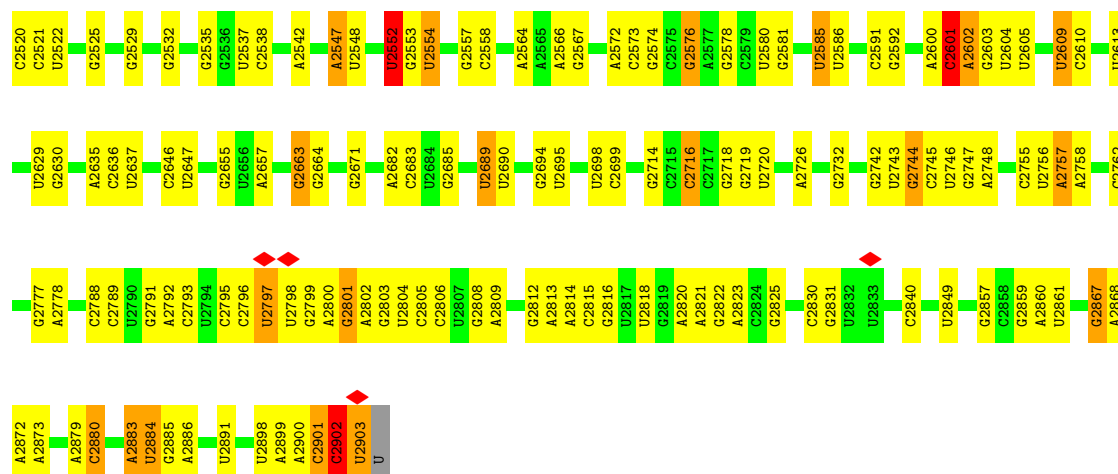
- Molecule 24: Phe-NH-tRNA(Phe) A-site



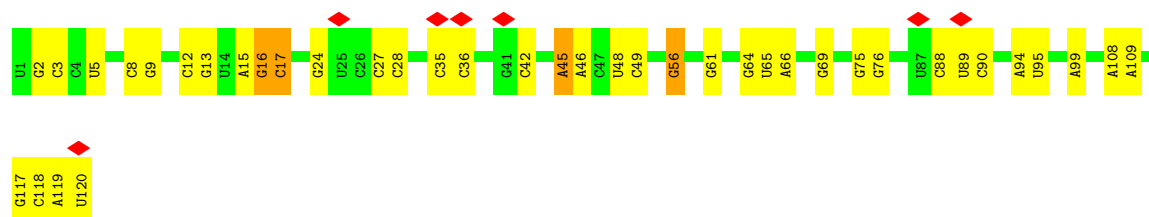
• Molecule 25: 23S ribosomal RNA



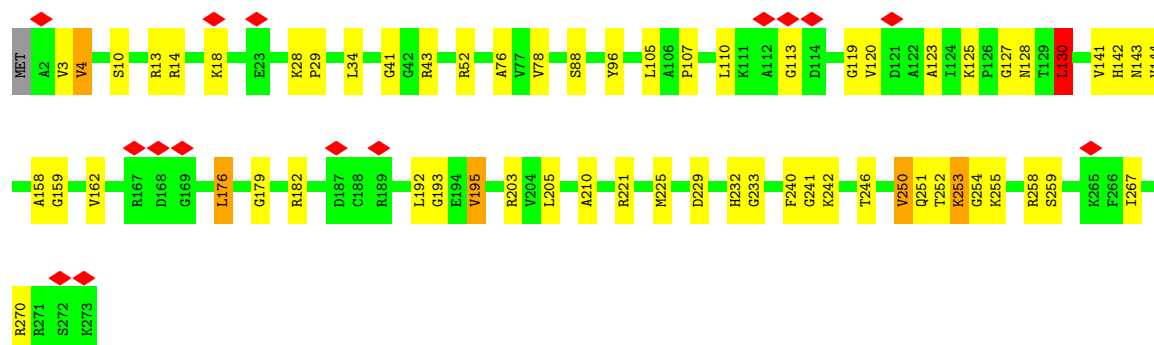
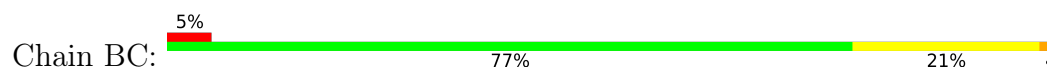




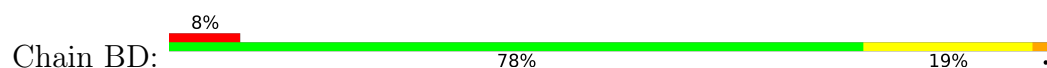
• Molecule 26: 5S ribosomal RNA

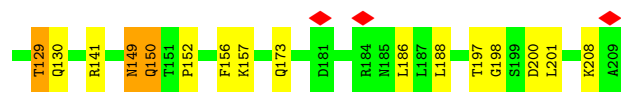


• Molecule 27: 50S ribosomal protein L2

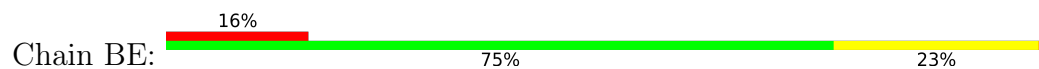


• Molecule 28: 50S ribosomal protein L3

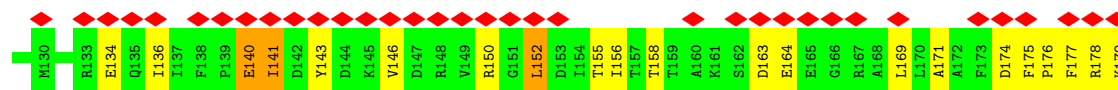
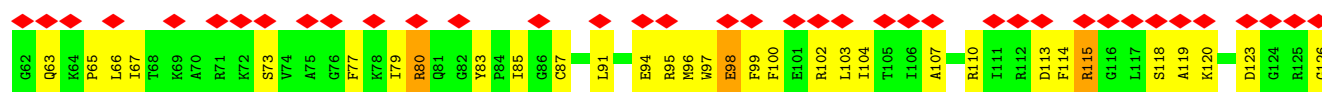




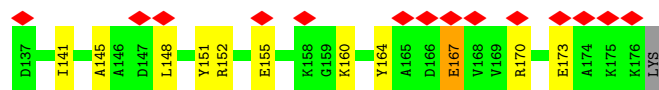
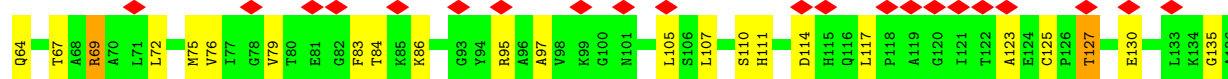
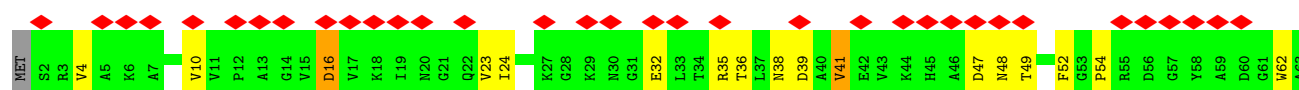
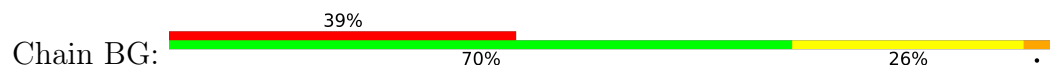
- Molecule 29: 50S ribosomal protein L4



- Molecule 30: 50S ribosomal protein L5

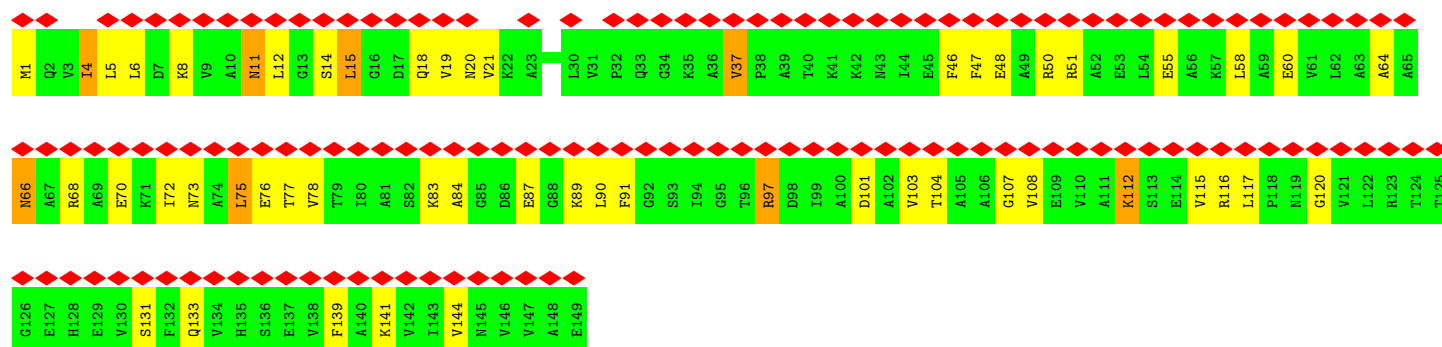


- Molecule 31: 50S ribosomal protein L6

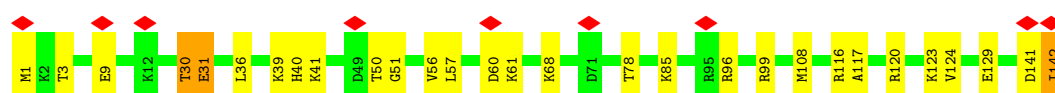
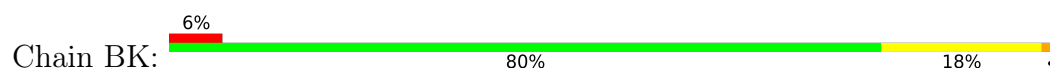


- Molecule 32: 50S ribosomal protein L9

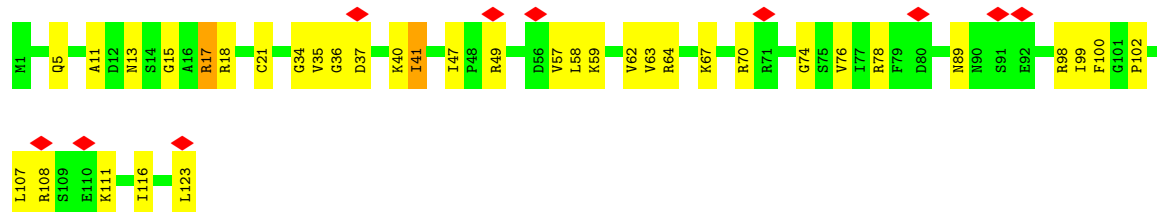




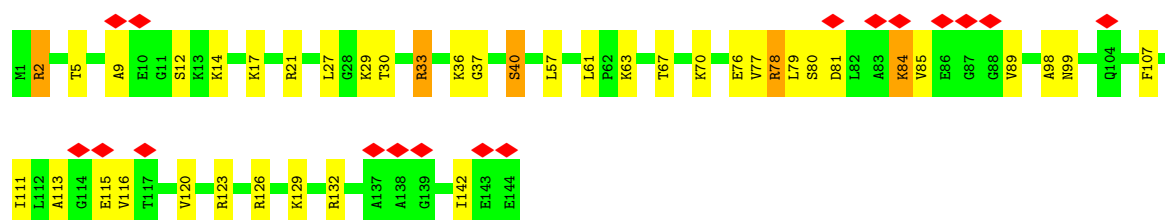
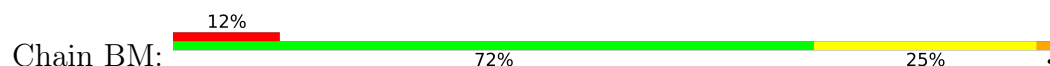
• Molecule 33: 50S ribosomal protein L13



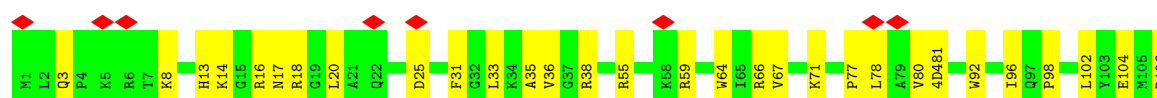
• Molecule 34: 50S ribosomal protein L14



• Molecule 35: 50S ribosomal protein L15

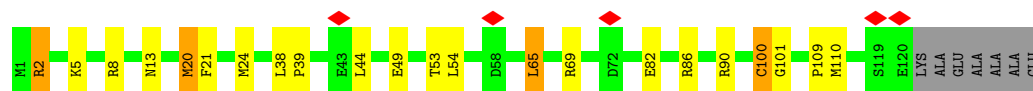
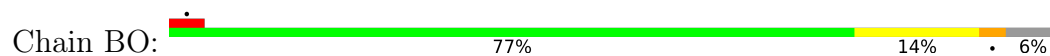


• Molecule 36: 50S ribosomal protein L16

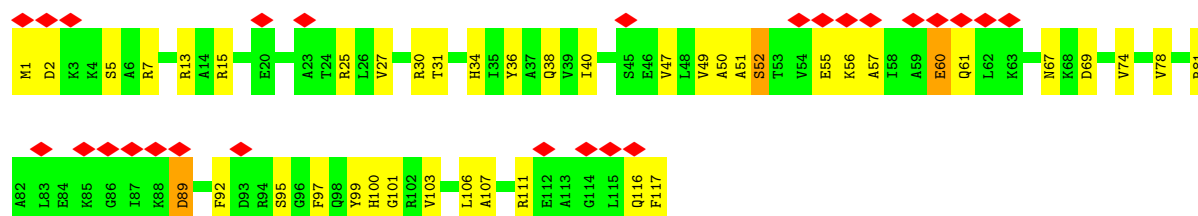




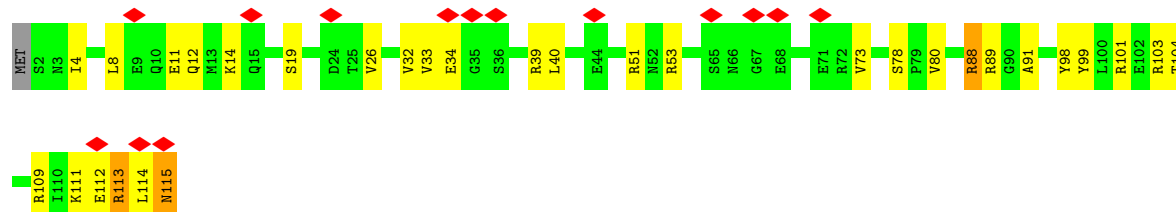
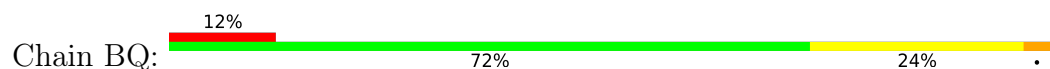
- Molecule 37: 50S ribosomal protein L17



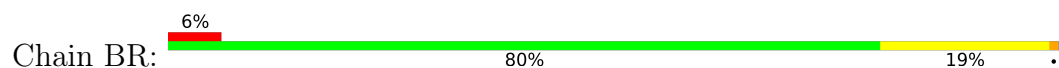
- Molecule 38: 50S ribosomal protein L18



- Molecule 39: 50S ribosomal protein L19



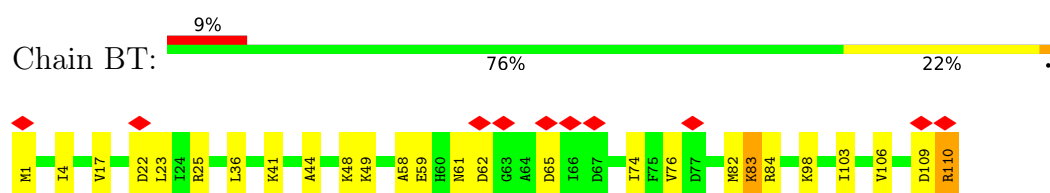
- Molecule 40: 50S ribosomal protein L20



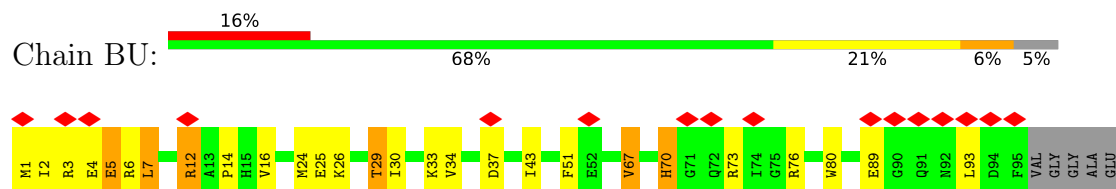
- Molecule 41: 50S ribosomal protein L21



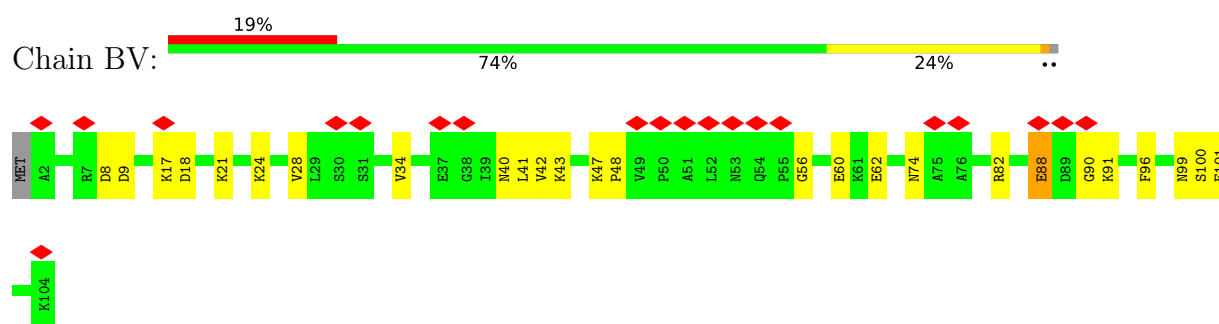
- Molecule 42: 50S ribosomal protein L22



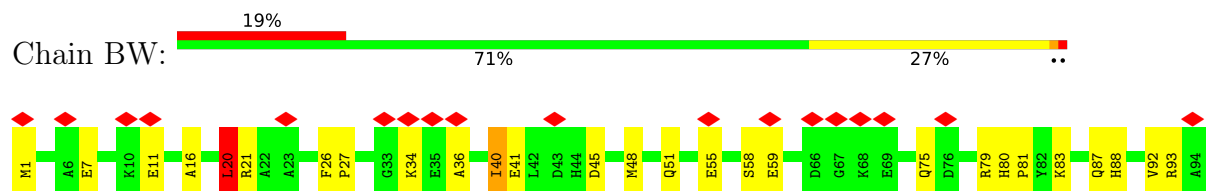
- Molecule 43: 50S ribosomal protein L23



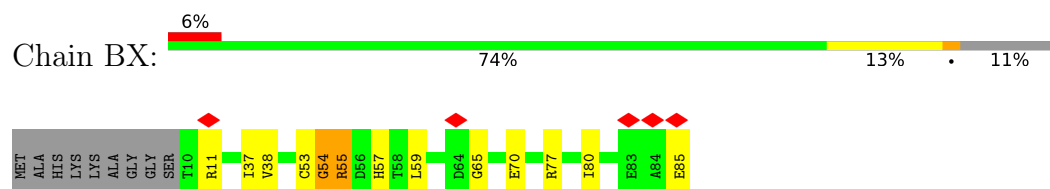
- Molecule 44: 50S ribosomal protein L24



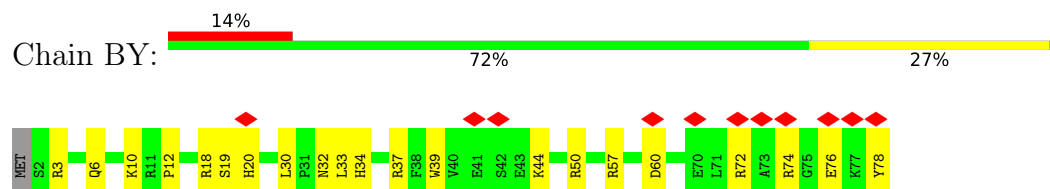
- Molecule 45: 50S ribosomal protein L25



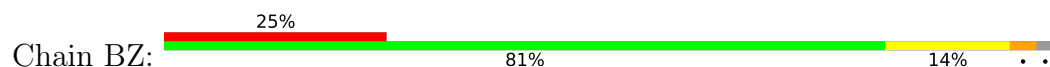
- Molecule 46: 50S ribosomal protein L27

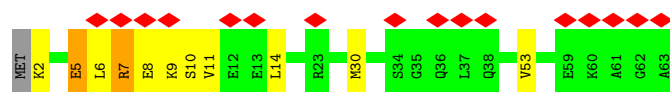


- Molecule 47: 50S ribosomal protein L28



- Molecule 48: 50S ribosomal protein L29

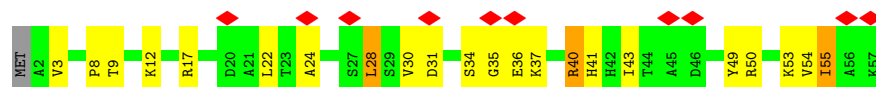




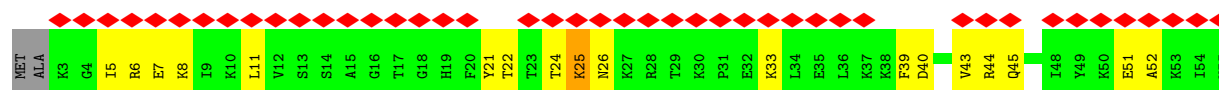
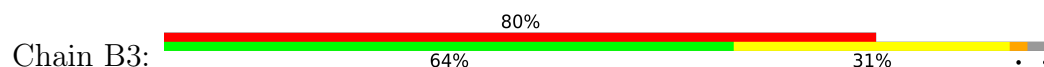
- Molecule 49: 50S ribosomal protein L30



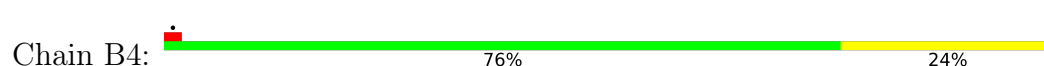
- Molecule 50: 50S ribosomal protein L32



- Molecule 51: 50S ribosomal protein L33



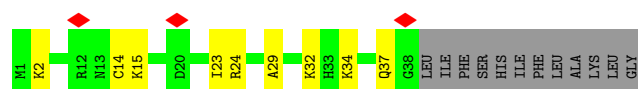
- Molecule 52: 50S ribosomal protein L34



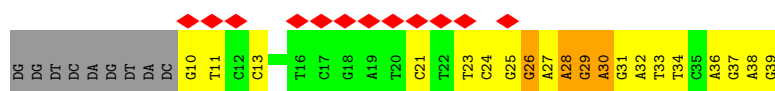
- Molecule 53: 50S ribosomal protein L35



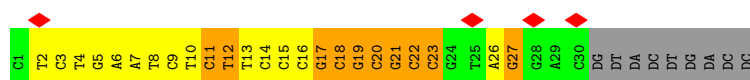
- Molecule 54: 50S ribosomal protein L36



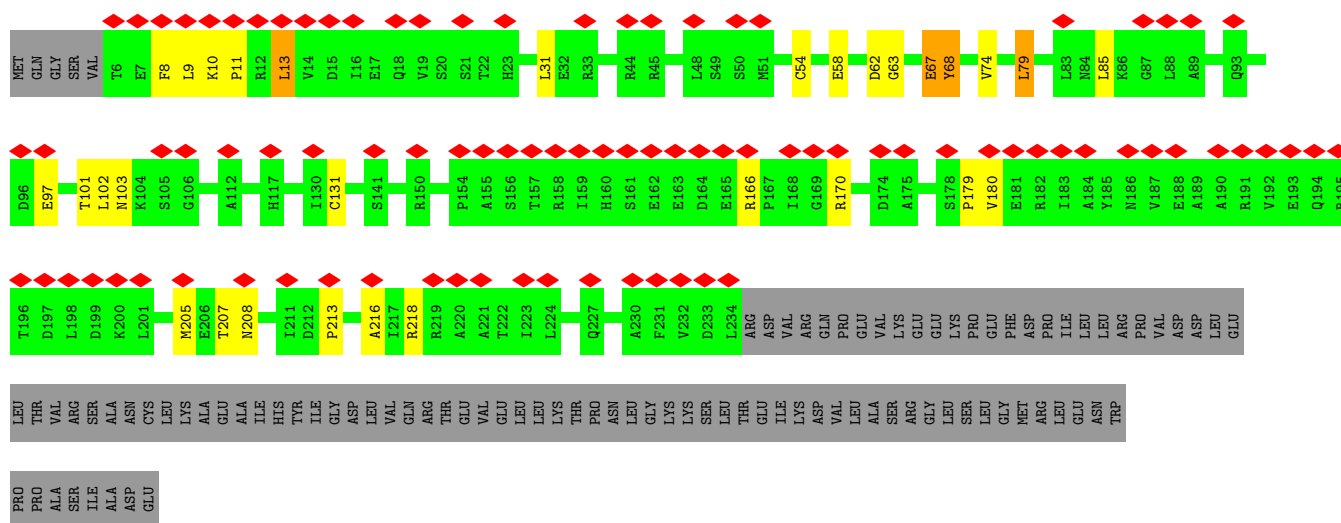
- Molecule 55: Non-template DNA strand



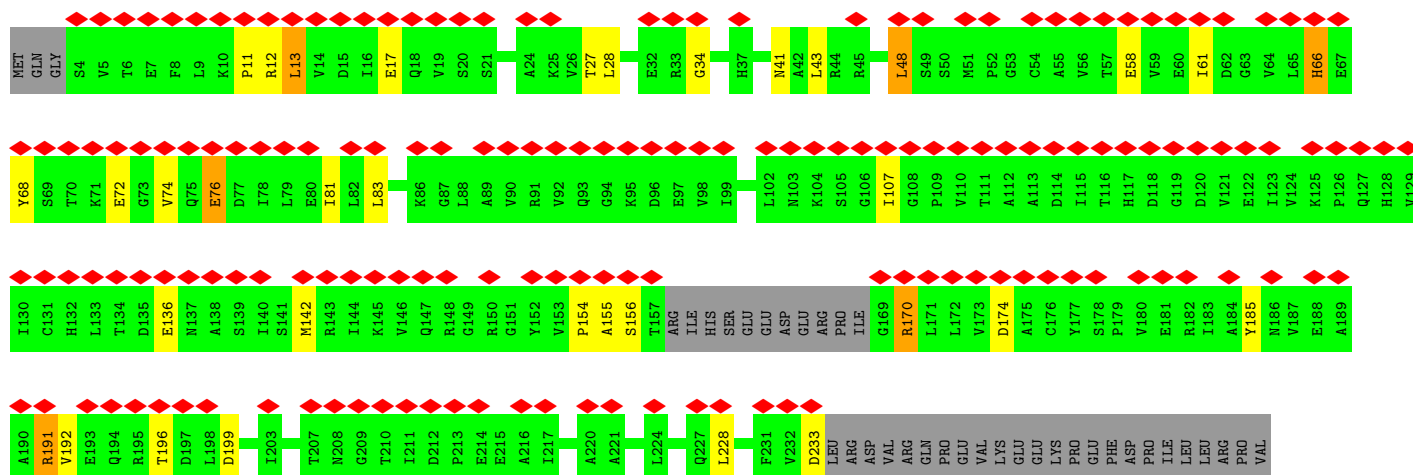
- Molecule 56: Template DNA strand



- Molecule 57: DNA-directed RNA polymerase subunit alpha




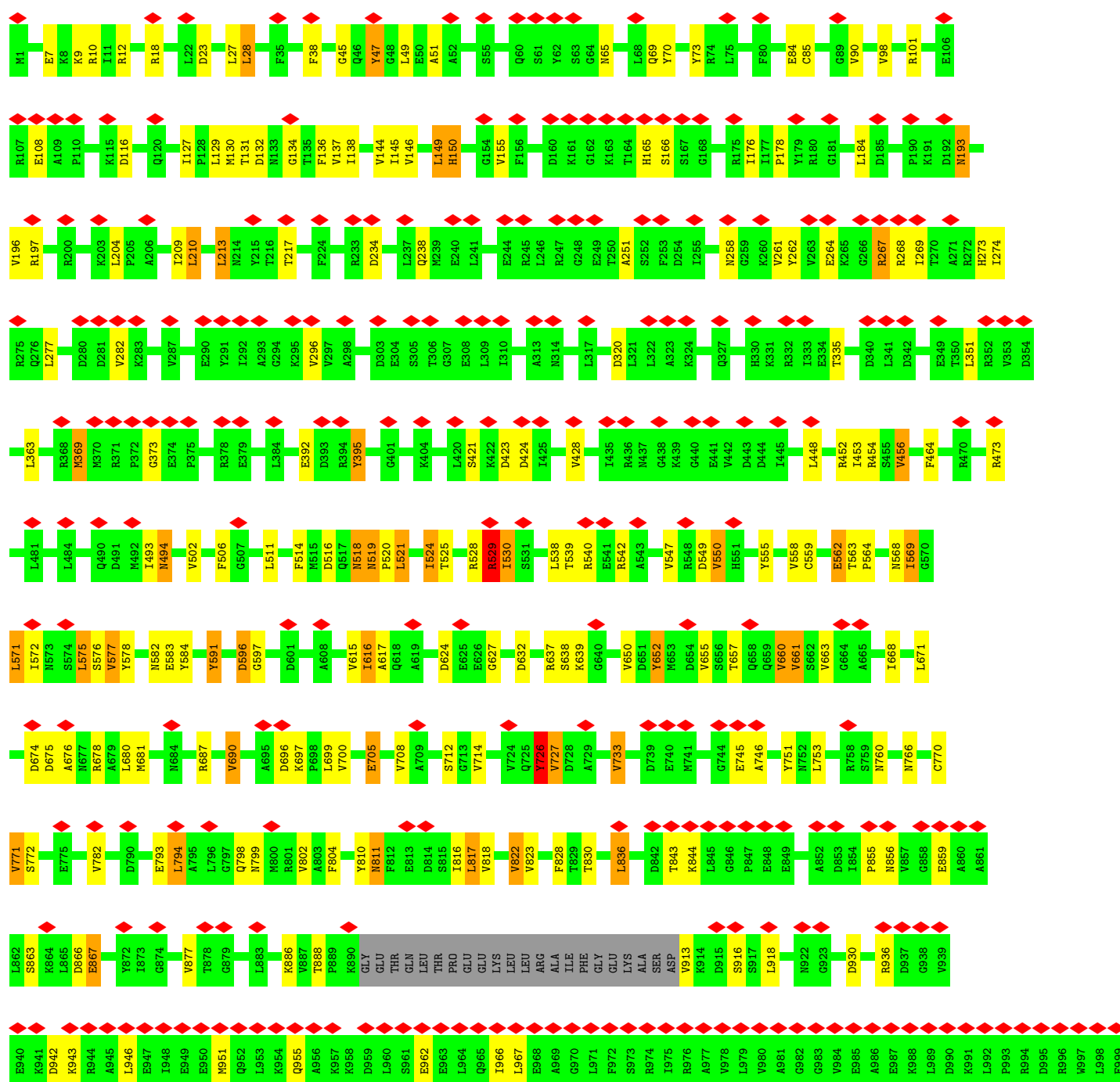
- Molecule 57: DNA-directed RNA polymerase subunit alpha

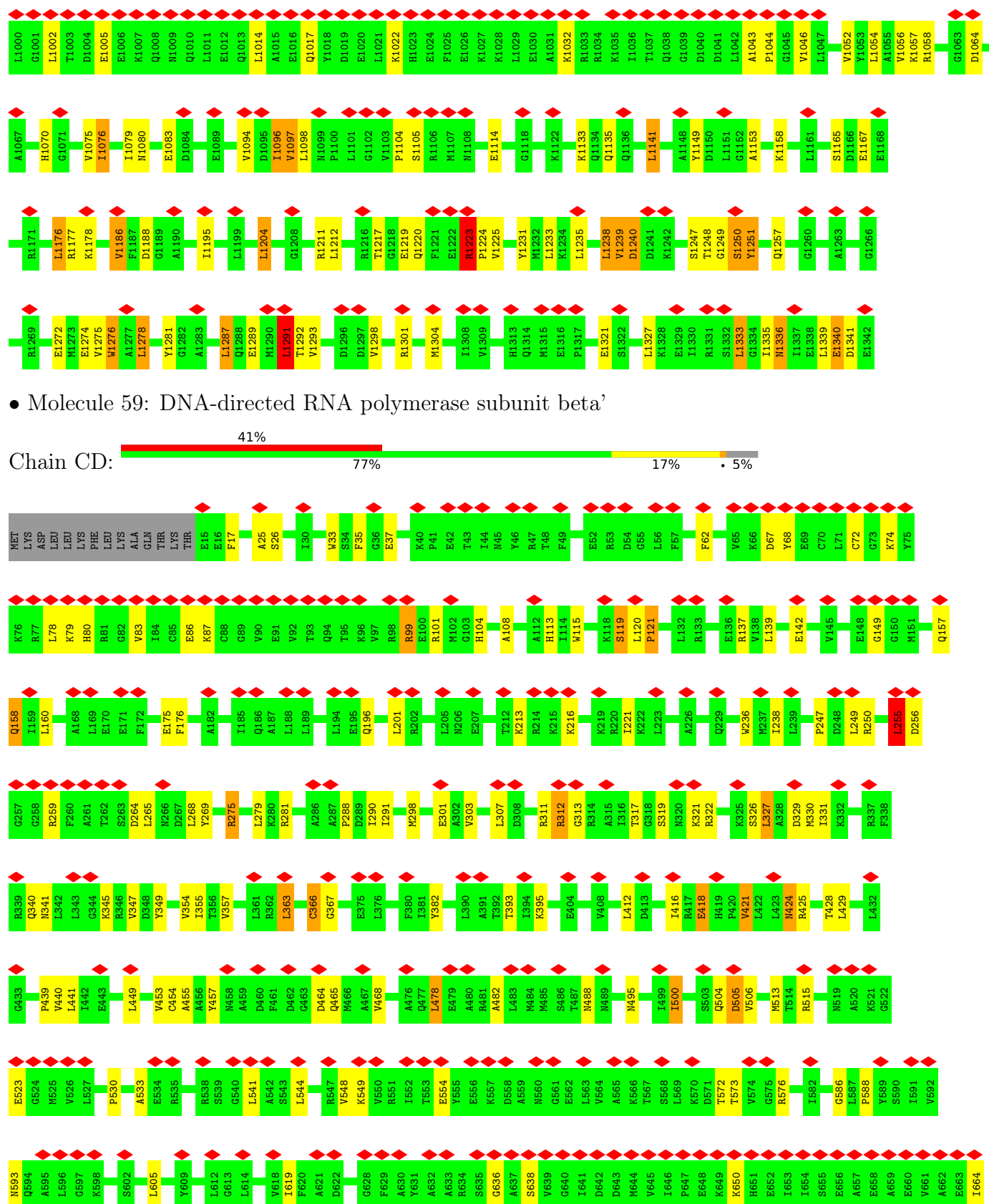


ASP	ASP	LEU	GLU	ASN	TRP	PRO	PRO	ALA	ALA	ALA	ASP	ASP	CYS	LEU	LYS	ALA	GLU	ALA	ILE	ILE	HIS	TYR	ILE	GLY	ASP	LEU	VAL	GLN	ARG	THR	GLU	VAL	GLU	LEU	LYS	THR	PRO	ASN	LEU	GLY	LYS	LYS	LYS	SER	SER	LEU	THR	GLU	ILE	LYS	LYS	ASP	VAL	LEU	ALA	SER	ARG	GLY	LEU	SER	LEU	GLY	MET	ARG
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• Molecule 58: DNA-directed RNA polymerase subunit beta

Chain CC: 





ALA	PRO	GLN	VAL	THR	ALA	GLU	ASP	SER	SER	LEU	ALA	GLU	LEU	ASN	ALA	GLY	LEU	GLY	GLY	SER	ASP	ASN	GLU																																				
M1260	L1261	A1269	G1270	S1271	S1272	D1273	E1278	K1286	L1292	E1293	A1294	K1297	L1307	G1308	I1309	T1310	S1313	F1325	V1331	L1332	T1333	D1342	K1348	E1349	N1350	V1351	I1352	L1356	I1357	P1358	Y1365	H1366	Q1367	D1368	R1369	M1370	R1371	R1372	R1373	ALA	ALA	GLY	GLU	ALA	PRO	ALA													
L1175	V1176	I1177	T1178	P1179	V1180	D1181	G1182	S1183	D1184	P1185	Y1186	E1187	E1188	M1189	I1190	P1191	K1192	W1193	R1194	Q1195	L1196	N1197	V1198	F1199	E1200	R1203	V1204	E1205	R1206	G1207	D1208	V1209	I1210	S1211	D1212	E1215	V1229	V1234	N1235	E1236	V1237	Q1238	D1239	V1240	Y1241	I1248	N1249	D1250	K1251	H1252	I1256	Q1259							
I1106	V1107	Q1108	L1109	E1110	D1111	G1112	V1113	Q1114	I1115	S1116	S1117	D1118	D1119	T1120	L1121	A1122	R1123	I1124	P1125	Q1126	GLU	SER	GLY	GLY	THR	LYS	ASP	ILE	T1135	G1136	G1137	L1138	V1141	A1142	D1143	L1144	F1145	P1150	K1151	A1157	E1158	I1159	S1160	V1163	S1164	F1165	G1166	K1167	E1168	T1169	K1170	G1171	K1172	R1173	R1174				
I1046	T1047	R1048	Q1049	T1050	D1051	E1052	L1053	T1054	G1055	L1056	S1057	S1058	L1059	V1060	V1061	L1062	D1063	S1064	A1065	E1066	R1067	T1068	A1069	G1070	G1071	K1072	D1073	L1074	R1075	P1076	A1077	L1078	K1079	I1080	V1081	D1082	A1083	Q1084	G1085	N1086	D1087	V1088	L1089	I1090	P1091	G1092	T1093	D1094	M1095	P1096	A1097	Q1098	Y1099	F1100	L1101	P1102	G1103	K1104	A1105
R978	N979	T980	E981	I985	D986	E987	F988	G989	R990	T991	K992	E993	S994	Y995	K996	Y999	G1000	A1001	V1002	L1003	A1004	K1005	G1006	D1007	G1008	E1009	Q1010	V1011	A1012	G1013	G1014	E1015	T1016	V1017	A1018	D1021	M1025	P1026	E1030	V1031	S1032	G1033	F1034	V1035	R1036	F1037	T1038	D1039	M1040	I1041	D1042	G1043	Q1044	T1045					
H907	I908	A914	V917	A920	G924	G927	T931	N932	R933	THR	PHE	HIS	ILE	GLY	GLY	ALA	ALA	SER	ARG	ALA	ALA	ALA	GLU	SER	SER	ILE	GLN	V952	K953	N954	K955	G956	S957	I958	K959	L960	S961	N962	V963	K964	S965	V966	V967	N968	S969	S970	G971	K972	L973	T976	S977								
L807	D813	T816	H817	E818	M822	T823	P824	V825	I826	E827	G828	G829	D830	V831	K832	R836	D837	R838	V839	L840	L849	K850	P851	G852	T853	A854	D855	I856	N861	D870	L871	L872	E873	E874	V877	D878	R883	S884	V885	C888	D889	T890	D891	A896	Y899	L903													
M725	A726	D727	S728	G729	A730	R731	G732	S733	A734	A735	Q736	I737	R738	Q739	L740	A741	G742	M743	R744	G745	L746	M747	A748	K749	P750	D751	G752	S753	I754	I755	E756	T757	P758	I759	T760	A761	N762	F763	L767	N768	V769	L770	Q771	Y772	L788	K789	Y795	L796	T797	V801	D802	V803	A804	Q805	D806				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18552	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.981	Depositor
Minimum map value	-0.434	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.068	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	688.0, 688.0, 688.0	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.075, 1.075, 1.075	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, 4D4, D2T, 4OC, 7MG, ZN, 1MG, OMC, 3TD, UR3, 6MZ, H2U, 3AU, 4SU, 2MG, MG, PSU, MEQ, OMG, G7M, MA6, 2MA, OMU, 5MU, MIA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	1.13	1/36569 (0.0%)	1.04	68/57044 (0.1%)
2	AB	0.35	0/1796	0.56	0/2420
3	AC	0.42	0/1667	0.58	0/2246
4	AD	0.51	0/1665	0.62	0/2227
5	AE	0.50	0/1161	0.68	1/1563 (0.1%)
6	AF	0.44	0/867	0.58	0/1171
7	AG	0.34	0/1219	0.61	1/1635 (0.1%)
8	AH	0.54	0/989	0.60	1/1326 (0.1%)
9	AI	0.43	0/1043	0.62	0/1387
10	AJ	0.41	0/810	0.70	1/1094 (0.1%)
11	AK	0.40	0/882	0.57	0/1191
12	AL	0.59	0/954	0.72	1/1279 (0.1%)
13	AM	0.36	0/900	0.55	0/1204
14	AN	0.40	0/817	0.52	0/1088
15	AO	0.45	0/722	0.56	0/964
16	AP	0.63	0/659	0.62	0/884
17	AQ	0.53	0/650	0.71	1/871 (0.1%)
18	AR	0.43	0/449	0.47	0/604
19	AS	0.42	0/680	0.58	0/915
20	AT	0.47	0/676	0.53	0/895
21	AU	0.37	0/598	0.57	1/792 (0.1%)
22	AV	1.89	28/709 (3.9%)	1.72	32/1099 (2.9%)
23	AW	0.73	1/1725 (0.1%)	1.04	2/2687 (0.1%)
24	AX	0.60	1/1584 (0.1%)	0.85	0/2463
25	BA	1.01	2/69187 (0.0%)	1.01	148/107927 (0.1%)
26	BB	0.72	0/2872	0.90	1/4478 (0.0%)
27	BC	0.50	0/2131	0.64	1/2863 (0.0%)
28	BD	0.47	0/1576	0.60	0/2119
29	BE	0.44	0/1571	0.65	2/2113 (0.1%)
30	BF	0.33	0/1444	0.59	0/1937
31	BG	0.38	0/1333	0.59	0/1805

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	0.30	0/1122	0.65	2/1515 (0.1%)
33	BK	0.47	0/1152	0.54	0/1551
34	BL	0.46	0/956	0.62	0/1279
35	BM	0.44	0/1061	0.64	0/1412
36	BN	0.43	0/1081	0.57	0/1443
37	BO	0.46	0/973	0.62	0/1301
38	BP	0.36	0/910	0.59	0/1219
39	BQ	0.43	0/929	0.58	0/1242
40	BR	0.59	0/960	0.56	0/1278
41	BS	0.48	0/829	0.67	0/1107
42	BT	0.43	0/864	0.58	0/1156
43	BU	0.41	0/764	0.57	0/1021
44	BV	0.41	0/797	0.58	0/1062
45	BW	0.42	0/766	0.61	1/1025 (0.1%)
46	BX	0.45	0/589	0.56	0/779
47	BY	0.46	0/635	0.52	0/848
48	BZ	0.34	0/502	0.51	0/667
49	B1	0.40	0/453	0.61	0/605
50	B2	0.47	0/450	0.73	0/599
51	B3	0.36	0/443	0.65	0/587
52	B4	0.48	0/380	0.61	0/498
53	B5	0.40	0/513	0.65	0/676
54	B6	0.47	0/302	0.65	0/397
55	CN	1.77	13/693 (1.9%)	1.24	3/1068 (0.3%)
56	CT	2.53	39/676 (5.8%)	1.33	9/1039 (0.9%)
57	CA	1.13	7/1797 (0.4%)	0.91	2/2436 (0.1%)
57	CB	0.80	1/1703 (0.1%)	0.86	3/2308 (0.1%)
58	CC	1.41	120/10581 (1.1%)	0.97	31/14275 (0.2%)
59	CD	1.12	58/10532 (0.6%)	0.91	15/14219 (0.1%)
All	All	0.98	271/183318 (0.1%)	0.94	327/270903 (0.1%)

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
1	AA	0	3
10	AJ	0	1
12	AL	0	1
13	AM	0	2
22	AV	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
25	BA	0	2
27	BC	0	1
37	BO	0	1
46	BX	0	1
53	B5	0	1
All	All	0	14

The worst 5 of 271 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	1	C	OP3-P	-10.65	1.48	1.61
24	AX	1	G	OP3-P	-10.51	1.48	1.61
56	CT	18	DC	C3'-O3'	-10.28	1.30	1.44
59	CD	1357	ILE	C-N	-9.69	1.15	1.34
56	CT	14	DC	C3'-O3'	-9.60	1.31	1.44

The worst 5 of 327 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1027	C	C6-N1-C2	-25.80	109.98	120.30
1	AA	1027	C	C2-N1-C1'	18.88	139.57	118.80
1	AA	1027	C	C5-C6-N1	18.21	130.11	121.00
1	AA	1027	C	C6-N1-C1'	-15.29	102.45	120.80
25	BA	2131	U	O4'-C1'-N1	-14.14	96.89	108.20

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1027	C	Sidechain
1	AA	1034	G	Sidechain
1	AA	884	U	Sidechain
10	AJ	42	LEU	Mainchain
12	AL	43	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32907	0	16571	400	0
2	AB	1765	0	1792	35	0
3	AC	1640	0	1713	99	0
4	AD	1643	0	1706	58	0
5	AE	1148	0	1195	40	0
6	AF	848	0	846	31	0
7	AG	1203	0	1254	34	0
8	AH	979	0	1031	26	0
9	AI	1031	0	1076	50	0
10	AJ	800	0	839	39	0
11	AK	866	0	874	17	0
12	AL	949	0	1008	24	0
13	AM	891	0	952	37	0
14	AN	805	0	844	21	0
15	AO	714	0	734	13	0
16	AP	649	0	666	4	0
17	AQ	641	0	682	13	0
18	AR	443	0	466	14	0
19	AS	663	0	688	21	0
20	AT	670	0	719	14	0
21	AU	590	0	629	19	0
22	AV	636	0	327	19	0
23	AW	1645	0	842	26	0
24	AX	1624	0	823	35	0
25	BA	62290	0	31344	614	0
26	BB	2569	0	1301	24	0
27	BC	2092	0	2167	40	0
28	BD	1566	0	1618	31	0
29	BE	1552	0	1618	28	0
30	BF	1420	0	1457	63	0
31	BG	1313	0	1358	34	0
32	BH	1111	0	1148	35	0
33	BK	1129	0	1162	17	0
34	BL	947	0	1023	25	0
35	BM	1052	0	1127	26	0
36	BN	1075	0	1153	23	0
37	BO	960	0	999	15	0
38	BP	900	0	935	26	0
39	BQ	917	0	962	23	0
40	BR	947	0	1019	20	0
41	BS	816	0	839	15	0
42	BT	857	0	922	17	0
43	BU	757	0	820	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BV	789	0	844	18	0
45	BW	753	0	780	17	0
46	BX	582	0	599	8	0
47	BY	625	0	652	13	0
48	BZ	501	0	531	7	0
49	B1	449	0	488	9	0
50	B2	444	0	458	17	0
51	B3	436	0	477	13	0
52	B4	377	0	418	10	0
53	B5	504	0	572	14	0
54	B6	301	0	341	7	0
55	CN	618	0	339	27	0
56	CT	606	0	338	36	0
57	CA	1775	0	1800	15	0
57	CB	1684	0	1713	19	0
58	CC	10415	0	10432	214	0
59	CD	10375	0	10597	176	0
60	AA	119	0	0	0	0
60	AW	2	0	0	0	0
60	B2	1	0	0	0	0
60	BA	294	0	0	0	0
60	BB	2	0	0	0	0
60	BC	1	0	0	0	0
60	BO	1	0	0	0	0
60	CD	1	0	0	0	0
61	AX	11	0	8	1	0
62	B6	1	0	0	0	0
62	CD	2	0	0	0	0
All	All	171689	0	122636	2452	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 9.

The worst 5 of 2452 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)
3:AC:109:PRO:HD2	58:CC:859:GLU:CG	1.58	1.34
4:AD:193:ALA:CA	59:CD:86:GLU:OE2	1.73	1.32
5:AE:10:GLU:HG3	59:CD:78:LEU:CD1	1.77	1.15
3:AC:109:PRO:HD2	58:CC:859:GLU:HG3	1.21	1.15
4:AD:191:LEU:O	59:CD:86:GLU:OE1	1.60	1.15

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	AB	224/241 (93%)	208 (93%)	15 (7%)	1 (0%)	34	66
3	AC	207/233 (89%)	194 (94%)	10 (5%)	3 (1%)	11	38
4	AD	203/206 (98%)	193 (95%)	9 (4%)	1 (0%)	29	61
5	AE	154/167 (92%)	143 (93%)	10 (6%)	1 (1%)	25	57
6	AF	102/131 (78%)	95 (93%)	7 (7%)	0	100	100
7	AG	151/156 (97%)	142 (94%)	8 (5%)	1 (1%)	22	54
8	AH	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	19	51
9	AI	126/130 (97%)	115 (91%)	9 (7%)	2 (2%)	9	36
10	AJ	98/103 (95%)	88 (90%)	7 (7%)	3 (3%)	4	23
11	AK	114/129 (88%)	99 (87%)	14 (12%)	1 (1%)	17	48
12	AL	119/124 (96%)	109 (92%)	8 (7%)	2 (2%)	9	35
13	AM	113/118 (96%)	106 (94%)	6 (5%)	1 (1%)	17	48
14	AN	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
15	AO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	AP	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
17	AQ	77/84 (92%)	70 (91%)	7 (9%)	0	100	100
18	AR	52/75 (69%)	50 (96%)	2 (4%)	0	100	100
19	AS	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
20	AT	84/87 (97%)	84 (100%)	0	0	100	100
21	AU	68/71 (96%)	66 (97%)	1 (2%)	1 (2%)	10	38
27	BC	270/273 (99%)	249 (92%)	18 (7%)	3 (1%)	14	45
28	BD	206/209 (99%)	195 (95%)	10 (5%)	1 (0%)	29	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	BE	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
30	BF	176/179 (98%)	162 (92%)	14 (8%)	0	100	100
31	BG	173/177 (98%)	158 (91%)	15 (9%)	0	100	100
32	BH	147/149 (99%)	132 (90%)	14 (10%)	1 (1%)	22	54
33	BK	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
34	BL	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
35	BM	142/144 (99%)	132 (93%)	8 (6%)	2 (1%)	11	38
36	BN	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
37	BO	118/127 (93%)	105 (89%)	13 (11%)	0	100	100
38	BP	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	17	48
39	BQ	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
40	BR	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
41	BS	101/103 (98%)	98 (97%)	2 (2%)	1 (1%)	15	46
42	BT	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
43	BU	93/100 (93%)	88 (95%)	5 (5%)	0	100	100
44	BV	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	15	46
45	BW	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
46	BX	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
47	BY	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
48	BZ	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
49	B1	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
50	B2	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
51	B3	51/55 (93%)	49 (96%)	2 (4%)	0	100	100
52	B4	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
53	B5	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	9	36
54	B6	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
57	CA	227/329 (69%)	217 (96%)	10 (4%)	0	100	100
57	CB	215/329 (65%)	204 (95%)	10 (5%)	1 (0%)	29	61
58	CC	1316/1342 (98%)	1197 (91%)	110 (8%)	9 (1%)	22	54
59	CD	1327/1407 (94%)	1222 (92%)	95 (7%)	10 (1%)	19	51
All	All	8623/9235 (93%)	8034 (93%)	540 (6%)	49 (1%)	29	57

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	AI	13	LYS
9	AI	56	ASP
11	AK	93	ARG
12	AL	88	LYS
27	BC	241	GLY

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	AB	187/199 (94%)	175 (94%)	12 (6%)	17	46
3	AC	171/190 (90%)	153 (90%)	18 (10%)	7	25
4	AD	172/173 (99%)	154 (90%)	18 (10%)	7	25
5	AE	118/126 (94%)	107 (91%)	11 (9%)	9	30
6	AF	91/112 (81%)	83 (91%)	8 (9%)	10	33
7	AG	126/129 (98%)	111 (88%)	15 (12%)	5	21
8	AH	104/105 (99%)	97 (93%)	7 (7%)	16	45
9	AI	106/107 (99%)	97 (92%)	9 (8%)	10	35
10	AJ	87/90 (97%)	75 (86%)	12 (14%)	3	16
11	AK	89/99 (90%)	85 (96%)	4 (4%)	27	58
12	AL	102/103 (99%)	90 (88%)	12 (12%)	5	21
13	AM	93/96 (97%)	86 (92%)	7 (8%)	13	39
14	AN	83/84 (99%)	77 (93%)	6 (7%)	14	41
15	AO	76/77 (99%)	67 (88%)	9 (12%)	5	21
16	AP	65/65 (100%)	63 (97%)	2 (3%)	40	67
17	AQ	73/78 (94%)	63 (86%)	10 (14%)	3	16
18	AR	47/65 (72%)	43 (92%)	4 (8%)	10	35
19	AS	72/79 (91%)	69 (96%)	3 (4%)	30	60
20	AT	65/66 (98%)	58 (89%)	7 (11%)	6	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	AU	60/61 (98%)	58 (97%)	2 (3%)	38	66
27	BC	217/218 (100%)	207 (95%)	10 (5%)	27	58
28	BD	163/163 (100%)	151 (93%)	12 (7%)	13	40
29	BE	165/165 (100%)	150 (91%)	15 (9%)	9	31
30	BF	149/150 (99%)	135 (91%)	14 (9%)	8	30
31	BG	136/138 (99%)	122 (90%)	14 (10%)	7	26
32	BH	114/114 (100%)	100 (88%)	14 (12%)	4	20
33	BK	116/116 (100%)	108 (93%)	8 (7%)	15	44
34	BL	104/104 (100%)	96 (92%)	8 (8%)	13	38
35	BM	103/103 (100%)	92 (89%)	11 (11%)	6	25
36	BN	108/108 (100%)	103 (95%)	5 (5%)	27	58
37	BO	100/103 (97%)	95 (95%)	5 (5%)	24	55
38	BP	87/87 (100%)	80 (92%)	7 (8%)	12	37
39	BQ	99/100 (99%)	91 (92%)	8 (8%)	11	36
40	BR	89/90 (99%)	84 (94%)	5 (6%)	21	52
41	BS	84/84 (100%)	78 (93%)	6 (7%)	14	42
42	BT	93/93 (100%)	88 (95%)	5 (5%)	22	53
43	BU	82/84 (98%)	73 (89%)	9 (11%)	6	24
44	BV	84/85 (99%)	81 (96%)	3 (4%)	35	63
45	BW	78/78 (100%)	72 (92%)	6 (8%)	13	38
46	BX	58/63 (92%)	55 (95%)	3 (5%)	23	54
47	BY	67/68 (98%)	66 (98%)	1 (2%)	65	81
48	BZ	54/55 (98%)	52 (96%)	2 (4%)	34	63
49	B1	48/49 (98%)	41 (85%)	7 (15%)	3	14
50	B2	47/48 (98%)	42 (89%)	5 (11%)	6	25
51	B3	48/49 (98%)	46 (96%)	2 (4%)	30	60
52	B4	38/38 (100%)	36 (95%)	2 (5%)	22	53
53	B5	51/52 (98%)	50 (98%)	1 (2%)	55	76
54	B6	34/44 (77%)	34 (100%)	0	100	100
57	CA	197/286 (69%)	193 (98%)	4 (2%)	55	76
57	CB	187/286 (65%)	177 (95%)	10 (5%)	22	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	CC	1139/1157 (98%)	1096 (96%)	43 (4%)	33	62
59	CD	1118/1168 (96%)	1097 (98%)	21 (2%)	57	77
All	All	7244/7650 (95%)	6802 (94%)	442 (6%)	22	48

5 of 442 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	BG	69	ARG
36	BN	127	LYS
59	CD	1167	LYS
58	CC	830	THR
31	BG	155	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
5	AE	70	ASN
6	AF	11	HIS
9	AI	31	ASN
39	BQ	115	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1529/1542 (99%)	288 (18%)	32 (2%)
22	AV	28/57 (49%)	12 (42%)	1 (3%)
23	AW	76/77 (98%)	21 (27%)	6 (7%)
24	AX	73/76 (96%)	18 (24%)	0
25	BA	2895/2904 (99%)	552 (19%)	66 (2%)
26	BB	119/120 (99%)	15 (12%)	0
All	All	4720/4776 (98%)	906 (19%)	105 (2%)

5 of 906 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	9	G
1	AA	19	A

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Mol	Chain	Res	Type
1	AA	22	G

5 of 105 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BA	884	U
25	BA	1344	U
25	BA	2601	C
25	BA	984	A
25	BA	1109	C

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

53 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	$\# Z > 2$
25	2MG	BA	1835	25	18,26,27	2.23	7 (38%)	16,38,41	1.57	4 (25%)
23	OMC	AW	32	23	19,22,23	2.90	8 (42%)	26,31,34	0.82	0
1	5MC	AA	1407	1	18,22,23	3.75	7 (38%)	26,32,35	1.03	1 (3%)
28	MEQ	BD	150	28	8,9,10	0.94	0	5,10,12	0.97	1 (20%)
25	5MU	BA	747	25	19,22,23	1.41	4 (21%)	28,32,35	2.25	6 (21%)
25	PSU	BA	2605	25	18,21,22	1.08	2 (11%)	22,30,33	1.88	3 (13%)
25	OMC	BA	2498	25,60	19,22,23	2.69	7 (36%)	26,31,34	0.84	1 (3%)
25	PSU	BA	2604	25	18,21,22	1.04	2 (11%)	22,30,33	1.90	5 (22%)
24	H2U	AX	16	24	18,21,22	2.99	5 (27%)	21,30,33	1.94	5 (23%)
1	2MG	AA	966	1	18,25,27	2.54	8 (44%)	19,37,41	1.69	5 (26%)
25	PSU	BA	2457	25	18,21,22	1.06	2 (11%)	22,30,33	2.09	6 (27%)
25	2MA	BA	2503	25,60	17,25,26	2.58	6 (35%)	17,37,40	1.45	4 (23%)
25	PSU	BA	746	25,60	18,21,22	1.12	3 (16%)	22,30,33	2.04	6 (27%)
1	G7M	AA	527	1	20,26,27	2.24	8 (40%)	17,39,42	1.31	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	2MG	BA	2445	25,29	18,26,27	2.18	7 (38%)	16,38,41	1.63	4 (25%)
25	5MC	BA	1962	25	18,22,23	3.70	7 (38%)	26,32,35	1.11	1 (3%)
25	PSU	BA	1917	25	18,21,22	1.00	3 (16%)	22,30,33	1.90	5 (22%)
24	4SU	AX	8	24	18,21,22	4.03	8 (44%)	26,30,33	2.20	4 (15%)
36	4D4	BN	81	36	9,11,12	2.47	3 (33%)	8,13,15	0.84	0
24	PSU	AX	32	24	18,21,22	1.03	1 (5%)	22,30,33	1.73	4 (18%)
25	OMG	BA	2251	23,25	18,26,27	2.54	8 (44%)	19,38,41	1.48	4 (21%)
24	H2U	AX	20	24	18,21,22	3.21	5 (27%)	21,30,33	1.90	5 (23%)
23	5MU	AW	54	23	19,22,23	1.38	5 (26%)	28,32,35	2.20	8 (28%)
25	6MZ	BA	2030	25	18,25,26	1.95	3 (16%)	16,36,39	2.61	4 (25%)
25	PSU	BA	2580	25	18,21,22	1.09	2 (11%)	22,30,33	2.27	8 (36%)
25	PSU	BA	955	25,36	18,21,22	1.17	3 (16%)	22,30,33	1.94	5 (22%)
25	6MZ	BA	1618	25	18,25,26	1.96	3 (16%)	16,36,39	2.19	3 (18%)
24	PSU	AX	55	24	18,21,22	1.01	1 (5%)	22,30,33	1.94	5 (22%)
24	PSU	AX	39	24	18,21,22	1.11	2 (11%)	22,30,33	1.86	4 (18%)
1	4OC	AA	1402	1,60	20,23,24	3.29	9 (45%)	26,32,35	1.05	3 (11%)
24	5MU	AX	54	24	19,22,23	1.37	4 (21%)	28,32,35	2.11	6 (21%)
12	D2T	AL	89	12	6,7,10	1.02	0	5,8,13	1.07	0
1	2MG	AA	1516	1	18,26,27	2.20	7 (38%)	16,38,41	1.65	4 (25%)
25	1MG	BA	745	25	18,26,27	2.55	4 (22%)	19,39,42	1.52	4 (21%)
25	PSU	BA	2504	25,60	18,21,22	1.12	3 (16%)	22,30,33	2.11	6 (27%)
1	MA6	AA	1518	1	19,26,27	1.39	3 (15%)	18,38,41	4.06	2 (11%)
1	PSU	AA	516	1,60	18,21,22	1.03	2 (11%)	22,30,33	2.04	7 (31%)
1	UR3	AA	1498	1	19,22,23	2.40	6 (31%)	26,32,35	1.29	1 (3%)
25	3TD	BA	1915	25	18,22,23	4.39	10 (55%)	22,32,35	2.04	4 (18%)
1	MA6	AA	1519	1	19,26,27	1.35	3 (15%)	18,38,41	4.63	2 (11%)
1	5MC	AA	967	1	18,22,23	3.85	7 (38%)	26,32,35	1.11	2 (7%)
25	OMU	BA	2552	25	19,22,23	2.80	6 (31%)	26,31,34	1.85	5 (19%)
25	PSU	BA	1911	25	18,21,22	1.11	2 (11%)	22,30,33	1.87	4 (18%)
25	5MU	BA	1939	25,60	19,22,23	1.45	3 (15%)	28,32,35	2.36	6 (21%)
1	2MG	AA	1207	1	18,25,27	2.49	8 (44%)	19,37,41	1.66	5 (26%)
23	4SU	AW	8	23	18,21,22	4.08	8 (44%)	26,30,33	2.21	5 (19%)
25	H2U	BA	2449	25	18,21,22	2.74	5 (27%)	21,30,33	2.10	5 (23%)
24	7MG	AX	46	24	20,25,27	3.16	10 (50%)	27,37,42	2.05	7 (25%)
23	H2U	AW	20	23	18,21,22	3.05	5 (27%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	3AU	AX	47	24	18,21,29	3.41	8 (44%)	26,30,43	1.66	4 (15%)
25	G7M	BA	2069	25	20,26,27	2.21	8 (40%)	17,39,42	1.24	1 (5%)
23	PSU	AW	55	23	18,21,22	1.03	1 (5%)	22,30,33	1.96	5 (22%)
24	MIA	AX	37	24	18,24,32	1.48	3 (16%)	18,35,47	1.53	2 (11%)

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
25	2MG	BA	1835	25	-	0/5/27/28	0/3/3/3
23	OMC	AW	32	23	-	0/9/27/28	0/2/2/2
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
28	MEQ	BD	150	28	-	3/8/9/11	-
25	5MU	BA	747	25	-	0/7/25/26	0/2/2/2
25	PSU	BA	2605	25	-	0/7/25/26	0/2/2/2
25	OMC	BA	2498	25,60	-	2/9/27/28	0/2/2/2
25	PSU	BA	2604	25	-	0/7/25/26	0/2/2/2
24	H2U	AX	16	24	-	1/7/38/39	0/2/2/2
1	2MG	AA	966	1	-	2/3/25/28	0/3/3/3
25	PSU	BA	2457	25	-	0/7/25/26	0/2/2/2
25	2MA	BA	2503	25,60	-	2/3/25/26	0/3/3/3
25	PSU	BA	746	25,60	-	1/7/25/26	0/2/2/2
1	G7M	AA	527	1	-	1/3/25/26	0/3/3/3
25	2MG	BA	2445	25,29	-	2/5/27/28	0/3/3/3
25	5MC	BA	1962	25	-	0/7/25/26	0/2/2/2
25	PSU	BA	1917	25	-	2/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
36	4D4	BN	81	36	-	7/11/12/14	-
24	PSU	AX	32	24	-	0/7/25/26	0/2/2/2
25	OMG	BA	2251	23,25	-	0/5/27/28	0/3/3/3
24	H2U	AX	20	24	-	5/7/38/39	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
25	6MZ	BA	2030	25	-	2/5/27/28	0/3/3/3
25	PSU	BA	2580	25	-	0/7/25/26	0/2/2/2
25	PSU	BA	955	25,36	-	0/7/25/26	0/2/2/2
25	6MZ	BA	1618	25	-	2/5/27/28	0/3/3/3
24	PSU	AX	55	24	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PSU	AX	39	24	-	0/7/25/26	0/2/2/2
1	4OC	AA	1402	1,60	-	0/9/29/30	0/2/2/2
24	5MU	AX	54	24	-	0/7/25/26	0/2/2/2
12	D2T	AL	89	12	-	1/5/6/14	-
1	2MG	AA	1516	1	-	0/5/27/28	0/3/3/3
25	1MG	BA	745	25	-	0/3/25/26	0/3/3/3
25	PSU	BA	2504	25,60	-	0/7/25/26	0/2/2/2
1	MA6	AA	1518	1	-	3/7/29/30	0/3/3/3
1	PSU	AA	516	1,60	-	2/7/25/26	0/2/2/2
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
25	3TD	BA	1915	25	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	6/7/29/30	0/3/3/3
1	5MC	AA	967	1	-	3/7/25/26	0/2/2/2
25	OMU	BA	2552	25	-	2/9/27/28	0/2/2/2
25	PSU	BA	1911	25	-	1/7/25/26	0/2/2/2
25	5MU	BA	1939	25,60	-	2/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	2/3/25/28	0/3/3/3
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
25	H2U	BA	2449	25	-	0/7/38/39	0/2/2/2
24	7MG	AX	46	24	-	4/7/34/38	0/3/3/3
23	H2U	AW	20	23	-	7/7/38/39	0/2/2/2
24	3AU	AX	47	24	-	0/7/25/35	0/2/2/2
25	G7M	BA	2069	25	-	2/3/25/26	0/3/3/3
23	PSU	AW	55	23	-	1/7/25/26	0/2/2/2
24	MIA	AX	37	24	-	0/3/25/34	0/3/3/3

The worst 5 of 255 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	1915	3TD	C6-C5	11.44	1.48	1.35
24	AX	20	H2U	C2-N1	10.34	1.50	1.35
25	BA	1915	3TD	C2-N1	9.65	1.49	1.37
23	AW	20	H2U	C2-N1	9.55	1.49	1.35
1	AA	967	5MC	C6-C5	9.49	1.50	1.34

The worst 5 of 207 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1519	MA6	N1-C6-N6	-18.57	97.51	117.06
1	AA	1518	MA6	N1-C6-N6	-16.24	99.97	117.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	8	4SU	C4-N3-C2	-7.77	119.79	127.34
24	AX	8	4SU	C4-N3-C2	-7.50	120.05	127.34
25	BA	2030	6MZ	C9-N6-C6	-7.37	116.52	122.87

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	966	2MG	O4'-C4'-C5'-O5'
1	AA	966	2MG	C3'-C4'-C5'-O5'
1	AA	1518	MA6	C5-C6-N6-C9
1	AA	1518	MA6	C5-C6-N6-C10
1	AA	1519	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

26 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	BD	150	MEQ	3	0
25	BA	747	5MU	1	0
24	AX	16	H2U	1	0
1	AA	966	2MG	2	0
1	AA	527	G7M	2	0
25	BA	2445	2MG	1	0
25	BA	1917	PSU	3	0
24	AX	8	4SU	2	0
24	AX	20	H2U	2	0
23	AW	54	5MU	1	0
25	BA	2030	6MZ	1	0
25	BA	955	PSU	1	0
1	AA	1516	2MG	1	0
25	BA	2504	PSU	1	0
1	AA	1518	MA6	2	0
1	AA	1498	UR3	1	0
25	BA	1915	3TD	3	0
1	AA	1519	MA6	1	0
1	AA	967	5MC	1	0
25	BA	2552	OMU	3	0
1	AA	1207	2MG	2	0
25	BA	2449	H2U	2	0
24	AX	46	7MG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	BA	2069	G7M	1	0
23	AW	55	PSU	1	0
24	AX	37	MIA	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 425 ligands modelled in this entry, 424 are monoatomic - leaving 1 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	$\# Z > 2$
61	PHE	AX	101	24	10,11,12	0.49	0	10,13,15	0.24	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
61	PHE	AX	101	24	-	2/5/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
61	AX	101	PHE	CA-CB-CG-CD1
61	AX	101	PHE	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	AX	101	PHE	1	0

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
59	CD	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CD	1357:ILE	C	1358:PRO	N	1.15

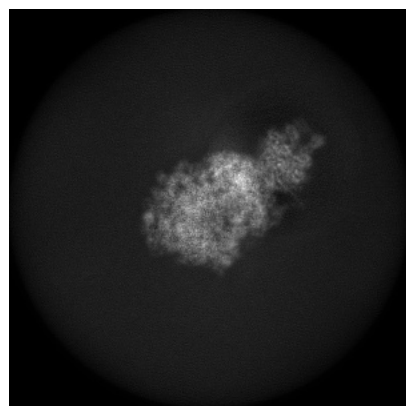
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11420. These allow visual inspection of the internal detail of the map and identification of artifacts.

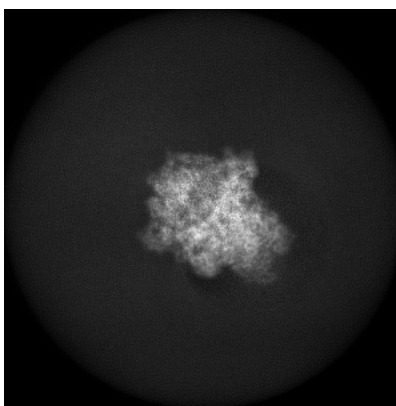
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

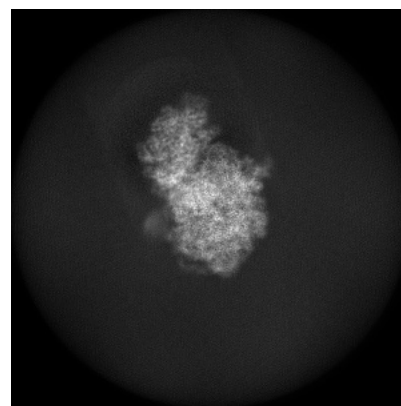
6.1.1 Primary map



X

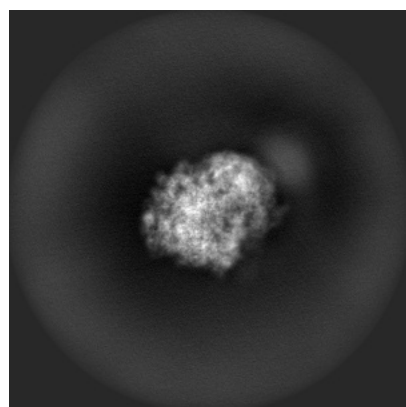


Y

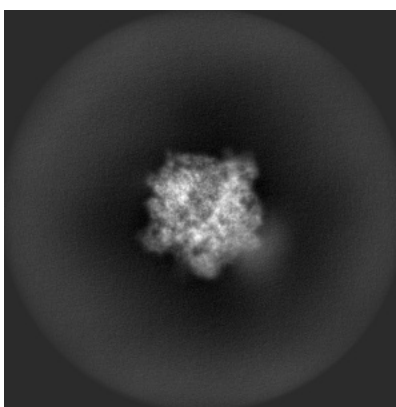


Z

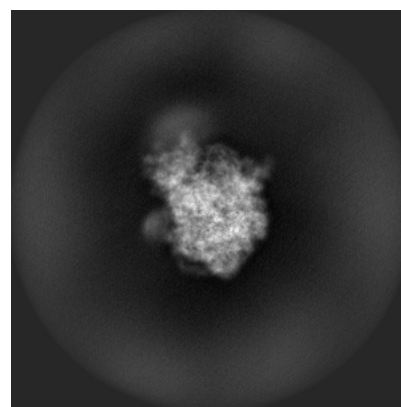
6.1.2 Raw map



X



Y

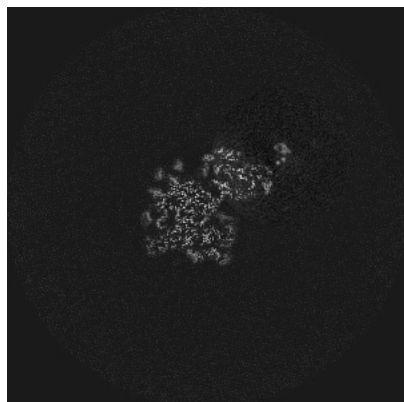


Z

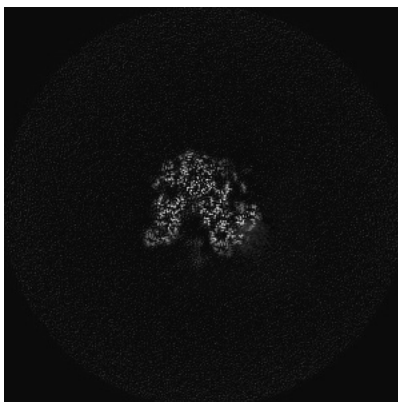
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

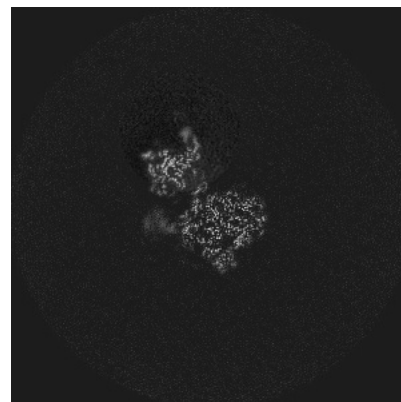
6.2.1 Primary map



X Index: 320

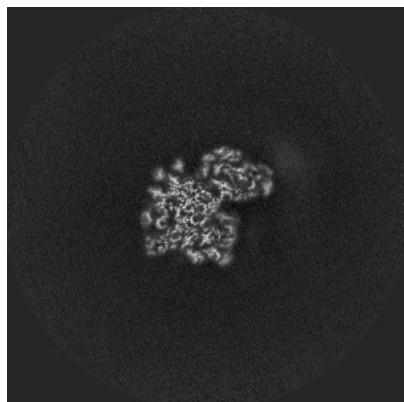


Y Index: 320

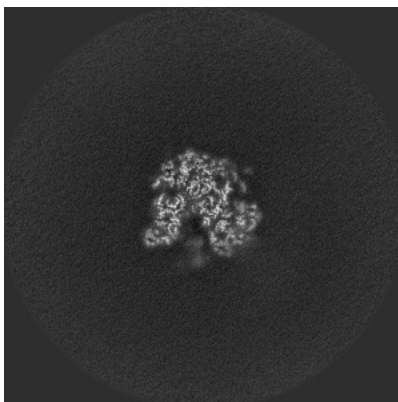


Z Index: 320

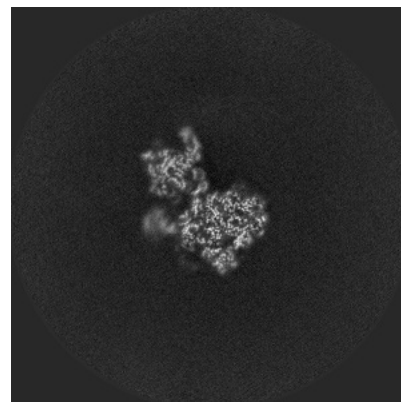
6.2.2 Raw map



X Index: 320



Y Index: 320

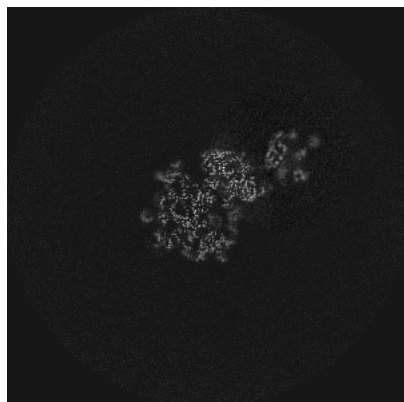


Z Index: 320

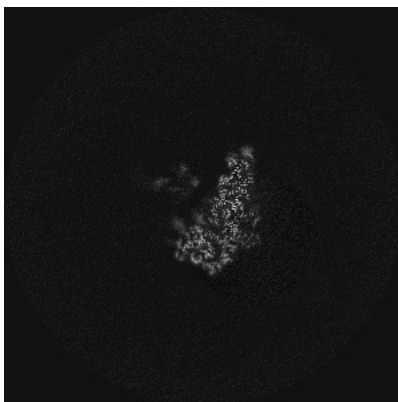
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

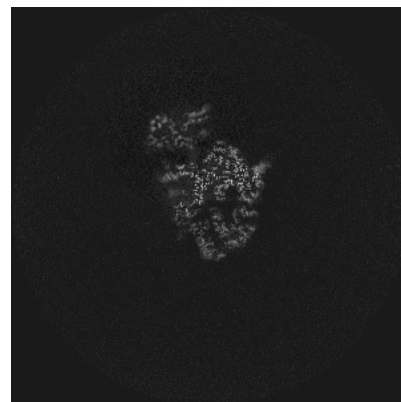
6.3.1 Primary map



X Index: 309

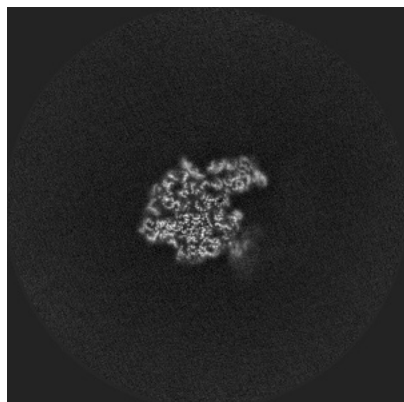


Y Index: 373

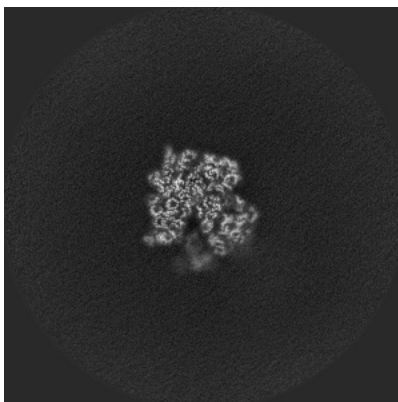


Z Index: 368

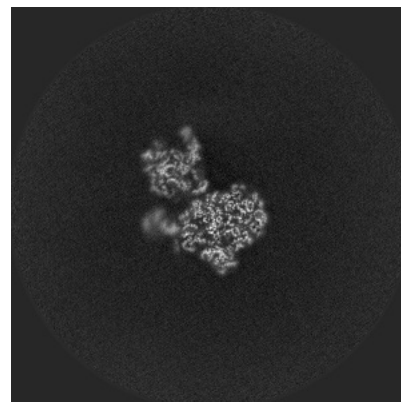
6.3.2 Raw map



X Index: 358



Y Index: 312

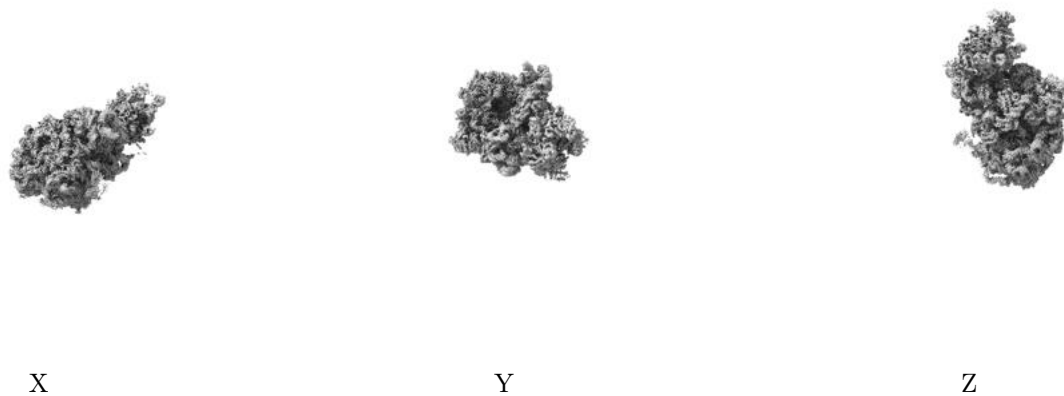


Z Index: 323

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

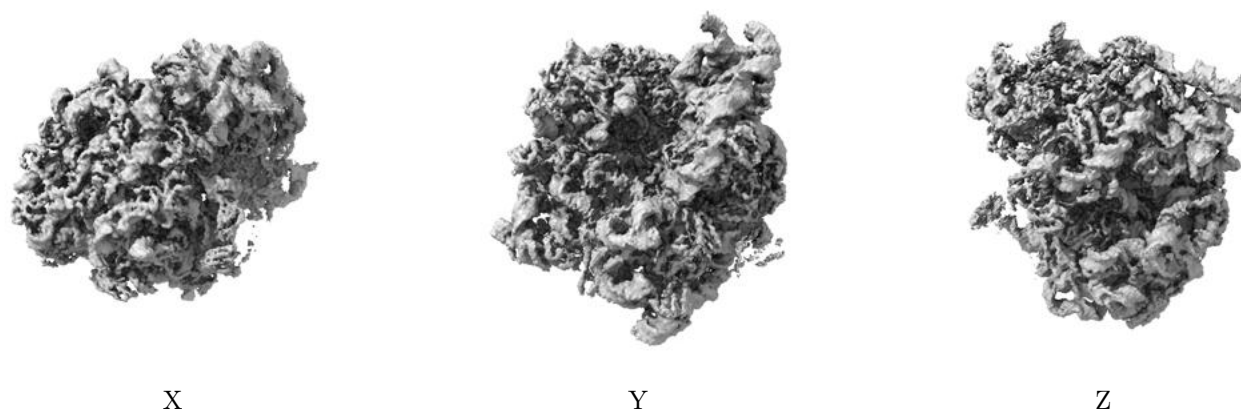
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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.

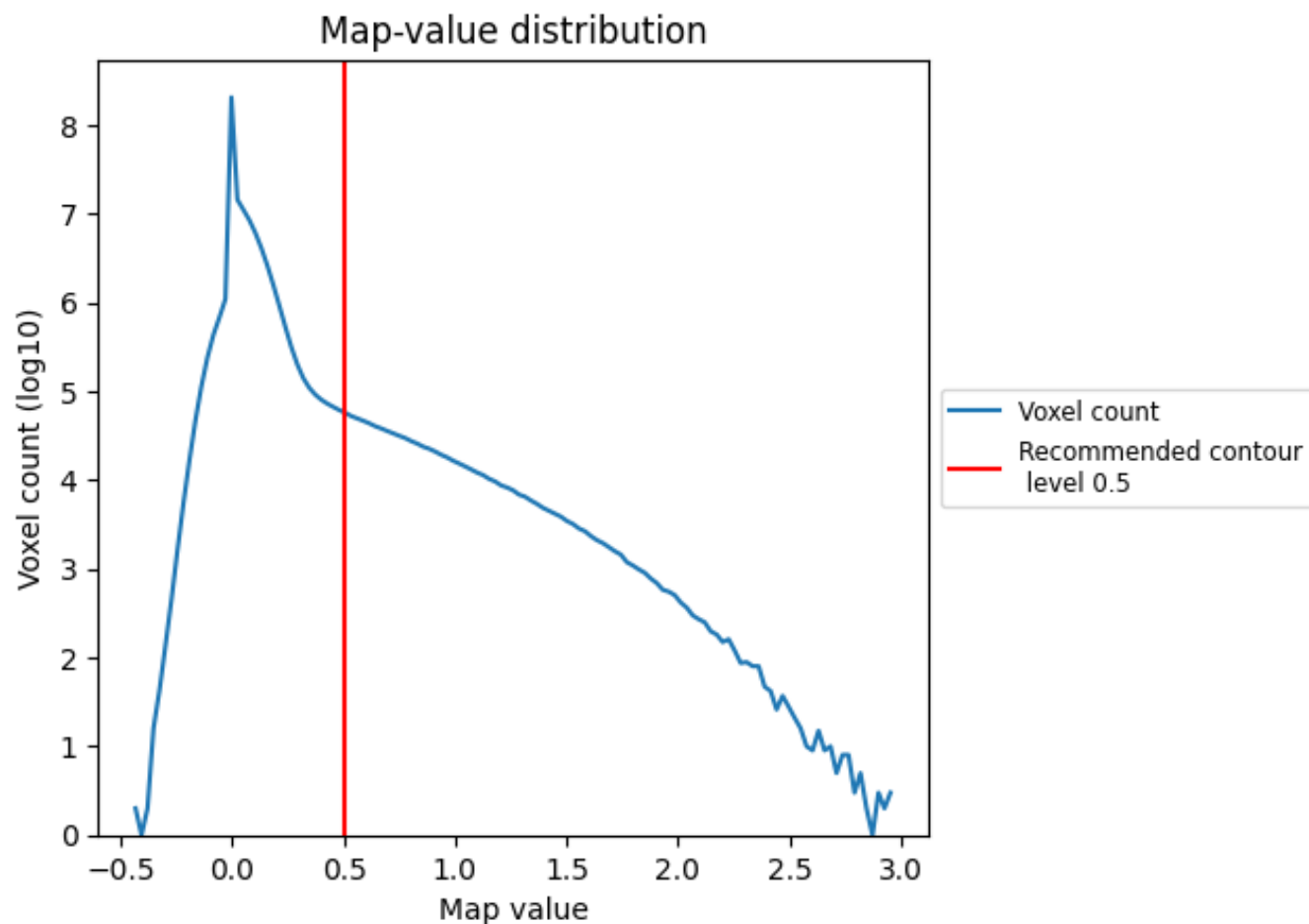
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

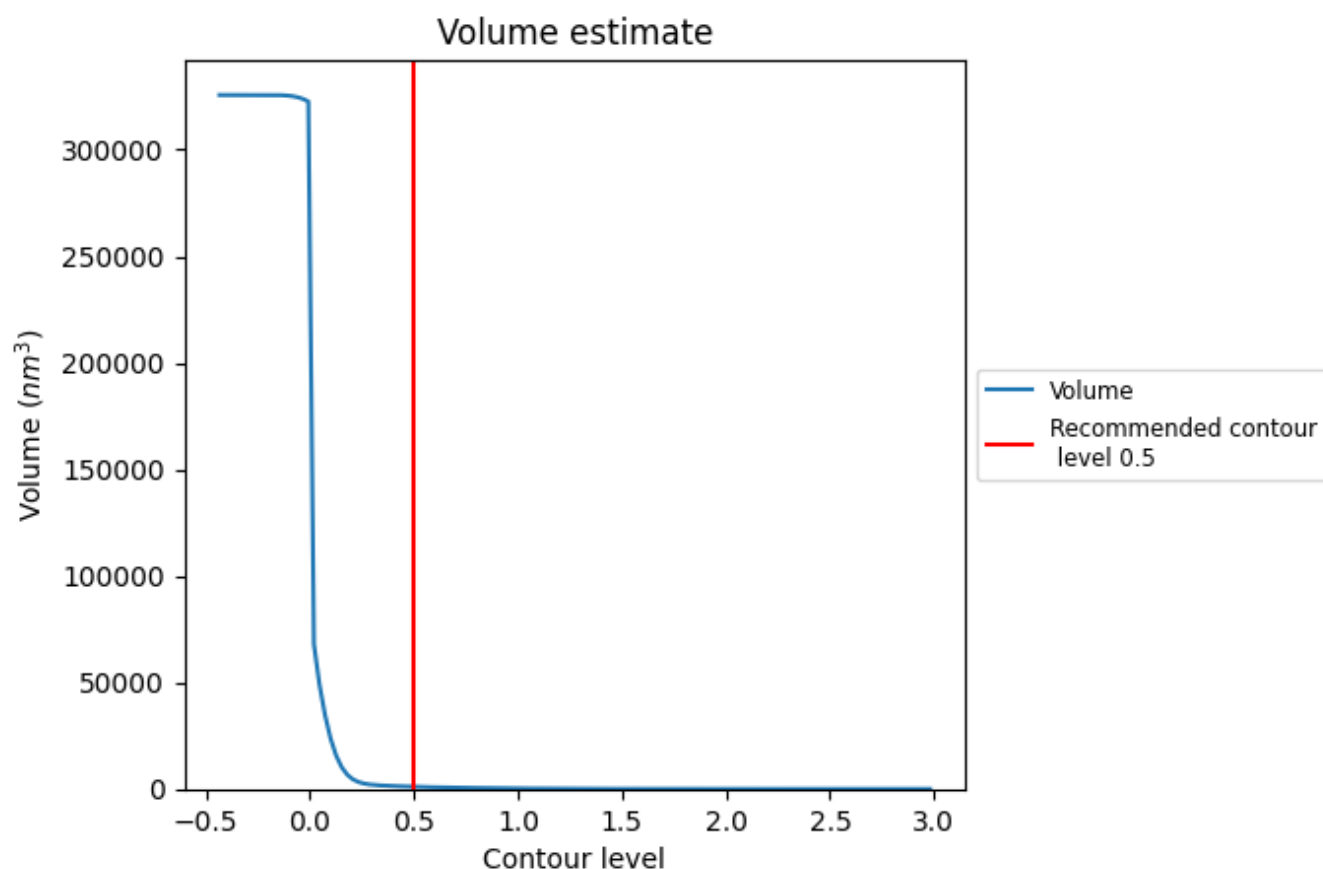
This section contains the results of statistical analysis of the map.

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.

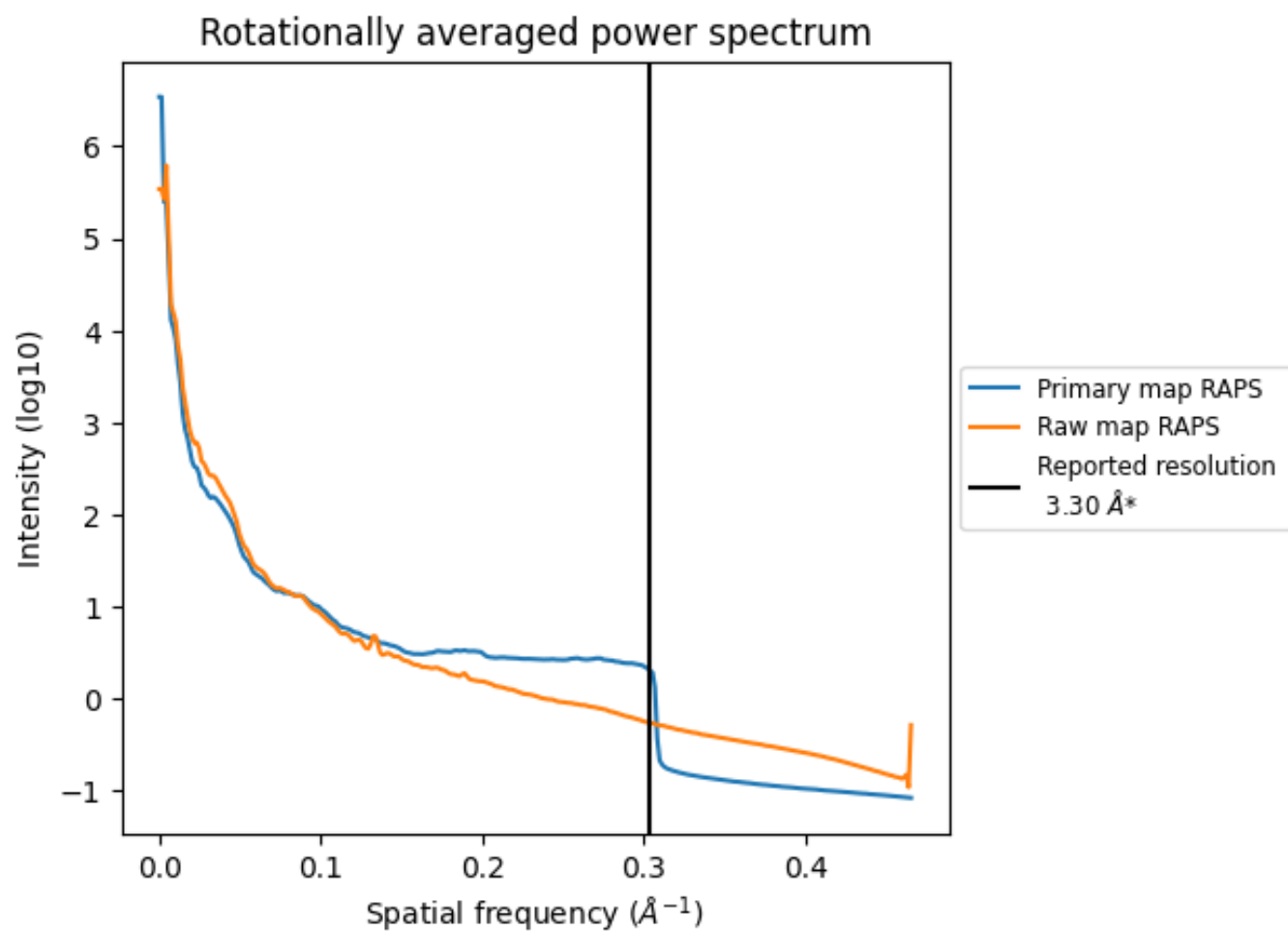
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1043 nm^3 ; this corresponds to an approximate mass of 942 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 ⓘ

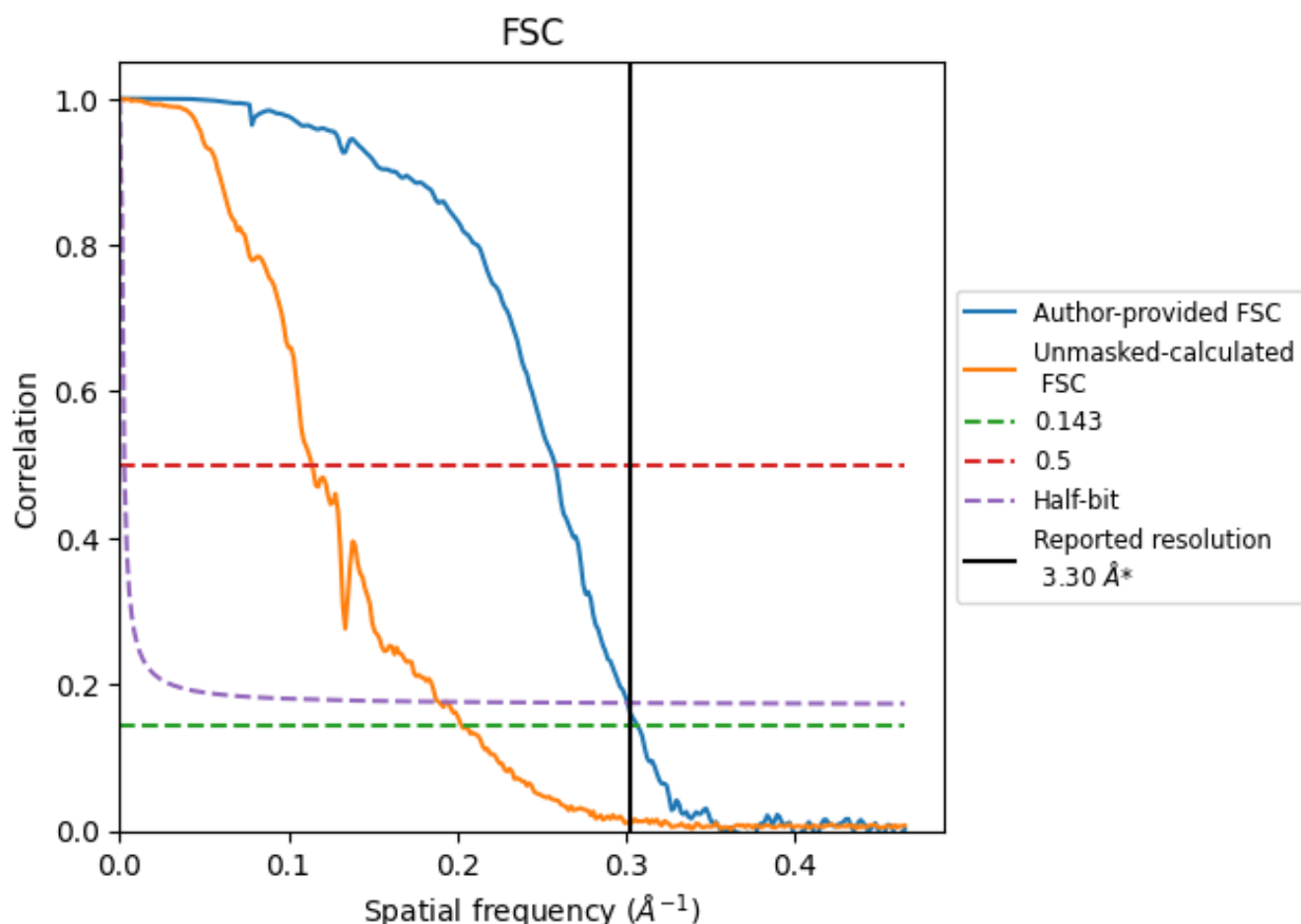


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

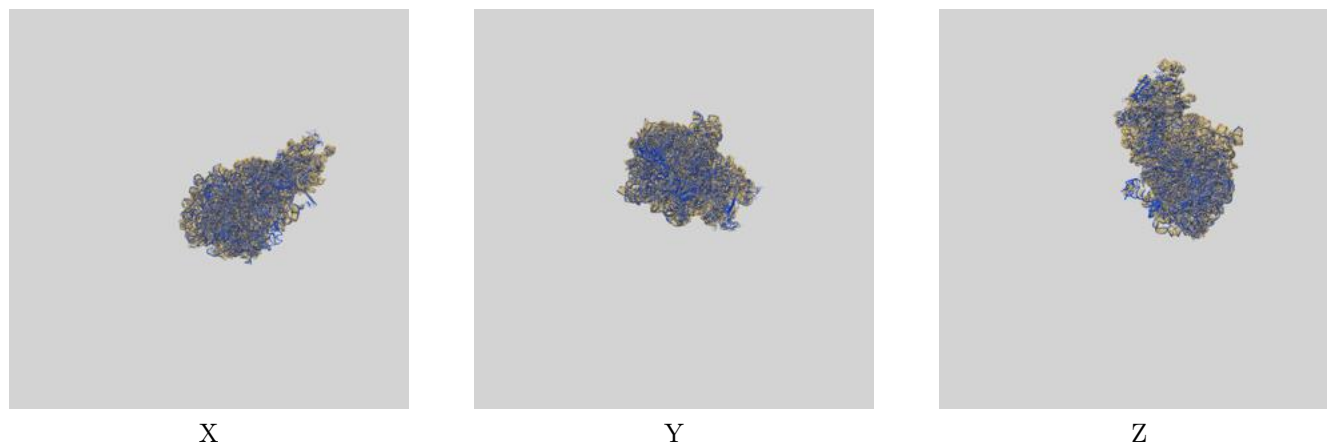
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.88	3.32
Unmasked-calculated*	4.93	8.78	5.29

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.93 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

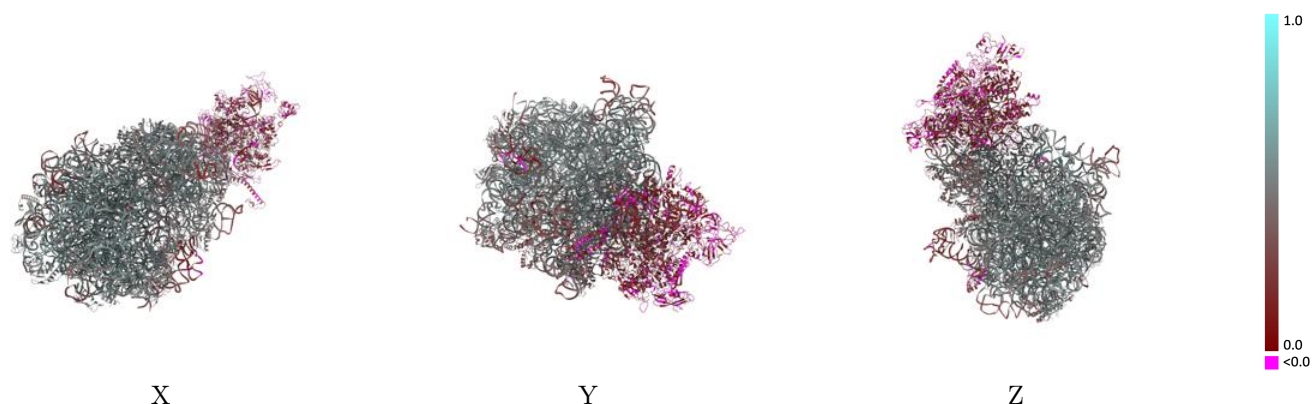
This section contains information regarding the fit between EMDB map EMD-11420 and PDB model 6ZTM. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



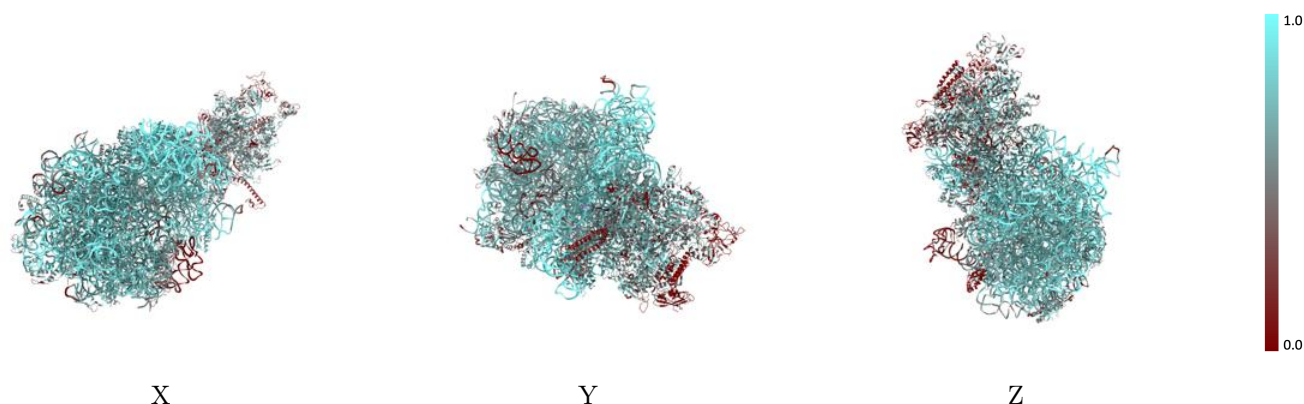
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



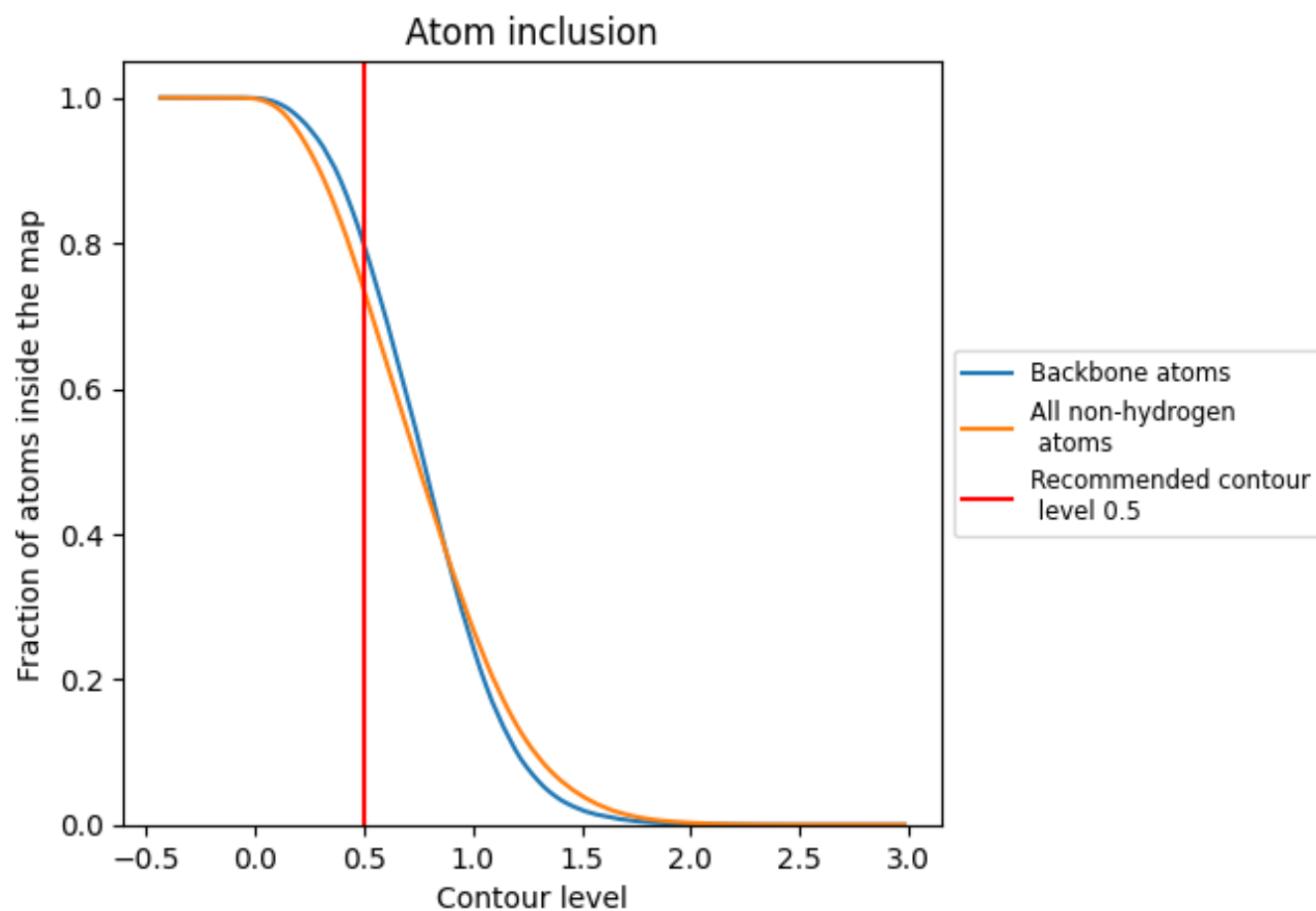
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 74% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7353	 0.4370
AA	 0.9357	 0.4900
AB	 0.3529	 0.3850
AC	 0.5941	 0.4560
AD	 0.5868	 0.4460
AE	 0.7398	 0.4930
AF	 0.6191	 0.4420
AG	 0.6489	 0.4010
AH	 0.7760	 0.5070
AI	 0.8006	 0.4310
AJ	 0.5806	 0.4130
AK	 0.6528	 0.4640
AL	 0.7836	 0.5210
AM	 0.7404	 0.3980
AN	 0.7623	 0.4590
AO	 0.7565	 0.4820
AP	 0.8517	 0.5230
AQ	 0.8032	 0.5060
AR	 0.7629	 0.5250
AS	 0.8331	 0.4470
AT	 0.8000	 0.4960
AU	 0.3411	 0.3650
AV	 0.5503	 0.3260
AW	 0.5999	 0.4060
AX	 0.4960	 0.4260
B1	 0.6613	 0.5180
B2	 0.6713	 0.5100
B3	 0.2079	 0.4270
B4	 0.7634	 0.5640
B5	 0.6680	 0.5390
B6	 0.6678	 0.5250
BA	 0.8218	 0.5010
BB	 0.7954	 0.4490
BC	 0.7055	 0.5340
BD	 0.6771	 0.5240



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Chain	Atom inclusion	Q-score
BE	 0.6309	 0.5020
BF	 0.3362	 0.3560
BG	 0.4483	 0.4220
BH	 0.0602	 0.2330
BK	 0.6864	 0.5180
BL	 0.6529	 0.5190
BM	 0.6579	 0.5060
BN	 0.6663	 0.5230
BO	 0.7259	 0.5270
BP	 0.5660	 0.4390
BQ	 0.6284	 0.4950
BR	 0.7456	 0.5320
BS	 0.6863	 0.5120
BT	 0.6627	 0.5180
BU	 0.5789	 0.4790
BV	 0.5766	 0.4730
BW	 0.6016	 0.4740
BX	 0.6873	 0.5390
BY	 0.6556	 0.5230
BZ	 0.5808	 0.4550
CA	 0.4572	 0.1670
CB	 0.2215	 0.1040
CC	 0.5237	 0.1740
CD	 0.4279	 0.1480
CN	 0.5049	 0.1520
CT	 0.7591	 0.2430