



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:22 PM UTC

PDB ID : 8CEH / pdb_00008ceh
EMDB ID : EMD-16609
Title : Translocation intermediate 4 (TI-4) of 80S *S. cerevisiae* ribosome with ligands and eEF2 in the presence of sordarin
Authors : Milicevic, N.; Jenner, L.; Myasnikov, A.; Yusupov, M.; Yusupova, G.
Deposited on : 2023-02-01
Resolution : 2.05 Å(reported)

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

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

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

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

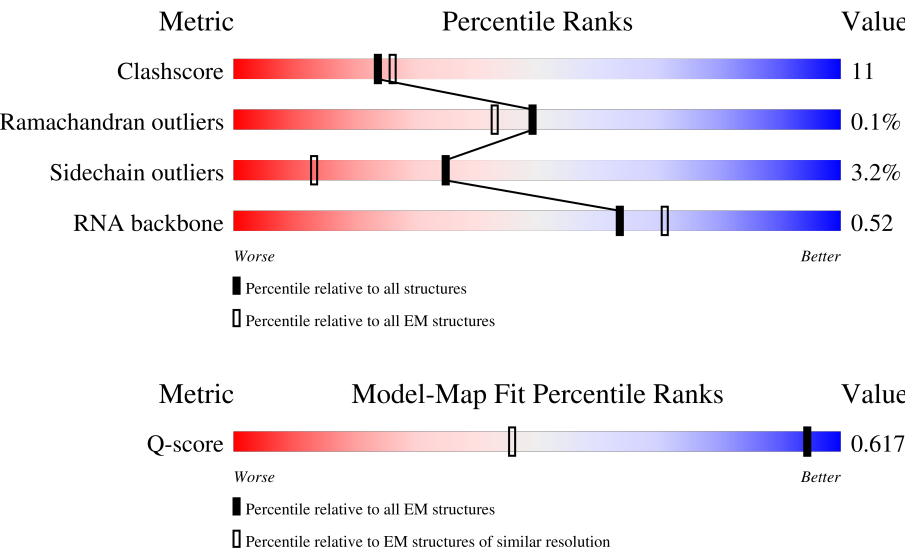
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.05 Å.

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



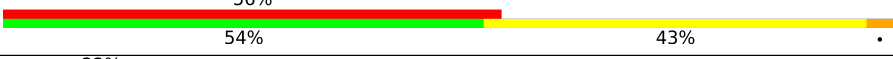
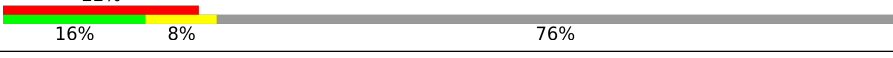
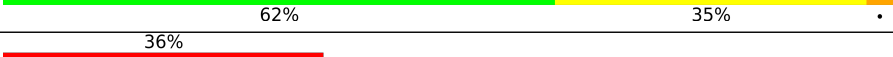
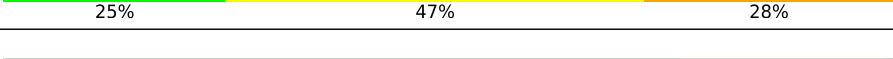
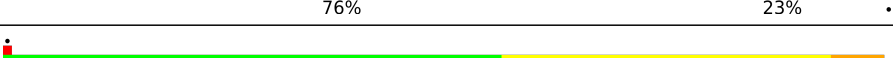
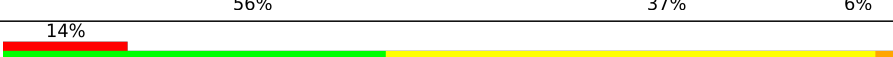
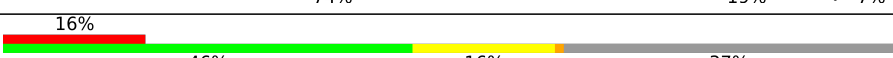
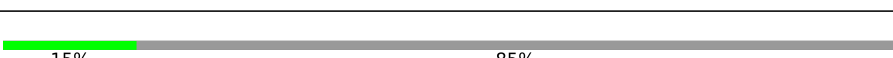
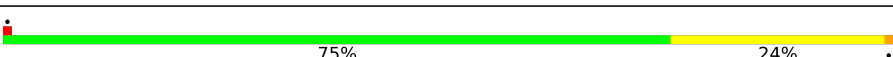
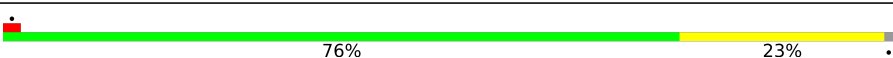
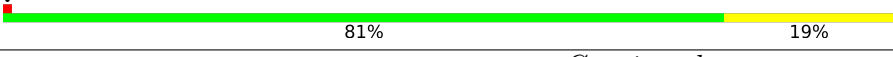
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1849 (1.55 - 2.55)

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	0	135	11% 60% 37% ..
2	1	108	63% 37% 24% 35%
3	2	119	65% 16% 18%

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Mol	Chain	Length	Quality of chain
4	3	82	
5	4	67	
6	5	56	
7	6	63	
8	7	319	
9	8	152	
10	A	199	
11	AA	3396	
12	Aa	842	
13	B	184	
14	BB	121	
15	Bb	76	
16	C	186	
17	CC	158	
18	Cc	77	
19	D	189	
20	DD	312	
21	Dd	39	
22	E	172	
23	EE	254	
24	Ee	165	
25	F	160	
26	FF	387	
27	G	121	
28	GG	362	

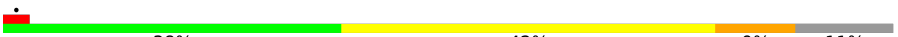
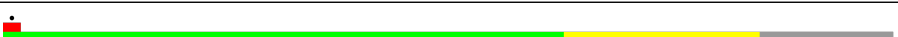
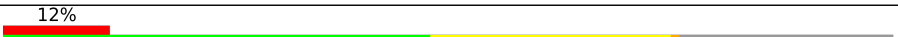
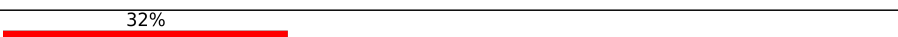
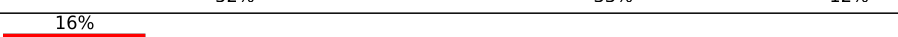
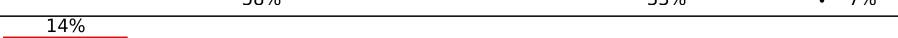
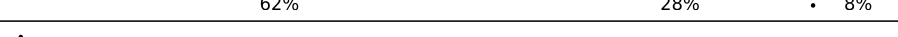
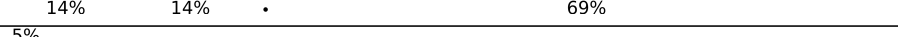
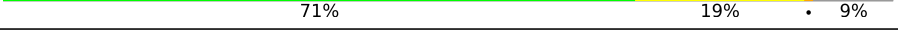
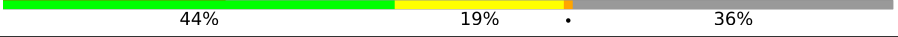
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Mol	Chain	Length	Quality of chain
29	H	137	
30	HH	297	
31	I	155	
32	II	176	
33	J	142	
34	JJ	244	
35	K	127	
36	KK	256	
37	L	136	
38	LL	191	
39	M	149	
40	MM	221	
41	N	59	
42	NN	174	
43	O	105	
44	OO	199	
45	P	113	
46	PP	138	
47	Pp	2	
48	Q	130	
49	QQ	204	
50	R	107	
51	S	121	
52	T	120	
53	U	100	

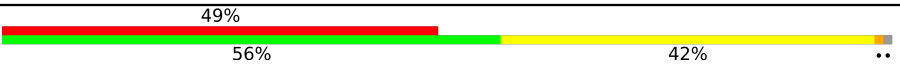
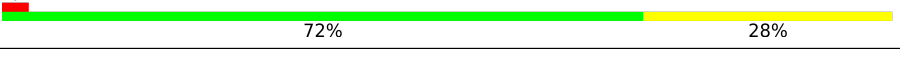
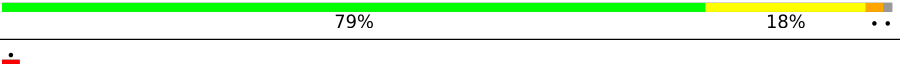
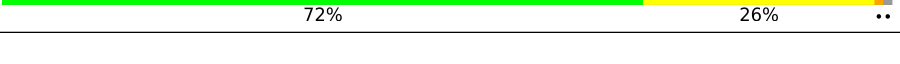
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Mol	Chain	Length	Quality of chain
54	V	88	
55	W	78	
56	X	51	
57	Y	128	
58	Z	25	
59	a	106	
60	b	92	
61	c	1800	
62	d	252	
63	e	255	
64	f	254	
65	g	240	
66	h	261	
67	i	225	
68	j	236	
69	k	190	
70	l	200	
71	m	197	
72	n	105	
73	o	156	
74	p	151	
75	q	137	
76	r	142	
77	s	143	
78	t	136	

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Mol	Chain	Length	Quality of chain
79	u	146	
80	v	144	
81	w	121	
82	x	87	
83	y	130	
84	z	145	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
90	PO4	Aa	1002	-	-	X	-

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 207126 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 2 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 3 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 4 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 5 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 6 is a protein called HLJ1_G0030400.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	49	Total	C	N	O	S	0	0
			404	249	86	65	4		

- Molecule 7 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	53	Total	C	N	O	S	0	0
			427	269	88	69	1		

- Molecule 8 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 9 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	36	Total	C	N	O	S	0	0
			276	173	54	45	4		

- Molecule 10 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 11 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	3197	Total	C	N	O	P	0	0
			68429	30589	12334	22309	3197		

- Molecule 12 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Aa	816	Total	C	N	O	S	0	0
			6368	4051	1088	1198	31		

- Molecule 13 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	B	154	Total	C	N	O	0	0
			1222	761	237	224		

- Molecule 14 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 15 is a RNA chain called Transfer RNA Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Bb	76	Total	C	N	O	P	0	0
			1638	736	294	533	75		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 17 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 18 is a RNA chain called Transfer RNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cc	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cc	18	C	U	conflict	GB 170517292

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	D	176	Total	C	N	O	0	0
			1423	875	308	240		

- Molecule 20 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	DD	197	Total	C	N	O	S	0	0
			1531	980	266	281	4		

- Molecule 21 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Dd	6	Total	C	N	O	P	0	0
			125	56	18	45	6		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	E	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 23 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	EE	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 24 is a protein called 60S ribosomal protein L12-A.

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

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

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

- Molecule 26 is a protein called 60S ribosomal protein L3.

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

- Molecule 27 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	G	97	Total	C	N	O	0	0
			770	499	126	145		

- Molecule 28 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	129	Total	C	N	O	S	0	0
			963	607	180	169	7		

- Molecule 30 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	HH	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 31 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	II	155	Total	C	N	O	S	0	0
			1230	795	221	213	1		

- Molecule 33 is a protein called 60S ribosomal protein L25.

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

- Molecule 34 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	JJ	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 35 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 36 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	KK	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 37 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L	135	Total	C	N	O	S	0	0
			1092	710	202	180			

- Molecule 38 is a protein called RPL9A isoform 1.

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

- Molecule 39 is a protein called 60S ribosomal protein L28.

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

- Molecule 40 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	MM	215	Total	C	N	O	S	0	0
			1743	1102	331	303	7		

- Molecule 41 is a protein called 60S ribosomal protein L29.

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

- Molecule 42 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	O	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 44 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	PP	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 47 is a protein called Polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Pp	2	Total	C	N	O	S	0	0
			19	14	2	2	1		

- Molecule 48 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Q	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 49 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S	109	Total	C	N	O	S	0	0
			861	533	175	149	4		

- Molecule 52 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	T	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 53 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	U	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 54 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 55 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	W	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 56 is a protein called 60S ribosomal protein L39.

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

- Molecule 57 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 58 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Z	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 59 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	a	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

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

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

- Molecule 61 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	c	1608	Total	C	N	O	P	0	0
			34321	15360	6093	11260	1608		

- Molecule 62 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	d	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 63 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	e	212	Total	C	N	O	S	0	0
			1689	1073	303	309	4		

- Molecule 64 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	f	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 65 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	g	183	Total	C	N	O	S	0	0
			1412	893	260	253	6		

- Molecule 66 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	h	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 67 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	i	199	Total	C	N	O	S	0	0
			1572	987	290	292	3		

- Molecule 68 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	j	219	Total	C	N	O	S	0	0
			1766	1108	341	314	3		

- Molecule 69 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	k	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 70 is a protein called 40S ribosomal protein S8-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	l	184	Total	C	N	O	S	0	0
			1457	906	291	258	2		

- Molecule 71 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	m	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 72 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	n	33	Total	C	N	O	0	0
			300	199	46	55		

- Molecule 73 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	o	142	Total	C	N	O	S	0	0
			1146	735	217	191	3		

- Molecule 74 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	p	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 75 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	q	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 76 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	r	91	Total	C	N	O	S	0	0
			732	469	138	120	5		

- Molecule 77 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	s	137	Total	C	N	O	S	0	0
			1080	692	199	189			

- Molecule 78 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	t	121	Total	C	N	O	S	0	0
			961	599	182	178	2		

- Molecule 79 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	u	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 80 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	v	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 81 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	w	100	Total	C	N	O	S	0	0
			800	509	144	146	1		

- Molecule 82 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	x	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 83 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	y	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 84 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	z	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	2	1	Total	Zn	0
			1	1	
85	5	1	Total	Zn	0
			1	1	
85	8	1	Total	Zn	0
			1	1	
85	S	1	Total	Zn	0
			1	1	
85	V	1	Total	Zn	0
			1	1	
85	Y	1	Total	Zn	0
			1	1	
85	a	1	Total	Zn	0
			1	1	
85	b	1	Total	Zn	0
			1	1	

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	AA	198	Total	Mg	0
			198	198	
86	Aa	1	Total	Mg	0
			1	1	
86	B	1	Total	Mg	0
			1	1	
86	BB	5	Total	Mg	0
			5	5	
86	Bb	1	Total	Mg	0
			1	1	

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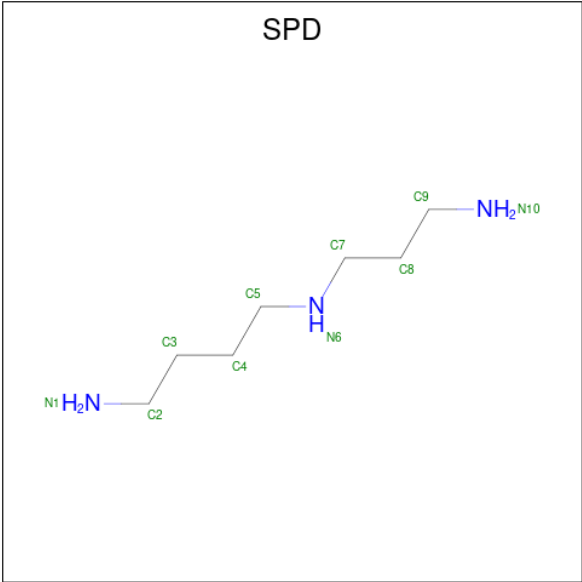
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Mol	Chain	Residues	Atoms		AltConf
86	CC	3	Total 3	Mg 3	0
86	Dd	1	Total 1	Mg 1	0
86	FF	1	Total 1	Mg 1	0
86	H	1	Total 1	Mg 1	0
86	QQ	1	Total 1	Mg 1	0
86	c	49	Total 49	Mg 49	0

- Molecule 87 is POTASSIUM ION (CCD ID: K) (formula: K).

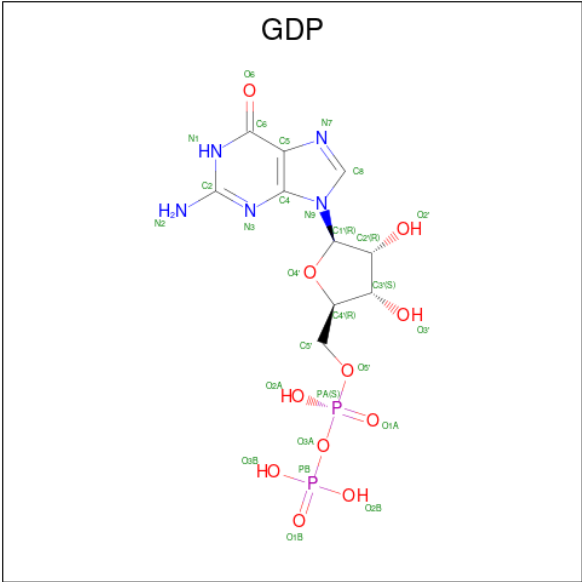
Mol	Chain	Residues	Atoms		AltConf
87	AA	14	Total 14	K 14	0
87	EE	1	Total 1	K 1	0
87	MM	1	Total 1	K 1	0
87	Q	1	Total 1	K 1	0
87	a	1	Total 1	K 1	0
87	c	2	Total 2	K 2	0
87	q	1	Total 1	K 1	0

- Molecule 88 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



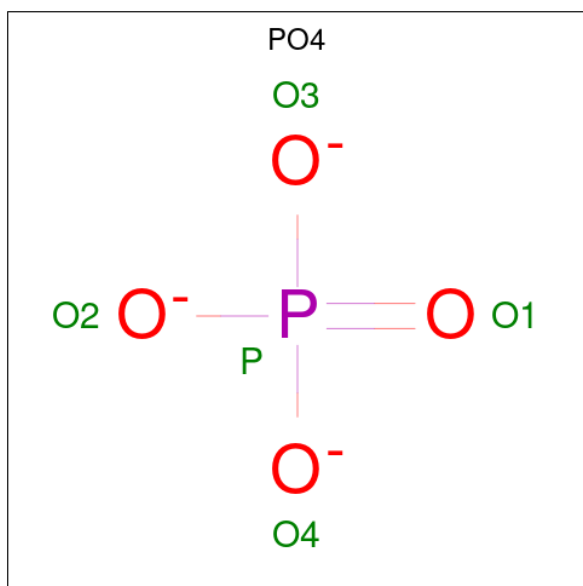
Mol	Chain	Residues	Atoms			AltConf
88	AA	1	Total	C	N	0
			10	7	3	
88	AA	1	Total	C	N	0
			10	7	3	
88	AA	1	Total	C	N	0
			10	7	3	

- Molecule 89 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).



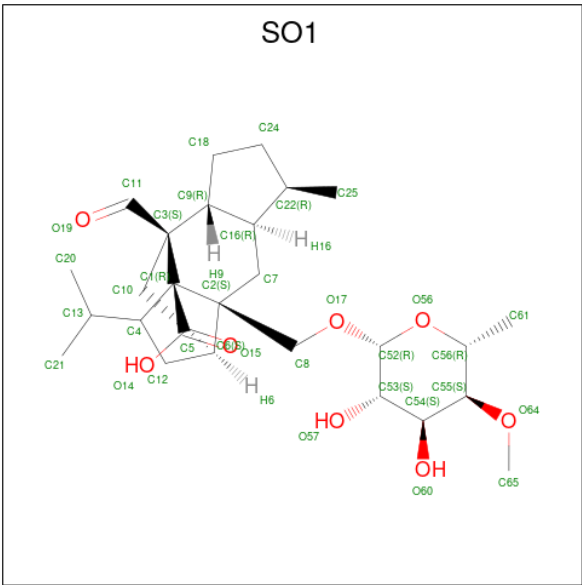
Mol	Chain	Residues	Atoms					AltConf
89	Aa	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 90 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			AltConf
90	Aa	1	Total	O	P	0
			5	4	1	

- Molecule 91 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: $C_{27}H_{42}O_8$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
91	Aa	1	Total	C	O	0
			35	27	8	

• Molecule 92 is water.

Mol	Chain	Residues	Atoms		AltConf
92	2	1	Total	O	0
			1	1	
92	A	2	Total	O	0
			2	2	
92	AA	778	Total	O	0
			778	778	
92	B	3	Total	O	0
			3	3	
92	BB	13	Total	O	0
			13	13	
92	CC	13	Total	O	0
			13	13	
92	Cc	1	Total	O	0
			1	1	
92	D	1	Total	O	0
			1	1	
92	EE	6	Total	O	0
			6	6	
92	F	4	Total	O	0
			4	4	
92	FF	3	Total	O	0
			3	3	

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Mol	Chain	Residues	Atoms		AltConf
92	GG	3	Total 3	O 3	0
92	H	3	Total 3	O 3	0
92	HH	1	Total 1	O 1	0
92	J	1	Total 1	O 1	0
92	JJ	1	Total 1	O 1	0
92	M	2	Total 2	O 2	0
92	MM	2	Total 2	O 2	0
92	N	1	Total 1	O 1	0
92	Q	4	Total 4	O 4	0
92	QQ	6	Total 6	O 6	0
92	V	2	Total 2	O 2	0
92	c	118	Total 118	O 118	0
92	h	2	Total 2	O 2	0
92	o	2	Total 2	O 2	0
92	p	2	Total 2	O 2	0

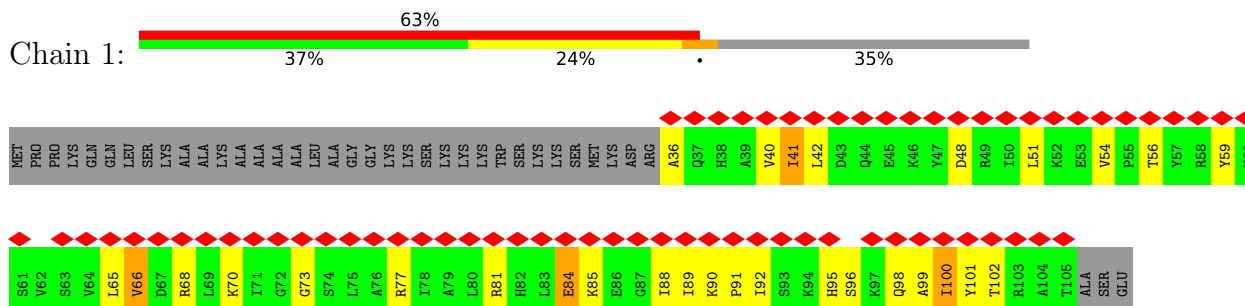
3 Residue-property plots [i](#)

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.

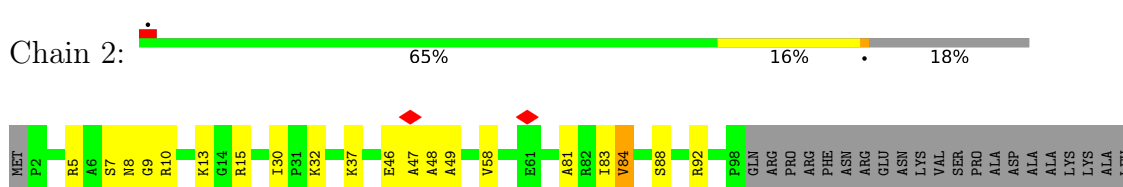
- Molecule 1: 40S ribosomal protein S24-A



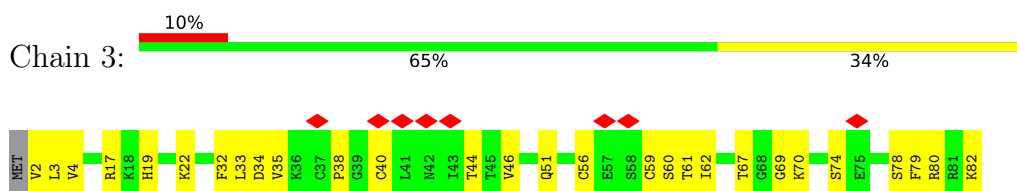
- Molecule 2: 40S ribosomal protein S25-A



- Molecule 3: 40S ribosomal protein S26

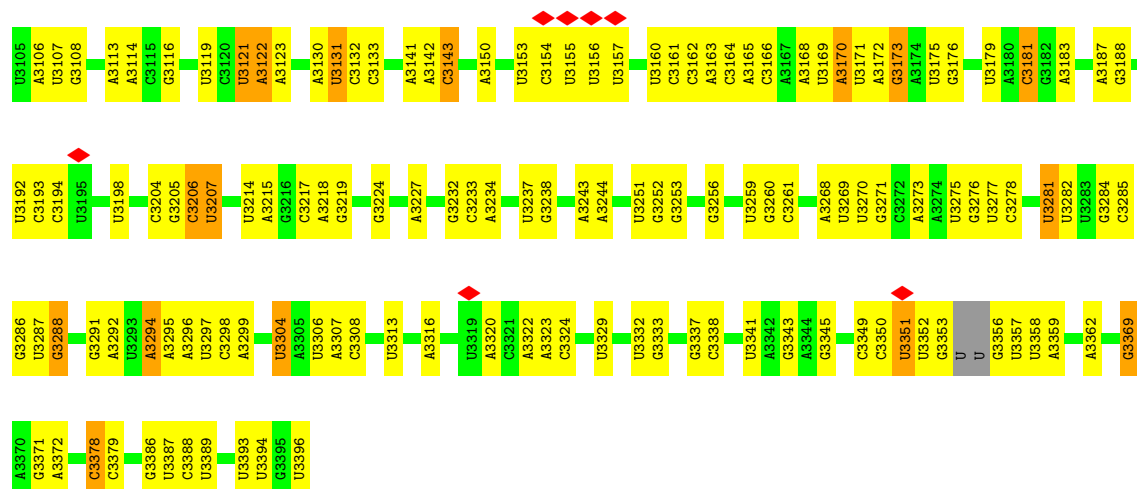


- Molecule 4: 40S ribosomal protein S27-A

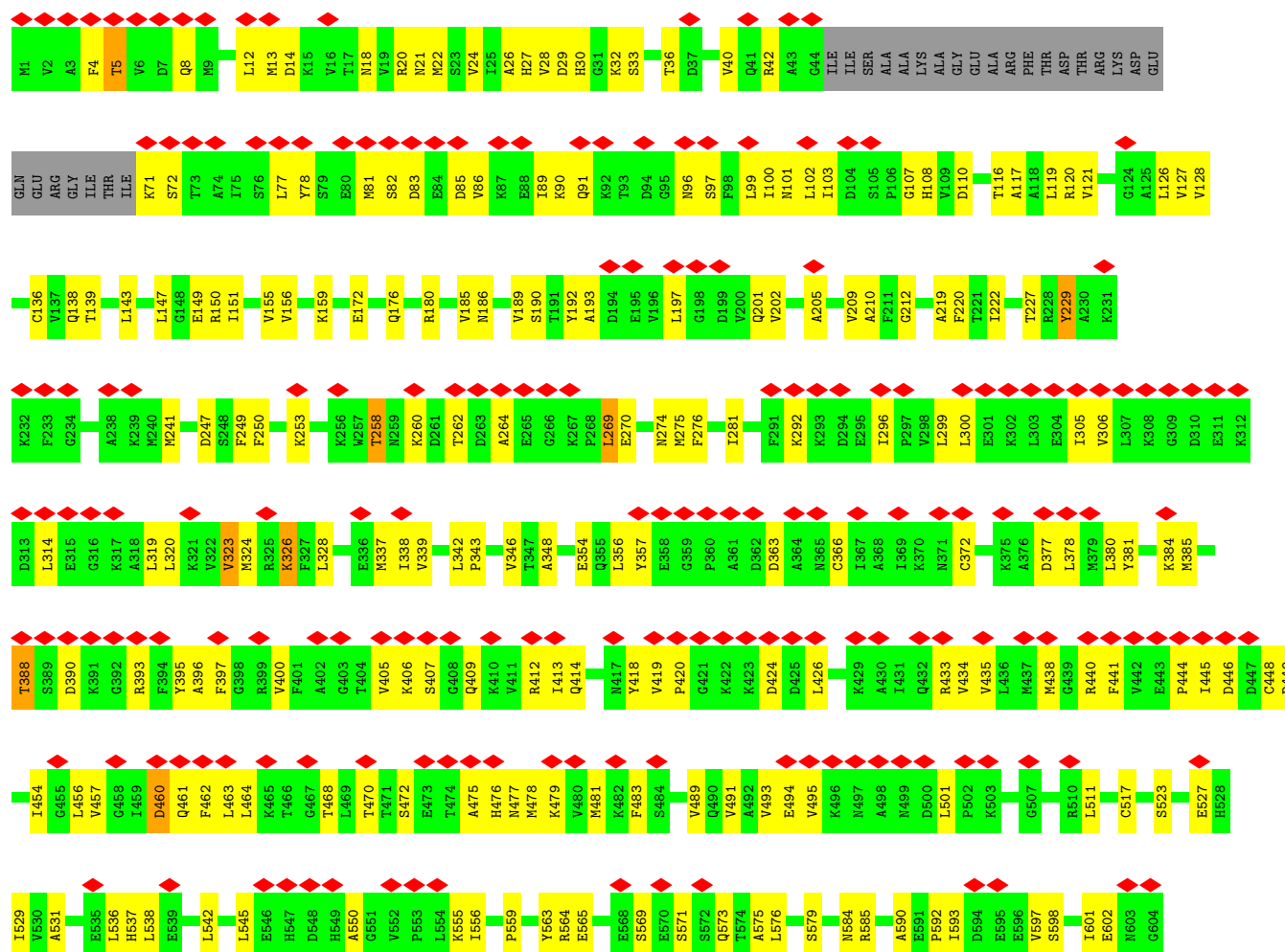


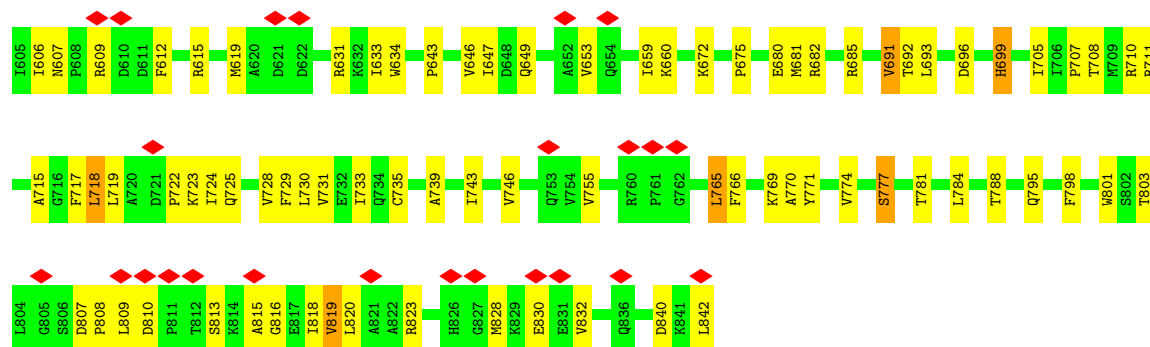


G3022	G2938	G2848	G2752	G2659	A2561	U2493	U2428	G2355	G2249	U2162	U	G
U3023	C2941	G2848	G2753	G2660	A2562	A2494	G2429	A2356	A2256	C2163	A	A
A3024	C2942	C2852	G2754	G2661	G2661	C2495	C2430	A2357	C2257	A2167	C	U
	G2943	A2853	G2755	G2662	C2566	C2496	C2431	C2358	C2257	A2168	A	U
G3031	U2944	A2854	G2756	G2663	C2567	C2497		A2361	U2258	C2169	U	C
U3038	G2945	U2855	U2757	G2672	C2568	U2498	G2435	C2362	G2261	U2171	U	C
U3041	G2946	G2856	C2760	A2674	A2569	U2499	U2436	C2363	A2262	G2171	A	U
U3042	C2947	C2857	G2761	A2673	U2570	U2500	G2437	G2364	A2263			
	U2948	U2861	U2762	A2674	U2571	U2501	A2442	C2365	U2264	U2176	A2093	G
G3045	G2950	U2862	G2763	G2677	C2572	A2502	A2443	C2366	U2265	C2177	G2095	C
A3046	U2953	C2867	G2764	U2681	G2574	G2503	A2445	A2367	A2270	C2178		C
U3047	U2954	U2868	U2765	C2682	U2575	U2504	U2446	A2368	A2271	C2179	C2101	G
A3048	U2955	U2869	U2766	C2683	U2576	U2505	U2447	G2370	A2272	G2180	U2102	C
A3049	A2956	G2870	U2767	C2684	G2579	U2506	G2448	G2371	G2273	C2181	A2103	C
U3050	C2959	A2871	G2768	A2689	G2585	U2507	A2449	A2372	G2185		A2104	G
U3051	C2960	A2872	G2769	G2690	U2588	U2508	G2450	A2373	A2280	U2186	U2112	U
G3052	G2963	U2880	U2770	A2691	U2589	U2509	G2451	C2374	A2281	G2187	A2113	U
G3053	G2964	C2881	G2771	A2692	G2592	A2510	G2452	G2375	U2282	A2188	C2114	U
U3056		U2882	G2772	A2696	C2593	C2511	G2453	G2376	U2283	U2191	G2115	G
G3059		U2883	G2773	A2697	C2594	U2512	G2454	C2377	C2284	C2192	A2116	U
C3063	A2967	C2884	U2774	G2700	U2597	U2514	G2455	U2379	C2285	U2193	A2117	A
U3064	G2968	A2887	G2775	G2701	C2598	A2515	A2456	U2380	U2289	G2194	A2120	U
G3065	A2969	G2888	G2776	A2704	C2599	U2520	A2457	U2388	C2290	C2195	G2121	C
U3066	C2970	G2889	U2777	G2705	U2599	U2521	G2458	C2389	U2301	C2196	G2122	U
C3067	A2971	G2890	G2778	G2706	C2600	A2523	A2459	A2390	U2203	U2127	A1914	G
U3068	G2972	A2897	U2779	C2707	G2606	G2524	U2460	G2393	G2305	C2204	A1915	G
G3069	U2973	C2898	A2799	C2708	G2607	U2525	A2461	G2396	G2306	U2205	C2128	C
A3070	A2974	G2900	G2800	C2709	U2610	C2526	A2462	A2397	C2307	G2206	U2129	A
U3071	G2975	G2901	A2801	C2711	G2611	G2527	A2463	U2403	U2310	A2207	G2130	U
C3072	U2976	U2904	G2802	G2712	U2612	U2532	U2464	A2402	G2311	U2211	U2133	G
A3073	U2977	U2905	A2803	G2713	U2613	G2533	G2465	A2403	C2312	C2212	C2136	A
G3074	C2978	A2910	C2809	U2714	G2614	G2534	G2466	A2404	A2313	A2213	U2137	G
U3075	A2983	G2911	A2810	U2715	G2615	A2535	G2467	C2405	U2314	A2214	A2138	U
U3078	C2984	A2912	A2811	U2722	C2616	A2536	G2468	C2406	G2315	G2215	A2139	C
U3079	G2985	G2913	G2812	U2723	U2631	U2537	A2469	C2407	U2328	U2217	U2140	U
G3080	A2986	C2914	G2813	U2724	U2634	U2538	C2470	U2408	G2329	G2218	A2142	C
C3084	G2990	U2915	G2814	U2725	U2637	C2539	U2471	U2411	A2332	A2219	A2143	U
G3085	G2997	U2916	G2815	C2726	A2637	A2540	U2472	G2412	C2333	A2220	A2144	G
U3089	U2997	G2921	A2816	G2727	C2638	U2541	C2473	A2413	U2334	G2221	A2145	A
U3090	A3000	U2922	G2817	G2728	G2639	U2542	G2474	G2414	A2222	A2223	C2146	U
A3091	C3001	U2923	A2820	U2729	A2640	U2543	G2475	C2415	A2224	A2248	U2148	A
C3092	A3006	U2924	G2823	A2738	U2641	C2544	C2476	U2416	U2225	U2226	A2149	C
C3093	U3007	G2925	G2824	A2739	A2642	C2545	C2477	G2418	C2227	C2227	A2152	C
A3094	C3009	U2926	U2828	U2744	G2648	A2546	U2478	A2419	A2228	U2153	U2153	G
U3095	U3012	C2929	G2830	G2745	C2547	U2547	C2479	C2420	A2346	A2229	C2156	U
C3096	A3013	A2930	U2835	A2746	G2549	U2548	A2480	U2421	U2347		A2158	A
C3097	U3014	C2931	C2836	A2747	U2651	G2549	A2481	U2423	A2348	A2230	G2157	G
	G3101	U2935	U2837	A2748	U2652	C2552	U2482	A2424	A2362	A2233	A2159	A
U3104	A3016	A2936	C2844	U2749	A2656	U2553	U2483	G2425	G2353	A2244	G2160	G
				U2750	A2657	A2554	A2484	U2426	G2354		G2161	C
				A2557	G2658	U2557	A2485	U2427				
				U2558		U2559	A2486					
				C2560			U2487					
							A2488					
							C2489					
							C2490					
							A2491					
							C2492					



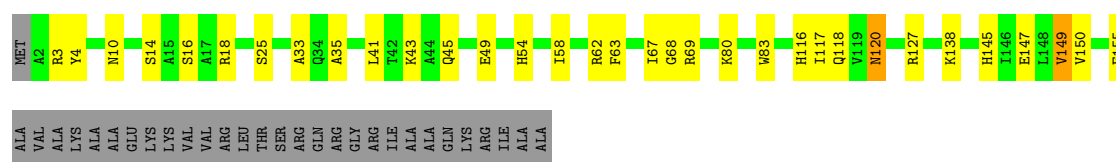
• Molecule 12: Elongation factor 2





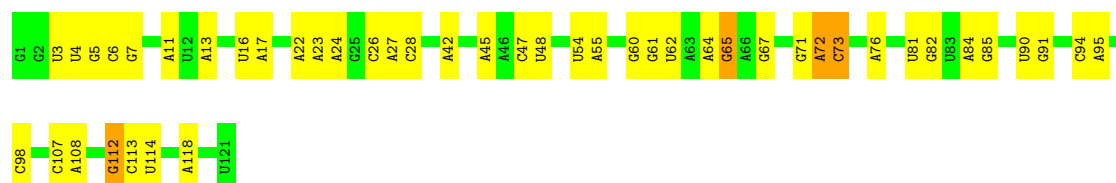
• Molecule 13: 60S ribosomal protein L17-A

Chain B: 66% 17% 16%



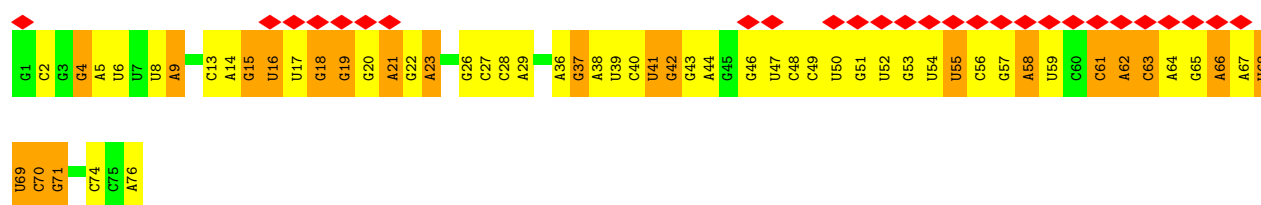
• Molecule 14: 5S ribosomal RNA

Chain BB: 62% 35%



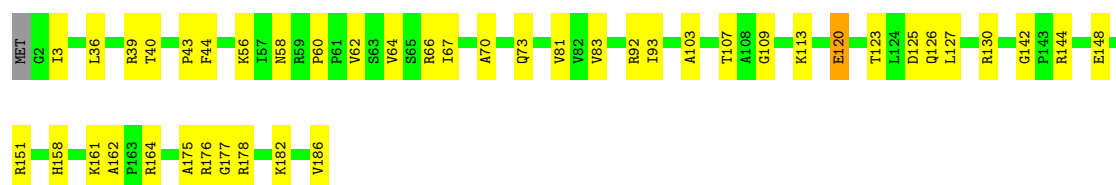
• Molecule 15: Transfer RNA Phe

Chain Bb: 25% 36% 47% 28%

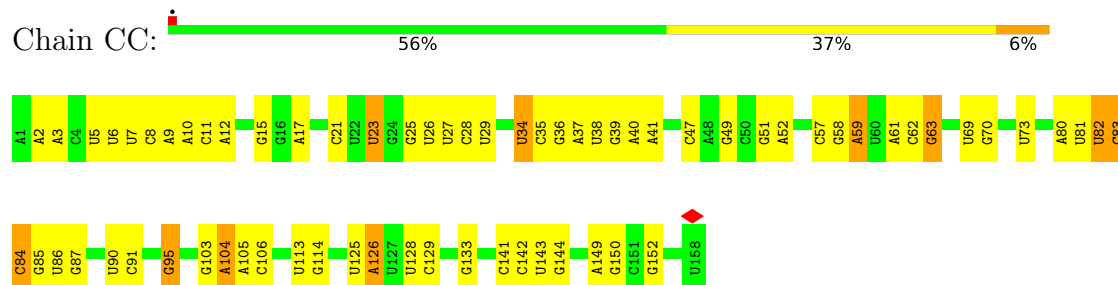


• Molecule 16: 60S ribosomal protein L18-A

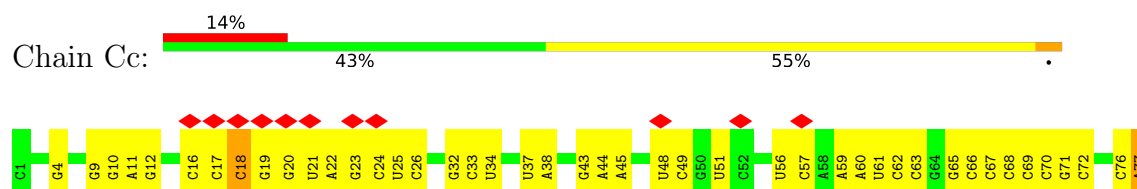
Chain C: 76% 23%



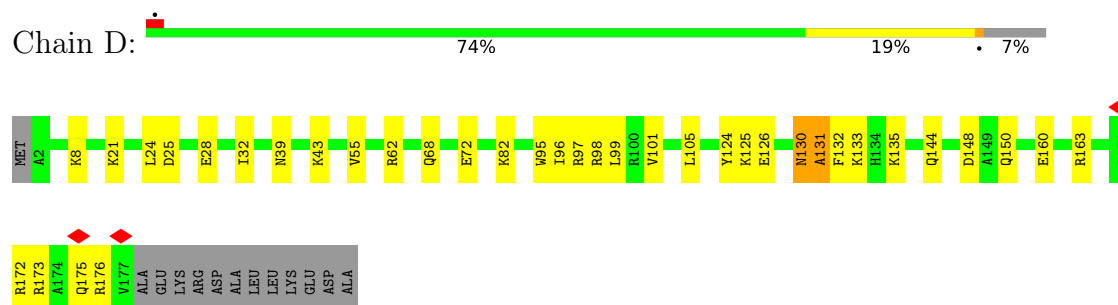
- Molecule 17: 5.8S ribosomal RNA



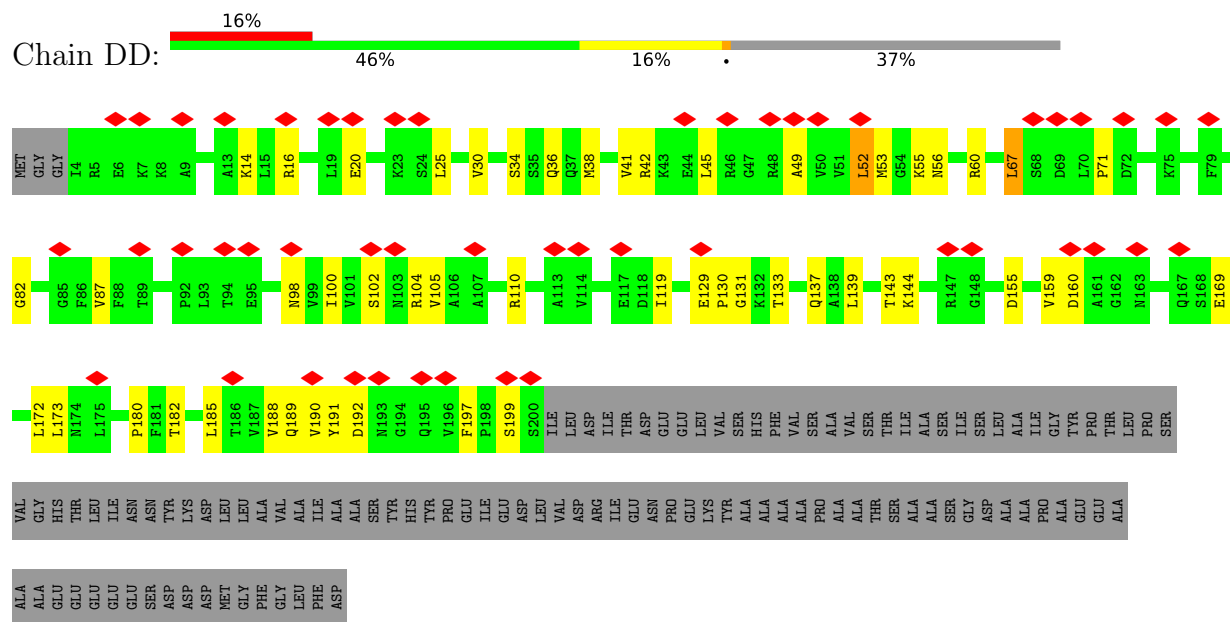
- Molecule 18: Transfer RNA fMet



- Molecule 19: 60S ribosomal protein L19-A



- Molecule 20: 60S acidic ribosomal protein P0



- Molecule 21: Messenger RNA

A A A A A G G A A A A A A A A A G C A A A A A A A A U¹⁹ U²⁴ U U U U G U G A A G G A A A A A G C A A A A

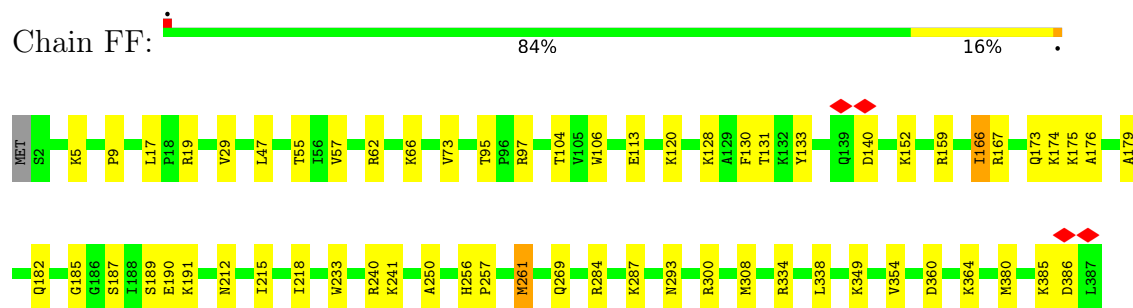
- Chain E:
-
- 75% 24%
- Legend: ◆ Red, ◆ Green, ◆ Yellow
- | Label | Color |
|-------|--------|
| M1 | Yellow |
| A2 | Yellow |
| E6 | Yellow |
| Y7 | Yellow |
| Q8 | Yellow |
| W9 | Yellow |
| I10 | Yellow |
| G11 | Yellow |
| R12 | Yellow |
| R13 | Yellow |
| L14 | Yellow |
| P15 | Yellow |
| P22 | Yellow |
| K23 | Green |
| L24 | Yellow |
| M27 | Yellow |
| S32 | Yellow |
| I36 | Yellow |
| Y43 | Yellow |
| F44 | Yellow |
| L45 | Yellow |
| Q46 | Yellow |
| K47 | Yellow |
| V51 | Yellow |
| G56 | Yellow |
| V59 | Yellow |
| S60 | Yellow |
| I61 | Yellow |
| N62 | Yellow |
| G63 | Green |
| I64 | Yellow |
| P69 | Yellow |
| T70 | Green |
| K71 | Yellow |
| V72 | Green |
| K73 | Yellow |
| V77 | Yellow |
| M90 | Yellow |
| I94 | Yellow |
| V97 | Yellow |
| S98 | Green |
| R99 | Yellow |
| L106 | Yellow |
| Y107 | Green |
| V126 | Green |
| T132 | Yellow |
| Q138 | Yellow |
| Y139 | Yellow |
| K149 | Yellow |
| K158 | Yellow |
| R167 | Yellow |
| Y172 | Green |

- Chain EE: 

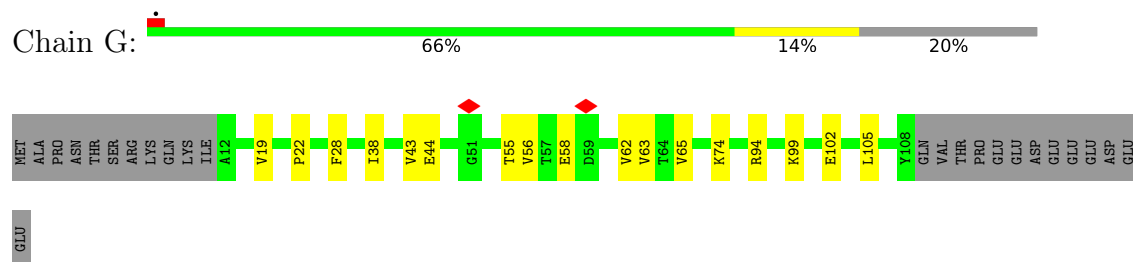
- Chain Ee:
-
- 76%
- 60%
- 32%
-
-
- MET PRO PRO PRO LYS PHE ASP PRO N8 E9 V10 K11 Y12 L13 Y14 L15 R16 A17 V18 G19 G20 E21 V22 G23 A24 S25 A26 A27 L28 A29 P30 K31 I32 G33 P34 L35 G36 L37 S38 P39 K40 K41 V42 G43 E44 D45 I46 A47 K48 A49 T50 K51 E52 F53 K54 G55 I56 K57 V60 D61 L62 K63 I64 Q65 N66 R67 Q68 A69 A70 V73 S78 S79 L80 V81 I82 T83 A84 L85 K86 E87 P88 P89 R90 D91 R92 K93 K94 D95 K96 N97 V98 K99 H100 S101 G102 N103 I104 Q105 L106 D107 E108 I109 I110 E111 I112 A113 R114 G115 M116 R117 D118 K119 R123 I124 L125 A126 S127

- Chain F:  82% 17%
- 
- | Category | Color | Marker |
|----------|--------|-------------|
| MET | Grey | |
| G2 | Green | |
| S9 | Yellow | |
| R12 | Yellow | |
| T13 | Green | |
| M14 | Yellow | |
| F15 | Yellow | |
| Q16 | Yellow | |
| R17 | Yellow | |
| D18 | Green | |
| F19 | Yellow | |
| S28 | Yellow | |
| K32 | Yellow | |
| G51 | Yellow | |
| T68 | Yellow | |
| I75 | Yellow | |
| K78 | Yellow | |
| R88 | Yellow | |
| R92 | Yellow | |
| K100 | Yellow | |
| G101 | Green | |
| R102 | Yellow | |
| Q103 | Yellow | |
| E104 | Red | Red Diamond |
| V109 | Yellow | |
| R116 | Yellow | |
| V124 | Green | Red Diamond |
| A125 | Green | Red Diamond |
| V126 | Yellow | |
| Q127 | Yellow | |
| P132 | Yellow | |
| R136 | Yellow | |
| R139 | Yellow | |
| E157 | Yellow | |
| T158 | Yellow | |
| F159 | Yellow | |

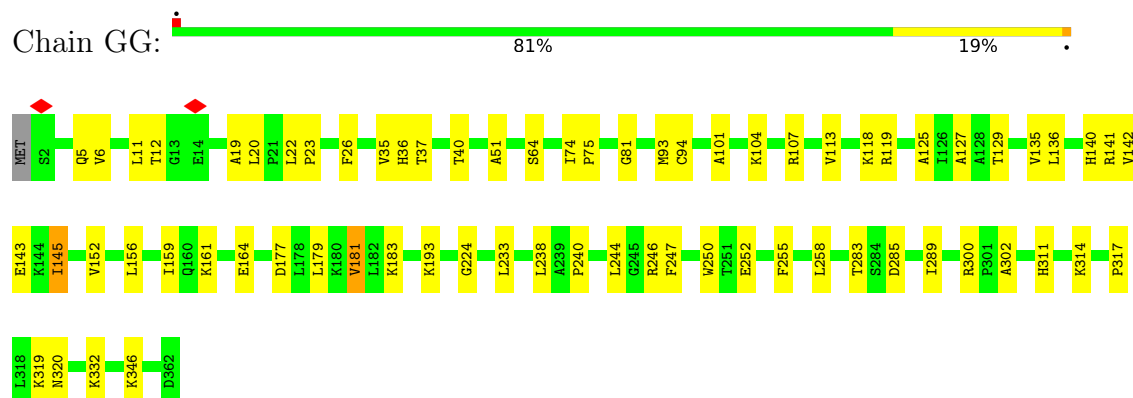
- 
- WORLDWIDE
PDB
PROTEIN DATA BANK



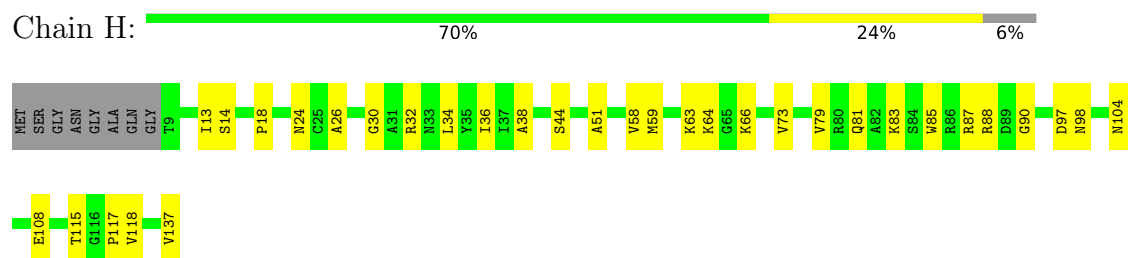
- Molecule 27: 60S ribosomal protein L22-A



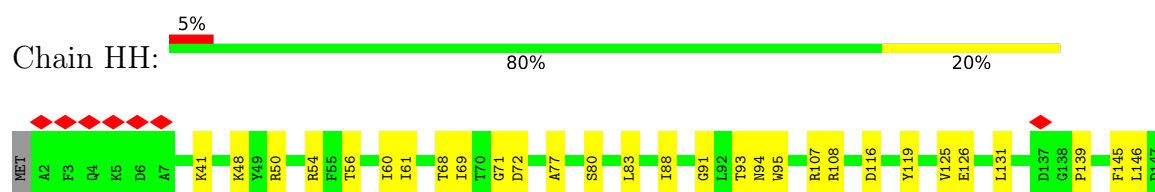
- Molecule 28: 60S ribosomal protein L4-A

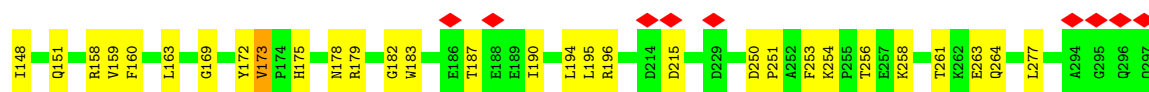


- Molecule 29: 60S ribosomal protein L23-A

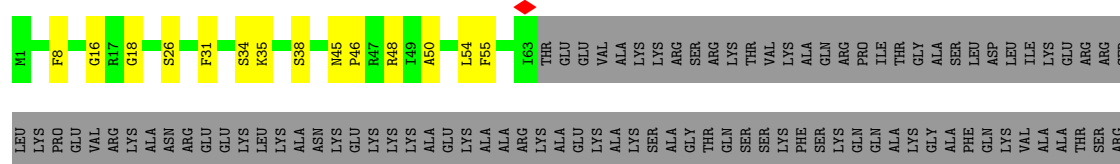


- Molecule 30: 60S ribosomal protein L5

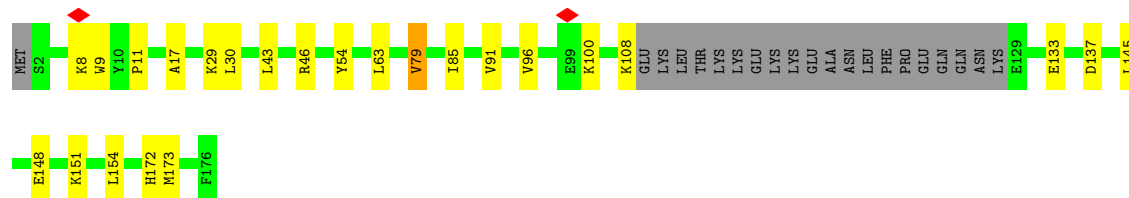
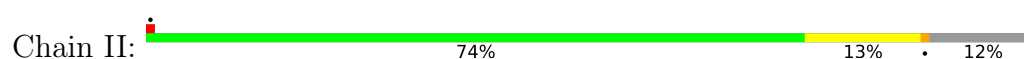




- Molecule 31: 60S ribosomal protein L24-A



- Molecule 32: 60S ribosomal protein L6-A



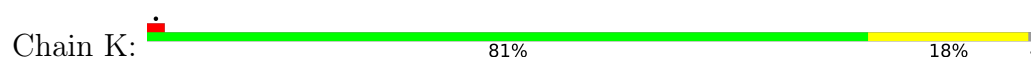
- Molecule 33: 60S ribosomal protein L25



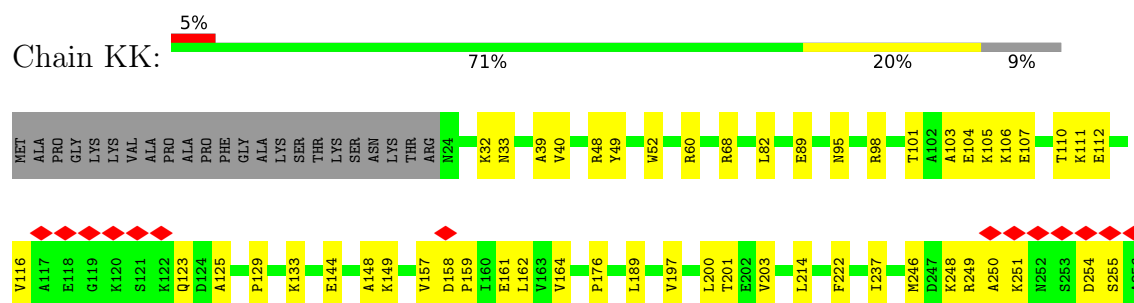
- Molecule 34: 60S ribosomal protein L7-A



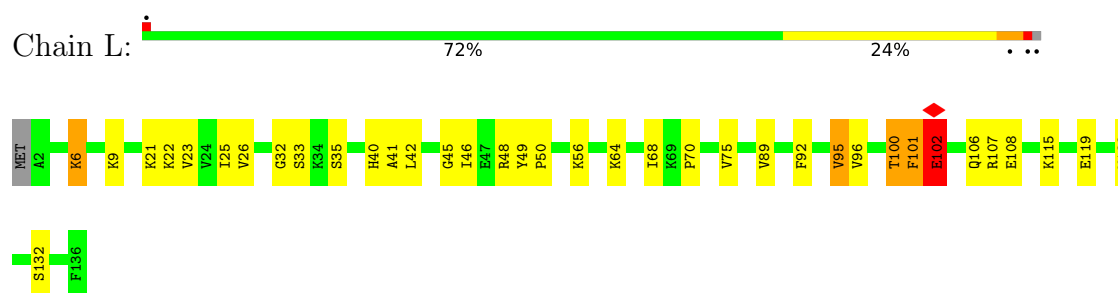
- Molecule 35: 60S ribosomal protein L26-A



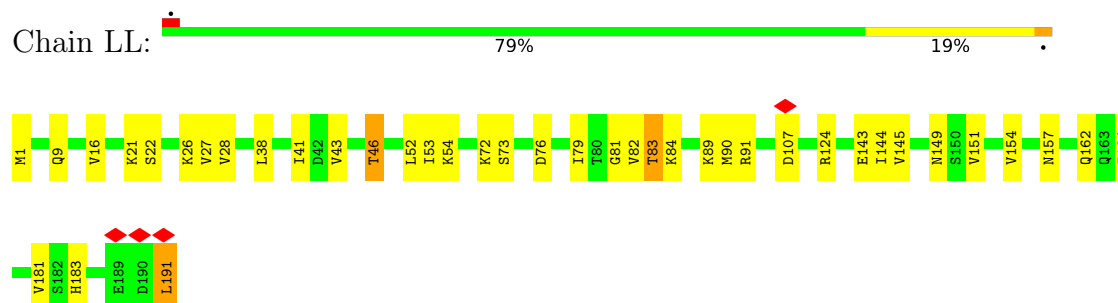
- Molecule 36: 60S ribosomal protein L8-A



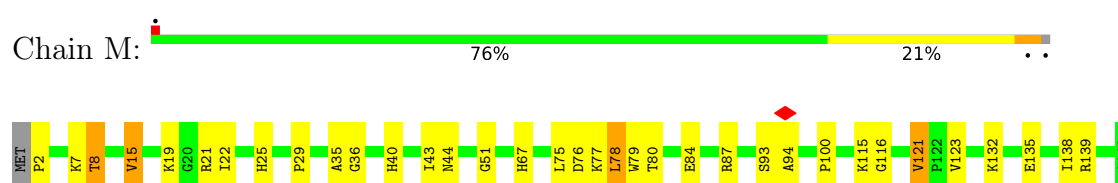
- Molecule 37: 60S ribosomal protein L27-A



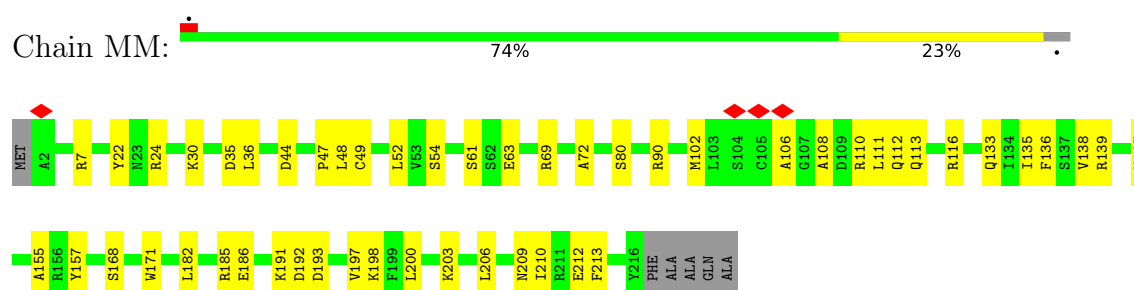
- Molecule 38: RPL9A isoform 1



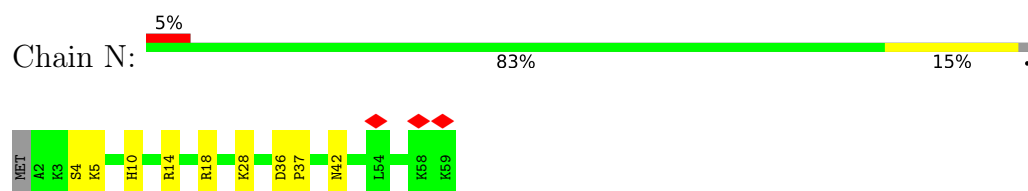
- Molecule 39: 60S ribosomal protein L28



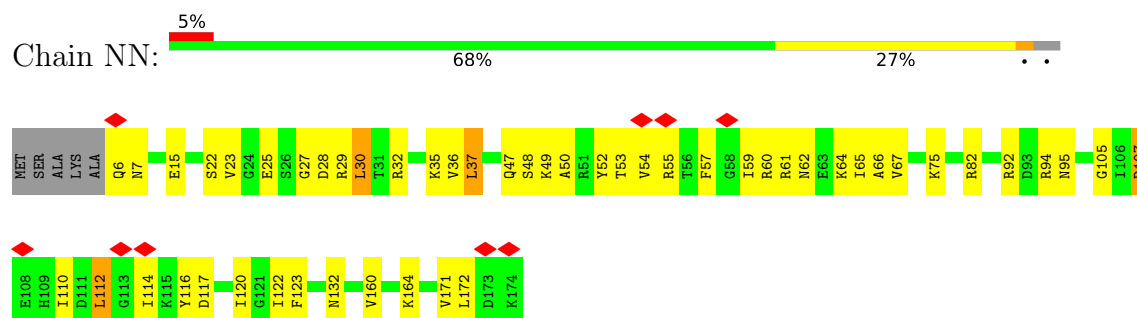
- Molecule 40: 60S ribosomal protein L10



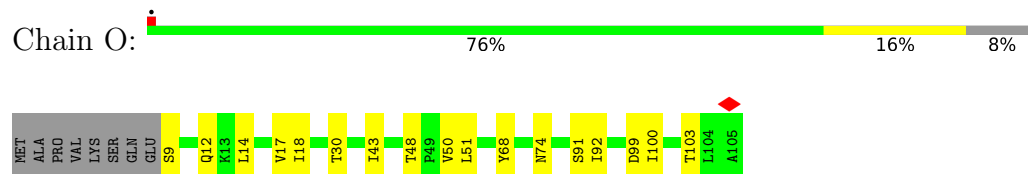
- Molecule 41: 60S ribosomal protein L29



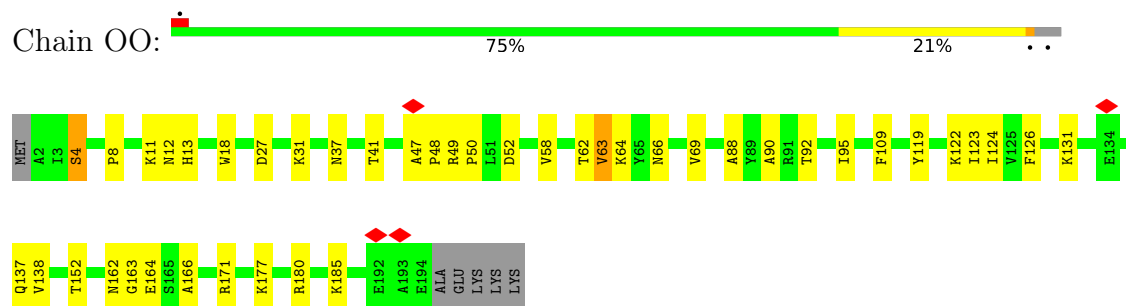
- Molecule 42: 60S ribosomal protein L11-A



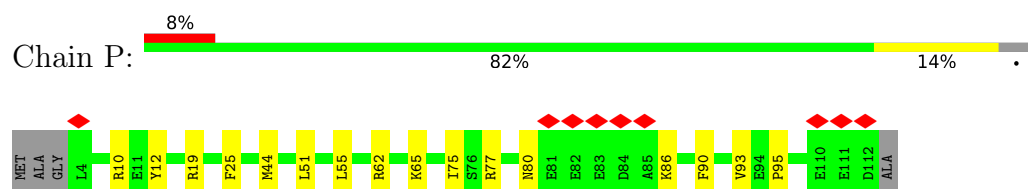
- Molecule 43: 60S ribosomal protein L30



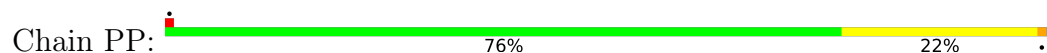
- Molecule 44: 60S ribosomal protein L13-A

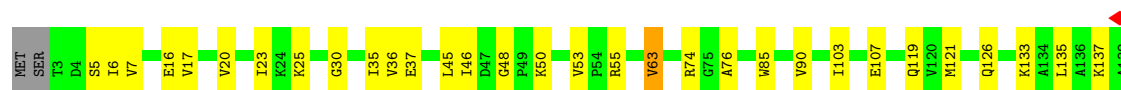


- Molecule 45: 60S ribosomal protein L31-A



- Molecule 46: 60S ribosomal protein L14-A

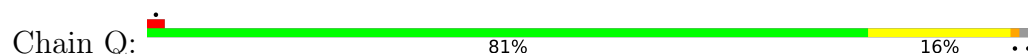




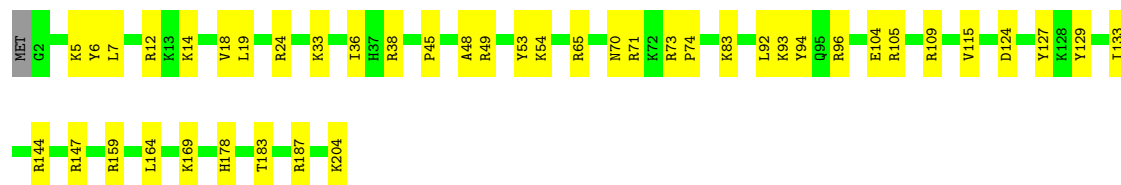
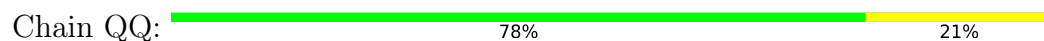
- Molecule 47: Polypeptide



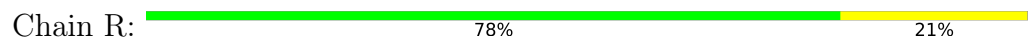
- Molecule 48: 60S ribosomal protein L32



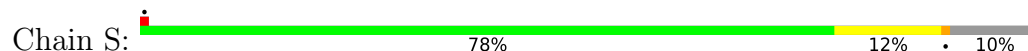
- Molecule 49: 60S ribosomal protein L15-A



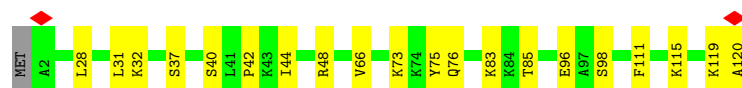
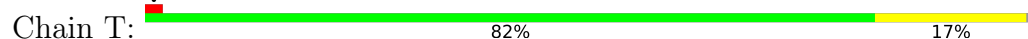
- Molecule 50: 60S ribosomal protein L33-A



- Molecule 51: 60S ribosomal protein L34-A



- Molecule 52: 60S ribosomal protein L35-A



- Molecule 53: 60S ribosomal protein L36-A

Chain U:  78% 21%



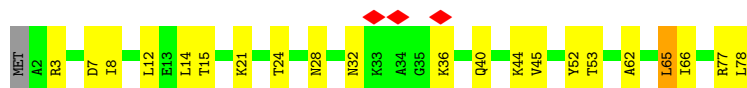
- Molecule 54: 60S ribosomal protein L37-A

Chain V:  69% 23% 5%



- Molecule 55: 60S ribosomal protein L38

Chain W:  72% 26%



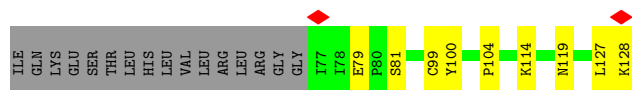
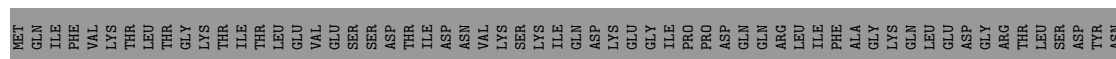
- Molecule 56: 60S ribosomal protein L39

Chain X:  75% 24%



- Molecule 57: Ubiquitin-60S ribosomal protein L40

Chain Y:  34% 7% 59%



- Molecule 58: 60S ribosomal protein L41

Chain Z:  84% 16%

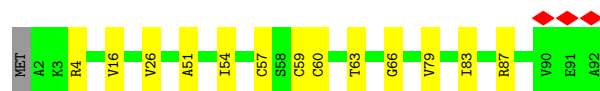
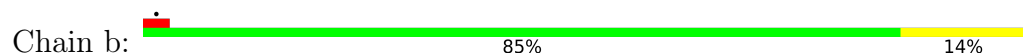


- Molecule 59: 60S ribosomal protein L42-A

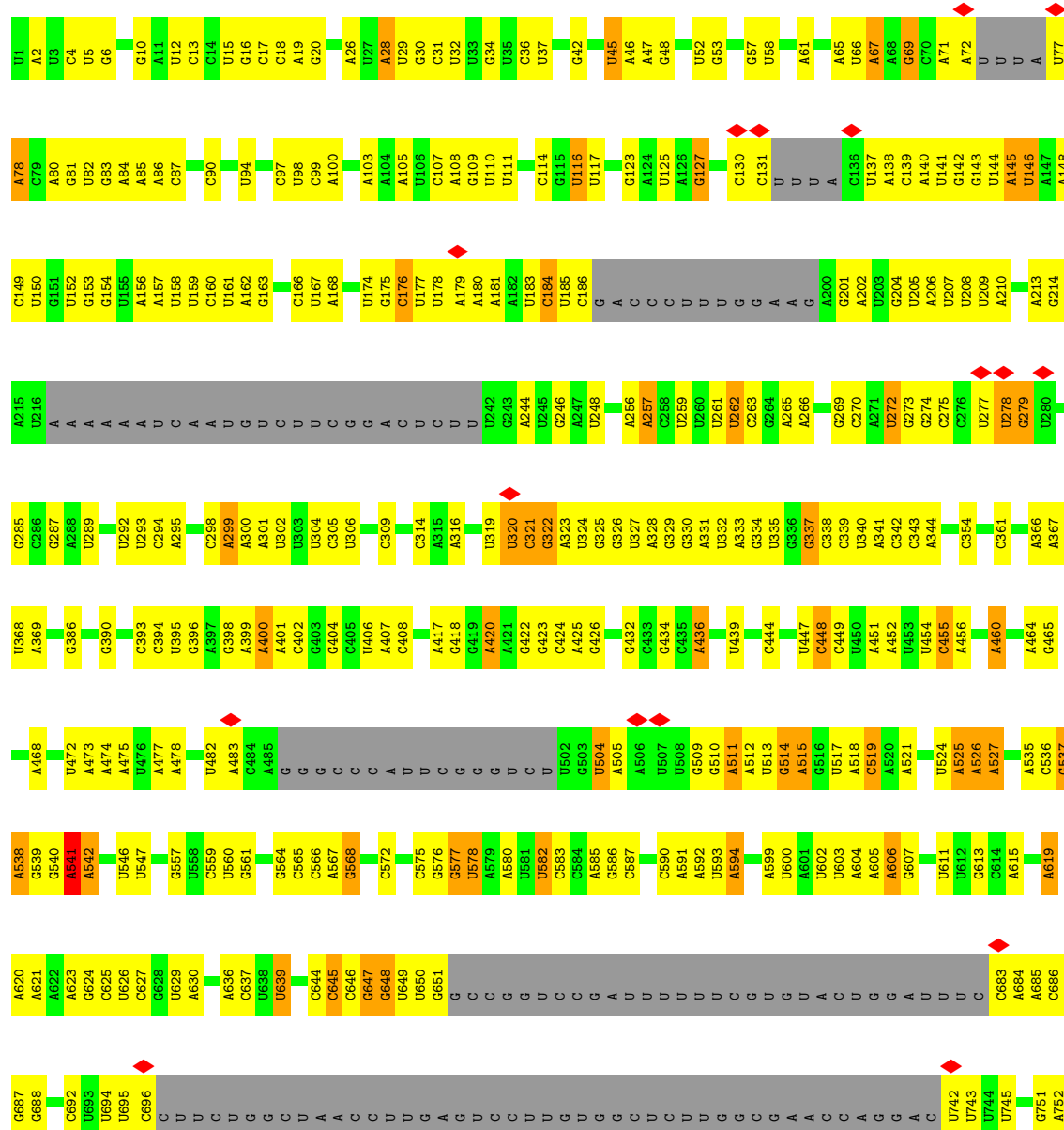
Chain a:  72% 25%



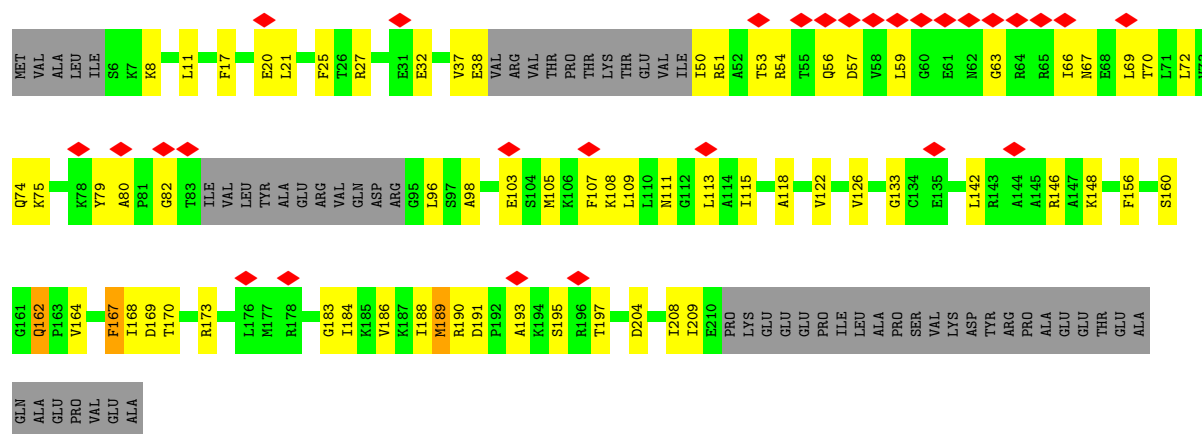
- Molecule 60: 60S ribosomal protein L43-A



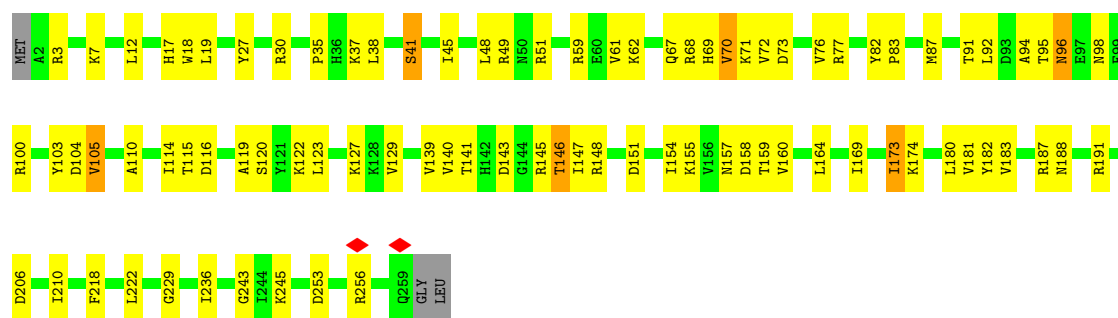
- Molecule 61: 18S ribosomal RNA



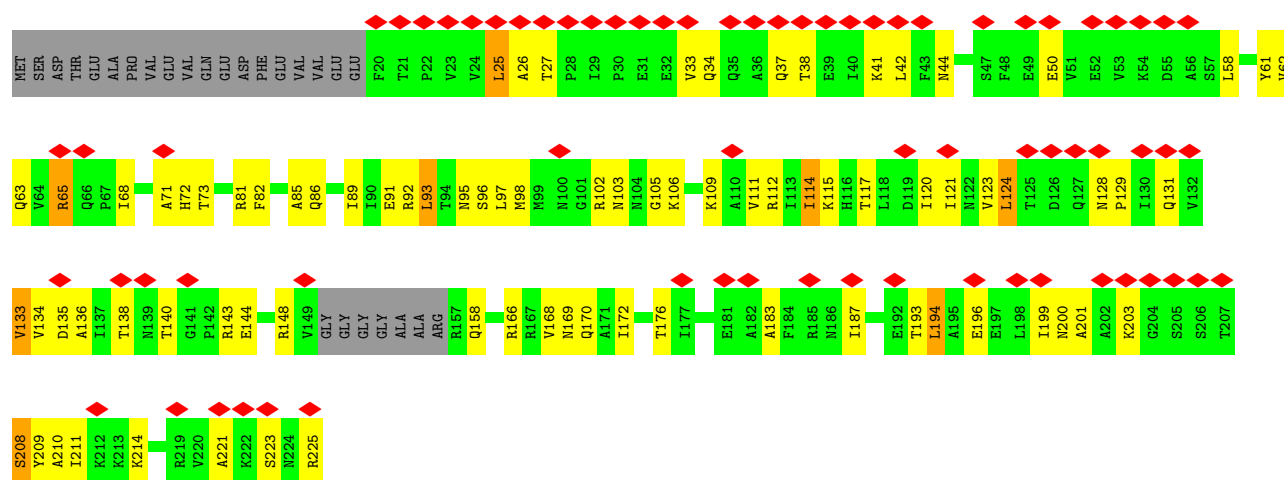




• Molecule 66: 40S ribosomal protein S4-A



• Molecule 67: 40S ribosomal protein S5

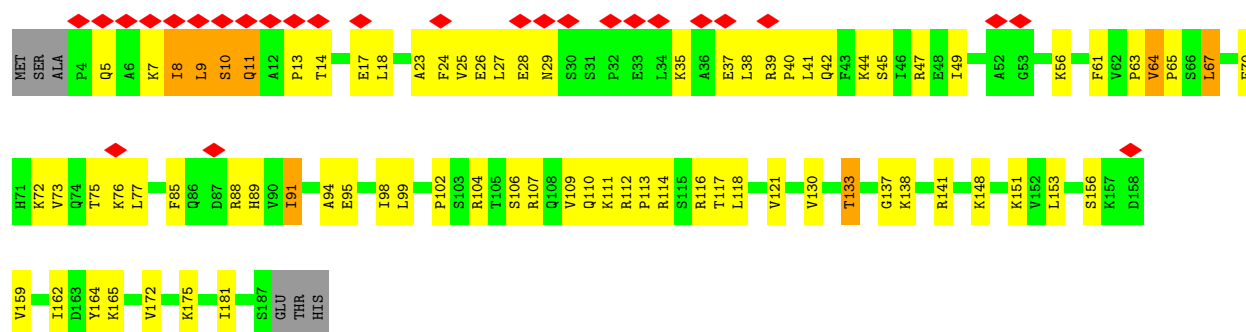


• Molecule 68: 40S ribosomal protein S6-A

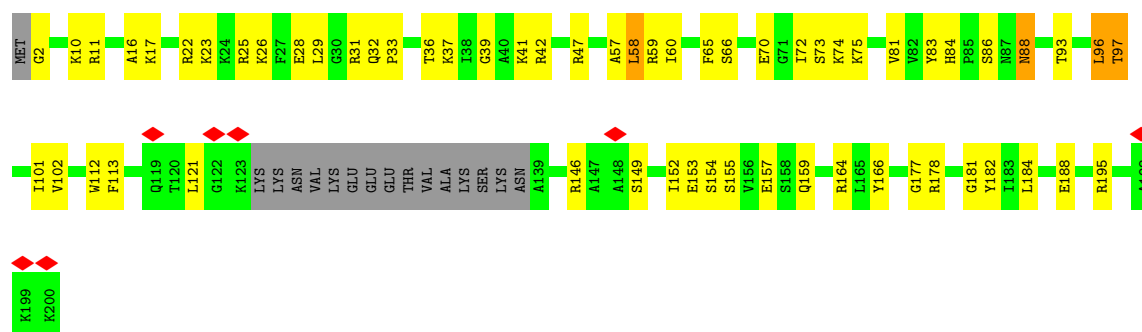




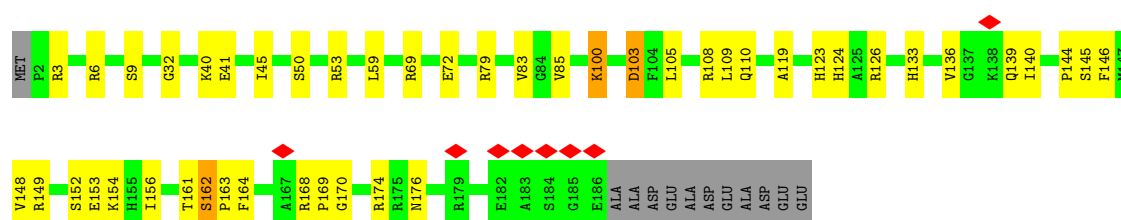
• Molecule 69: 40S ribosomal protein S7-A



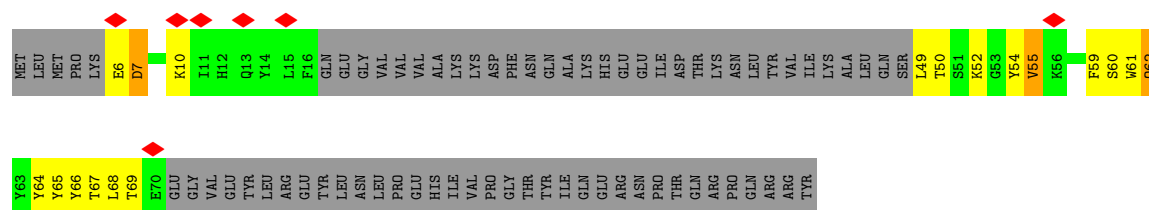
• Molecule 70: 40S ribosomal protein S8-B



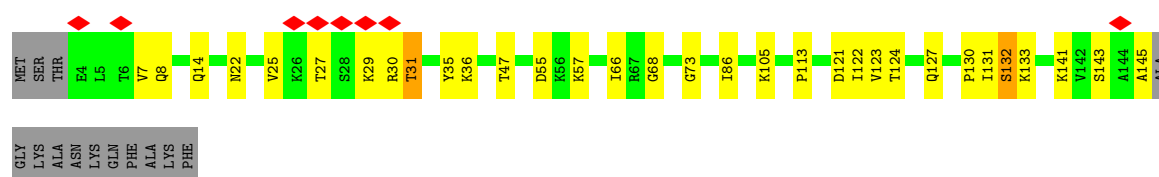
• Molecule 71: 40S ribosomal protein S9-A



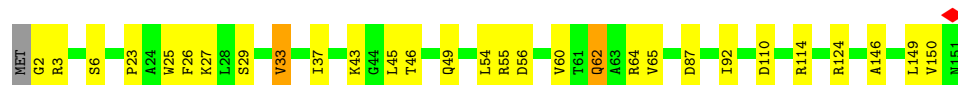
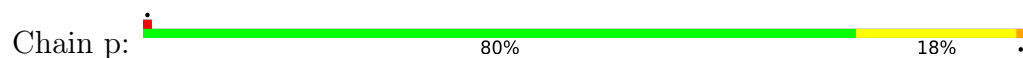
- Molecule 72: 40S ribosomal protein S10-A



- Molecule 73: 40S ribosomal protein S11-A



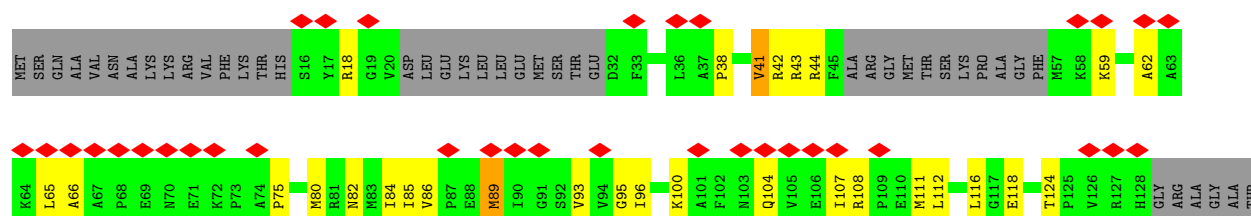
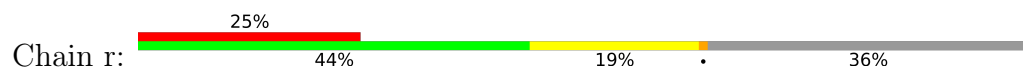
- Molecule 74: 40S ribosomal protein S13



- Molecule 75: 40S ribosomal protein S14-A



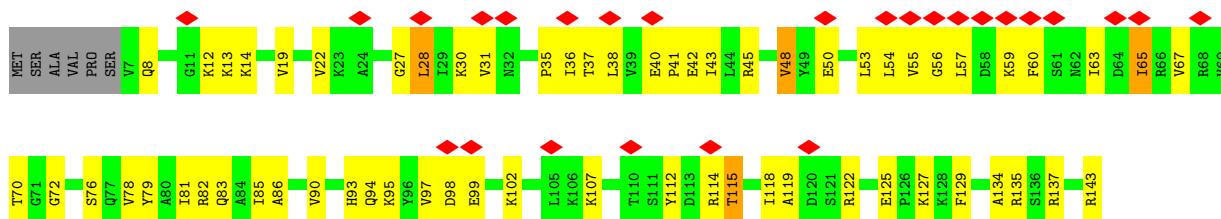
- Molecule 76: 40S ribosomal protein S15



THR
SER
SER
ARG
VAL
PHE
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PRO
LEU
LYS

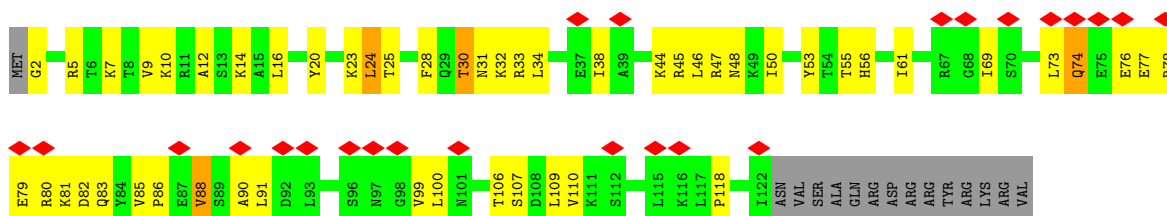
• Molecule 77: 40S ribosomal protein S16-A

Chain s: 18% 52% 41%



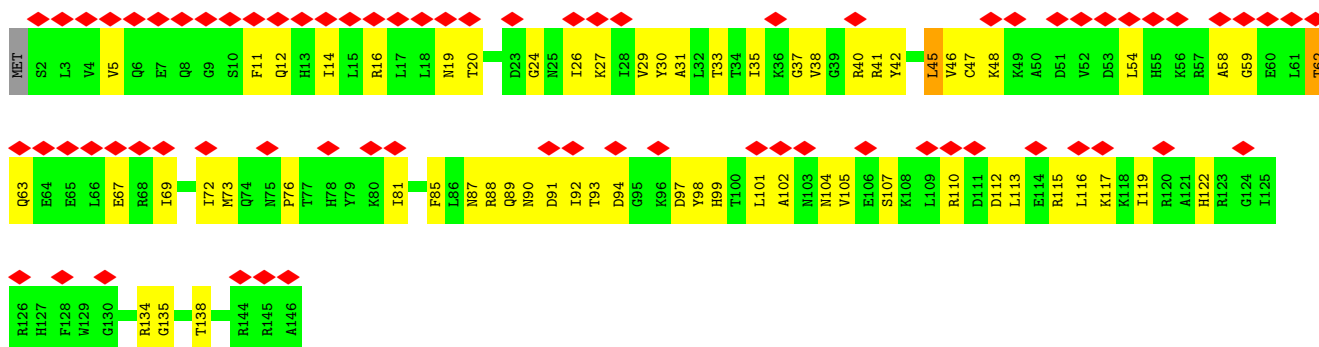
• Molecule 78: 40S ribosomal protein S17-A

Chain t: 18% 51% 35% 11%



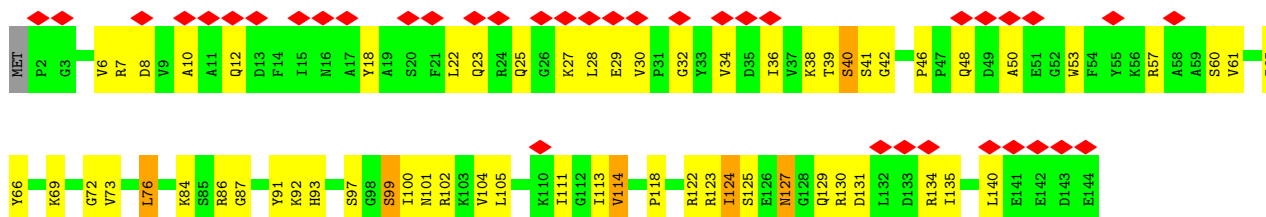
• Molecule 79: 40S ribosomal protein S18-A

Chain u: 49% 56% 42%

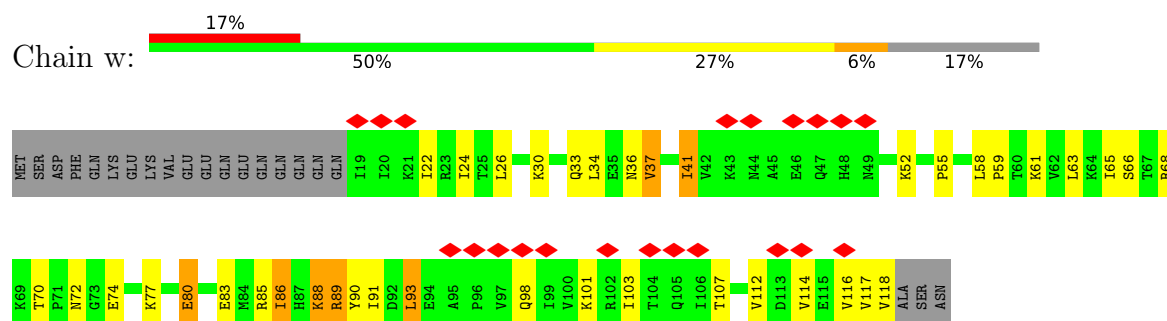


• Molecule 80: 40S ribosomal protein S19-A

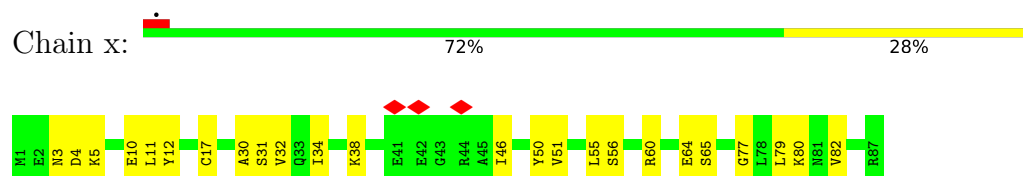
Chain v: 26% 56% 39%



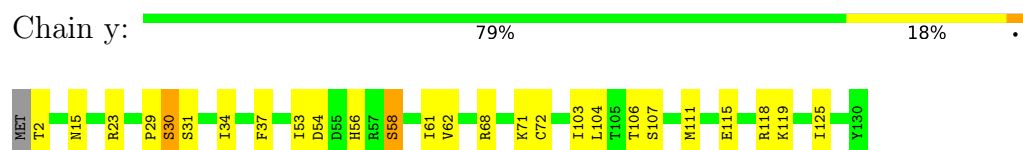
- Molecule 81: 40S ribosomal protein S20



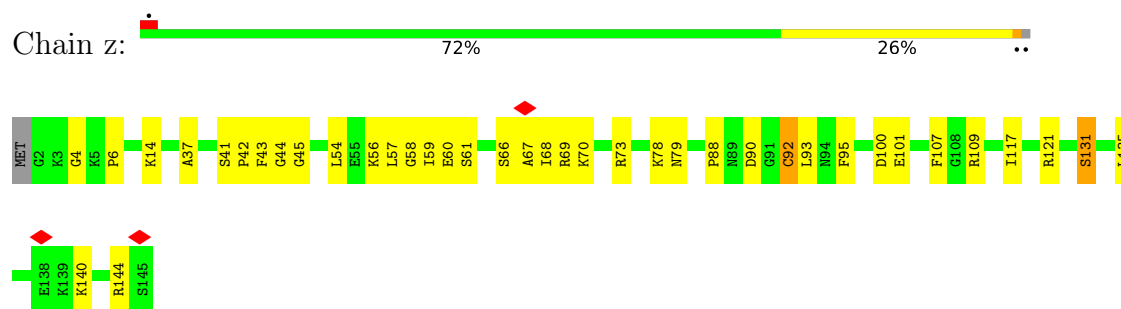
- Molecule 82: 40S ribosomal protein S21-A



- Molecule 83: 40S ribosomal protein S22-A



- Molecule 84: 40S ribosomal protein S23-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58351	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	270000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.697	Depositor
Minimum map value	-0.518	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.161	Depositor
Map size (Å)	540.0, 540.0, 540.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9, 0.9, 0.9	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, G7M, 1MA, MG, 5MC, PO4, DDE, GDP, MA6, 4AC, A2M, OMG, SO1, OMC, K, UR3, YYG, B8N, OMU, ZN

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	0	0.16	0/1087	0.39	0/1449
2	1	0.12	0/571	0.43	0/768
3	2	0.17	0/782	0.41	0/1047
4	3	0.14	0/620	0.41	0/838
5	4	0.15	0/499	0.39	0/670
6	5	0.13	0/412	0.33	0/544
7	6	0.13	0/433	0.43	0/575
8	7	0.14	0/2489	0.42	0/3389
9	8	0.12	0/279	0.44	0/369
10	A	0.20	0/1585	0.35	0/2128
11	AA	0.28	6/75545 (0.0%)	0.30	0/117782
12	Aa	0.14	0/6470	0.38	0/8759
13	B	0.20	0/1245	0.34	0/1676
14	BB	0.17	0/2883	0.24	0/4491
15	Bb	0.13	0/1788	0.33	0/2786
16	C	0.17	0/1465	0.34	0/1965
17	CC	0.20	0/3746	0.29	0/5832
18	Cc	0.11	0/1836	0.23	0/2859
19	D	0.16	0/1440	0.34	0/1921
20	DD	0.14	0/1558	0.38	0/2107
21	Dd	0.17	0/138	0.31	0/212
22	E	0.18	0/1481	0.38	0/1990
23	EE	0.19	0/1948	0.36	0/2617
24	Ee	0.72	2/1210 (0.2%)	0.71	1/1627 (0.1%)
25	F	0.16	0/1300	0.32	0/1743
26	FF	0.18	0/3146	0.35	0/4228
27	G	0.14	0/786	0.36	0/1065
28	GG	0.17	0/2800	0.36	0/3790
29	H	0.17	0/978	0.34	0/1316
30	HH	0.15	0/2425	0.33	0/3271
31	I	0.16	0/533	0.30	0/707

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	II	0.16	0/1251	0.36	0/1682
33	J	0.17	0/974	0.34	0/1314
34	JJ	0.19	0/1821	0.48	2/2451 (0.1%)
35	K	0.16	0/1004	0.30	0/1341
36	KK	0.16	0/1836	0.33	0/2481
37	L	0.16	0/1118	0.35	0/1497
38	LL	0.17	0/1539	0.38	0/2073
39	M	0.18	0/1204	0.39	0/1612
40	MM	0.17	0/1779	0.35	0/2386
41	N	0.16	0/473	0.32	0/629
42	NN	0.16	0/1374	0.38	0/1842
43	O	0.14	0/750	0.27	0/1008
44	OO	0.17	0/1568	0.38	0/2106
45	P	0.16	0/897	0.34	0/1205
46	PP	0.17	0/1068	0.32	0/1438
47	Pp	0.21	0/19	0.55	0/23
48	Q	0.16	0/1041	0.29	0/1394
49	QQ	0.19	0/1757	0.36	0/2354
50	R	0.19	0/868	0.34	0/1168
51	S	0.18	0/871	0.33	0/1164
52	T	0.15	0/978	0.30	0/1301
53	U	0.17	0/778	0.38	0/1034
54	V	0.19	0/680	0.47	0/901
55	W	0.18	0/618	0.36	0/826
56	X	0.19	0/443	0.45	0/588
57	Y	0.13	0/423	0.27	0/562
58	Z	0.18	0/234	0.26	0/300
59	a	0.18	0/831	0.39	0/1097
60	b	0.16	0/701	0.37	0/934
61	c	0.18	0/37760	0.29	0/58811
62	d	0.15	0/1623	0.36	0/2222
63	e	0.16	0/1714	0.42	0/2308
64	f	0.18	0/1665	0.42	0/2263
65	g	0.15	0/1429	0.39	0/1913
66	h	0.15	0/2097	0.36	0/2823
67	i	0.17	0/1591	0.43	0/2151
68	j	0.12	0/1790	0.34	0/2393
69	k	0.18	0/1506	0.51	2/2028 (0.1%)
70	l	0.16	0/1482	0.37	0/1980
71	m	0.14	0/1519	0.33	0/2035
72	n	0.12	0/309	0.41	0/416
73	o	0.15	0/1172	0.32	0/1580
74	p	0.15	0/1215	0.30	0/1638

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	q	0.16	0/901	0.45	1/1217 (0.1%)
76	r	0.13	0/747	0.36	0/1002
77	s	0.14	0/1099	0.44	0/1473
78	t	0.14	0/971	0.39	0/1303
79	u	0.12	0/1211	0.35	0/1628
80	v	0.14	0/1130	0.39	0/1517
81	w	0.17	0/810	0.41	0/1095
82	x	0.17	0/693	0.41	0/935
83	y	0.19	0/1038	0.42	0/1395
84	z	0.15	0/1139	0.38	0/1518
All	All	0.22	8/218987 (0.0%)	0.33	6/320876 (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
19	D	0	1
26	FF	0	1
34	JJ	0	2
37	L	0	2
54	V	0	1
59	a	0	1
63	e	0	2
67	i	0	1
69	k	0	3
77	s	0	1
84	z	0	1
All	All	0	16

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	AA	1236	G	C2-N3	26.21	1.85	1.32
11	AA	1236	G	N3-C4	25.66	1.86	1.35
11	AA	1236	G	N1-C2	18.83	1.75	1.37
24	Ee	16	ARG	CD-NE	18.75	1.72	1.46
11	AA	1236	G	C6-N1	18.56	1.76	1.39

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	Ee	16	ARG	CD-NE-CZ	20.62	153.26	124.40
34	JJ	157	ASN	CA-C-N	8.99	138.71	121.54
34	JJ	157	ASN	C-N-CA	8.99	138.71	121.54
69	k	9	LEU	CA-C-N	5.66	132.36	121.54
69	k	9	LEU	C-N-CA	5.66	132.36	121.54

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	D	130	ASN	Peptide
26	FF	349	LYS	Peptide
34	JJ	158	LYS	Peptide
34	JJ	232	ARG	Peptide
37	L	101	PHE	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	0	1073	0	1132	40	0
2	1	563	0	603	27	0
3	2	769	0	814	12	0
4	3	610	0	633	19	0
5	4	497	0	535	23	0
6	5	404	0	399	17	0
7	6	427	0	475	18	0
8	7	2436	0	2386	106	0
9	8	276	0	289	8	0
10	A	1555	0	1659	27	0
11	AA	68429	0	34441	1138	0
12	Aa	6368	0	6435	209	0
13	B	1222	0	1231	24	0
14	BB	2579	0	1304	37	0
15	Bb	1638	0	835	42	0
16	C	1441	0	1543	36	0
17	CC	3353	0	1695	64	0
18	Cc	1644	0	837	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	D	1423	0	1510	26	0
20	DD	1531	0	1571	39	0
21	Dd	125	0	63	0	0
22	E	1445	0	1487	32	0
23	EE	1914	0	1981	43	0
24	Ee	1196	0	1257	77	0
25	F	1276	0	1323	19	0
26	FF	3075	0	3142	51	0
27	G	770	0	780	9	0
28	GG	2748	0	2859	49	0
29	H	963	0	1015	21	0
30	HH	2375	0	2325	44	0
31	I	521	0	551	10	0
32	II	1230	0	1320	17	0
33	J	959	0	1023	16	0
34	JJ	1784	0	1862	42	0
35	K	993	0	1081	19	0
36	KK	1804	0	1877	35	0
37	L	1092	0	1155	24	0
38	LL	1518	0	1587	26	0
39	M	1173	0	1215	36	0
40	MM	1743	0	1785	36	0
41	N	462	0	491	9	0
42	NN	1353	0	1383	38	0
43	O	742	0	797	10	0
44	OO	1543	0	1608	33	0
45	P	883	0	918	12	0
46	PP	1053	0	1149	19	0
47	Pp	19	0	20	4	0
48	Q	1020	0	1090	16	0
49	QQ	1720	0	1779	36	0
50	R	850	0	880	15	0
51	S	861	0	918	9	0
52	T	969	0	1078	19	0
53	U	771	0	849	15	0
54	V	665	0	668	19	0
55	W	612	0	682	12	0
56	X	436	0	475	11	0
57	Y	417	0	455	7	0
58	Z	233	0	284	4	0
59	a	819	0	886	20	0
60	b	694	0	734	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	c	34321	0	17285	729	0
62	d	1583	0	1578	51	0
63	e	1689	0	1763	52	0
64	f	1635	0	1723	39	0
65	g	1412	0	1473	49	0
66	h	2056	0	2140	67	0
67	i	1572	0	1639	73	0
68	j	1766	0	1859	70	0
69	k	1481	0	1572	67	0
70	l	1457	0	1488	55	0
71	m	1494	0	1573	42	0
72	n	300	0	279	16	0
73	o	1146	0	1213	20	0
74	p	1192	0	1255	20	0
75	q	891	0	883	25	0
76	r	732	0	760	31	0
77	s	1080	0	1140	58	0
78	t	961	0	999	45	0
79	u	1192	0	1222	44	0
80	v	1112	0	1124	54	0
81	w	800	0	869	33	0
82	x	684	0	672	22	0
83	y	1021	0	1060	22	0
84	z	1121	0	1196	27	0
85	2	1	0	0	0	0
85	5	1	0	0	0	0
85	8	1	0	0	0	0
85	S	1	0	0	0	0
85	V	1	0	0	0	0
85	Y	1	0	0	0	0
85	a	1	0	0	0	0
85	b	1	0	0	0	0
86	AA	198	0	0	0	0
86	Aa	1	0	0	0	0
86	B	1	0	0	0	0
86	BB	5	0	0	0	0
86	Bb	1	0	0	0	0
86	CC	3	0	0	0	0
86	Dd	1	0	0	0	0
86	FF	1	0	0	0	0
86	H	1	0	0	0	0
86	QQ	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	c	49	0	0	0	0
87	AA	14	0	0	0	0
87	EE	1	0	0	0	0
87	MM	1	0	0	0	0
87	Q	1	0	0	0	0
87	a	1	0	0	0	0
87	c	2	0	0	0	0
87	q	1	0	0	0	0
88	AA	30	0	57	5	0
89	Aa	28	0	12	3	0
90	Aa	5	0	0	6	0
91	Aa	35	0	41	7	0
92	2	1	0	0	0	0
92	A	2	0	0	0	0
92	AA	778	0	0	9	0
92	B	3	0	0	0	0
92	BB	13	0	0	0	0
92	CC	13	0	0	0	0
92	Cc	1	0	0	0	0
92	D	1	0	0	0	0
92	EE	6	0	0	0	0
92	F	4	0	0	0	0
92	FF	3	0	0	0	0
92	GG	3	0	0	0	0
92	H	3	0	0	0	0
92	HH	1	0	0	0	0
92	J	1	0	0	0	0
92	JJ	1	0	0	0	0
92	M	2	0	0	0	0
92	MM	2	0	0	0	0
92	N	1	0	0	0	0
92	Q	4	0	0	0	0
92	QQ	6	0	0	0	0
92	V	2	0	0	0	0
92	c	118	0	0	4	0
92	h	2	0	0	0	0
92	o	2	0	0	0	0
92	p	2	0	0	0	0
All	All	207126	0	154034	3892	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 11.

The worst 5 of 3892 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)
11:AA:1236:G:C6	11:AA:1236:G:C5	1.77	1.61
11:AA:1236:G:C2	24:Ee:16:ARG:NE	1.76	1.53
11:AA:1236:G:C2	11:AA:1236:G:N1	1.75	1.53
24:Ee:16:ARG:NE	24:Ee:16:ARG:CD	1.72	1.53
11:AA:1236:G:C6	11:AA:1236:G:N1	1.76	1.51

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	132/135 (98%)	127 (96%)	5 (4%)	0	100	100
2	1	68/108 (63%)	62 (91%)	6 (9%)	0	100	100
3	2	95/119 (80%)	88 (93%)	6 (6%)	1 (1%)	11	5
4	3	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
5	4	61/67 (91%)	61 (100%)	0	0	100	100
6	5	47/56 (84%)	47 (100%)	0	0	100	100
7	6	51/63 (81%)	50 (98%)	1 (2%)	0	100	100
8	7	316/319 (99%)	297 (94%)	19 (6%)	0	100	100
9	8	32/152 (21%)	20 (62%)	12 (38%)	0	100	100
10	A	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
12	Aa	811/842 (96%)	787 (97%)	24 (3%)	0	100	100
13	B	152/184 (83%)	149 (98%)	3 (2%)	0	100	100
16	C	183/186 (98%)	180 (98%)	3 (2%)	0	100	100
19	D	174/189 (92%)	170 (98%)	3 (2%)	1 (1%)	21	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	DD	195/312 (62%)	194 (100%)	1 (0%)	0	100	100
22	E	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
23	EE	250/254 (98%)	245 (98%)	5 (2%)	0	100	100
24	Ee	156/165 (94%)	154 (99%)	2 (1%)	0	100	100
25	F	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
26	FF	384/387 (99%)	375 (98%)	9 (2%)	0	100	100
27	G	95/121 (78%)	94 (99%)	1 (1%)	0	100	100
28	GG	359/362 (99%)	344 (96%)	15 (4%)	0	100	100
29	H	127/137 (93%)	125 (98%)	2 (2%)	0	100	100
30	HH	294/297 (99%)	287 (98%)	7 (2%)	0	100	100
31	I	61/155 (39%)	61 (100%)	0	0	100	100
32	II	151/176 (86%)	146 (97%)	5 (3%)	0	100	100
33	J	118/142 (83%)	115 (98%)	3 (2%)	0	100	100
34	JJ	220/244 (90%)	212 (96%)	7 (3%)	1 (0%)	24	16
35	K	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
36	KK	231/256 (90%)	226 (98%)	5 (2%)	0	100	100
37	L	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
38	LL	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
39	M	146/149 (98%)	139 (95%)	6 (4%)	1 (1%)	18	10
40	MM	213/221 (96%)	206 (97%)	7 (3%)	0	100	100
41	N	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
42	NN	167/174 (96%)	158 (95%)	9 (5%)	0	100	100
43	O	95/105 (90%)	95 (100%)	0	0	100	100
44	OO	191/199 (96%)	176 (92%)	14 (7%)	1 (0%)	24	16
45	P	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
46	PP	134/138 (97%)	132 (98%)	2 (2%)	0	100	100
48	Q	125/130 (96%)	125 (100%)	0	0	100	100
49	QQ	201/204 (98%)	194 (96%)	7 (4%)	0	100	100
50	R	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
51	S	107/121 (88%)	106 (99%)	1 (1%)	0	100	100
52	T	117/120 (98%)	114 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	U	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
54	V	82/88 (93%)	77 (94%)	4 (5%)	1 (1%)	10	4
55	W	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
56	X	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
57	Y	50/128 (39%)	50 (100%)	0	0	100	100
58	Z	23/25 (92%)	23 (100%)	0	0	100	100
59	a	100/106 (94%)	95 (95%)	5 (5%)	0	100	100
60	b	89/92 (97%)	89 (100%)	0	0	100	100
62	d	204/252 (81%)	193 (95%)	11 (5%)	0	100	100
63	e	210/255 (82%)	199 (95%)	11 (5%)	0	100	100
64	f	215/254 (85%)	204 (95%)	11 (5%)	0	100	100
65	g	177/240 (74%)	168 (95%)	9 (5%)	0	100	100
66	h	256/261 (98%)	247 (96%)	9 (4%)	0	100	100
67	i	195/225 (87%)	186 (95%)	9 (5%)	0	100	100
68	j	217/236 (92%)	207 (95%)	10 (5%)	0	100	100
69	k	182/190 (96%)	172 (94%)	10 (6%)	0	100	100
70	l	180/200 (90%)	169 (94%)	11 (6%)	0	100	100
71	m	183/197 (93%)	176 (96%)	7 (4%)	0	100	100
72	n	29/105 (28%)	25 (86%)	4 (14%)	0	100	100
73	o	140/156 (90%)	132 (94%)	8 (6%)	0	100	100
74	p	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
75	q	125/137 (91%)	115 (92%)	10 (8%)	0	100	100
76	r	85/142 (60%)	84 (99%)	1 (1%)	0	100	100
77	s	135/143 (94%)	127 (94%)	8 (6%)	0	100	100
78	t	119/136 (88%)	112 (94%)	7 (6%)	0	100	100
79	u	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
80	v	141/144 (98%)	137 (97%)	4 (3%)	0	100	100
81	w	98/121 (81%)	98 (100%)	0	0	100	100
82	x	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
83	y	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
84	z	142/145 (98%)	129 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11673/13056 (89%)	11237 (96%)	430 (4%)	6 (0%)	49	43

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	JJ	159	GLN
39	M	78	LEU
44	OO	63	VAL
54	V	65	ARG
3	2	47	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	112/113 (99%)	107 (96%)	5 (4%)	24	18
2	1	61/89 (68%)	56 (92%)	5 (8%)	10	5
3	2	83/101 (82%)	79 (95%)	4 (5%)	23	16
4	3	70/71 (99%)	69 (99%)	1 (1%)	59	60
5	4	56/60 (93%)	51 (91%)	5 (9%)	9	4
6	5	43/49 (88%)	40 (93%)	3 (7%)	14	7
7	6	46/54 (85%)	43 (94%)	3 (6%)	15	9
8	7	259/262 (99%)	244 (94%)	15 (6%)	18	11
9	8	30/135 (22%)	27 (90%)	3 (10%)	7	3
10	A	160/162 (99%)	158 (99%)	2 (1%)	61	63
12	Aa	694/714 (97%)	664 (96%)	30 (4%)	26	20
13	B	125/146 (86%)	121 (97%)	4 (3%)	34	29
16	C	150/151 (99%)	149 (99%)	1 (1%)	76	80
19	D	143/154 (93%)	140 (98%)	3 (2%)	47	46
20	DD	167/254 (66%)	160 (96%)	7 (4%)	26	20
22	E	156/156 (100%)	152 (97%)	4 (3%)	40	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	EE	193/196 (98%)	190 (98%)	3 (2%)	55	56
24	Ee	129/136 (95%)	121 (94%)	8 (6%)	16	9
25	F	136/137 (99%)	134 (98%)	2 (2%)	57	58
26	FF	320/323 (99%)	316 (99%)	4 (1%)	61	63
27	G	84/107 (78%)	82 (98%)	2 (2%)	43	40
28	GG	288/289 (100%)	284 (99%)	4 (1%)	59	60
29	H	101/105 (96%)	100 (99%)	1 (1%)	68	72
30	HH	244/245 (100%)	238 (98%)	6 (2%)	42	39
31	I	55/129 (43%)	54 (98%)	1 (2%)	51	51
32	II	133/153 (87%)	131 (98%)	2 (2%)	57	58
33	J	104/118 (88%)	103 (99%)	1 (1%)	68	72
34	JJ	186/205 (91%)	184 (99%)	2 (1%)	65	68
35	K	109/110 (99%)	109 (100%)	0	100	100
36	KK	187/208 (90%)	184 (98%)	3 (2%)	55	56
37	L	115/116 (99%)	110 (96%)	5 (4%)	26	20
38	LL	171/171 (100%)	166 (97%)	5 (3%)	37	33
39	M	118/119 (99%)	115 (98%)	3 (2%)	42	39
40	MM	184/187 (98%)	183 (100%)	1 (0%)	81	85
41	N	46/47 (98%)	46 (100%)	0	100	100
42	NN	147/150 (98%)	140 (95%)	7 (5%)	23	16
43	O	81/88 (92%)	80 (99%)	1 (1%)	63	65
44	OO	154/159 (97%)	149 (97%)	5 (3%)	34	29
45	P	94/97 (97%)	94 (100%)	0	100	100
46	PP	107/109 (98%)	104 (97%)	3 (3%)	38	34
47	Pp	2/2 (100%)	2 (100%)	0	100	100
48	Q	109/111 (98%)	108 (99%)	1 (1%)	70	75
49	QQ	175/176 (99%)	174 (99%)	1 (1%)	78	83
50	R	90/91 (99%)	89 (99%)	1 (1%)	65	68
51	S	94/103 (91%)	92 (98%)	2 (2%)	47	46
52	T	104/105 (99%)	103 (99%)	1 (1%)	68	72
53	U	81/82 (99%)	79 (98%)	2 (2%)	42	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	V	69/71 (97%)	68 (99%)	1 (1%)	59	60
55	W	68/69 (99%)	63 (93%)	5 (7%)	13	6
56	X	45/46 (98%)	45 (100%)	0	100	100
57	Y	47/116 (40%)	47 (100%)	0	100	100
58	Z	23/23 (100%)	22 (96%)	1 (4%)	26	20
59	a	87/91 (96%)	86 (99%)	1 (1%)	65	68
60	b	71/72 (99%)	70 (99%)	1 (1%)	59	60
62	d	165/210 (79%)	164 (99%)	1 (1%)	78	83
63	e	189/224 (84%)	180 (95%)	9 (5%)	23	16
64	f	176/205 (86%)	170 (97%)	6 (3%)	32	27
65	g	145/195 (74%)	138 (95%)	7 (5%)	23	16
66	h	220/222 (99%)	212 (96%)	8 (4%)	31	26
67	i	172/191 (90%)	162 (94%)	10 (6%)	18	11
68	j	188/201 (94%)	179 (95%)	9 (5%)	23	16
69	k	165/170 (97%)	155 (94%)	10 (6%)	17	10
70	l	146/161 (91%)	140 (96%)	6 (4%)	27	21
71	m	158/166 (95%)	154 (98%)	4 (2%)	42	39
72	n	32/98 (33%)	29 (91%)	3 (9%)	8	3
73	o	127/137 (93%)	122 (96%)	5 (4%)	28	23
74	p	127/128 (99%)	123 (97%)	4 (3%)	35	30
75	q	81/105 (77%)	77 (95%)	4 (5%)	22	15
76	r	77/118 (65%)	74 (96%)	3 (4%)	28	23
77	s	114/119 (96%)	105 (92%)	9 (8%)	11	5
78	t	105/124 (85%)	96 (91%)	9 (9%)	10	4
79	u	128/129 (99%)	121 (94%)	7 (6%)	19	12
80	v	115/116 (99%)	108 (94%)	7 (6%)	17	10
81	w	94/114 (82%)	83 (88%)	11 (12%)	5	1
82	x	74/74 (100%)	71 (96%)	3 (4%)	27	21
83	y	110/111 (99%)	107 (97%)	3 (3%)	39	36
84	z	119/120 (99%)	116 (98%)	3 (2%)	42	39
All	All	9933/10971 (90%)	9611 (97%)	322 (3%)	35	29

5 of 322 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	k	8	ILE
78	t	88	VAL
69	k	133	THR
74	p	43	LYS
80	v	124	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
55	W	76	ASN
69	k	161	GLN
62	d	33	GLN
66	h	216	ASN
73	o	81	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	AA	3194/3396 (94%)	474 (14%)	24 (0%)
14	BB	120/121 (99%)	8 (6%)	1 (0%)
15	Bb	75/76 (98%)	36 (48%)	0
17	CC	157/158 (99%)	20 (12%)	0
18	Cc	76/77 (98%)	17 (22%)	0
21	Dd	5/39 (12%)	0	0
61	c	1598/1800 (88%)	323 (20%)	0
All	All	5225/5667 (92%)	878 (16%)	25 (0%)

5 of 878 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	AA	4	U
11	AA	6	A
11	AA	14	U
11	AA	26	A
11	AA	40	A

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	AA	2487	U
11	AA	2501	U
14	BB	72	A
11	AA	2500	A
11	AA	2535	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

68 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$
61	OMG	c	1428	61	23,26,27	0.47	0	32,38,41	0.46	0
11	OMC	AA	1437	11,86	19,22,23	0.57	0	25,31,34	0.90	1 (4%)
11	OMU	AA	2421	11	19,22,23	3.06	8 (42%)	25,31,34	1.88	5 (20%)
11	OMG	AA	2922	11	23,26,27	0.54	0	32,38,41	0.57	0
61	OMG	c	1271	61	23,26,27	0.45	0	32,38,41	0.45	0
61	A2M	c	420	61	22,25,26	3.21	10 (45%)	30,36,39	2.93	10 (33%)
11	OMU	AA	1888	11	19,22,23	3.06	8 (42%)	25,31,34	1.94	6 (24%)
11	A2M	AA	2281	11	22,25,26	3.22	10 (45%)	30,36,39	3.12	14 (46%)
11	OMC	AA	2948	11	19,22,23	0.55	0	25,31,34	0.75	1 (4%)
11	OMC	AA	2337	11	19,22,23	0.54	0	25,31,34	0.62	0
11	OMG	AA	908	11	23,26,27	0.53	0	32,38,41	0.52	0
11	OMU	AA	2921	11,86	19,22,23	3.08	8 (42%)	25,31,34	1.82	5 (20%)
61	OMC	c	1639	86,61	19,22,23	0.54	0	25,31,34	0.55	0
11	A2M	AA	817	11,86	22,25,26	3.19	10 (45%)	30,36,39	2.94	11 (36%)
11	OMU	AA	2724	11	19,22,23	3.04	8 (42%)	25,31,34	1.80	5 (20%)
61	MA6	c	1781	61	23,26,27	1.42	4 (17%)	33,38,41	3.18	12 (36%)
11	OMC	AA	650	11	19,22,23	0.59	0	25,31,34	0.69	0
11	OMU	AA	2729	11	19,22,23	3.03	8 (42%)	25,31,34	1.74	5 (20%)
11	A2M	AA	2946	11,86	22,25,26	3.22	10 (45%)	30,36,39	2.96	11 (36%)
61	B8N	c	1191	61	25,29,30	3.39	7 (28%)	28,42,45	2.00	8 (28%)
11	OMG	AA	2619	11,15	23,26,27	0.50	0	32,38,41	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
61	OMG	c	1572	61	23,26,27	0.52	0	32,38,41	0.59	0
11	A2M	AA	2220	11	22,25,26	3.21	10 (45%)	30,36,39	2.87	10 (33%)
11	A2M	AA	2280	11	22,25,26	3.21	10 (45%)	30,36,39	2.92	10 (33%)
11	OMC	AA	2959	11,86	19,22,23	0.56	0	25,31,34	0.68	0
11	A2M	AA	1449	11,86	22,25,26	3.21	9 (40%)	30,36,39	2.88	10 (33%)
61	A2M	c	28	61	22,25,26	3.21	10 (45%)	30,36,39	2.96	11 (36%)
61	A2M	c	100	86,61	22,25,26	3.22	10 (45%)	30,36,39	2.95	10 (33%)
61	A2M	c	436	61	22,25,26	3.21	10 (45%)	30,36,39	2.88	10 (33%)
11	1MA	AA	2142	11,86	21,25,26	0.52	0	30,37,40	0.83	1 (3%)
15	YYG	Bb	37	15	38,42,43	2.42	11 (28%)	45,62,65	2.12	13 (28%)
11	1MA	AA	645	11,86	21,25,26	0.52	0	30,37,40	0.76	1 (3%)
61	OMG	c	1126	61	23,26,27	0.52	0	32,38,41	0.56	0
61	G7M	c	1575	18,61	23,26,27	2.65	8 (34%)	34,39,42	2.37	10 (29%)
61	A2M	c	974	61	22,25,26	3.22	10 (45%)	30,36,39	2.92	11 (36%)
61	A2M	c	619	86,61	22,25,26	3.21	10 (45%)	30,36,39	2.91	10 (33%)
61	OMU	c	1269	61	19,22,23	3.15	8 (42%)	25,31,34	1.82	5 (20%)
11	A2M	AA	807	11	22,25,26	3.21	10 (45%)	30,36,39	2.99	11 (36%)
11	A2M	AA	2256	11	22,25,26	3.21	10 (45%)	30,36,39	3.10	15 (50%)
11	OMU	AA	898	11	19,22,23	3.03	8 (42%)	25,31,34	1.80	5 (20%)
61	OMC	c	414	61	19,22,23	0.52	0	25,31,34	0.67	0
61	A2M	c	796	61	22,25,26	3.24	10 (45%)	30,36,39	2.93	11 (36%)
11	OMG	AA	867	11,87	23,26,27	0.54	0	32,38,41	0.53	0
11	OMU	AA	2417	11	19,22,23	3.03	8 (42%)	25,31,34	1.81	5 (20%)
61	OMC	c	1007	61	19,22,23	0.54	0	25,31,34	0.66	0
61	4AC	c	1280	61	21,24,25	3.54	10 (47%)	28,34,37	1.73	6 (21%)
61	OMU	c	578	61	19,22,23	3.14	8 (42%)	25,31,34	1.78	5 (20%)
11	OMC	AA	2197	11,87	19,22,23	0.55	0	25,31,34	0.57	0
11	OMG	AA	805	11	23,26,27	0.50	0	32,38,41	0.56	0
11	OMC	AA	663	11	19,22,23	0.56	0	25,31,34	0.76	0
11	OMG	AA	2288	11	23,26,27	0.51	0	32,38,41	0.48	0
61	OMG	c	562	61	23,26,27	0.45	0	32,38,41	0.48	0
61	A2M	c	541	61	22,25,26	3.20	9 (40%)	30,36,39	2.93	11 (36%)
11	5MC	AA	2870	11,87	19,22,23	0.67	0	26,32,35	0.62	0
11	5MC	AA	2278	11,86	19,22,23	0.55	0	26,32,35	0.66	0
11	OMG	AA	1450	11	23,26,27	0.50	0	32,38,41	0.42	0
11	A2M	AA	1133	11,86	22,25,26	3.23	10 (45%)	30,36,39	3.01	11 (36%)
11	OMG	AA	2791	11	23,26,27	0.48	0	32,38,41	0.48	0
11	OMU	AA	2347	11	19,22,23	3.09	8 (42%)	25,31,34	1.84	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
61	MA6	c	1782	61	23,26,27	1.40	4 (17%)	33,38,41	3.24	12 (36%)
11	OMG	AA	2793	11	23,26,27	0.50	0	32,38,41	0.49	0
11	A2M	AA	649	11	22,25,26	3.20	10 (45%)	30,36,39	2.88	10 (33%)
11	A2M	AA	2640	11	22,25,26	3.21	10 (45%)	30,36,39	2.90	10 (33%)
61	4AC	c	1773	61	21,24,25	3.36	10 (47%)	28,34,37	1.61	6 (21%)
11	A2M	AA	876	11	22,25,26	3.21	10 (45%)	30,36,39	2.87	10 (33%)
11	OMG	AA	2815	11	23,26,27	0.49	0	32,38,41	0.47	0
12	DDE	Aa	699	12	18,20,21	0.98	1 (5%)	17,28,30	0.86	1 (5%)
11	UR3	AA	2634	11	19,22,23	2.87	6 (31%)	26,32,35	1.64	2 (7%)

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	OMG	c	1428	61	-	1/9/27/28	0/3/3/3
11	OMC	AA	1437	11,86	-	1/9/27/28	0/2/2/2
11	OMU	AA	2421	11	-	1/9/27/28	0/2/2/2
11	OMG	AA	2922	11	-	2/9/27/28	0/3/3/3
61	OMG	c	1271	61	-	1/9/27/28	0/3/3/3
61	A2M	c	420	61	-	2/9/27/28	0/3/3/3
11	OMU	AA	1888	11	-	0/9/27/28	0/2/2/2
11	A2M	AA	2281	11	-	3/9/27/28	0/3/3/3
11	OMC	AA	2948	11	-	0/9/27/28	0/2/2/2
11	OMC	AA	2337	11	-	0/9/27/28	0/2/2/2
11	OMG	AA	908	11	-	1/9/27/28	0/3/3/3
11	OMU	AA	2921	11,86	-	0/9/27/28	0/2/2/2
61	OMC	c	1639	86,61	-	0/9/27/28	0/2/2/2
11	A2M	AA	817	11,86	-	1/9/27/28	0/3/3/3
11	OMU	AA	2724	11	-	1/9/27/28	0/2/2/2
61	MA6	c	1781	61	-	0/11/29/30	0/3/3/3
11	OMC	AA	650	11	-	0/9/27/28	0/2/2/2
11	OMU	AA	2729	11	-	0/9/27/28	0/2/2/2
11	A2M	AA	2946	11,86	-	0/9/27/28	0/3/3/3
61	B8N	c	1191	61	-	5/16/34/35	0/2/2/2
11	OMG	AA	2619	11,15	-	1/9/27/28	0/3/3/3
61	OMG	c	1572	61	-	3/9/27/28	0/3/3/3
11	A2M	AA	2220	11	-	1/9/27/28	0/3/3/3
11	A2M	AA	2280	11	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	OMC	AA	2959	11,86	-	0/9/27/28	0/2/2/2
11	A2M	AA	1449	11,86	-	0/9/27/28	0/3/3/3
61	A2M	c	28	61	-	2/9/27/28	0/3/3/3
61	A2M	c	100	86,61	-	1/9/27/28	0/3/3/3
61	A2M	c	436	61	-	0/9/27/28	0/3/3/3
11	1MA	AA	2142	11,86	-	1/7/25/26	0/3/3/3
15	YYG	Bb	37	15	-	14/24/42/43	0/4/4/4
11	1MA	AA	645	11,86	-	1/7/25/26	0/3/3/3
61	OMG	c	1126	61	-	0/9/27/28	0/3/3/3
61	G7M	c	1575	18,61	-	3/7/25/26	0/3/3/3
61	A2M	c	974	61	-	0/9/27/28	0/3/3/3
61	A2M	c	619	86,61	-	5/9/27/28	0/3/3/3
61	OMU	c	1269	61	-	3/9/27/28	0/2/2/2
11	A2M	AA	807	11	-	1/9/27/28	0/3/3/3
11	A2M	AA	2256	11	-	1/9/27/28	0/3/3/3
11	OMU	AA	898	11	-	0/9/27/28	0/2/2/2
61	OMC	c	414	61	-	1/9/27/28	0/2/2/2
61	A2M	c	796	61	-	0/9/27/28	0/3/3/3
11	OMG	AA	867	11,87	-	2/9/27/28	0/3/3/3
11	OMU	AA	2417	11	-	1/9/27/28	0/2/2/2
61	OMC	c	1007	61	-	0/9/27/28	0/2/2/2
61	4AC	c	1280	61	-	4/11/29/30	0/2/2/2
61	OMU	c	578	61	-	2/9/27/28	0/2/2/2
11	OMC	AA	2197	11,87	-	4/9/27/28	0/2/2/2
11	OMG	AA	805	11	-	0/9/27/28	0/3/3/3
11	OMC	AA	663	11	-	1/9/27/28	0/2/2/2
11	OMG	AA	2288	11	-	0/9/27/28	0/3/3/3
61	OMG	c	562	61	-	1/9/27/28	0/3/3/3
61	A2M	c	541	61	-	4/9/27/28	0/3/3/3
11	5MC	AA	2870	11,87	-	4/7/25/26	0/2/2/2
11	5MC	AA	2278	11,86	-	0/7/25/26	0/2/2/2
11	OMG	AA	1450	11	-	2/9/27/28	0/3/3/3
11	A2M	AA	1133	11,86	-	0/9/27/28	0/3/3/3
11	OMG	AA	2791	11	-	0/9/27/28	0/3/3/3
11	OMU	AA	2347	11	-	0/9/27/28	0/2/2/2
61	MA6	c	1782	61	-	1/11/29/30	0/3/3/3
11	OMG	AA	2793	11	-	1/9/27/28	0/3/3/3
11	A2M	AA	649	11	-	1/9/27/28	0/3/3/3
11	A2M	AA	2640	11	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	4AC	c	1773	61	-	2/11/29/30	0/2/2/2
11	A2M	AA	876	11	-	0/9/27/28	0/3/3/3
11	OMG	AA	2815	11	-	0/9/27/28	0/3/3/3
12	DDE	Aa	699	12	-	3/20/21/23	0/1/1/1
11	UR3	AA	2634	11	-	0/7/25/26	0/2/2/2

The worst 5 of 339 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	c	28	A2M	C3'-C4'	-9.14	1.29	1.53
11	AA	807	A2M	C3'-C4'	-8.96	1.30	1.53
61	c	541	A2M	C3'-C4'	-8.93	1.30	1.53
11	AA	2280	A2M	C3'-C4'	-8.93	1.30	1.53
61	c	619	A2M	C3'-C4'	-8.92	1.30	1.53

The worst 5 of 342 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	c	1782	MA6	N1-C6-N6	-11.84	102.43	116.86
61	c	1781	MA6	N1-C6-N6	-11.44	102.92	116.86
61	c	1782	MA6	C5-C6-N6	7.82	137.72	125.33
61	c	1781	MA6	C5-C6-N6	7.71	137.53	125.33
15	Bb	37	YYG	C5-C4-N3	-7.24	118.11	123.99

There are no chirality outliers.

5 of 90 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	AA	649	A2M	C1'-C2'-O2'-CM'
11	AA	663	OMC	C1'-C2'-O2'-CM2
11	AA	1437	OMC	C1'-C2'-O2'-CM2
11	AA	1450	OMG	O4'-C4'-C5'-O5'
11	AA	2197	OMC	C2'-C1'-N1-C6

There are no ring outliers.

38 monomers are involved in 62 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	c	1428	OMG	2	0
11	AA	1437	OMC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	2421	OMU	1	0
11	AA	2922	OMG	2	0
61	c	1271	OMG	1	0
61	c	420	A2M	2	0
11	AA	2281	A2M	1	0
11	AA	2948	OMC	1	0
11	AA	2337	OMC	1	0
11	AA	908	OMG	1	0
61	c	1639	OMC	1	0
11	AA	817	A2M	2	0
11	AA	2724	OMU	4	0
61	c	1781	MA6	1	0
11	AA	650	OMC	2	0
61	c	1572	OMG	1	0
11	AA	2220	A2M	2	0
11	AA	2959	OMC	1	0
11	AA	1449	A2M	1	0
61	c	436	A2M	1	0
15	Bb	37	YYG	7	0
61	c	1575	G7M	2	0
61	c	1269	OMU	1	0
11	AA	898	OMU	1	0
11	AA	2417	OMU	1	0
61	c	1280	4AC	4	0
11	AA	805	OMG	1	0
11	AA	663	OMC	3	0
61	c	541	A2M	1	0
11	AA	2870	5MC	2	0
11	AA	1133	A2M	1	0
11	AA	2347	OMU	1	0
11	AA	2793	OMG	1	0
11	AA	649	A2M	1	0
11	AA	2640	A2M	1	0
61	c	1773	4AC	4	0
11	AA	2815	OMG	1	0
12	Aa	699	DDE	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 297 ligands modelled in this entry, 291 are monoatomic - leaving 6 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
88	SPD	AA	3615	-	9,9,9	0.29	0	8,8,8	0.77	0
88	SPD	AA	3614	-	9,9,9	0.33	0	8,8,8	0.93	0
90	PO4	Aa	1002	86	4,4,4	1.06	0	6,6,6	0.54	0
91	SO1	Aa	1003	-	34,39,39	1.19	3 (8%)	38,64,64	1.15	3 (7%)
88	SPD	AA	3613	-	9,9,9	0.32	0	8,8,8	0.89	0
89	GDP	Aa	1001	86	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)

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
88	SPD	AA	3615	-	-	3/7/7/7	-
88	SPD	AA	3614	-	-	0/7/7/7	-
91	SO1	Aa	1003	-	-	10/21/104/104	0/7/5/5
88	SPD	AA	3613	-	-	1/7/7/7	-
89	GDP	Aa	1001	86	-	5/16/32/32	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	Aa	1003	SO1	C2-C6	-4.05	1.49	1.55
89	Aa	1001	GDP	C5-C4	3.05	1.47	1.38
91	Aa	1003	SO1	C16-C22	-2.44	1.50	1.54
89	Aa	1001	GDP	C6-N1	-2.44	1.34	1.38
91	Aa	1003	SO1	C3-C9	-2.16	1.51	1.56

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	Aa	1001	GDP	C5-C4-N3	-5.91	118.98	128.39
89	Aa	1001	GDP	C2-N3-C4	4.99	120.90	112.30
89	Aa	1001	GDP	N9-C4-N3	4.37	134.69	125.95
89	Aa	1001	GDP	C6-C5-N7	3.38	136.44	130.29
91	Aa	1003	SO1	C52-O56-C56	-2.98	108.54	113.63

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

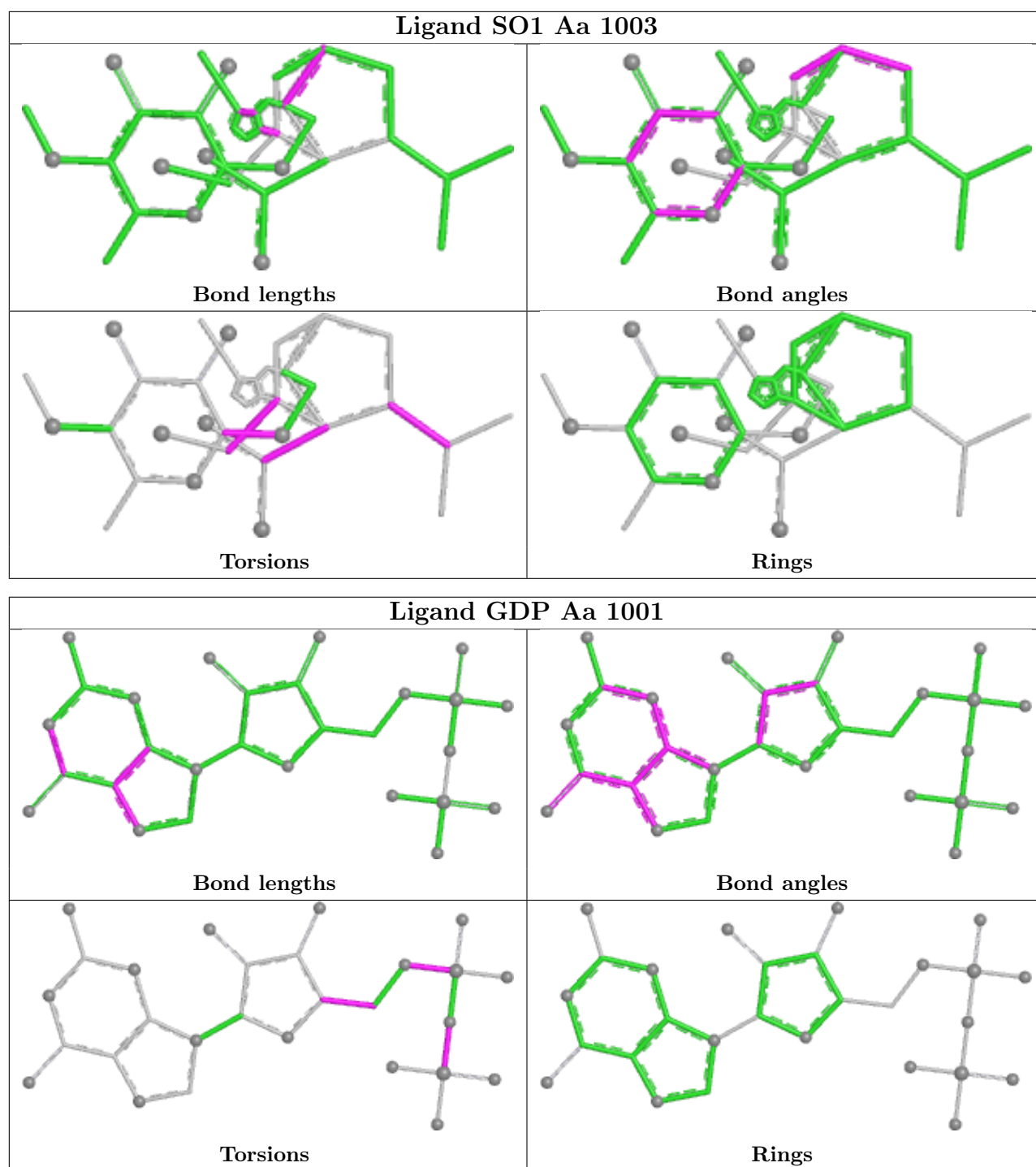
Mol	Chain	Res	Type	Atoms
89	Aa	1001	GDP	O4'-C4'-C5'-O5'
91	Aa	1003	SO1	C2-C1-C5-O14
91	Aa	1003	SO1	C2-C1-C5-O15
91	Aa	1003	SO1	C20-C13-C4-C1
91	Aa	1003	SO1	C21-C13-C4-C1

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	AA	3615	SPD	3	0
88	AA	3614	SPD	1	0
90	Aa	1002	PO4	6	0
91	Aa	1003	SO1	7	0
88	AA	3613	SPD	1	0
89	Aa	1001	GDP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

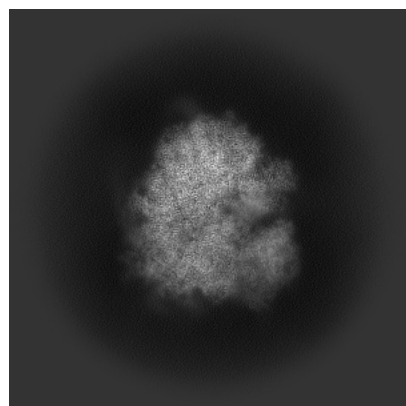
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16609. These allow visual inspection of the internal detail of the map and identification of artifacts.

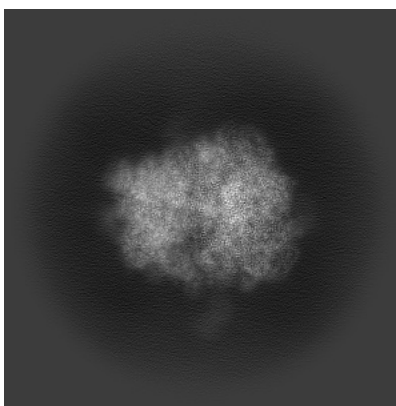
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

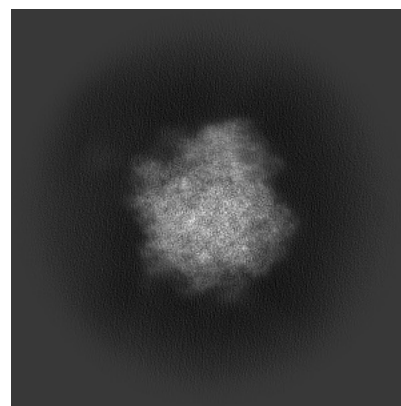
6.1.1 Primary map



X

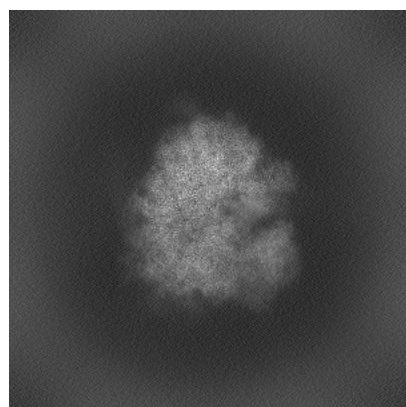


Y

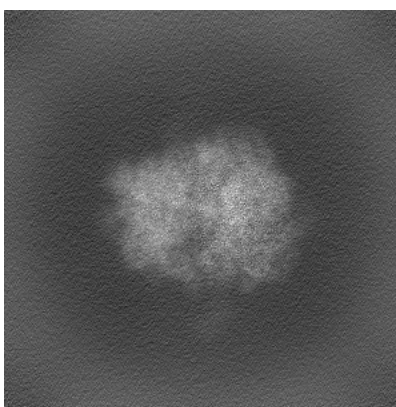


Z

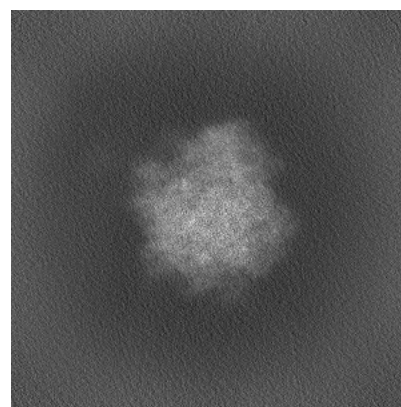
6.1.2 Raw map



X



Y

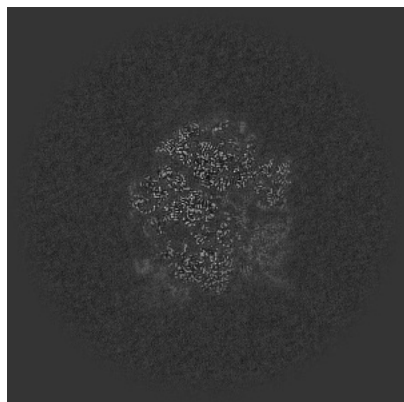


Z

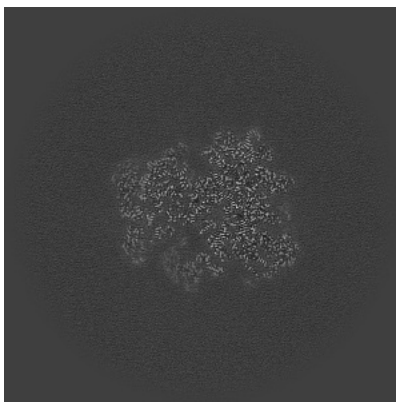
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

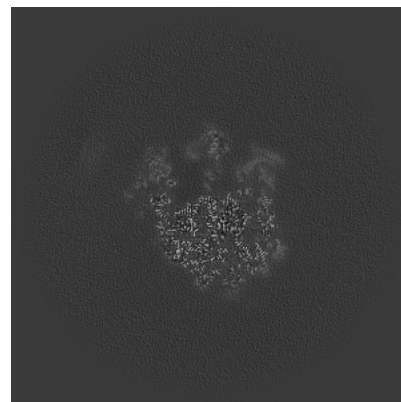
6.2.1 Primary map



X Index: 300

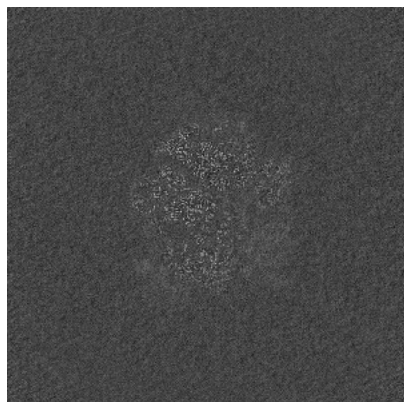


Y Index: 300

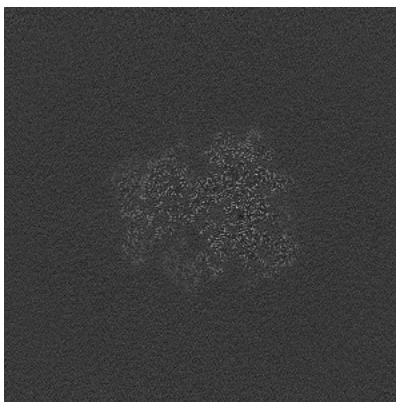


Z Index: 300

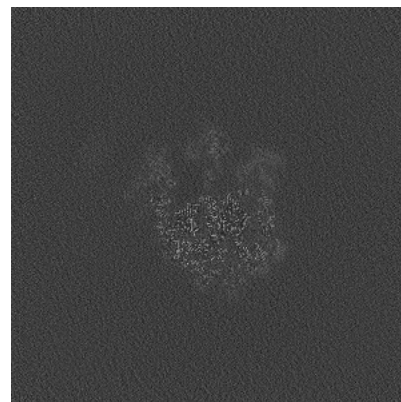
6.2.2 Raw map



X Index: 300



Y Index: 300

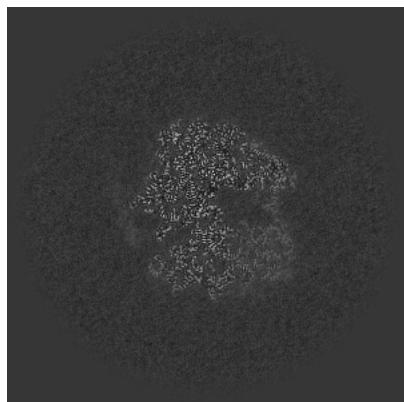


Z Index: 300

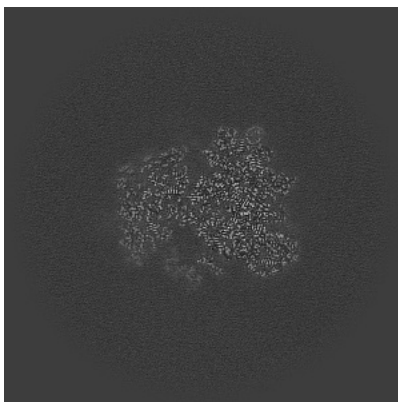
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

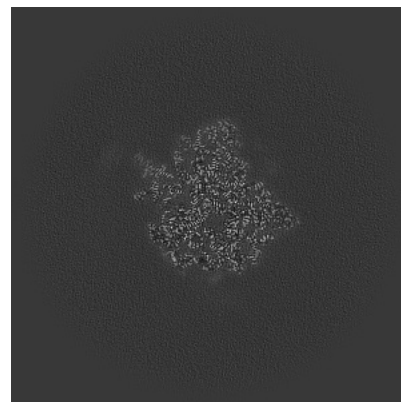
6.3.1 Primary map



X Index: 324

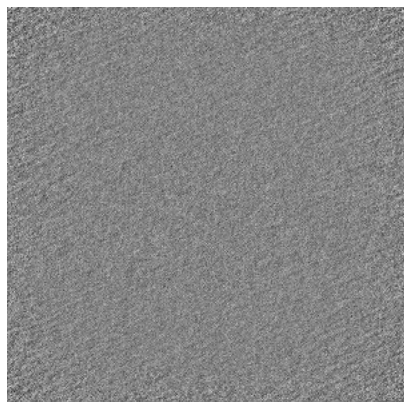


Y Index: 295

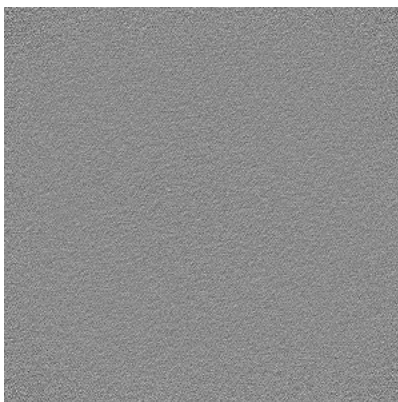


Z Index: 340

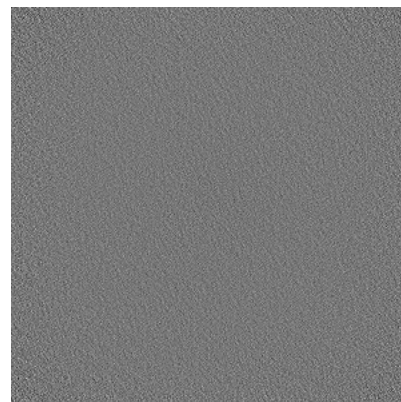
6.3.2 Raw map



X Index: 0



Y Index: 0

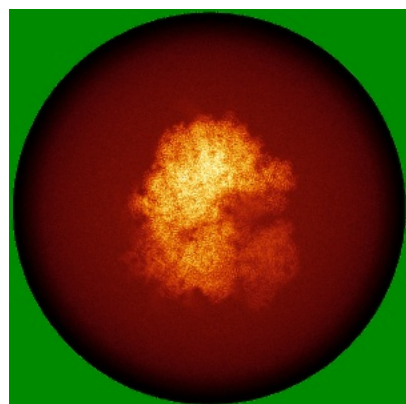


Z Index: 0

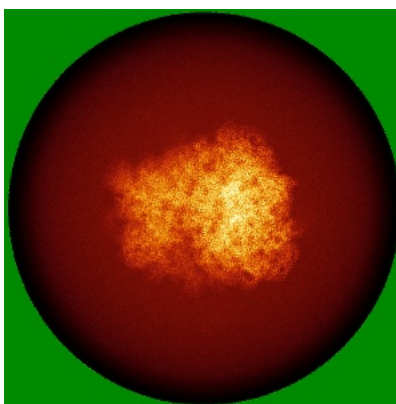
The images above show the largest variance slices of the map in three orthogonal directions.

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

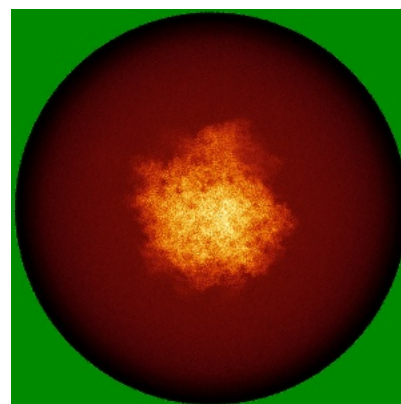
6.4.1 Primary map



X

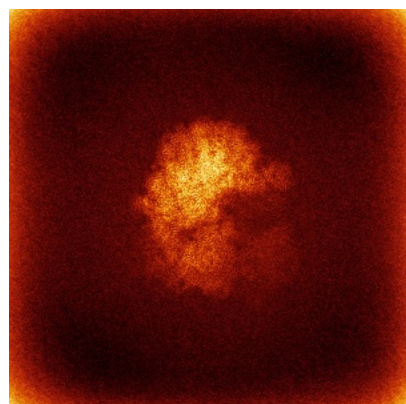


Y

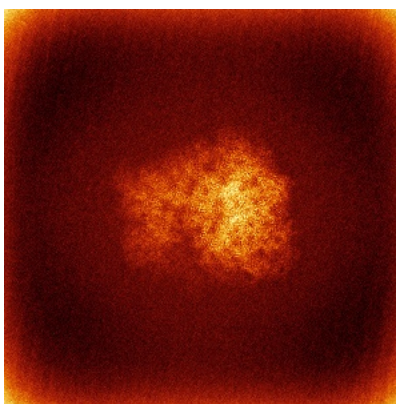


Z

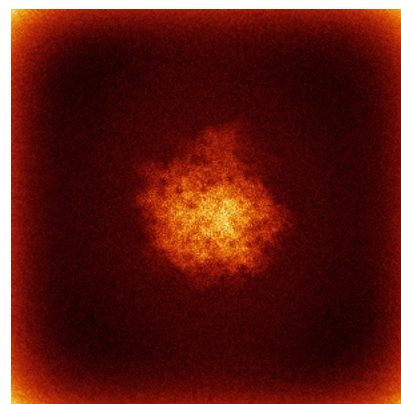
6.4.2 Raw map



X



Y

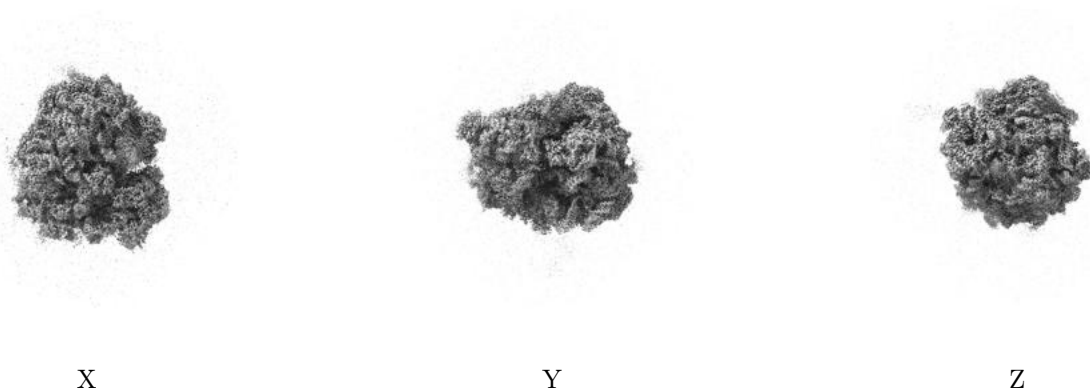


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

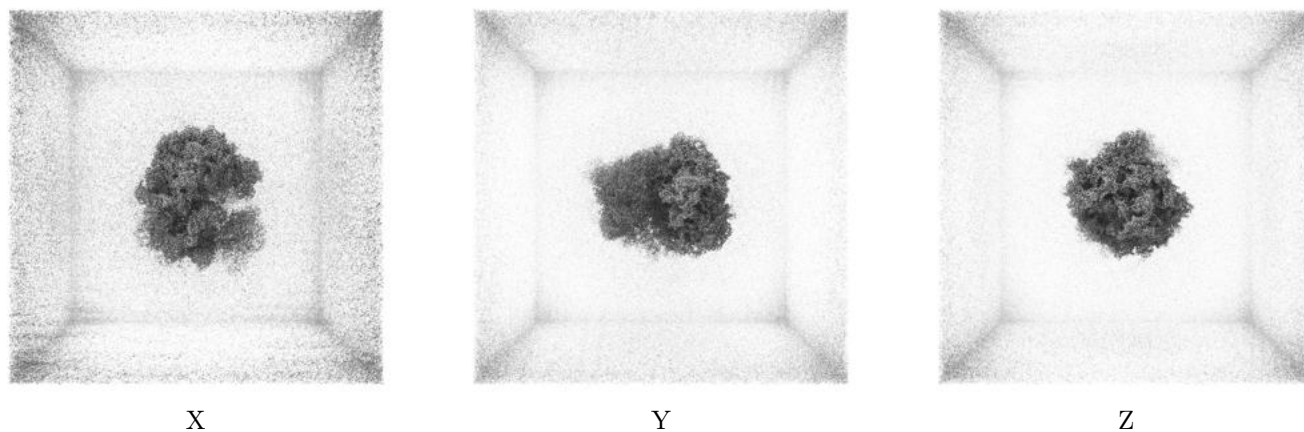
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.161. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

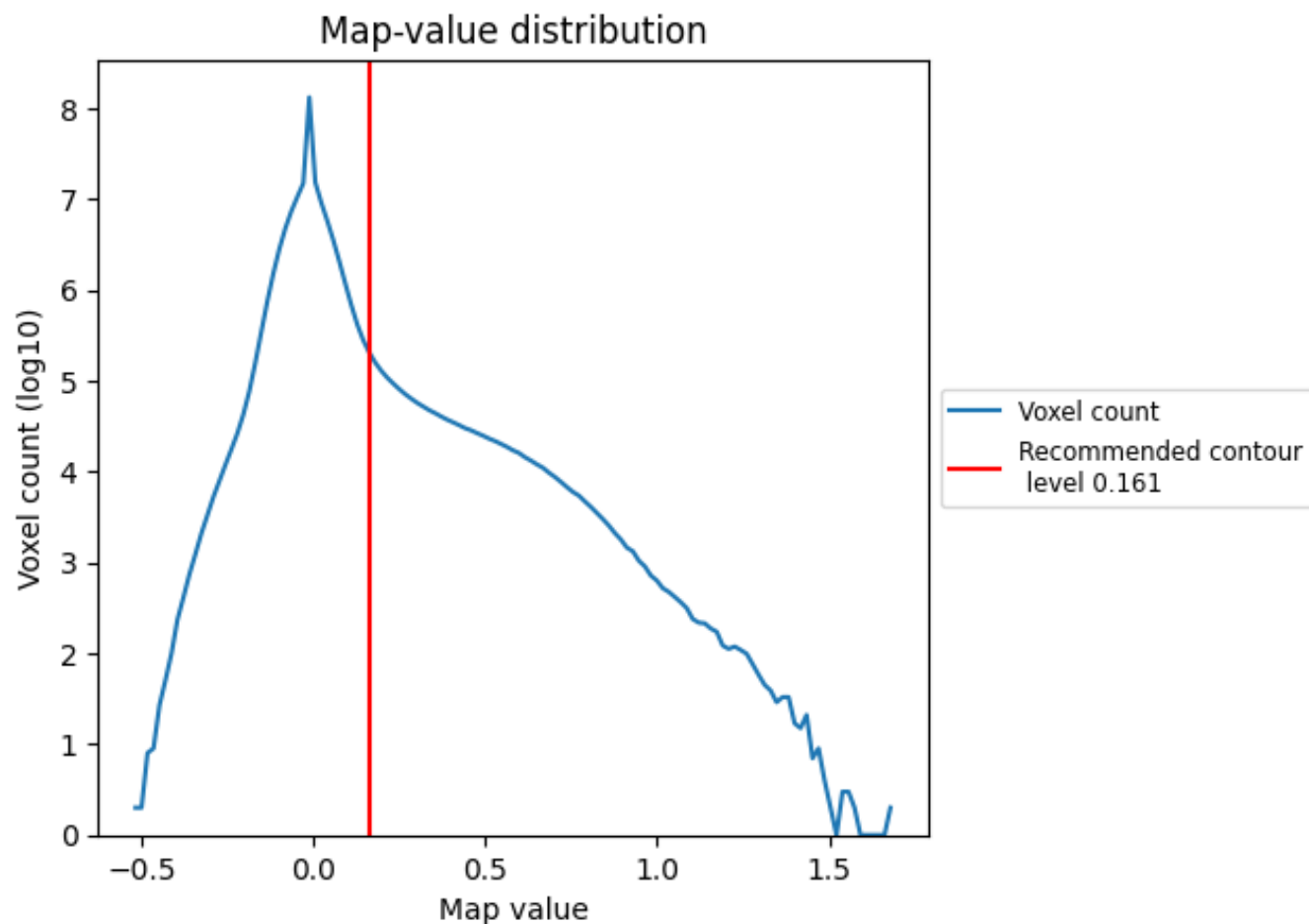
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

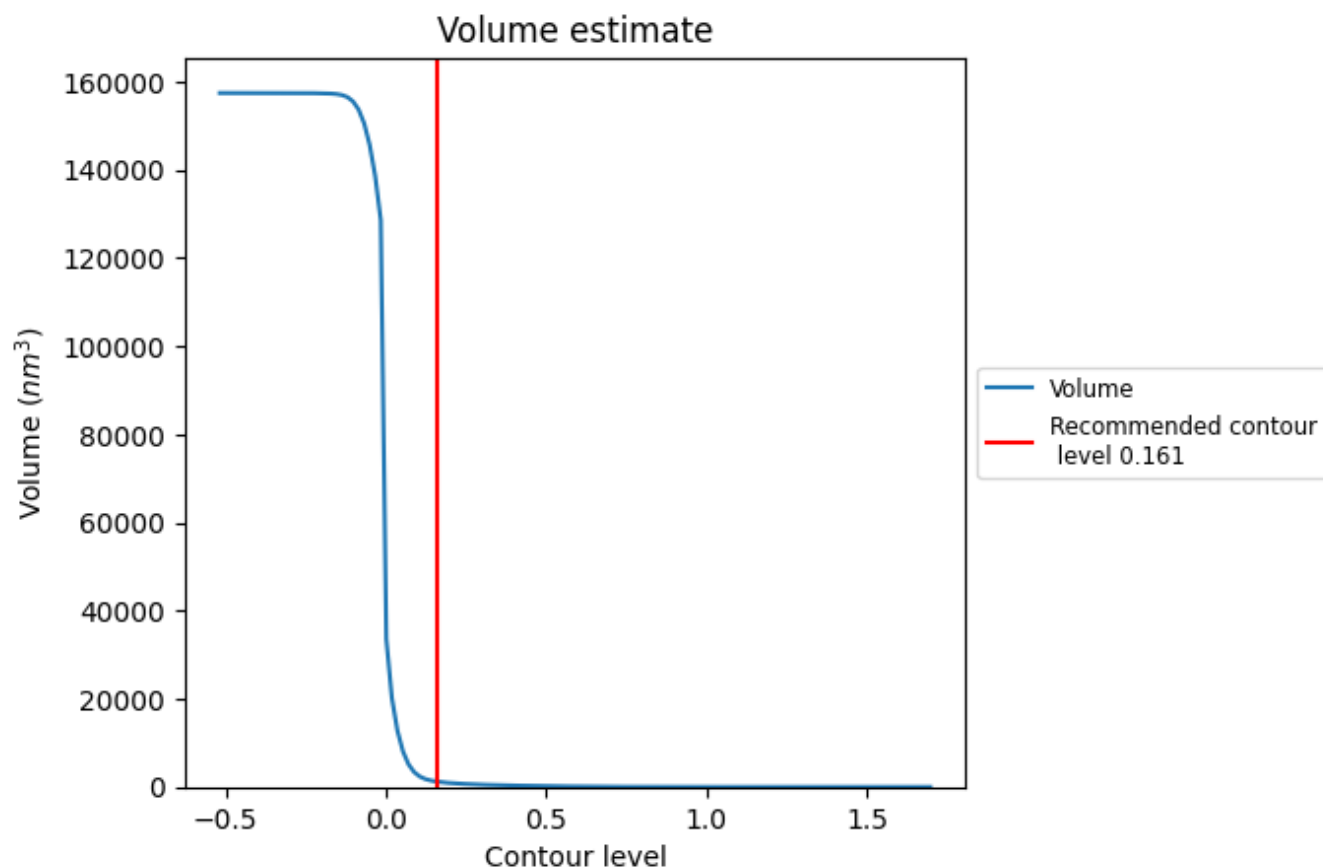
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

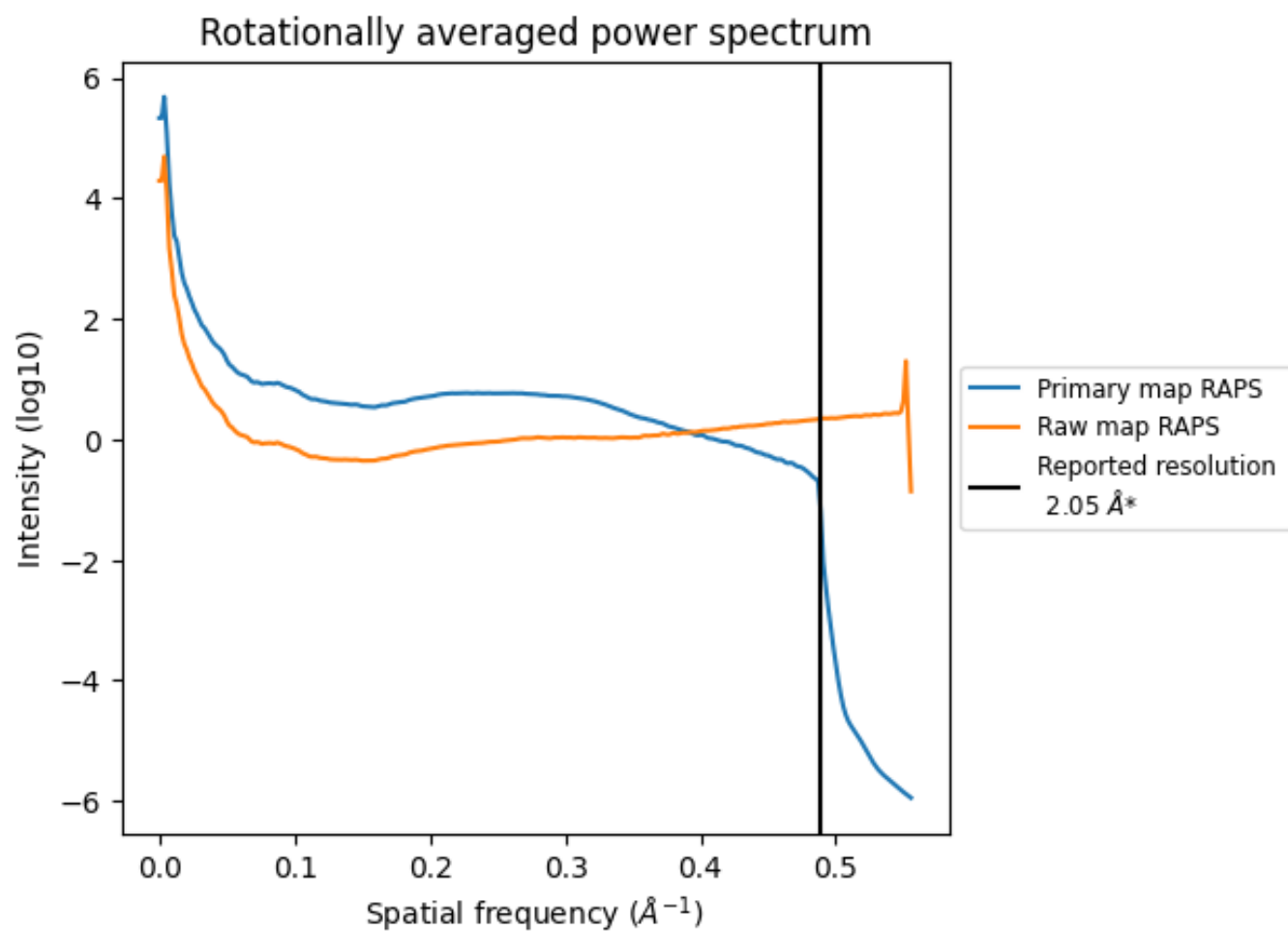
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1195 nm^3 ; this corresponds to an approximate mass of 1079 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 ⓘ

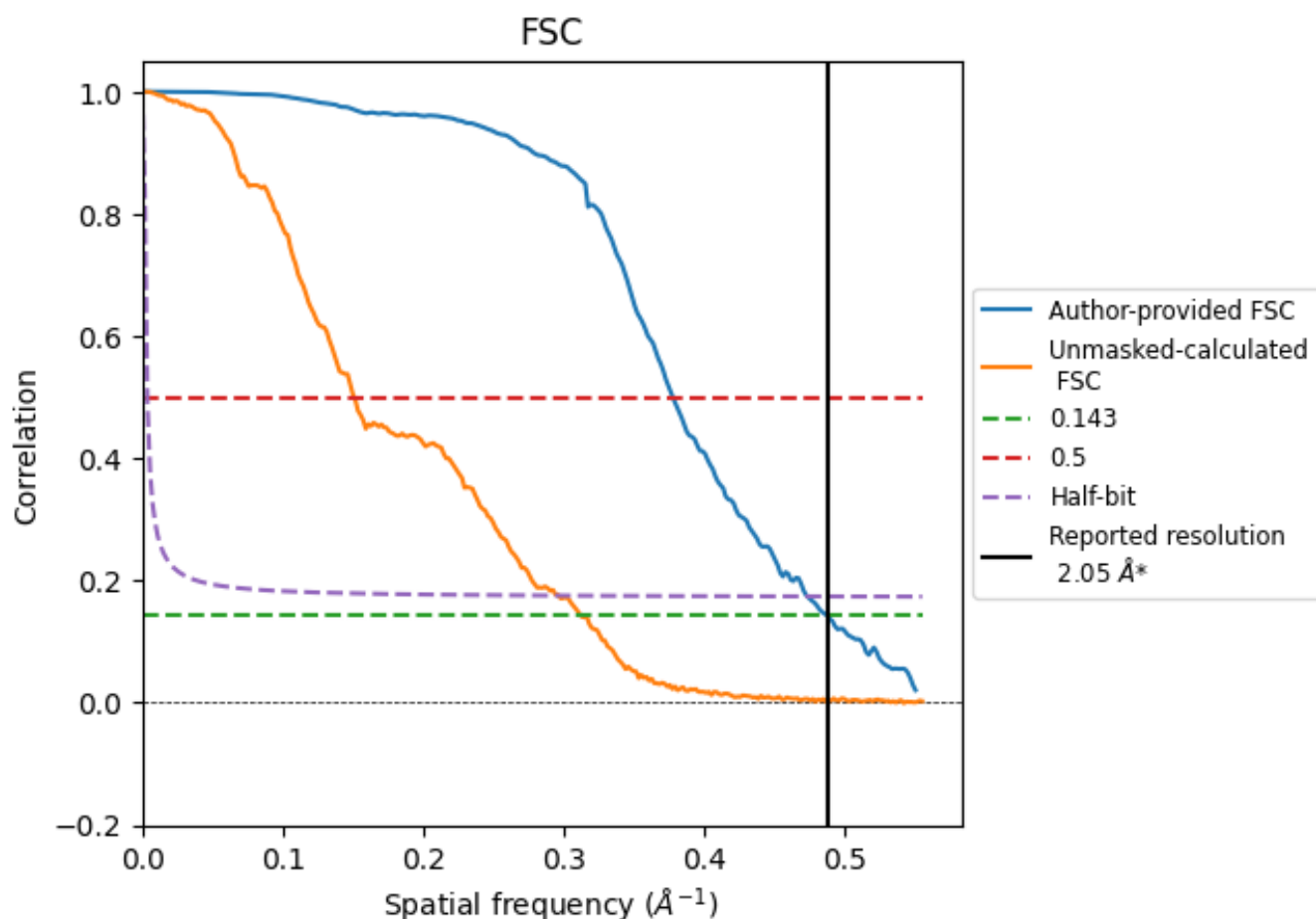


*Reported resolution corresponds to spatial frequency of 0.488 $\text{\AA}^{-1}$

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 0.488 Å⁻¹

8.2 Resolution estimates [i](#)

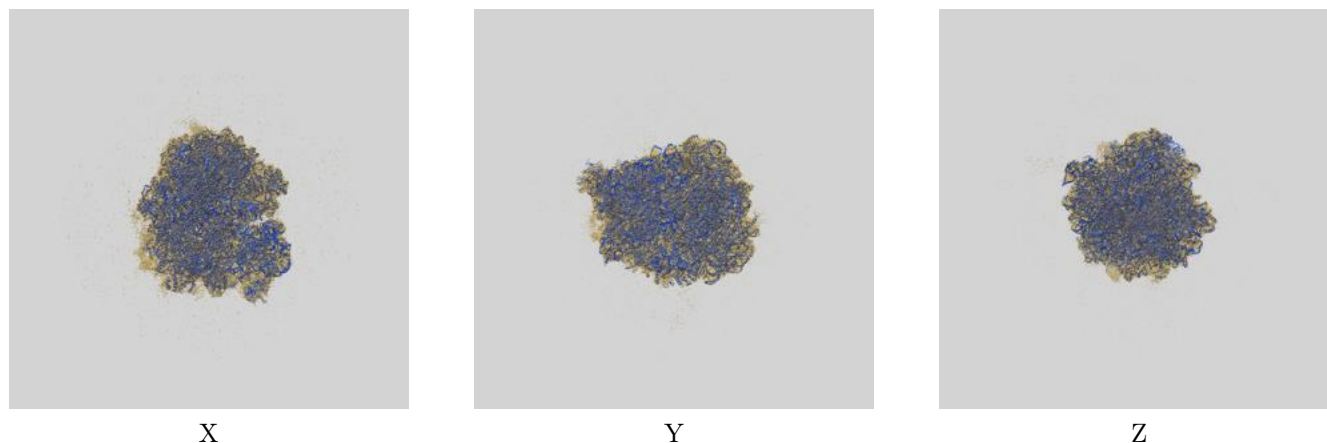
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.05	-	-
Author-provided FSC curve	2.05	2.65	2.11
Unmasked-calculated*	3.20	6.63	3.37

*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 3.20 differs from the reported value 2.05 by more than 10 %

9 Map-model fit [i](#)

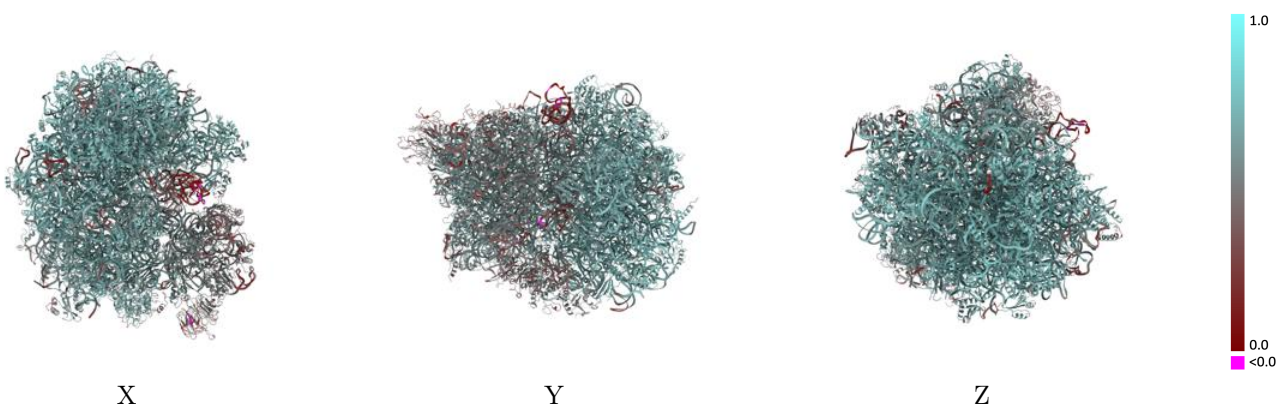
This section contains information regarding the fit between EMDB map EMD-16609 and PDB model 8CEH. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



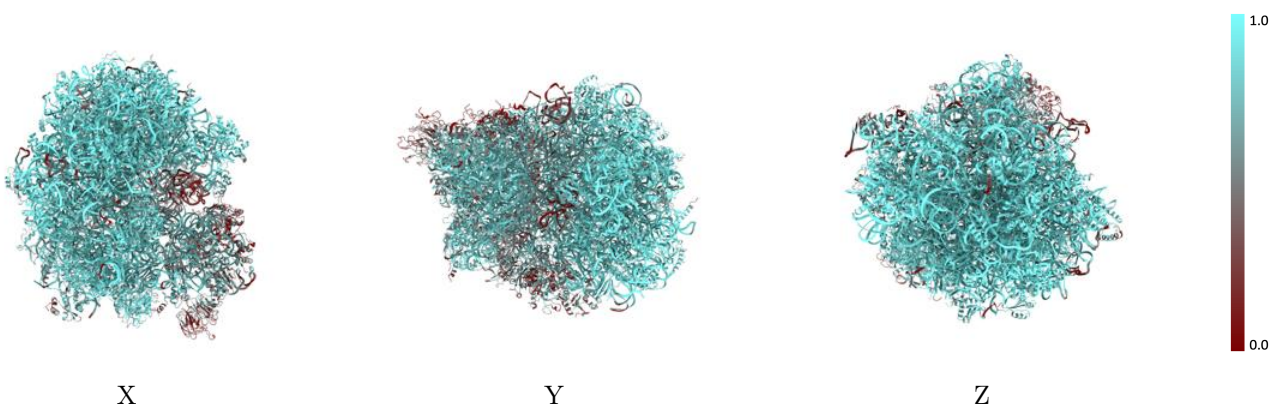
The images above show the 3D surface view of the map at the recommended contour level 0.161 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



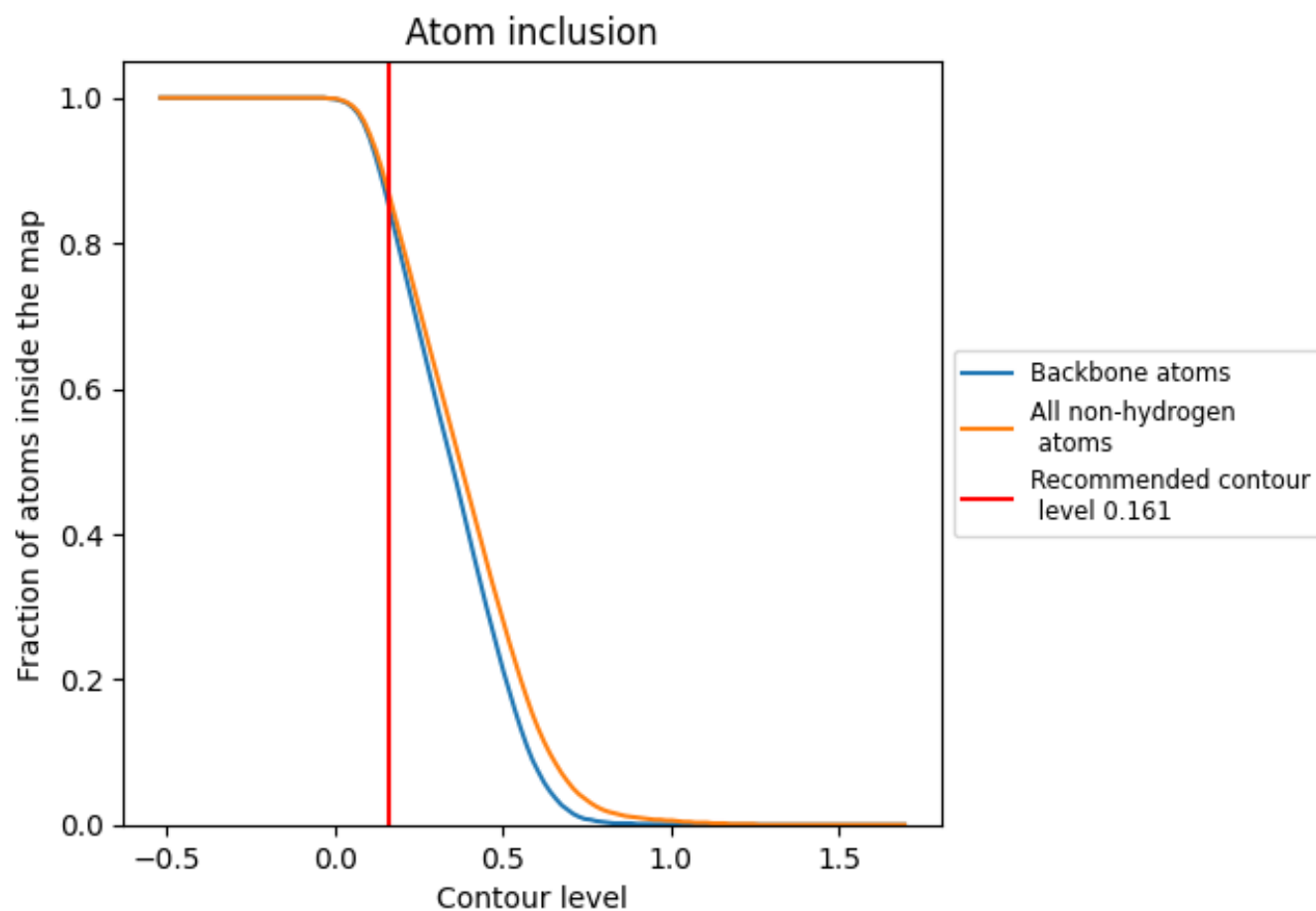
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.161).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 87% 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 (0.161) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8700	 0.6170
0	 0.7540	 0.5610
1	 0.0770	 0.3350
2	 0.9190	 0.6460
3	 0.8290	 0.6120
4	 0.4760	 0.4890
5	 0.8400	 0.5540
6	 0.7660	 0.5470
7	 0.3680	 0.3870
8	 0.1620	 0.3330
A	 0.9720	 0.6990
AA	 0.9430	 0.6480
Aa	 0.5790	 0.5000
B	 0.9750	 0.7100
BB	 0.9880	 0.6610
Bb	 0.5280	 0.4710
C	 0.9750	 0.7010
CC	 0.9790	 0.6760
Cc	 0.6390	 0.4500
D	 0.9200	 0.6740
DD	 0.5460	 0.5050
Dd	 0.9440	 0.6290
E	 0.9630	 0.6920
EE	 0.9720	 0.7070
Ee	 0.2220	 0.3650
F	 0.9330	 0.6750
FF	 0.9630	 0.6930
G	 0.8690	 0.6200
GG	 0.9640	 0.6970
H	 0.9670	 0.7020
HH	 0.8640	 0.6280
I	 0.9510	 0.6930
II	 0.9290	 0.6700
J	 0.9460	 0.6840
JJ	 0.9570	 0.6890



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Chain	Atom inclusion	Q-score
K	 0.9560	 0.6880
KK	 0.8840	 0.6480
L	 0.9320	 0.6650
LL	 0.9270	 0.6690
M	 0.9570	 0.6890
MM	 0.9280	 0.6760
N	 0.8920	 0.6320
NN	 0.7960	 0.5810
O	 0.9360	 0.6800
OO	 0.9190	 0.6680
P	 0.9030	 0.6550
PP	 0.9550	 0.6810
Pp	 0.4210	 0.5790
Q	 0.9680	 0.7080
QQ	 0.9920	 0.7100
R	 0.9930	 0.7180
S	 0.9540	 0.6890
T	 0.9460	 0.6700
U	 0.8980	 0.6410
V	 0.9890	 0.7080
W	 0.8350	 0.6320
X	 0.9690	 0.6830
Y	 0.9550	 0.6950
Z	 0.9430	 0.6750
a	 0.9300	 0.6730
b	 0.9400	 0.6970
c	 0.8830	 0.5730
d	 0.8700	 0.6060
e	 0.8680	 0.6250
f	 0.9160	 0.6460
g	 0.6420	 0.4980
h	 0.8810	 0.6060
i	 0.4930	 0.4690
j	 0.6650	 0.5120
k	 0.7110	 0.5520
l	 0.8730	 0.6200
m	 0.8680	 0.6050
n	 0.5600	 0.4460
o	 0.8940	 0.6490
p	 0.9300	 0.6640
q	 0.9360	 0.6420
r	 0.4970	 0.4680

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Chain	Atom inclusion	Q-score
s	 0.6440	 0.5120
t	 0.6260	 0.5000
u	 0.4110	 0.4570
v	 0.5780	 0.4670
w	 0.6060	 0.4890
x	 0.8890	 0.6340
y	 0.9730	 0.6910
z	 0.8740	 0.6230