



wwPDB EM Validation Summary Report ⓘ

Jul 21, 2025 – 08:12 PM EDT

PDB ID : 8VVQ / pdb_00008vvq
EMDB ID : EMD-43565
Title : Codon sampling state of elongation inhibitor-treated mammalian ribosomes
obtained from merged datasets
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.
Deposited on : 2024-01-31
Resolution : 2.70 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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

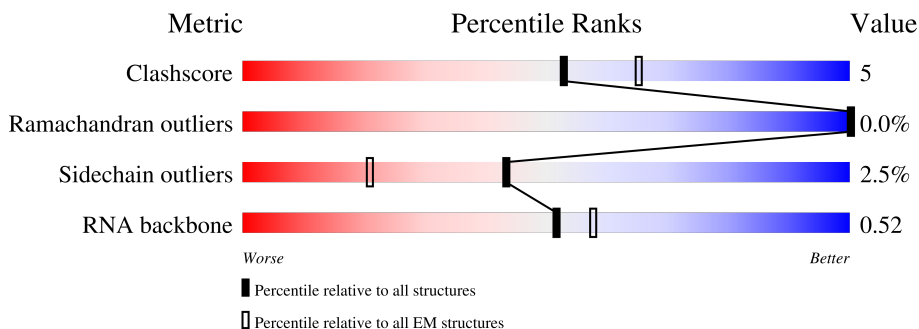
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

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





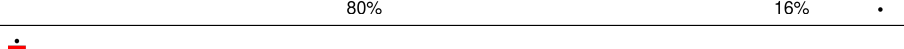
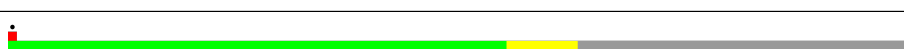



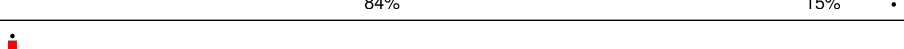



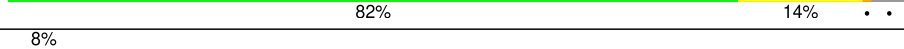

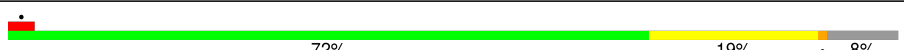


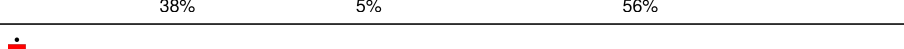







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	413	
4	D	297	
5	E	291	
6	F	249	
7	G	319	






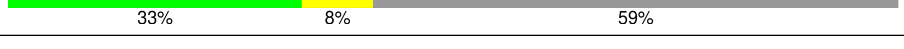
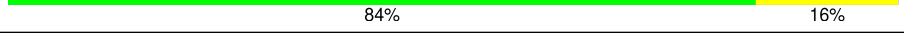
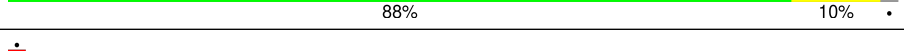
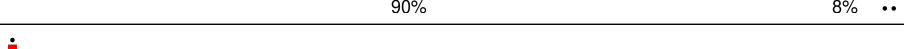

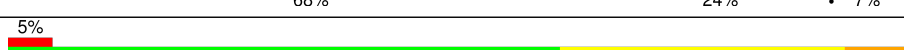

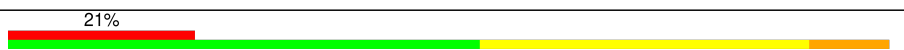

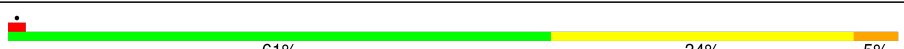





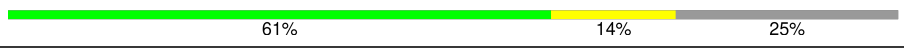
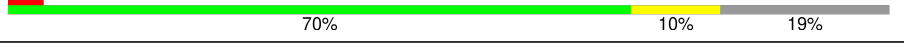



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Mol	Chain	Length	Quality of chain
8	H	192	
9	I	214	
10	J	178	
11	K	211	
12	L	218	
13	M	204	
14	N	203	
15	O	213	
16	P	188	
17	Q	212	
18	R	224	
19	S	160	
20	T	128	
21	U	140	
22	V	157	
23	W	156	
24	X	145	
25	Y	136	
26	Z	148	
27	AA	245	
28	BA	115	
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	

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Mol	Chain	Length	Quality of chain
33	GA	123	
34	HA	105	
35	IA	97	
36	JA	70	
37	KA	51	
38	LA	128	
39	MA	25	
40	NA	106	
41	OA	92	
42	PA	137	
43	RA	165	
44	SA	76	
45	TA	76	
46	UA	75	
47	VA	12	
48	WA	3584	
49	XA	120	
50	YA	156	
51	ZA	1869	
52	AB	295	
53	BB	264	
54	CB	293	
55	DB	281	
56	EB	263	
57	FB	204	

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Mol	Chain	Length	Quality of chain
58	GB	249	
59	HB	432	
60	IB	208	
61	JB	194	
62	KB	165	
63	LB	158	
64	MB	132	
65	NB	151	
66	OB	151	
67	PB	145	
68	QB	172	
69	RB	135	
70	SB	152	
71	TB	145	
72	UB	119	
73	VB	83	
74	WB	130	
75	XB	143	
76	YB	131	
77	ZB	124	
78	AC	115	
79	BC	84	
80	CC	69	
81	DC	56	
82	EC	133	

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Mol	Chain	Length	Quality of chain
83	FC	188	
84	GC	317	
85	HC	462	
86	IC	4	
87	b	318	
88	c	14	

2 Entry composition

There are 96 unique types of molecules in this entry. The entry contains 222430 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	250	Total	C	N	O	S	0	0
			1914	1199	392	317	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	397	Total	C	N	O	S	0	0
			3196	2035	603	545	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2395	1514	439	428	14		

- Molecule 5 is a protein called L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1823	1173	349	298	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1897	1217	366	305	9		

- Molecule 7 is a protein called L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	229	Total	C	N	O	S	0	0
			1850	1181	356	309	4		

- Molecule 8 is a protein called L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	171	Total	C	N	O	S	0	0
			1372	867	256	243	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	46	ILE	-	insertion	UNP G1TPV0
K	47	ALA	-	insertion	UNP G1TPV0
K	48	PRO	-	insertion	UNP G1TPV0
K	49	ARG	-	insertion	UNP G1TPV0
K	50	PRO	-	insertion	UNP G1TPV0
K	51	ALA	-	insertion	UNP G1TPV0
K	52	ALA	-	insertion	UNP G1TPV0
K	53	GLY	-	insertion	UNP G1TPV0
K	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	156	Total	C	N	O	S	0	0
			1266	793	245	219	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	43	SER	ALA	conflict	UNP G1TVT6

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	4	ASP	ASN	conflict	UNP G1TFE0
P	14	ARG	TRP	conflict	UNP G1TFE0
P	53	MET	LEU	conflict	UNP G1TFE0
P	58	ARG	TRP	conflict	UNP G1TFE0
P	75	ARG	GLN	conflict	UNP G1TFE0
P	80	ALA	PRO	conflict	UNP G1TFE0
P	86	VAL	ILE	conflict	UNP G1TFE0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	104	ARG	HIS	conflict	UNP G1TFE0
P	110	ARG	CYS	conflict	UNP G1TFE0
P	137	VAL	GLY	conflict	UNP G1TFE0
P	157	GLY	ARG	conflict	UNP G1TFE0
P	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	101	Total	C	N	O	S	0	0
			826	530	144	150	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	18	LEU	VAL	conflict	UNP G1TSG1
T	32	GLY	ARG	conflict	UNP G1TSG1
T	36	ALA	GLU	conflict	UNP G1TSG1
T	39	PHE	SER	conflict	UNP G1TSG1
T	54	GLY	ARG	conflict	UNP G1TSG1
T	60	VAL	ALA	conflict	UNP G1TSG1
T	62	SER	THR	conflict	UNP G1TSG1
T	63	LEU	ILE	conflict	UNP G1TSG1

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Chain	Residue	Modelled	Actual	Comment	Reference
T	97	ARG	HIS	conflict	UNP G1TSG1
T	106	THR	SER	conflict	UNP G1TSG1
T	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	135	Total	C	N	O	S	0	0
			1004	631	191	177	5		

- Molecule 22 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	110	Total	C	N	O	S	0	0
			887	555	179	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	78	SER	PHE	conflict	UNP G1SE28

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	107	Total	C	N	O	S	0	0
			873	542	195	133	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	99	Total	C	N	O	S	0	0
			769	486	135	141	7		

- Molecule 29 is a protein called L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	108	Total	C	N	O	S	0	0
			893	563	172	156	2		

- Molecule 30 is a protein called L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	GA	121	Total	C	N	O	S	0	0
			1008	637	203	167	1		

- Molecule 34 is a protein called L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	HA	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IA	87	Total	C	N	O	S	0	0
			716	440	159	112	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JA	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	MA	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NA	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	OA	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	PA	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	RA	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 44 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SA	76	Total	C	N	O	P	0	0
			1622	726	300	521	75		

- Molecule 45 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	TA	76	Total	C	N	O	P	0	0
			1615	722	286	532	75		

- Molecule 46 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	UA	75	Total	C	N	O	P	0	0
			1586	711	279	521	75		

- Molecule 47 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	VA	12	Total	C	N	O	P	0	0
			249	114	42	81	12		

- Molecule 48 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	WA	3578	Total	C	N	O	P	0	0
			76735	34173	14061	24923	3578		

- Molecule 49 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	XA	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XA	2	U	N	conflict	GB X06789.1
XA	36	C	N	conflict	GB X06789.1
XA	102	U	N	conflict	GB X06789.1
XA	112	U	N	conflict	GB X06789.1
XA	114	U	N	conflict	GB X06789.1
XA	119	U	C	conflict	GB X06789.1
XA	120	U	N	conflict	GB X06789.1

- Molecule 50 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	YA	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 51 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	ZA	1716	Total	C	N	O	P	0	0
			36623	16347	6572	11989	1715		

- Molecule 52 is a protein called RPSA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 53 is a protein called S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 54 is a protein called S2-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CB	220	Total	C	N	O	S	0	0
			1707	1105	293	300	9		

- Molecule 55 is a protein called S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DB	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 56 is a protein called S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	EB	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EB	25	GLY	SER	conflict	UNP G1TK17
EB	51	ARG	LYS	conflict	UNP G1TK17
EB	78	THR	ALA	conflict	UNP G1TK17
EB	156	VAL	MET	conflict	UNP G1TK17

- Molecule 57 is a protein called S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FB	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 58 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	GB	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 59 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	HB	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 60 is a protein called S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	IB	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	JB	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 62 is a protein called S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	KB	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 63 is a protein called S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LB	144	Total	C	N	O	S	0	0
			1180	752	223	199	6		

- Molecule 64 is a protein called S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	MB	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 65 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	NB	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 66 is a protein called S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	OB	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 67 is a protein called S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PB	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 68 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	QB	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RB	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 70 is a protein called S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SB	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 71 is a protein called S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	TB	142	Total	C	N	O	S	0	0
			1104	693	212	196	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TB	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	UB	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 73 is a protein called S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	VB	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VB	3	ASN	SER	conflict	UNP G1TM82
VB	4	ASP	ASN	conflict	UNP G1TM82
VB	33	GLN	PRO	conflict	UNP G1TM82
VB	50	PHE	SER	conflict	UNP G1TM82
VB	75	ALA	SER	conflict	UNP G1TM82
VB	76	ASP	HIS	conflict	UNP G1TM82
VB	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 74 is a protein called S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	WB	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 75 is a protein called S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	XB	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 76 is a protein called S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	YB	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	ZB	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 78 is a protein called S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AC	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	28	ARG	CYS	conflict	UNP G1TFE8
AC	56	ALA	VAL	conflict	UNP G1TFE8
AC	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 79 is a protein called S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BC	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CC	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 81 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	DC	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 82 is a protein called S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EC	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 83 is a protein called S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	FC	69	Total	C	N	O	S	0	0
			564	357	105	95	7		

- Molecule 84 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	GC	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 85 is a protein called eukaryotic elongation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	HC	440	Total	C	N	O	S	0	0
			3371	2143	581	630	17		

- Molecule 86 is a protein called peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
86	IC	4	Total	C	N	O	0	0
			20	12	4	4		

- Molecule 87 is a protein called RPLP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	b	167	Total	C	N	O	S	0	0
			1279	813	228	229	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	82	LEU	ILE	conflict	UNP G1SPK4

- Molecule 88 is a protein called RPLP peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	c	11	Total	C	N	O	S	0	0
			86	53	11	21	1		

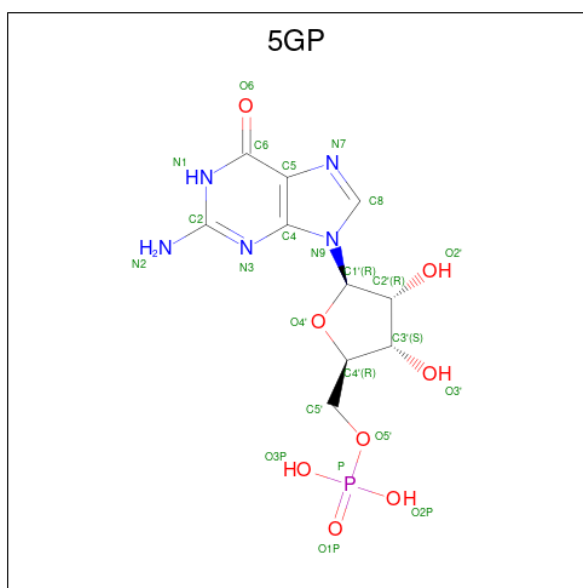
- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	A	1	Total	Mg	0
			1	1	
89	B	1	Total	Mg	0
			1	1	
89	I	1	Total	Mg	0
			1	1	
89	O	1	Total	Mg	0
			1	1	
89	U	1	Total	Mg	0
			1	1	
89	Z	1	Total	Mg	0
			1	1	
89	DA	1	Total	Mg	0
			1	1	
89	FA	1	Total	Mg	0
			1	1	
89	IA	1	Total	Mg	0
			1	1	
89	SA	1	Total	Mg	0
			1	1	
89	WA	186	Total	Mg	0
			186	186	
89	XA	6	Total	Mg	0
			6	6	
89	YA	4	Total	Mg	0
			4	4	
89	ZA	80	Total	Mg	0
			80	80	
89	LB	1	Total	Mg	0
			1	1	
89	AC	1	Total	Mg	0
			1	1	
89	HC	1	Total	Mg	0
			1	1	
89	b	1	Total	Mg	0
			1	1	

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

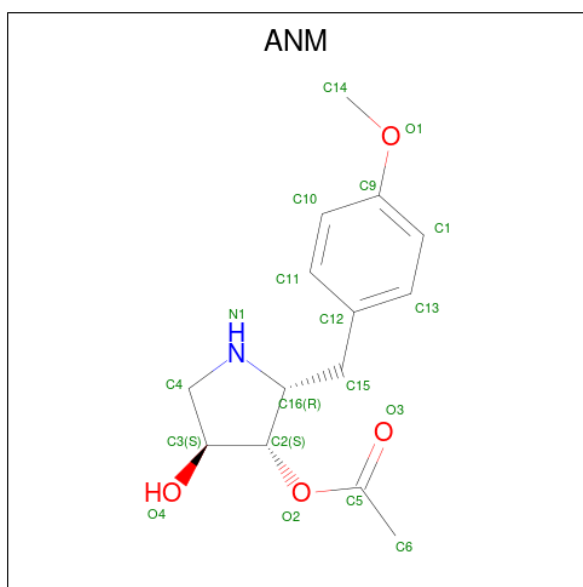
Mol	Chain	Residues	Atoms		AltConf
90	FA	1	Total	Zn	0
			1	1	
90	IA	1	Total	Zn	0
			1	1	
90	LA	1	Total	Zn	0
			1	1	
90	NA	1	Total	Zn	0
			1	1	
90	OA	1	Total	Zn	0
			1	1	
90	AC	1	Total	Zn	0
			1	1	
90	DC	1	Total	Zn	0
			1	1	
90	FC	1	Total	Zn	0
			1	1	

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



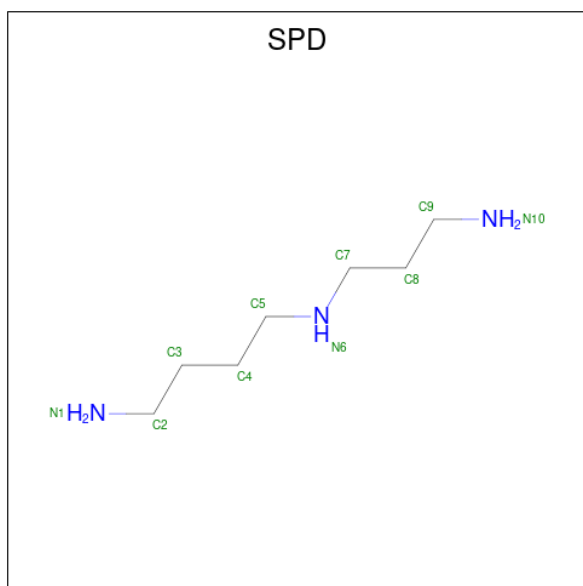
Mol	Chain	Residues	Atoms					AltConf
91	UA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 92 is ANISOMYCIN (CCD ID: ANM) (formula: $C_{14}H_{19}NO_4$).



Mol	Chain	Residues	Atoms				AltConf
92	WA	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 93 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).

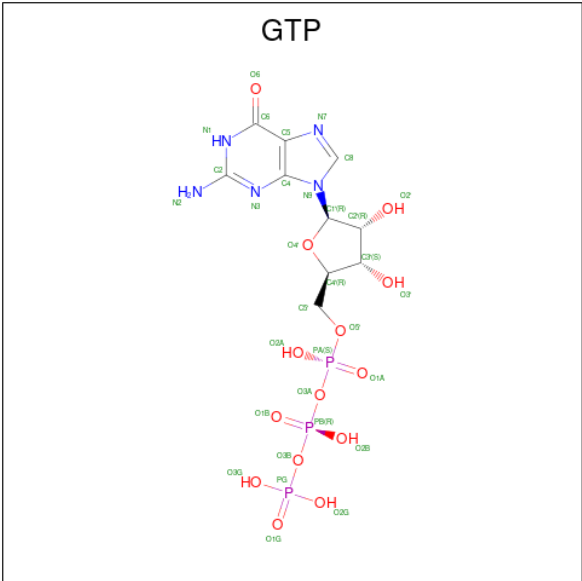


Mol	Chain	Residues	Atoms			AltConf
93	WA	1	Total	C	N	0
			10	7	3	

- Molecule 94 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
94	WA	1	Total	K	0
			1	1	

- Molecule 95 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

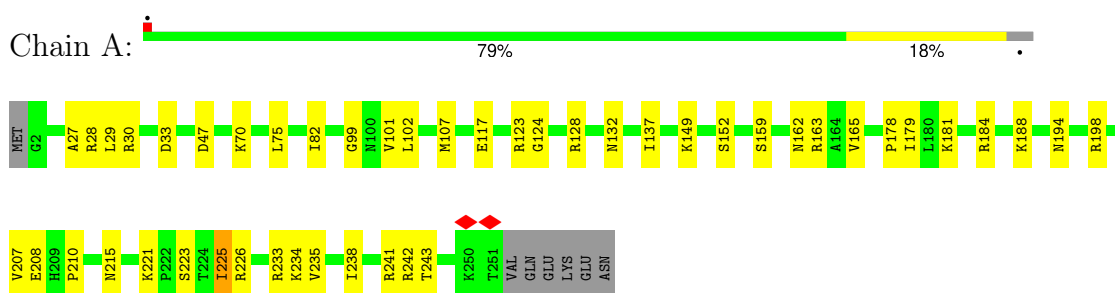


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
96	HC	1	6	3	1	2	0

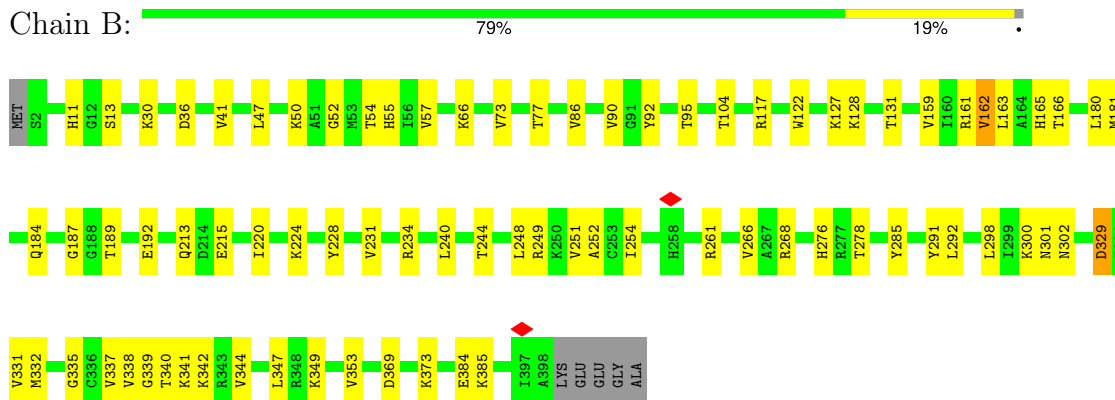
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

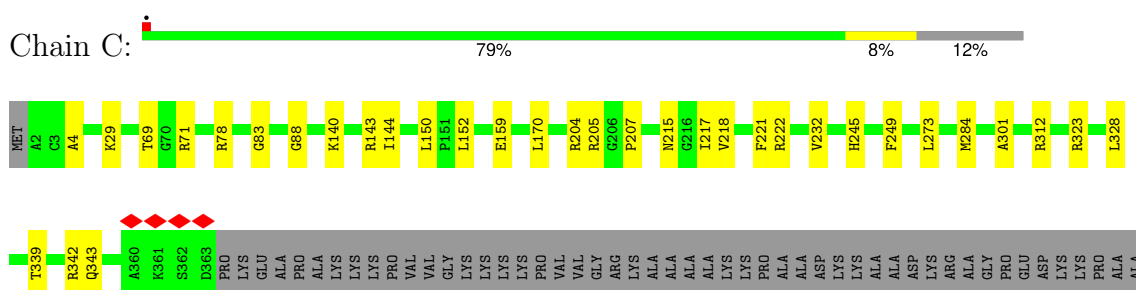
• Molecule 1: uL2



• Molecule 2: uL3



• Molecule 3: uL4



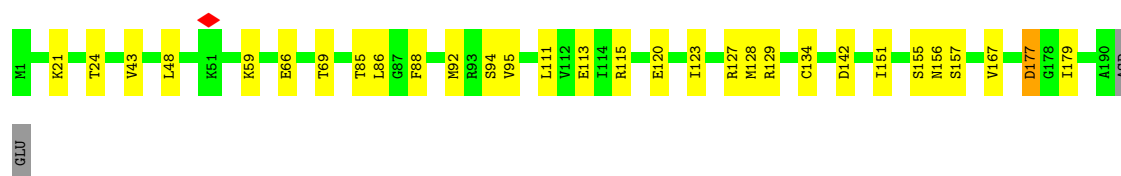
• Molecule 4: uL18

Protein	Residue	Score	Rank	Position
PHE	K242	0.99	1	1
ASP	Q253	0.98	2	2
THR	K265	0.97	3	3
GLU	L274	0.96	4	4
GLU	R275	0.95	5	5
GLU	V290	0.94	6	6
GLU	F291	0.93	7	7
ARG	R90	0.92	8	8
GLU	T96	0.91	9	9
PRO	V109	0.90	10	10
ALA	M115	0.89	11	11
PRO	D123	0.88	12	12
ASP	R126	0.87	13	13
THR	F136	0.86	14	14
LYS	R141	0.85	15	15
LYS	R144	0.84	16	16
LYS	L156	0.83	17	17
ASP	R159	0.82	18	18
HIS	H160	0.81	19	19
ARG	K163	0.80	20	20
GLY	R164	0.79	21	21
LYS	S172	0.78	22	22
LYS	V178	0.77	23	23
LEU	L184	0.76	24	24
LEU	N185	0.75	25	25
ALA	R186	0.74	26	26
LYS	L189	0.73	27	27
LYS	H193	0.72	28	28
GLY	Q194	0.71	29	29
LYS	K195	0.70	30	30
THR	F196	0.69	31	31
LYS	V197	0.68	32	32
LYS	I198	0.67	33	33
GLU	T216	0.66	34	34
GLU	D217	0.65	35	35
LYS	K224	0.64	36	36
LEU	A77	0.63	37	37
ARG	P78	0.62	38	38
PRO	K79	0.61	39	39
ARG	S80	0.60	40	40
HIS	R81	0.59	41	41
GLU	I82	0.58	42	42
GLU	GLU	0.57	43	43
ARG	ARG	0.56	44	44
LYS	LYS	0.55	45	45
LYS	LYS	0.54	46	46
LYS	LYS	0.53	47	47
LYS	LYS	0.52	48	48
LYS	LYS	0.51	49	49
LYS	LYS	0.50	50	50

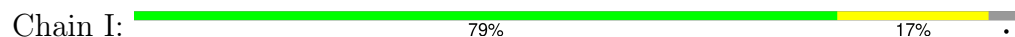
Sequence logo for the 22nd position of the 22-residue peptide. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows the 22 positions. The 22nd position is highly conserved, with a peak at 'R' (Arginine) and 'D' (Aspartic acid). Other positions show varying degrees of conservation, with 'K' (Lysine) and 'N' (Asparagine) being prominent in positions 1-10 and 15-20. The logo is color-coded: red for high conservation, yellow for moderate, and green for low.

[illegible]

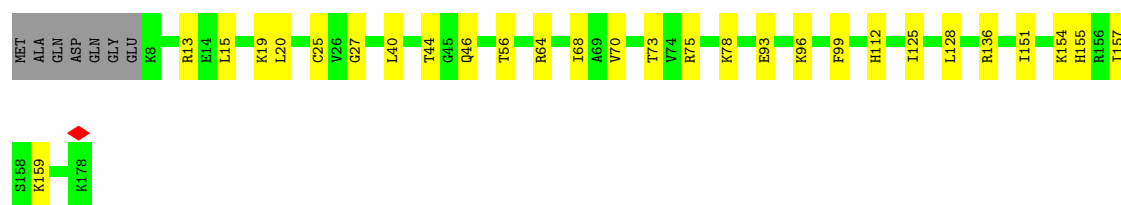
Chain H: 83% 15%



• Molecule 9: L10



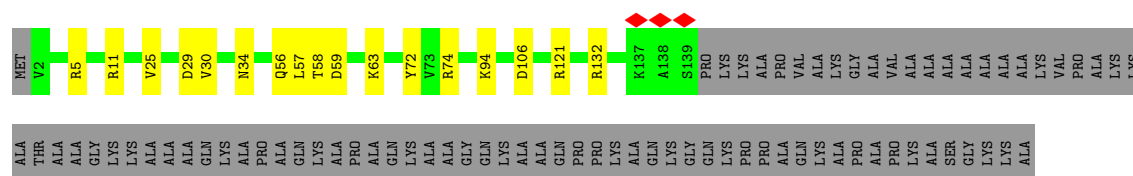
• Molecule 10: uL5



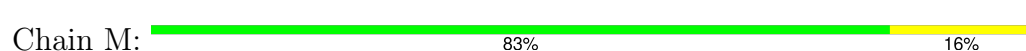
• Molecule 11: eL13



• Molecule 12: eL14



• Molecule 13: L15





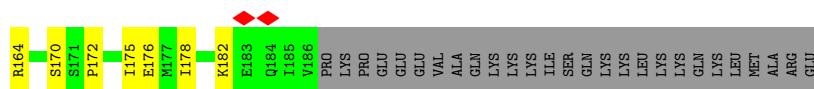
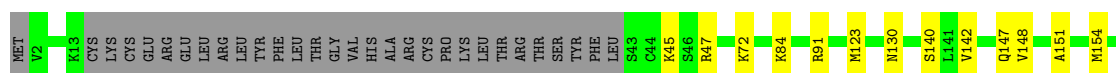
• Molecule 14: uL13

Chain N: 84% 13%



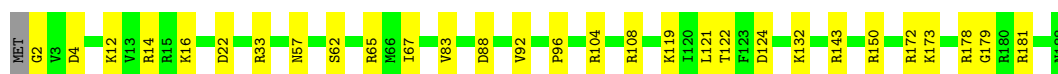
• Molecule 15: uL22

Chain O: 64% 9% 27%



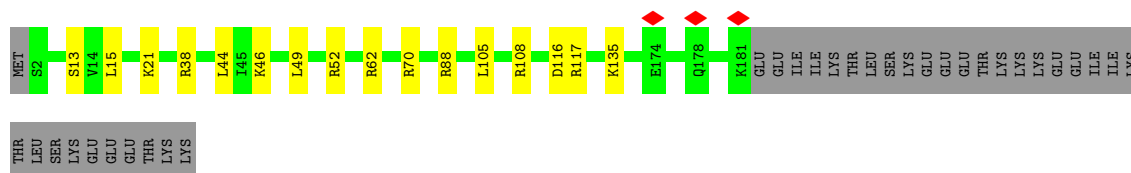
• Molecule 16: eL18

Chain P: 84% 15%



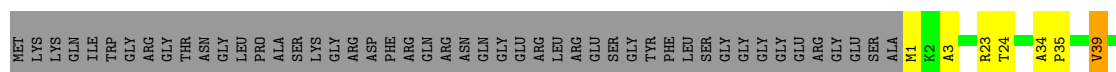
• Molecule 17: eL19

Chain Q: 77% 8% 15%



• Molecule 18: L18A

Chain R: 67% 10% 21%



• Molecule 19: eL21

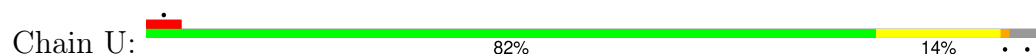
Chain S: 84% 15%



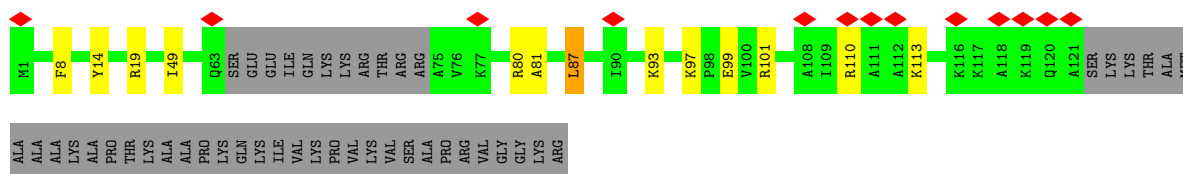
- Molecule 20: eL22



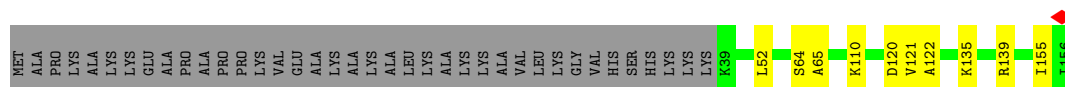
- Molecule 21: L23



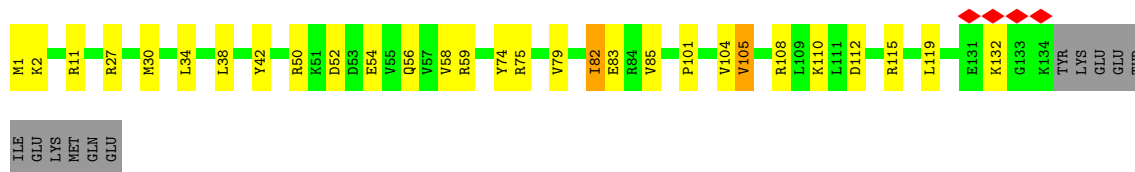
- Molecule 22: uL24



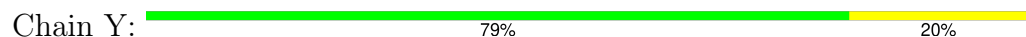
- Molecule 23: uL23

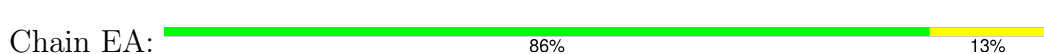


- Molecule 24: L26



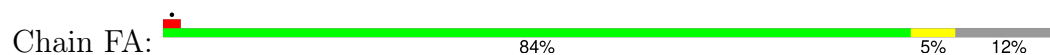
- Molecule 25: L27



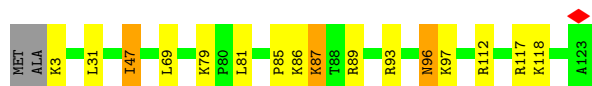
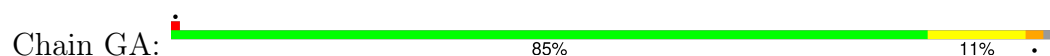




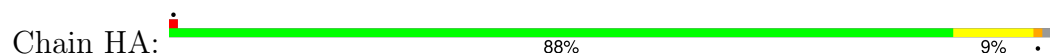
- Molecule 32: L34



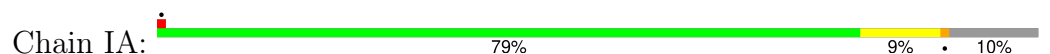
- Molecule 33: L35



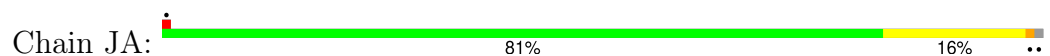
- Molecule 34: L36



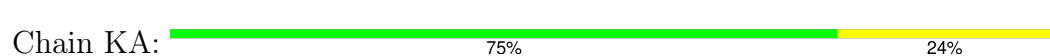
- Molecule 35: L37



- Molecule 36: eL38



- Molecule 37: eL39



- Molecule 38: eL40



MET GLN ILE PHE VAL THR THR THR GLY LYS THR ILE THR LEU GLY VAL GLU VAL GLU PRO SER ASP THR ILE GLU ASN VAL LYS LYS LYS ILE GLN ASP LYS GLY GLY ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS VAL LEU ARG THR ILE HIS GLY ILE1 Q68 L59 A60 N64 Y74 R85 K86 K87 K88 T92 N93 N94 K99 K102

• Molecule 39: eL41

Chain MA: 84% 16%

M1 R2 W5 R9 K25

• Molecule 40: eL42

Chain NA: 88% 10%

MET V2 N3 V4 C15 Q19 Y26 T63 K64 V67 C72 R81 R87 G94 Q105 PHE

• Molecule 41: eL43

Chain OA: 90% 8% ..

MET A2 K3 R4 K13 Y14 V26 E30 Q33 V52 I83 D91 Q92

• Molecule 42: L28

Chain PA: 72% 18% 9%

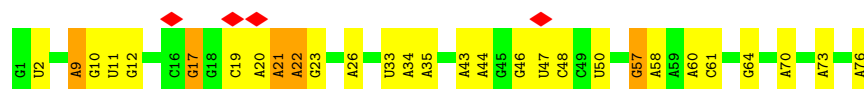
MET S2 Q6 L17 I18 K19 Y25 N31 R35 F38 R39 I44 H45 V49 K65 R66 R67 R87 T25 L90 I97 Y102 H103 P104 D105 L106 R107 I111 R112 V124 M125 VAL LYS ARG LYS THR ARG PRO LYS SER

• Molecule 43: L12

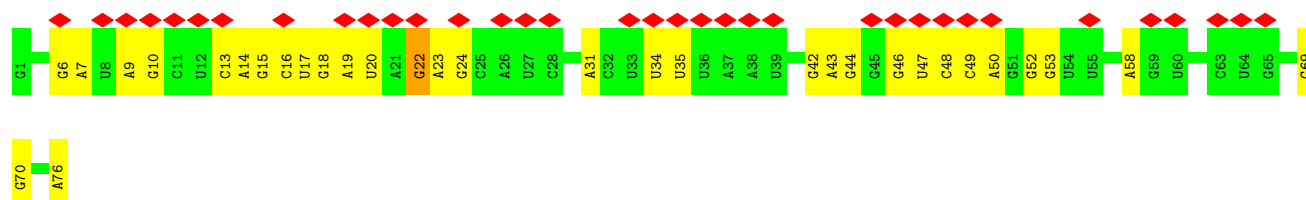
Chain RA: 67% 68% 24% 7%

MET PRO PRO LYS PHE ASP PRO ASN E9 I10 K11 V12 V13 Y14 Y15 L16 C17 T18 G19 G20 E21 V22 G23 A24 T25 S26 A27 K31 I32 G33 P34 L35 G36 L37 S38 P39 K40 K41 V42 G43 D44 D45 I46 A47 K48 A49 T50 G51 D52 W53 K54 G55 L56 R57 I58 T59 V60 K61 L62 T63 I64 Q65 N66 R67 Q68 A69 Q70 I71 E72 V73 V74 P75 S76 A77 A78 A79 L80 I81 I82 K83 A84 L85 K86 E87 P88 P89 R90 D91 G92 R93 K94 Q95 Q96 N97 I98 K99 H100 S101 G102 N103 I104 T105 F106 D107 E108 I109 V110 N111 R114 Q115 M116 R117 H118 R119 V120 S120 A122 R123 E124 L125 S126 G127 K130 L133 G134 T135 A136 Q137 S138 V139 G140 C141 S142 N143 D144 G145 R146 H147 P148 H149 D150 I151 I152 P153 D154 I155 N156 S157 V160 E161 CYS PRO ALA SER

• Molecule 44: P-site tRNA



- Molecule 45: E-site tRNA



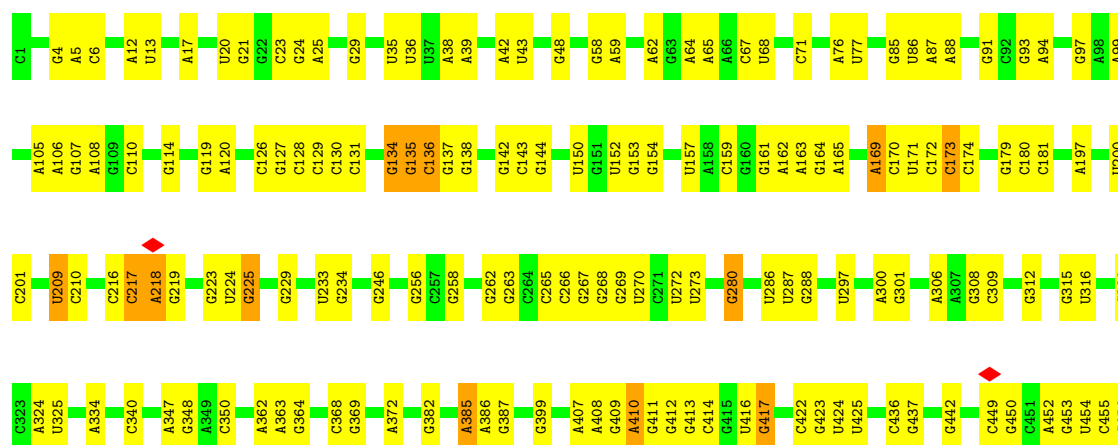
- Molecule 46: A-site tRNA

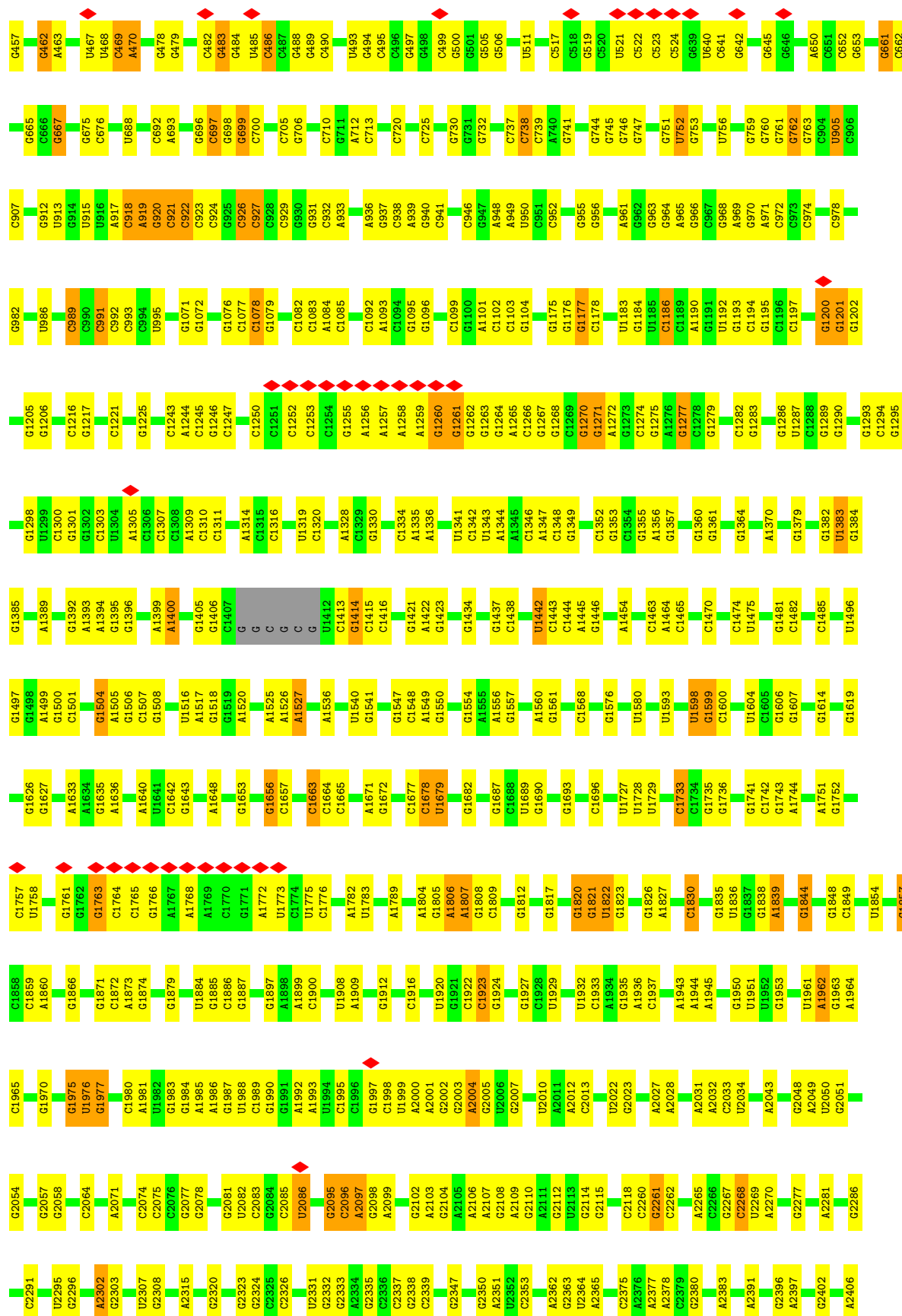


- Molecule 47: mRNA

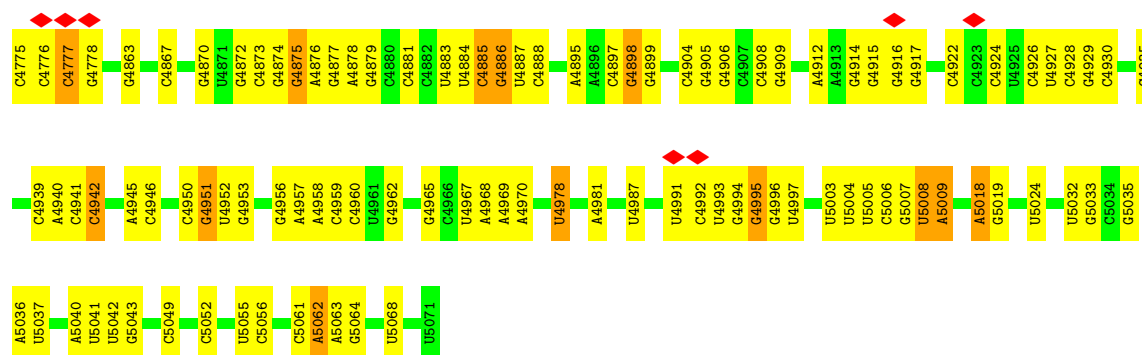


- Molecule 48: 28S rRNA





A4548	A4550	A4553	A4554	C4562	A4565	A4566	A4567	A4568	A4569	A4570	A4571	A4572	A4573	A4574	A4575	A4576	A4577	A4578	A4579	A4580	A4581	A4586	A4587	A4588	A4592	A4593	A4594	A4595	A4596	A4597	A4601	A4602	A4603	A4604	A4613	A4620	A4624	A4629	A4632	A4633	A4637	A4638	A4639	A4640	A4641	A4646																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
G4436	U4440	U4440	C4446	G4450	A4451	U4454	U4459	C4460	U4461	U4462	C4463	A4466	U4467	C4468	A4469	G4474	A4475	A4476	G4477	A4478	A4479	A4480	A4487	C4488	A4489	A4492	A4493	A4494	A4495	A4496	A4497	A4501	A4502	A4503	A4504	A4509	C4510	A4511	A4512	A4513	U4514	A4515	C4521	A4522	U4523	A4524	A4525	G4526	C4527	G4531	U4532	U4533	A4534	C4539	U4540	U4541	G4546																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
G4306	G4307	U4308	C4316	C4321	G4322	G4323	G4324	A4327	G4328	C4329	G4330	G4331	G4332	G4333	C4334	A4338	A4350	C4351	C4352	U4355	U4356	G4372	G4375	G4379	A4380	A4381	C4389	A4392	G4395	U4396	U4397	A4398	G4403	G4407	A4417	U4421	U4422	C4423	A4424	C4431	U4433	U4436	U4437	U4438	U4439	U4440	U4441	U4442	U4443	U4444	U4445	U4446	U4447	U4448	U4449	U4450	U4451	U4452	U4453	U4454	U4455	U4456	U4457	U4458	U4459	U4460	U4461	U4462	U4463	U4464	U4465	U4466	U4467	U4468	U4469	U4470	U4471	U4472	U4473	U4474	U4475	U4476	U4477	U4478	U4479	U4480	U4481	U4482	U4483	U4484	U4485	U4486	U4487	U4488	U4489	U4490	U4491	U4492	U4493	U4494	U4495	U4496	U4497	U4498	U4499	U4500	U4501	U4502	U4503	U4504	U4505	U4506	U4507	U4508	U4509	U4510	U4511	U4512	U4513	U4514	U4515	U4516	U4517	U4518	U4519	U4520	U4521	U4522	U4523	U4524	U4525	U4526	U4527	U4528	U4529	U4530	U4531	U4532	U4533	U4534	U4535	U4536	U4537	U4538	U4539	U4540	U4541	U4542	U4543	U4544	U4545	U4546	U4547	U4548	U4549	U4550	U4551	U4552	U4553	U4554	U4555	U4556	U4557	U4558	U4559	U4560	U4561	U4562	U4563	U4564	U4565	U4566	U4567	U4568	U4569	U4570	U4571	U4572	U4573	U4574	U4575	U4576	U4577	U4578	U4579	U4580	U4581	U4582	U4583	U4584	U4585	U4586	U4587	U4588	U4589	U4590	U4591	U4592	U4593	U4594	U4595	U4596	U4597	U4598	U4599	U4600	U4601	U4602	U4603	U4604	U4605	U4606	U4607	U4608	U4609	U4610	U4611	U4612	U4613	U4614	U4615	U4616	U4617	U4618	U4619	U4620	U4621	U4622	U4623	U4624	U4625	U4626	U4627	U4628	U4629	U4630	U4631	U4632	U4633	U4634	U4635	U4636	U4637	U4638	U4639	U4640	U4641	U4642	U4643	U4644	U4645	U4646	U4647	U4648	U4649	U4650	U4651	U4652	U4653	U4654	U4655	U4656	U4657	U4658	U4659	U4660	U4661	U4662	U4663	U4664	U4665	U4666	U4667	U4668	U4669	U4670	U4671	U4672	U4673	U4674	U4675	U4676	U4677	U4678	U4679	U4680	U4681	U4682	U4683	U4684	U4685	U4686	U4687	U4688	U4689	U4690	U4691	U4692	U4693	U4694	U4695	U4696	U4697	U4698	U4699	U4700	U4701	U4702	U4703	U4704	U4705	U4706	U4707	U4708	U4709	U4710	U4711	U4712	U4713	U4714	U4715	U4716	U4717	U4718	U4719	U4720	U4721	U4722	U4723	U4724	U4725	U4726	U4727	U4728	U4729	U4730	U4731	U4732	U4733	U4734	U4735	U4736	U4737	U4738	U4739	U4740	U4741	U4742	U4743	U4744	U4745	U4746	U4747	U4748	U4749	U4750	U4751	U4752	U4753	U4754	U4755	U4756	U4757	U4758	U4759	U4760	U4761	U4762	U4763	U4764	U4765	U4766	U4767	U4768	U4769	U4770	U4771	U4772	U4773	U4774	U4775	U4776	U4777	U4778	U4779	U4780	U4781	U4782	U4783	U4784	U4785	U4786	U4787	U4788	U4789	U4790	U4791	U4792	U4793	U4794	U4795	U4796	U4797	U4798	U4799	U4800	U4801	U4802	U4803	U4804	U4805	U4806	U4807	U4808	U4809	U4810	U4811	U4812	U4813	U4814	U4815	U4816	U4817	U4818	U4819	U4820	U4821	U4822	U4823	U4824	U4825	U4826	U4827	U4828	U4829	U4830	U4831	U4832	U4833	U4834	U4835	U4836	U4837	U4838	U4839	U4840	U4841	U4842	U4843	U4844	U4845	U4846	U4847	U4848	U4849	U4850	U4851	U4852	U4853	U4854	U4855	U4856	U4857	U4858	U4859	U4860	U4861	U4862	U4863	U4864	U4865	U4866	U4867	U4868	U4869	U4870	U4871	U4872	U4873	U4874	U4875	U4876	U4877	U4878	U4879	U4880	U4881	U4882	U4883	U4884	U4885	U4886	U4887	U4888	U4889	U4890	U4891	U4892	U4893	U4894	U4895	U4896	U4897	U4898	U4899	U4900	U4901	U4902	U4903	U4904	U4905	U4906	U4907	U4908	U4909	U4910	U4911	U4912	U4913	U4914	U4915	U4916	U4917	U4918	U4919	U4920	U4921	U4922	U4923	U4924	U4925	U4926	U4927	U4928	U4929	U4930	U4931	U4932	U4933	U4934	U4935	U4936	U4937	U4938	U4939	U4940	U4941	U4942	U4943	U4944	U4945	U4946	U4947	U4948	U4949	U4950	U4951	U4952	U4953	U4954	U4955	U4956	U4957	U4958	U4959	U4960	U4961	U4962	U4963	U4964	U4965	U4966	U4967	U4968	U4969	U4970	U4971	U4972	U4973	U4974	U4975	U4976	U4977	U4978	U4979	U4980	U4981	U4982	U4983	U4984	U4985	U4986	U4987	U4988	U4989	U4990	U4991	U4992	U4993	U4994	U4995	U4996	U4997	U4998	U4999	U5000	U5001	U5002	U5003	U5004	U5005	U5006	U5007	U5008	U5009	U5010	U5011	U5012	U5013	U5014	U5015	U5016	U5017	U5018	U5019	U5020	U5021	U5022	U5023	U5024	U5025	U5026	U5027	U5028	U5029	U5030	U5031	U5032	U5033	U5034	U5035	U5036	U5037	U5038	U5039	U5040	U5041	U5042	U5043	U5044	U5045	U5046	U5047	U5048	U5049	U5050	U5051	U5052	U5053	U5054	U5055	U5056	U5057	U5058	U5059	U5060	U5061	U5062	U5063	U5064	U5065	U5066	U5067	U5068	U5069	U5070	U5071	U5072	U5073	U5074	U5075	U5076	U5077	U5078	U5079	U5080	U5081	U5082	U5083	U5084	U5085	U5086	U5087	U5088	U5089	U5090	U5091	U5092	U5093	U5094	U5095	U5096	U5097	U5098	U5099	U5100	U5101	U5102	U5103	U5104	U5105	U5106	U5107	U5108	U5109	U5110	U5111	U5112	U5113	U5114	U5115	U5116	U5117	U5118	U5119	U5120	U5121	U5122	U5123	U5124	U5125	U5126	U5127	U5128	U5129	U5130	U5131	U5132	U5133	U5134	U5135	U5136	U5137	U5138	U5139	U5140	U5141	U5142	U5143	U5144	U5145	U5146	U5147	U5148	U5149	U5150	U5151	U5152	U5153	U5154	U5155	U5156	U5157	U5158	U5159	U5160	U5161	U5162	U5163	U5164	U5165	U5166	U5167	U5168	U5169	U5170	U5171	U5172	U5173	U5174	U5175	U5176	U5177	U5178	U5179	U5180	U5181	U5182	U5183	U5184	U5185	U5186	U5187	U5188	U5189	U5190	U5191	U5192	U5193	U5194	U5195	U5196	U5197	U5198	U5199	U5200	U5201	U5202	U5203	U5204	U5205	U5206	U5207	U5208	U5209	U5210	U5211	U5212	U5213	U5214	U5215	U5216	U5217	U5218	U5219	U5220	U5221	U5222	U5223	U5224	U5225	U5226	U5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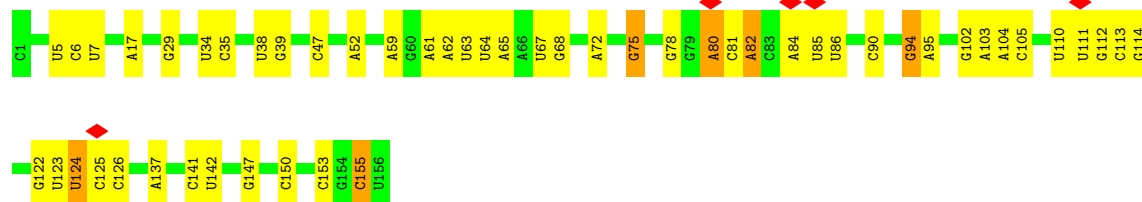
• Molecule 49: 5S rRNA

Chain XA: 72% 23%



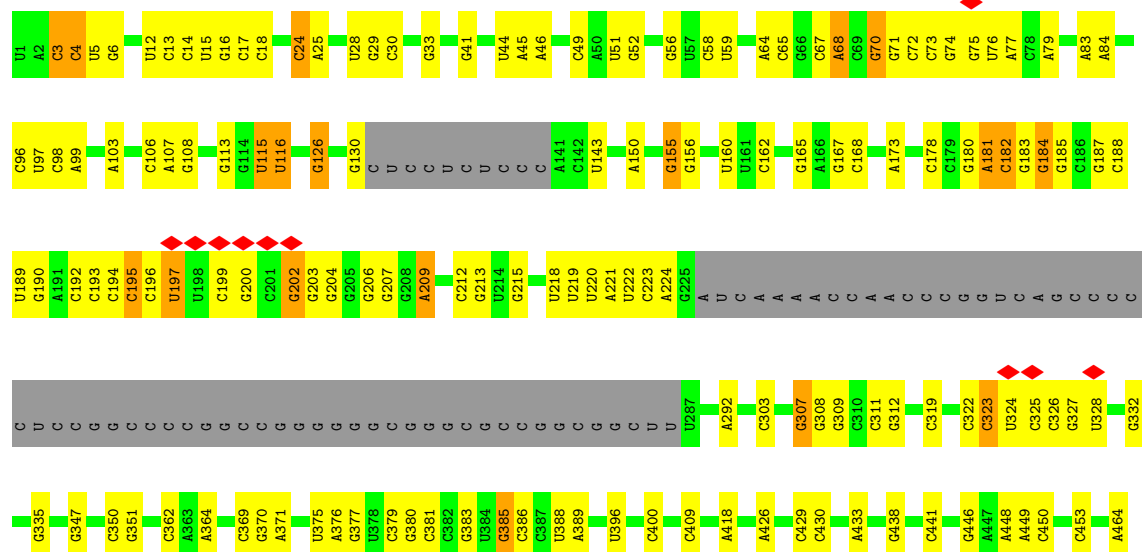
• Molecule 50: 5.8S rRNA

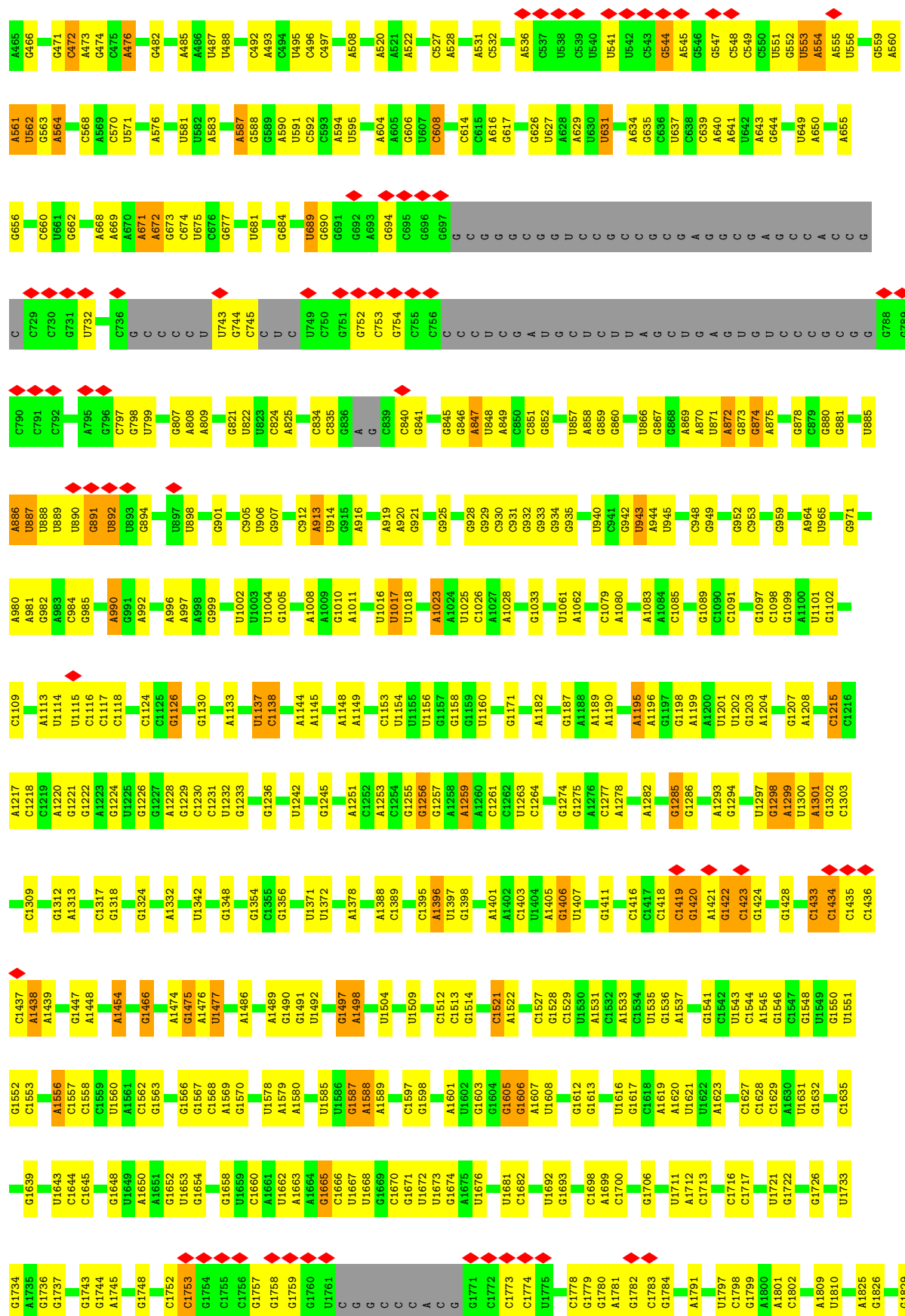
Chain YA: 67% 29%



• Molecule 51: 18S rRNA

Chain ZA: 57% 31% 8%

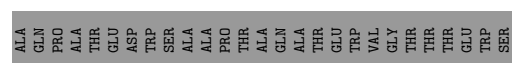
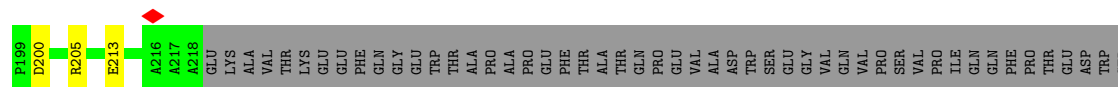






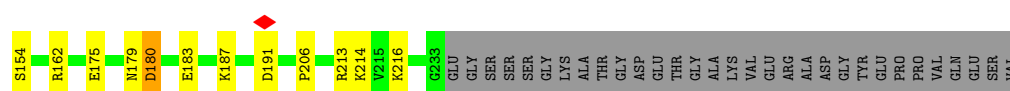
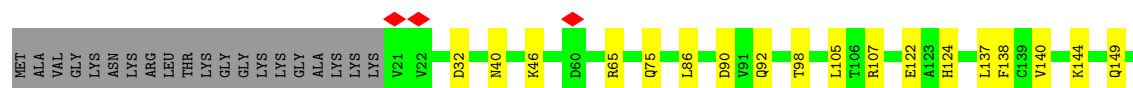
• Molecule 52: RPSA

Chain AB: 61% 12% 26%



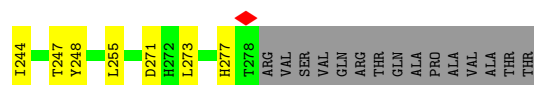
• Molecule 53: S3A

Chain BB: 69% 11% 19%



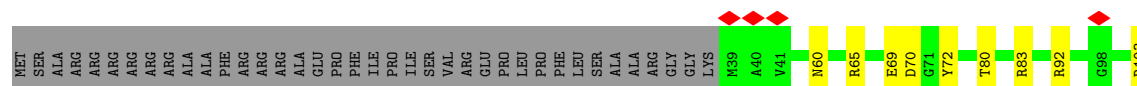
• Molecule 54: S2-like

Chain CB: 61% 14% 25%



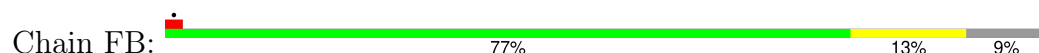
• Molecule 55: S3

Chain DB: 70% 10% 19%

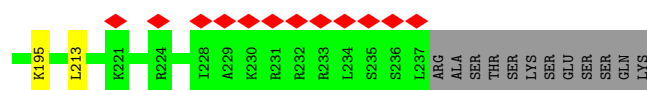
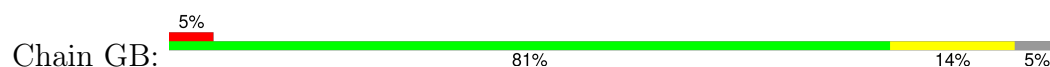




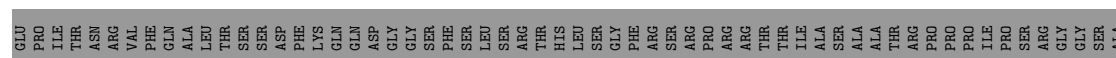
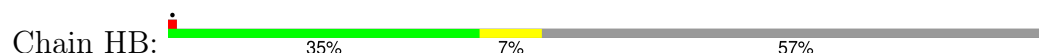
- Molecule 57: S5

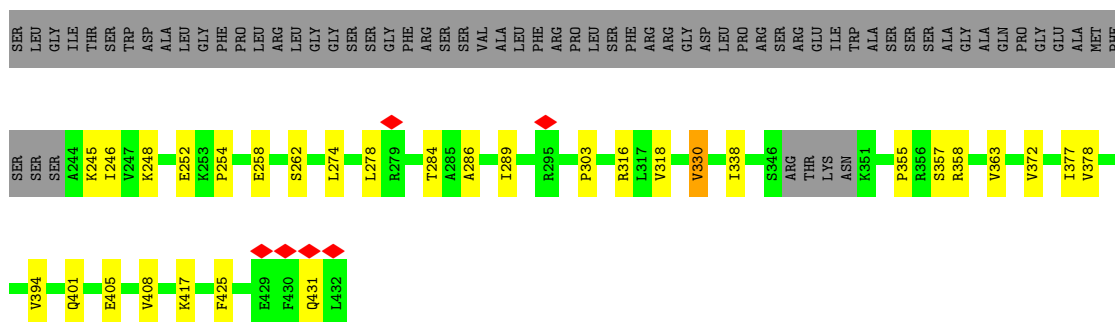


- Molecule 58: eS6

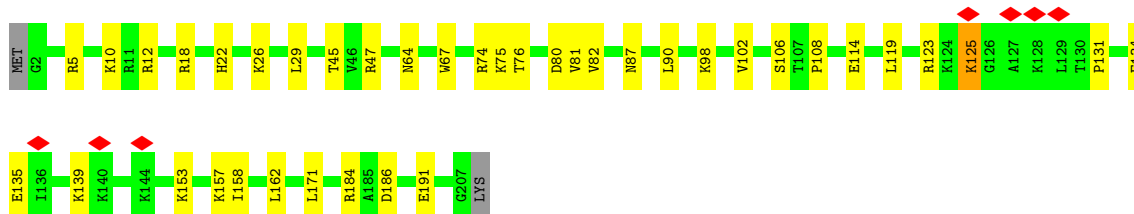
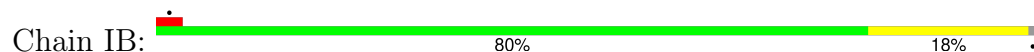


- Molecule 59: eS7

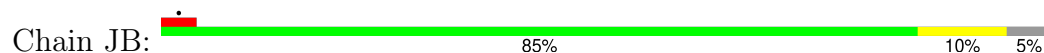




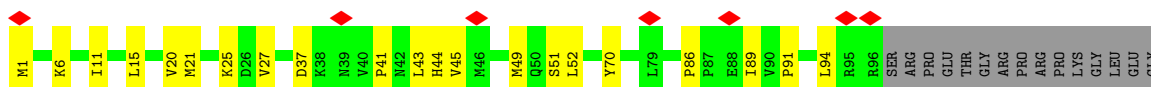
• Molecule 60: S8



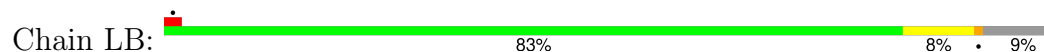
• Molecule 61: S9



• Molecule 62: S10

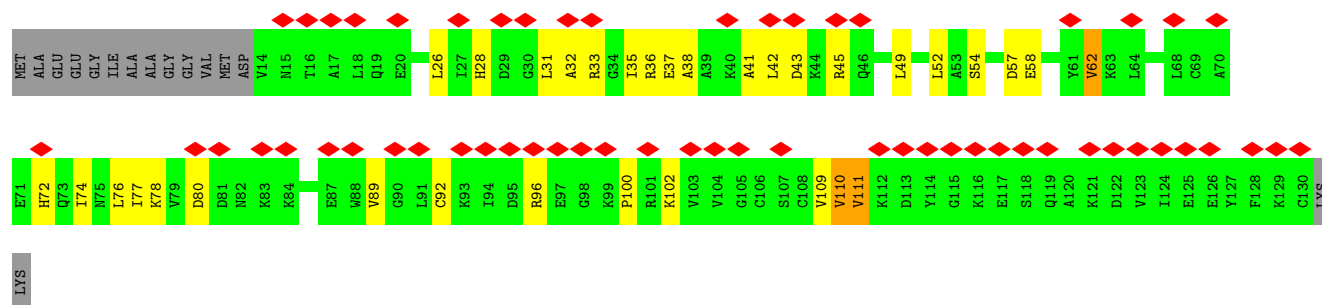


• Molecule 63: S11



• Molecule 64: S12





• Molecule 65: uS15

Chain NB: 85% 14%



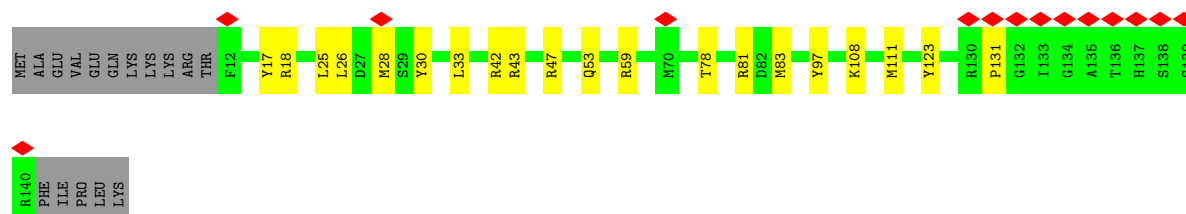
• Molecule 66: S14

Chain OB: 76% 14% 10%



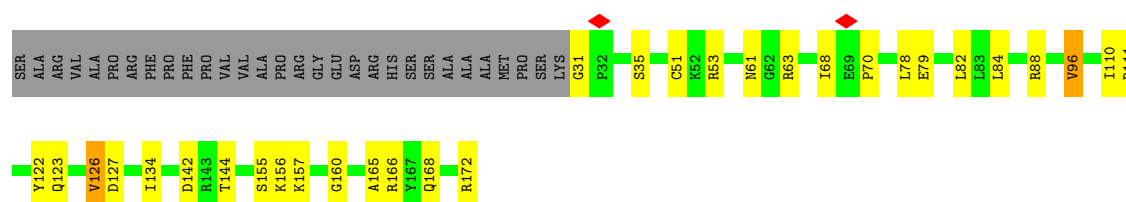
• Molecule 67: S15

Chain PB: 10% 75% 14% 11%



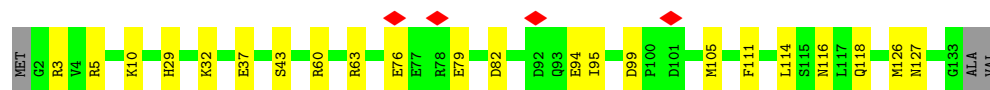
• Molecule 68: uS9

Chain QB: 65% 17% 17%

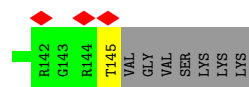
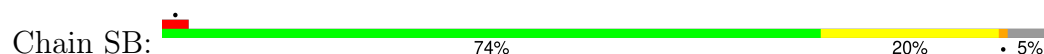


• Molecule 69: eS17

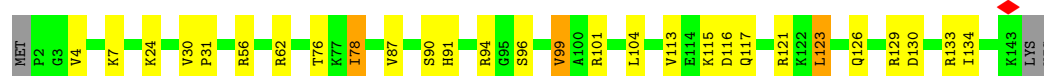
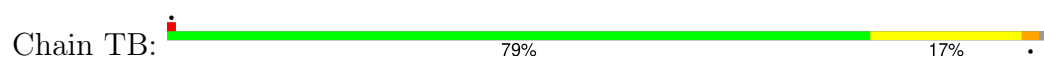
Chain RB: 81% 16%



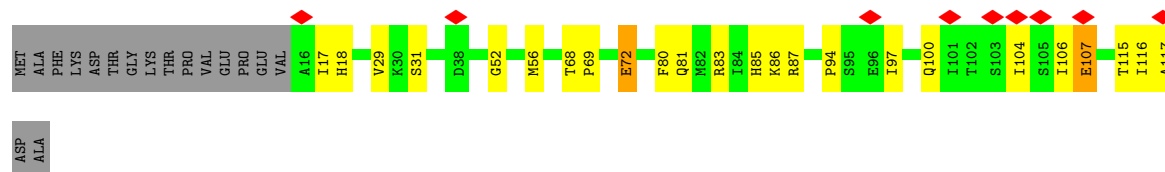
- Molecule 70: S18



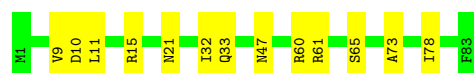
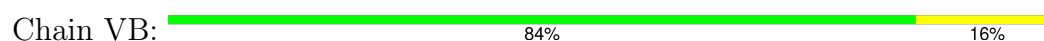
- Molecule 71: S19



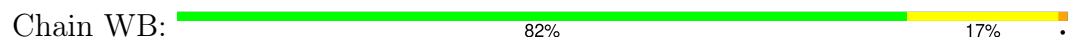
- Molecule 72: uS10



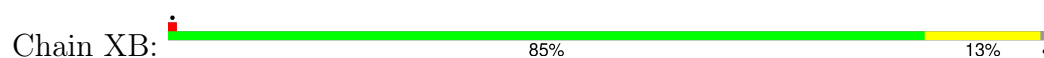
- Molecule 73: S21

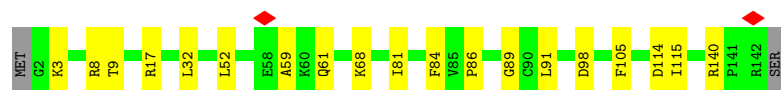


- Molecule 74: S15A

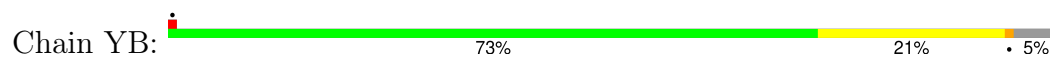


- Molecule 75: S23

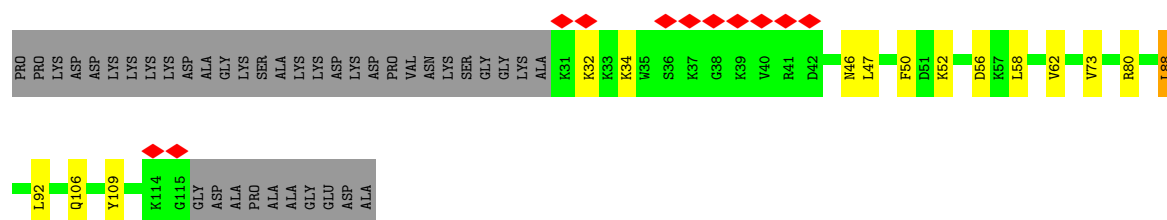




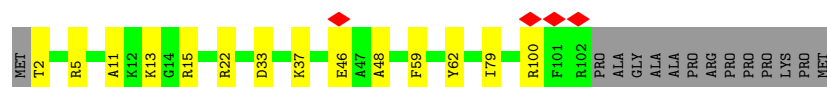
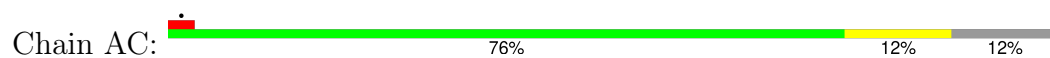
- Molecule 76: S24



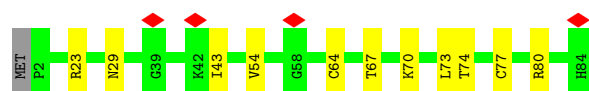
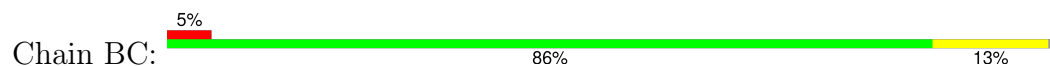
- Molecule 77: eS25



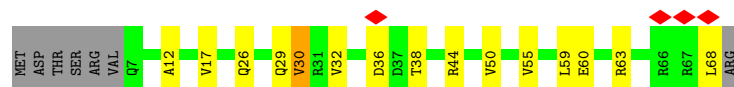
- Molecule 78: S26



- Molecule 79: S27

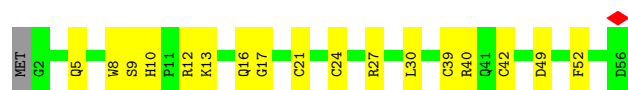


- Molecule 80: S28

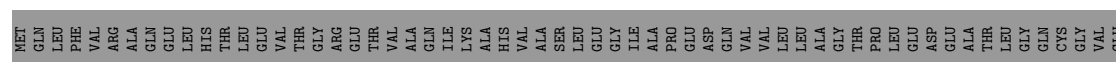


- Molecule 81: uS14

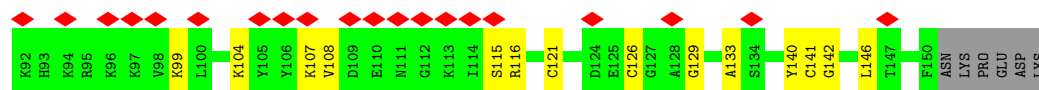
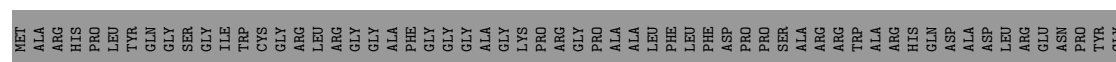




• Molecule 82: S30



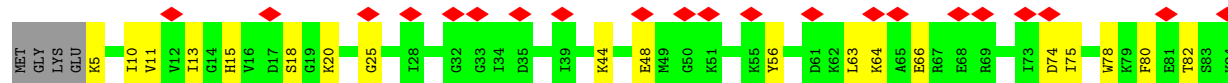
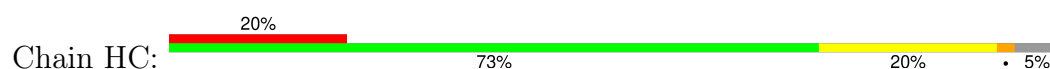
• Molecule 83: S27A

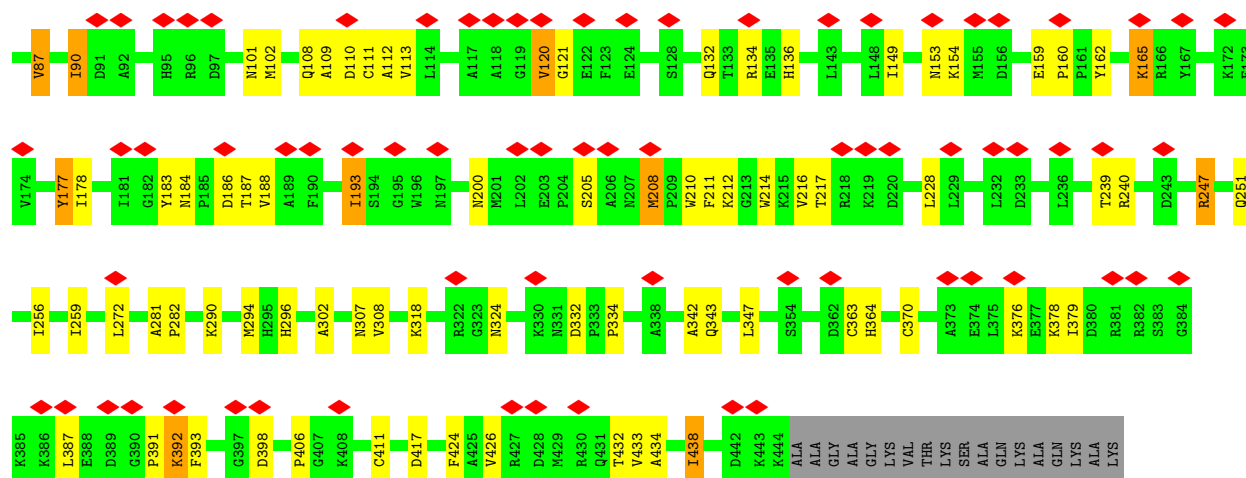


• Molecule 84: RACK1



• Molecule 85: eukaryotic elongation factor 1A

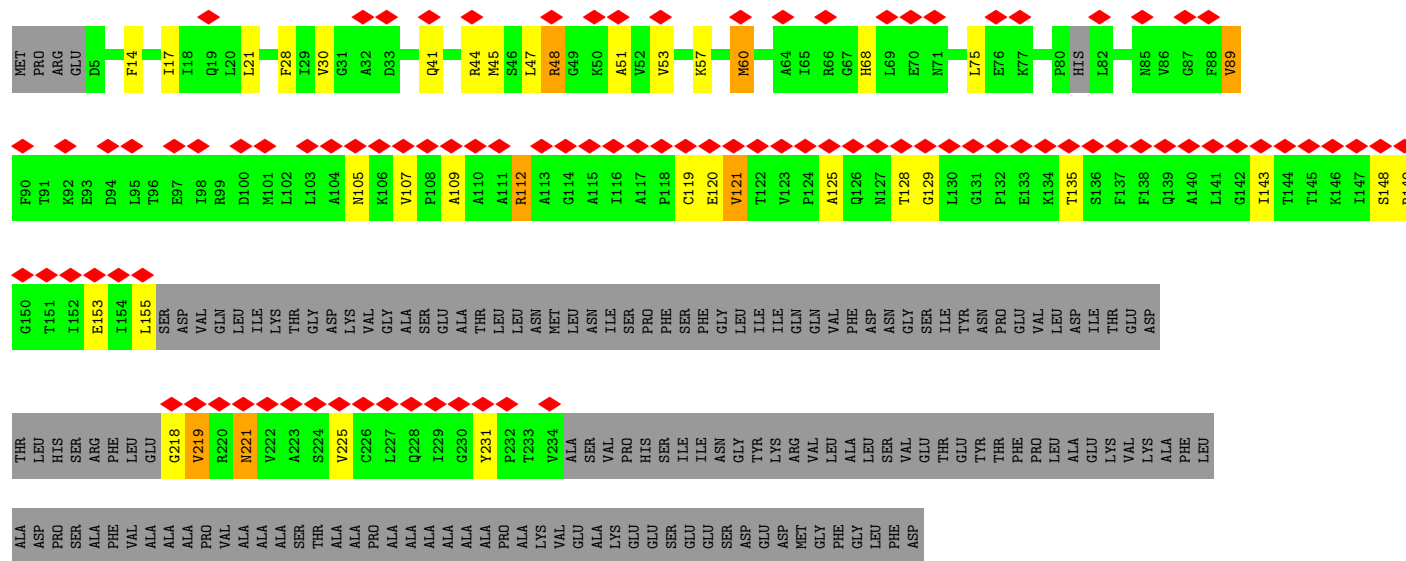
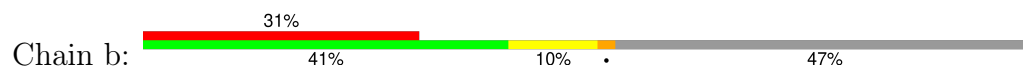




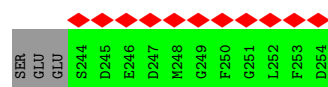
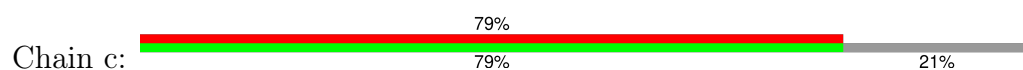
- Molecule 86: peptide



- Molecule 87: RPLP0



- Molecule 88: RPLP peptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37882	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 ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	43.279	Depositor
Minimum map value	-20.542	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.217	Depositor
Recommended contour level	4.45	Depositor
Map size (Å)	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SPD, K, GTP, ANM, 5GP, 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	A	0.22	0/1952	0.33	0/2617
2	B	0.20	0/3264	0.30	0/4371
3	C	0.19	0/2937	0.29	0/3946
4	D	0.16	0/2441	0.27	0/3269
5	E	0.16	0/1859	0.30	0/2491
6	F	0.19	0/1933	0.29	0/2577
7	G	0.17	0/1881	0.29	0/2532
8	H	0.17	0/1535	0.27	0/2063
9	I	0.18	0/1702	0.27	0/2272
10	J	0.16	0/1395	0.30	0/1863
11	K	0.17	0/1733	0.26	0/2316
12	L	0.18	0/1158	0.30	0/1547
13	M	0.22	0/1746	0.31	0/2338
14	N	0.20	0/1662	0.31	0/2222
15	O	0.19	0/1292	0.31	0/1733
16	P	0.21	0/1539	0.30	0/2054
17	Q	0.17	0/1524	0.26	0/2013
18	R	0.20	0/1501	0.30	0/2012
19	S	0.19	0/1326	0.26	0/1770
20	T	0.16	0/840	0.31	0/1127
21	U	0.21	0/1018	0.31	0/1364
22	V	0.15	0/900	0.28	0/1194
23	W	0.18	0/984	0.27	0/1323
24	X	0.16	0/1132	0.26	0/1504
25	Y	0.18	0/1130	0.28	0/1507
26	Z	0.21	0/1191	0.31	0/1590
27	AA	0.15	0/886	0.22	0/1171
28	BA	0.18	0/779	0.25	0/1044
29	CA	0.19	0/908	0.31	0/1223
30	DA	0.21	0/1082	0.27	0/1443
31	EA	0.22	0/895	0.31	0/1198
32	FA	0.19	0/916	0.30	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	0.17	0/1016	0.26	0/1341
34	HA	0.16	0/841	0.27	0/1112
35	IA	0.20	0/731	0.31	0/966
36	JA	0.16	0/575	0.26	0/761
37	KA	0.19	0/459	0.28	0/608
38	LA	0.18	0/435	0.30	0/575
39	MA	0.18	0/240	0.25	0/305
40	NA	0.19	0/864	0.26	0/1140
41	OA	0.20	0/718	0.33	0/953
42	PA	0.18	0/1010	0.31	0/1354
43	RA	0.11	0/1174	0.29	0/1582
44	SA	0.15	0/1815	0.27	0/2828
45	TA	0.12	0/1804	0.24	0/2810
46	UA	0.12	0/1771	0.29	0/2754
47	VA	0.13	0/278	0.24	0/428
48	WA	0.22	0/85840	0.29	0/133885
49	XA	0.20	0/2836	0.25	0/4421
50	YA	0.21	0/3701	0.26	0/5766
51	ZA	0.19	0/40949	0.28	0/63819
52	AB	0.16	0/1747	0.27	0/2374
53	BB	0.16	0/1756	0.28	0/2350
54	CB	0.18	0/1744	0.31	0/2358
55	DB	0.13	0/1796	0.26	0/2417
56	EB	0.16	0/2118	0.30	0/2849
57	FB	0.15	0/1492	0.30	0/2005
58	GB	0.13	0/1946	0.24	0/2590
59	HB	0.14	0/1511	0.28	0/2022
60	IB	0.17	0/1715	0.30	0/2287
61	JB	0.15	0/1550	0.27	0/2069
62	KB	0.12	0/834	0.26	0/1125
63	LB	0.18	0/1200	0.26	0/1604
64	MB	0.11	0/918	0.28	0/1233
65	NB	0.16	0/1226	0.25	0/1649
66	OB	0.18	0/1029	0.29	0/1380
67	PB	0.12	0/1079	0.26	0/1441
68	QB	0.16	0/1146	0.30	0/1534
69	RB	0.13	0/1082	0.26	0/1452
70	SB	0.13	0/1208	0.28	0/1618
71	TB	0.13	0/1123	0.26	0/1504
72	UB	0.14	0/818	0.28	0/1099
73	VB	0.15	0/643	0.27	0/860
74	WB	0.20	0/1051	0.35	0/1406
75	XB	0.18	0/1116	0.27	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	YB	0.14	0/1028	0.28	0/1366
77	ZB	0.12	0/691	0.27	0/922
78	AC	0.19	0/828	0.29	0/1109
79	BC	0.15	0/665	0.24	0/891
80	CC	0.14	0/490	0.28	0/656
81	DC	0.15	0/470	0.29	0/623
82	EC	0.14	0/447	0.28	0/587
83	FC	0.09	0/576	0.24	0/764
84	GC	0.13	0/2493	0.31	0/3394
85	HC	0.12	0/3441	0.30	0/4657
86	IC	0.09	0/19	0.14	0/25
87	b	0.16	0/1298	0.36	0/1752
88	c	0.08	0/87	0.28	0/113
All	All	0.19	0/238479	0.29	0/349897

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
85	HC	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
85	HC	159	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1914	0	2013	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3196	0	3339	54	0
3	C	2883	0	3053	21	0
4	D	2395	0	2427	27	0
5	E	1823	0	1995	25	0
6	F	1897	0	2021	22	0
7	G	1850	0	1991	19	0
8	H	1516	0	1597	18	0
9	I	1664	0	1712	20	0
10	J	1372	0	1412	15	0
11	K	1702	0	1820	15	0
12	L	1137	0	1211	12	0
13	M	1701	0	1749	25	0
14	N	1630	0	1778	18	0
15	O	1266	0	1302	13	0
16	P	1515	0	1634	25	0
17	Q	1508	0	1664	14	0
18	R	1462	0	1508	23	0
19	S	1298	0	1366	19	0
20	T	826	0	852	10	0
21	U	1004	0	1063	14	0
22	V	887	0	935	9	0
23	W	967	0	1040	7	0
24	X	1115	0	1205	17	0
25	Y	1107	0	1182	16	0
26	Z	1162	0	1209	18	0
27	AA	873	0	949	11	0
28	BA	769	0	803	6	0
29	CA	893	0	932	12	0
30	DA	1064	0	1160	21	0
31	EA	876	0	912	9	0
32	FA	906	0	998	6	0
33	GA	1008	0	1142	15	0
34	HA	830	0	916	6	0
35	IA	716	0	750	8	0
36	JA	569	0	637	9	0
37	KA	447	0	480	9	0
38	LA	429	0	465	6	0
39	MA	239	0	289	3	0
40	NA	851	0	920	7	0
41	OA	708	0	757	6	0
42	PA	994	0	1051	17	0
43	RA	1160	0	1218	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	SA	1622	0	825	15	0
45	TA	1615	0	820	15	0
46	UA	1586	0	805	9	0
47	VA	249	0	125	1	0
48	WA	76735	0	38762	652	0
49	XA	2538	0	1286	20	0
50	YA	3314	0	1683	21	0
51	ZA	36623	0	18504	331	0
52	AB	1710	0	1711	25	0
53	BB	1729	0	1803	17	0
54	CB	1707	0	1793	24	0
55	DB	1768	0	1863	17	0
56	EB	2076	0	2177	38	0
57	FB	1471	0	1522	18	0
58	GB	1923	0	2089	21	0
59	HB	1489	0	1582	17	0
60	IB	1686	0	1772	26	0
61	JB	1525	0	1640	17	0
62	KB	810	0	836	12	0
63	LB	1180	0	1254	10	0
64	MB	908	0	939	21	0
65	NB	1202	0	1289	14	0
66	OB	1016	0	1039	14	0
67	PB	1058	0	1104	13	0
68	QB	1128	0	1195	21	0
69	RB	1068	0	1121	16	0
70	SB	1190	0	1249	20	0
71	TB	1104	0	1140	19	0
72	UB	808	0	878	13	0
73	VB	636	0	637	8	0
74	WB	1034	0	1080	16	0
75	XB	1098	0	1167	13	0
76	YB	1011	0	1083	17	0
77	ZB	683	0	761	10	0
78	AC	814	0	864	11	0
79	BC	651	0	672	4	0
80	CC	488	0	514	11	0
81	DC	459	0	449	11	0
82	EC	443	0	492	7	0
83	FC	564	0	577	10	0
84	GC	2436	0	2393	44	0
85	HC	3371	0	3428	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	IC	20	0	10	0	0
87	b	1279	0	1344	18	0
88	c	86	0	66	0	0
89	A	1	0	0	0	0
89	AC	1	0	0	0	0
89	B	1	0	0	0	0
89	DA	1	0	0	0	0
89	FA	1	0	0	0	0
89	HC	1	0	0	0	0
89	I	1	0	0	0	0
89	IA	1	0	0	0	0
89	LB	1	0	0	0	0
89	O	1	0	0	0	0
89	SA	1	0	0	0	0
89	U	1	0	0	0	0
89	WA	186	0	0	0	0
89	XA	6	0	0	0	0
89	YA	4	0	0	0	0
89	Z	1	0	0	0	0
89	ZA	80	0	0	0	0
89	b	1	0	0	0	0
90	AC	1	0	0	0	0
90	DC	1	0	0	0	0
90	FA	1	0	0	0	0
90	FC	1	0	0	0	0
90	IA	1	0	0	0	0
90	LA	1	0	0	0	0
90	NA	1	0	0	0	0
90	OA	1	0	0	0	0
91	UA	24	0	12	0	0
92	WA	19	0	19	3	0
93	WA	10	0	19	0	0
94	WA	1	0	0	0	0
95	HC	32	0	12	1	0
96	HC	6	0	4	1	0
All	All	222430	0	165866	1937	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 5.

The worst 5 of 1937 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)
44:SA:50:U:H3	44:SA:64:G:H1	0.90	0.87
48:WA:2847:A:H61	48:WA:3845:C:H42	1.16	0.87
48:WA:986:U:H3	48:WA:1277:G:H1	1.22	0.86
48:WA:3694:A:H62	48:WA:3825:G:H21	1.24	0.85
48:WA:1761:G:H1	48:WA:1775:U:H3	1.24	0.83

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	A	248/257 (96%)	235 (95%)	13 (5%)	0	100	100
2	B	395/403 (98%)	382 (97%)	13 (3%)	0	100	100
3	C	360/413 (87%)	349 (97%)	11 (3%)	0	100	100
4	D	292/297 (98%)	288 (99%)	4 (1%)	0	100	100
5	E	222/291 (76%)	212 (96%)	10 (4%)	0	100	100
6	F	225/249 (90%)	219 (97%)	6 (3%)	0	100	100
7	G	225/319 (70%)	220 (98%)	5 (2%)	0	100	100
8	H	188/192 (98%)	182 (97%)	6 (3%)	0	100	100
9	I	201/214 (94%)	193 (96%)	8 (4%)	0	100	100
10	J	169/178 (95%)	168 (99%)	1 (1%)	0	100	100
11	K	208/211 (99%)	204 (98%)	4 (2%)	0	100	100
12	L	136/218 (62%)	131 (96%)	5 (4%)	0	100	100
13	M	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
14	N	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
15	O	154/213 (72%)	151 (98%)	3 (2%)	0	100	100
16	P	185/188 (98%)	178 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	178/212 (84%)	173 (97%)	5 (3%)	0	100	100
18	R	174/224 (78%)	167 (96%)	7 (4%)	0	100	100
19	S	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
20	T	99/128 (77%)	96 (97%)	3 (3%)	0	100	100
21	U	133/140 (95%)	128 (96%)	5 (4%)	0	100	100
22	V	106/157 (68%)	105 (99%)	1 (1%)	0	100	100
23	W	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
24	X	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
25	Y	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
26	Z	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
27	AA	103/245 (42%)	100 (97%)	3 (3%)	0	100	100
28	BA	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
29	CA	106/125 (85%)	102 (96%)	4 (4%)	0	100	100
30	DA	127/135 (94%)	123 (97%)	4 (3%)	0	100	100
31	EA	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
32	FA	112/129 (87%)	108 (96%)	4 (4%)	0	100	100
33	GA	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
34	HA	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
35	IA	85/97 (88%)	84 (99%)	1 (1%)	0	100	100
36	JA	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
37	KA	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
38	LA	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
39	MA	23/25 (92%)	23 (100%)	0	0	100	100
40	NA	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
41	OA	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
42	PA	122/137 (89%)	114 (93%)	8 (7%)	0	100	100
43	RA	151/165 (92%)	143 (95%)	8 (5%)	0	100	100
52	AB	215/295 (73%)	207 (96%)	8 (4%)	0	100	100
53	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
54	CB	218/293 (74%)	214 (98%)	4 (2%)	0	100	100
55	DB	226/281 (80%)	225 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	EB	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
57	FB	181/204 (89%)	176 (97%)	5 (3%)	0	100	100
58	GB	235/249 (94%)	234 (100%)	1 (0%)	0	100	100
59	HB	181/432 (42%)	175 (97%)	6 (3%)	0	100	100
60	IB	204/208 (98%)	199 (98%)	5 (2%)	0	100	100
61	JB	183/194 (94%)	182 (100%)	1 (0%)	0	100	100
62	KB	94/165 (57%)	90 (96%)	4 (4%)	0	100	100
63	LB	140/158 (89%)	139 (99%)	1 (1%)	0	100	100
64	MB	115/132 (87%)	108 (94%)	7 (6%)	0	100	100
65	NB	147/151 (97%)	147 (100%)	0	0	100	100
66	OB	134/151 (89%)	130 (97%)	4 (3%)	0	100	100
67	PB	127/145 (88%)	127 (100%)	0	0	100	100
68	QB	140/172 (81%)	136 (97%)	4 (3%)	0	100	100
69	RB	130/135 (96%)	125 (96%)	5 (4%)	0	100	100
70	SB	142/152 (93%)	141 (99%)	1 (1%)	0	100	100
71	TB	140/145 (97%)	135 (96%)	5 (4%)	0	100	100
72	UB	100/119 (84%)	95 (95%)	5 (5%)	0	100	100
73	VB	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
74	WB	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
75	XB	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
76	YB	122/131 (93%)	120 (98%)	2 (2%)	0	100	100
77	ZB	83/124 (67%)	83 (100%)	0	0	100	100
78	AC	99/115 (86%)	95 (96%)	4 (4%)	0	100	100
79	BC	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
80	CC	60/69 (87%)	60 (100%)	0	0	100	100
81	DC	53/56 (95%)	53 (100%)	0	0	100	100
82	EC	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
83	FC	67/188 (36%)	65 (97%)	2 (3%)	0	100	100
84	GC	311/317 (98%)	299 (96%)	12 (4%)	0	100	100
85	HC	438/462 (95%)	418 (95%)	19 (4%)	1 (0%)	44	68
86	IC	2/4 (50%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
87	b	165/318 (52%)	150 (91%)	14 (8%)	1 (1%)	22	45
88	c	9/14 (64%)	8 (89%)	1 (11%)	0	100	100
All	All	12000/14293 (84%)	11655 (97%)	343 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
85	HC	160	PRO
87	b	225	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/199 (96%)	187 (97%)	5 (3%)	41	70
2	B	344/348 (99%)	337 (98%)	7 (2%)	50	78
3	C	302/337 (90%)	299 (99%)	3 (1%)	73	89
4	D	247/250 (99%)	244 (99%)	3 (1%)	67	86
5	E	201/251 (80%)	198 (98%)	3 (2%)	60	83
6	F	198/218 (91%)	197 (100%)	1 (0%)	86	95
7	G	197/273 (72%)	194 (98%)	3 (2%)	60	83
8	H	169/171 (99%)	164 (97%)	5 (3%)	36	65
9	I	175/181 (97%)	169 (97%)	6 (3%)	32	61
10	J	144/149 (97%)	140 (97%)	4 (3%)	38	68
11	K	175/176 (99%)	174 (99%)	1 (1%)	84	94
12	L	117/161 (73%)	115 (98%)	2 (2%)	56	81
13	M	171/172 (99%)	170 (99%)	1 (1%)	84	94
14	N	171/173 (99%)	168 (98%)	3 (2%)	54	80
15	O	137/190 (72%)	136 (99%)	1 (1%)	81	93
16	P	164/165 (99%)	162 (99%)	2 (1%)	67	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Q	159/191 (83%)	159 (100%)	0	100	100
18	R	157/192 (82%)	153 (98%)	4 (2%)	42	72
19	S	139/140 (99%)	138 (99%)	1 (1%)	81	93
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	101 (98%)	2 (2%)	52	79
22	V	89/126 (71%)	88 (99%)	1 (1%)	70	87
23	W	106/134 (79%)	104 (98%)	2 (2%)	52	79
24	X	124/135 (92%)	119 (96%)	5 (4%)	27	55
25	Y	117/118 (99%)	116 (99%)	1 (1%)	75	90
26	Z	119/120 (99%)	118 (99%)	1 (1%)	79	91
27	AA	87/184 (47%)	85 (98%)	2 (2%)	45	74
28	BA	85/98 (87%)	84 (99%)	1 (1%)	67	86
29	CA	98/110 (89%)	95 (97%)	3 (3%)	35	64
30	DA	115/121 (95%)	113 (98%)	2 (2%)	56	81
31	EA	88/89 (99%)	87 (99%)	1 (1%)	70	87
32	FA	98/109 (90%)	98 (100%)	0	100	100
33	GA	109/110 (99%)	105 (96%)	4 (4%)	29	58
34	HA	86/89 (97%)	84 (98%)	2 (2%)	45	74
35	IA	74/80 (92%)	73 (99%)	1 (1%)	62	84
36	JA	64/65 (98%)	63 (98%)	1 (2%)	58	82
37	KA	47/48 (98%)	46 (98%)	1 (2%)	48	76
38	LA	48/116 (41%)	47 (98%)	1 (2%)	48	76
39	MA	24/24 (100%)	24 (100%)	0	100	100
40	NA	92/94 (98%)	92 (100%)	0	100	100
41	OA	74/75 (99%)	72 (97%)	2 (3%)	40	69
42	PA	108/121 (89%)	105 (97%)	3 (3%)	38	68
43	RA	126/137 (92%)	117 (93%)	9 (7%)	12	30
52	AB	180/244 (74%)	178 (99%)	2 (1%)	70	87
53	BB	194/231 (84%)	191 (98%)	3 (2%)	60	83
54	CB	186/225 (83%)	183 (98%)	3 (2%)	58	82
55	DB	190/232 (82%)	186 (98%)	4 (2%)	48	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	EB	224/225 (100%)	218 (97%)	6 (3%)	40	69
57	FB	158/170 (93%)	154 (98%)	4 (2%)	42	72
58	GB	207/218 (95%)	202 (98%)	5 (2%)	44	73
59	HB	165/360 (46%)	163 (99%)	2 (1%)	67	86
60	IB	178/180 (99%)	176 (99%)	2 (1%)	70	87
61	JB	161/168 (96%)	159 (99%)	2 (1%)	67	86
62	KB	87/136 (64%)	85 (98%)	2 (2%)	45	74
63	LB	130/142 (92%)	128 (98%)	2 (2%)	60	83
64	MB	99/108 (92%)	93 (94%)	6 (6%)	15	36
65	NB	130/131 (99%)	129 (99%)	1 (1%)	79	91
66	OB	106/119 (89%)	104 (98%)	2 (2%)	52	79
67	PB	115/130 (88%)	113 (98%)	2 (2%)	56	81
68	QB	117/140 (84%)	115 (98%)	2 (2%)	56	81
69	RB	119/121 (98%)	117 (98%)	2 (2%)	56	81
70	SB	125/132 (95%)	123 (98%)	2 (2%)	58	82
71	TB	112/115 (97%)	106 (95%)	6 (5%)	18	42
72	UB	93/107 (87%)	86 (92%)	7 (8%)	11	28
73	VB	67/67 (100%)	65 (97%)	2 (3%)	36	65
74	WB	112/113 (99%)	110 (98%)	2 (2%)	54	80
75	XB	113/115 (98%)	107 (95%)	6 (5%)	19	43
76	YB	107/113 (95%)	105 (98%)	2 (2%)	52	79
77	ZB	75/102 (74%)	72 (96%)	3 (4%)	27	55
78	AC	88/98 (90%)	87 (99%)	1 (1%)	70	87
79	BC	75/76 (99%)	72 (96%)	3 (4%)	27	55
80	CC	55/62 (89%)	53 (96%)	2 (4%)	30	59
81	DC	48/49 (98%)	45 (94%)	3 (6%)	15	35
82	EC	46/106 (43%)	46 (100%)	0	100	100
83	FC	62/154 (40%)	60 (97%)	2 (3%)	34	63
84	GC	272/275 (99%)	246 (90%)	26 (10%)	7	17
85	HC	366/379 (97%)	342 (93%)	24 (7%)	14	33
87	b	138/258 (54%)	122 (88%)	16 (12%)	4	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
88	c	9/12 (75%)	9 (100%)	0	100	100
All	All	10440/12074 (86%)	10181 (98%)	259 (2%)	43	72

5 of 259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
85	HC	239	THR
85	HC	392	LYS
43	RA	147	HIS
43	RA	56	LEU
87	b	28	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
58	GB	187	HIS
74	WB	91	ASN
60	IB	22	HIS
64	MB	19	GLN
75	XB	92	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	SA	75/76 (98%)	16 (21%)	3 (4%)
45	TA	75/76 (98%)	16 (21%)	0
46	UA	74/75 (98%)	26 (35%)	1 (1%)
47	VA	11/12 (91%)	3 (27%)	0
48	WA	3558/3584 (99%)	701 (19%)	20 (0%)
49	XA	118/120 (98%)	11 (9%)	0
50	YA	155/156 (99%)	33 (21%)	0
51	ZA	1707/1869 (91%)	317 (18%)	7 (0%)
All	All	5773/5968 (96%)	1123 (19%)	31 (0%)

5 of 1123 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	SA	9	A
44	SA	17	G

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Mol	Chain	Res	Type
44	SA	19	C
44	SA	20	A
44	SA	21	A

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	WA	2048	G
51	ZA	752	G
48	WA	3627	G
51	ZA	874	G
51	ZA	24	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 304 ligands modelled in this entry, 299 are monoatomic - leaving 5 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	$\# Z > 2$
93	SPD	WA	5276	-	9,9,9	0.28	0	8,8,8	0.33	0
92	ANM	WA	5275	94	20,20,20	4.09	7 (35%)	24,27,27	1.42	1 (4%)
95	GTP	HC	601	89	29,34,34	1.23	2 (6%)	35,54,54	1.28	4 (11%)
96	SER	HC	603	-	4,5,6	0.57	0	1,5,7	0.55	0
91	5GP	UA	101	-	22,26,26	1.28	2 (9%)	24,40,40	1.28	4 (16%)

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
93	SPD	WA	5276	-	-	0/7/7/7	-
92	ANM	WA	5275	94	-	6/10/23/23	0/2/2/2
95	GTP	HC	601	89	-	8/18/38/38	0/3/3/3
96	SER	HC	603	-	-	0/2/4/6	-
91	5GP	UA	101	-	-	1/6/26/26	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	WA	5275	ANM	C3-C2	-11.90	1.32	1.53
92	WA	5275	ANM	C16-N1	-8.84	1.30	1.47
92	WA	5275	ANM	C2-C16	7.41	1.68	1.53
91	UA	101	5GP	C5-C6	-4.27	1.39	1.47
95	HC	601	GTP	C5-C6	-4.21	1.39	1.47

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	WA	5275	ANM	O2-C5-C6	5.44	120.79	111.09
95	HC	601	GTP	C8-N7-C5	3.52	108.55	102.55
95	HC	601	GTP	C2-N1-C6	-2.97	119.67	125.11
95	HC	601	GTP	C5-C6-N1	2.95	119.69	114.07
91	UA	101	5GP	C5-C6-N1	2.85	119.51	114.07

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

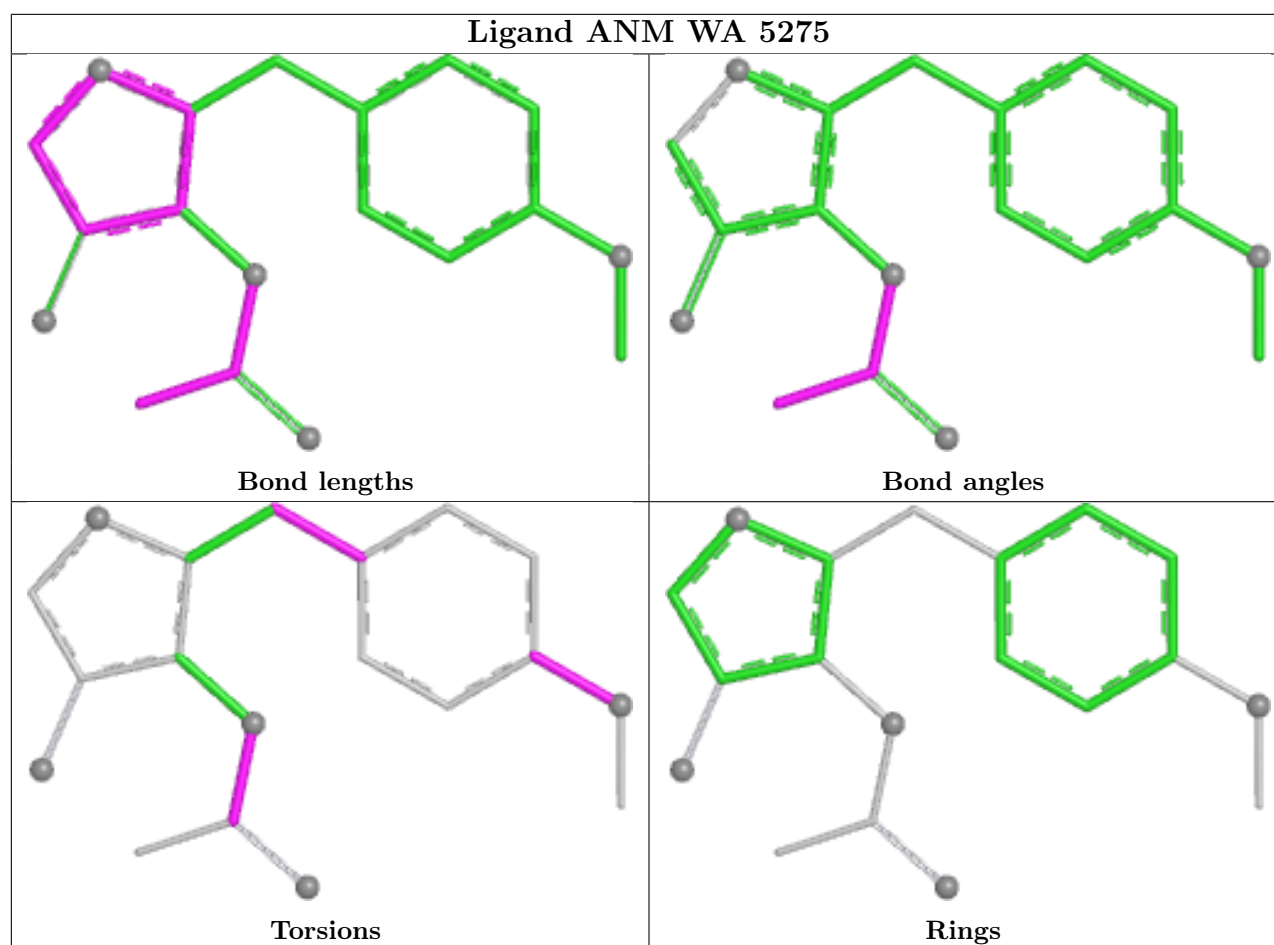
Mol	Chain	Res	Type	Atoms
95	HC	601	GTP	C5'-O5'-PA-O3A
95	HC	601	GTP	C5'-O5'-PA-O1A
95	HC	601	GTP	C5'-O5'-PA-O2A
92	WA	5275	ANM	C6-C5-O2-C2
92	WA	5275	ANM	O3-C5-O2-C2

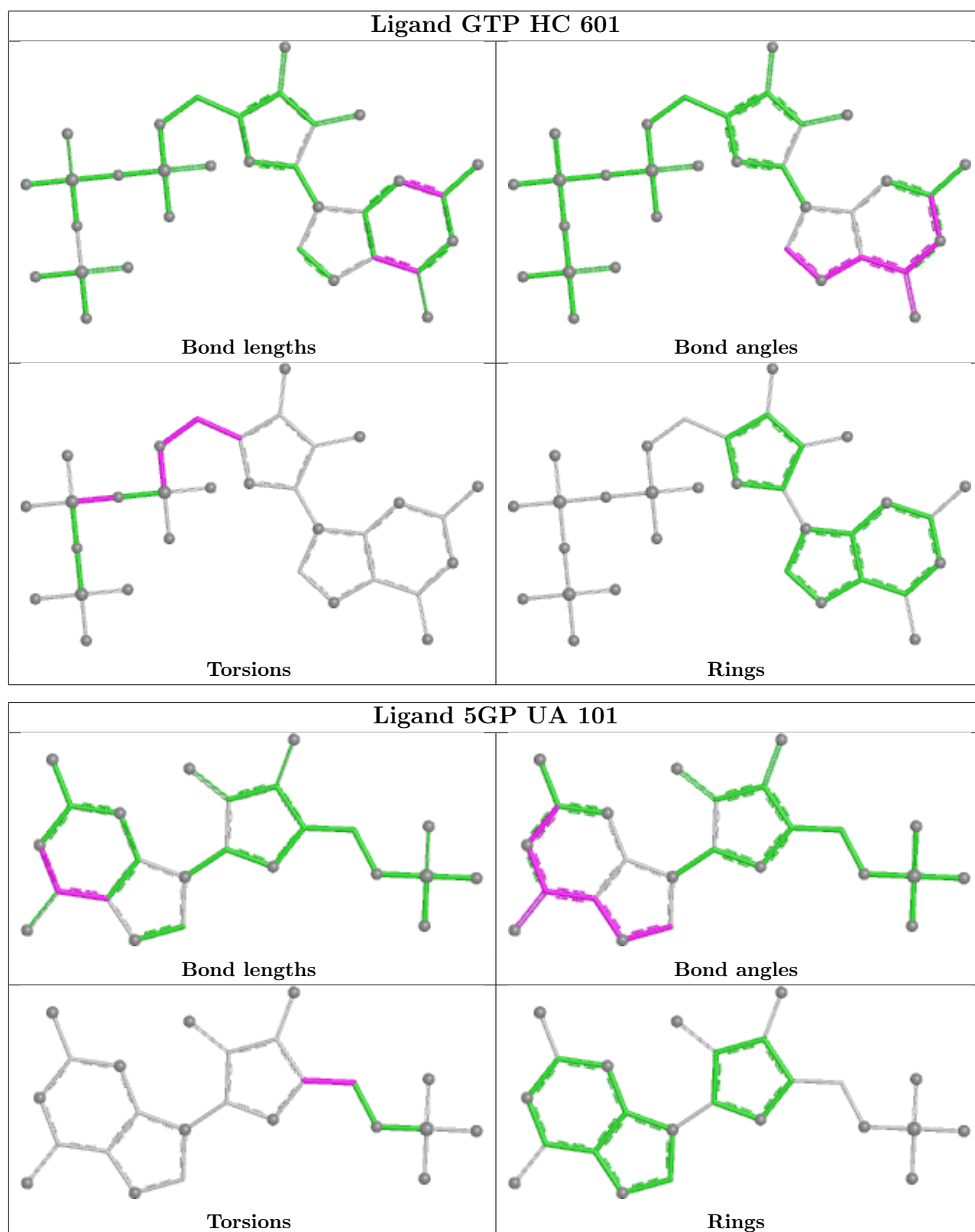
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
92	WA	5275	ANM	3	0
95	HC	601	GTP	1	0
96	HC	603	SER	1	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
48	WA	20

The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	2118:C	O3'	2260:C	P	36.21
1	WA	1225:G	O3'	1239:G	P	21.47
1	WA	4103:C	O3'	4109:G	P	19.88
1	WA	524:C	O3'	639:G	P	17.34
1	WA	996:C	O3'	1070:G	P	16.49

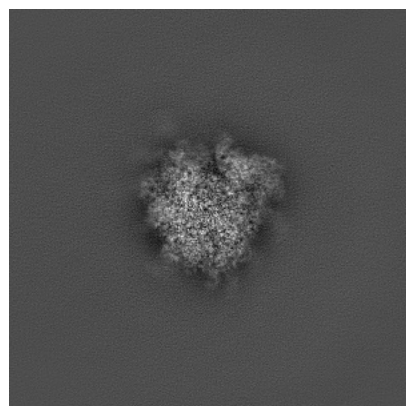
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43565. These allow visual inspection of the internal detail of the map and identification of artifacts.

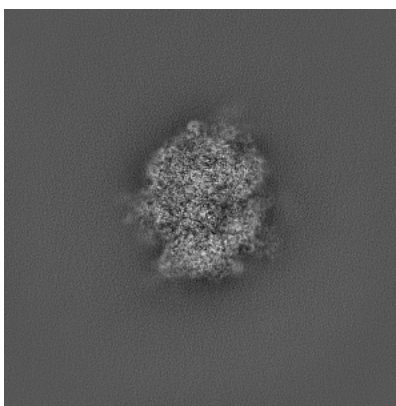
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

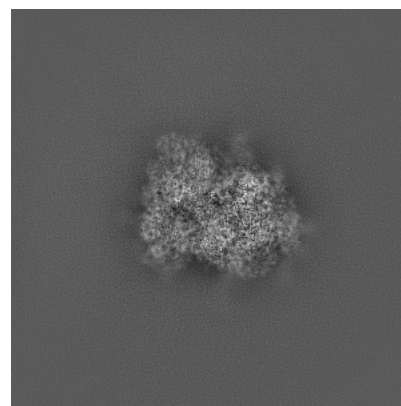
6.1.1 Primary map



X

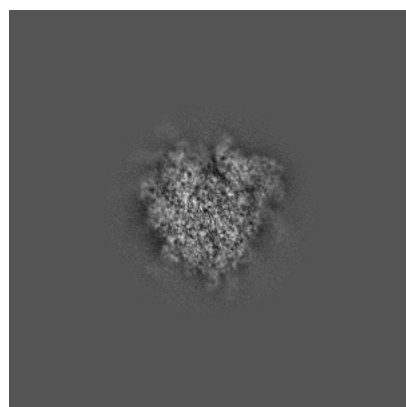


Y

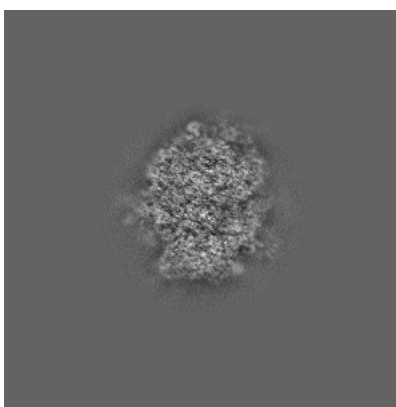


Z

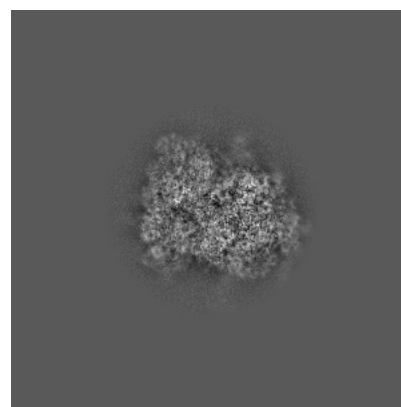
6.1.2 Raw map



X



Y

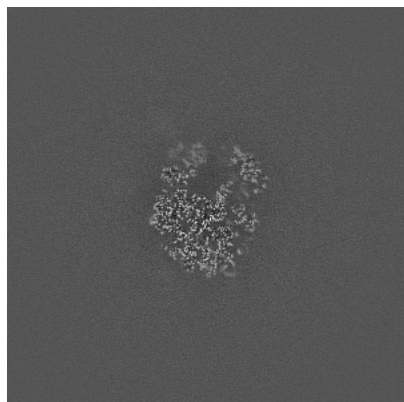


Z

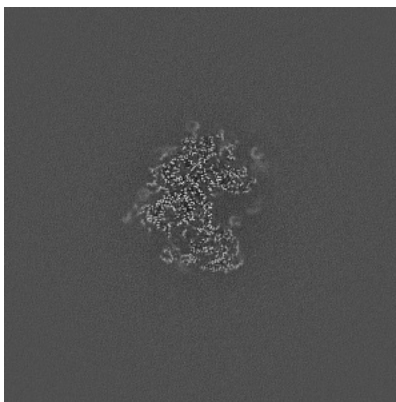
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

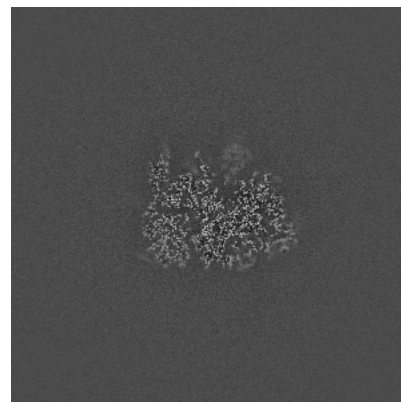
6.2.1 Primary map



X Index: 324

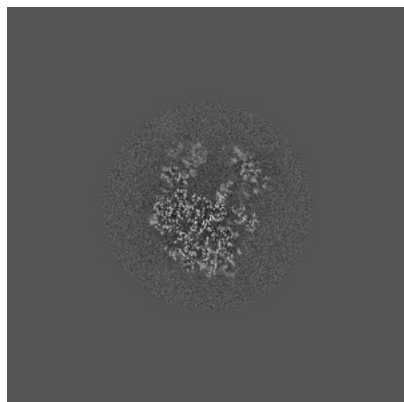


Y Index: 324

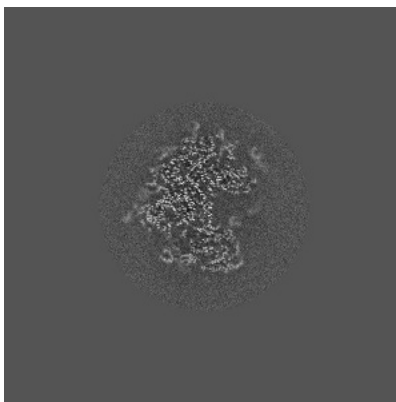


Z Index: 324

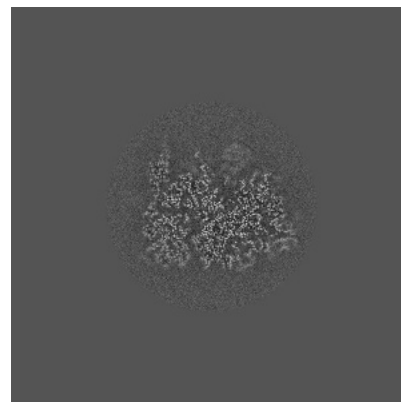
6.2.2 Raw map



X Index: 324



Y Index: 324

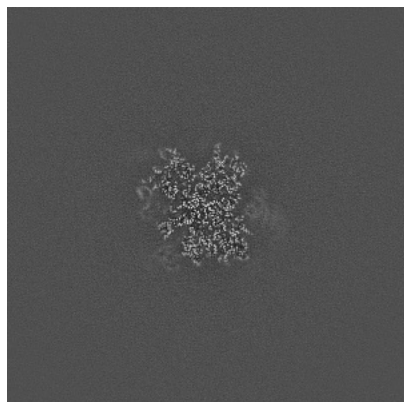


Z Index: 324

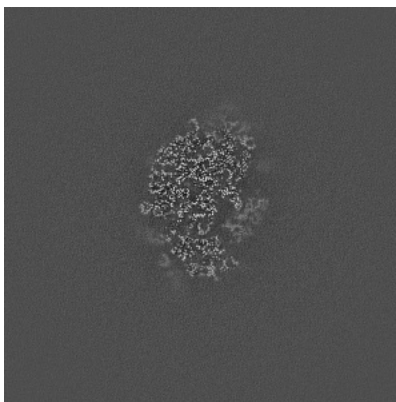
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

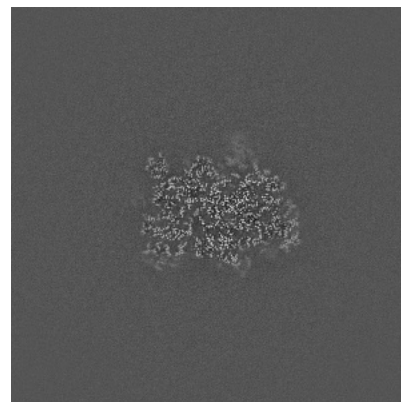
6.3.1 Primary map



X Index: 376

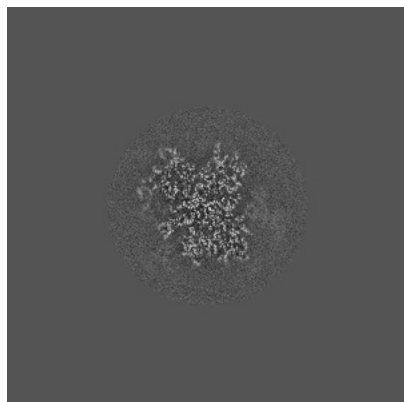


Y Index: 300

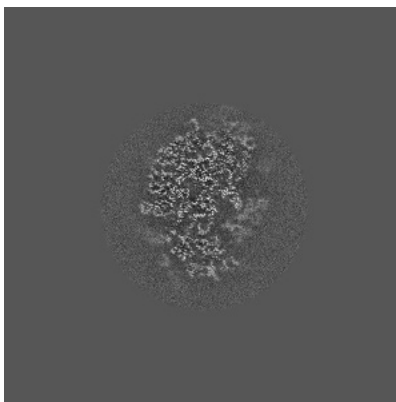


Z Index: 313

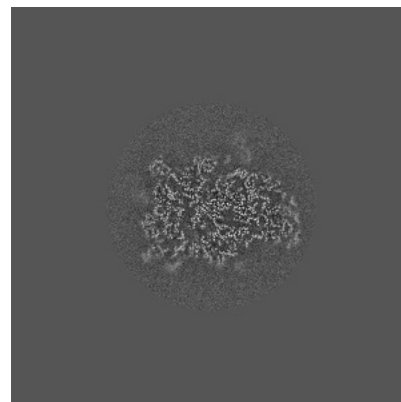
6.3.2 Raw map



X Index: 376



Y Index: 300

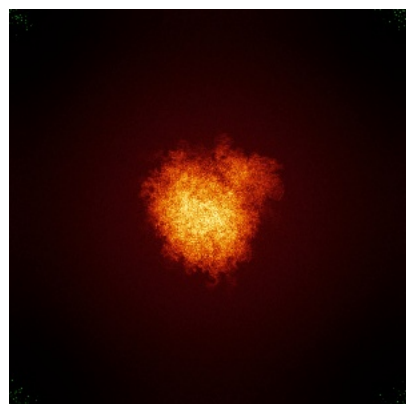


Z Index: 306

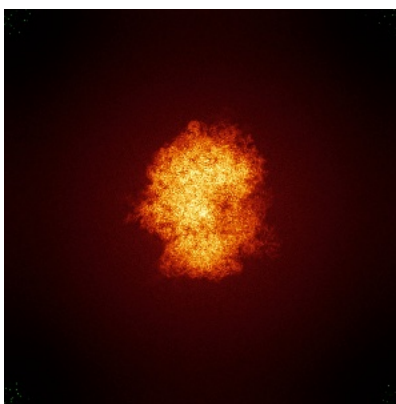
The images above show the largest variance slices of the map in three orthogonal directions.

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

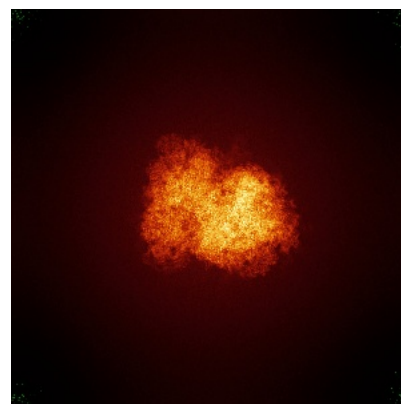
6.4.1 Primary map



X

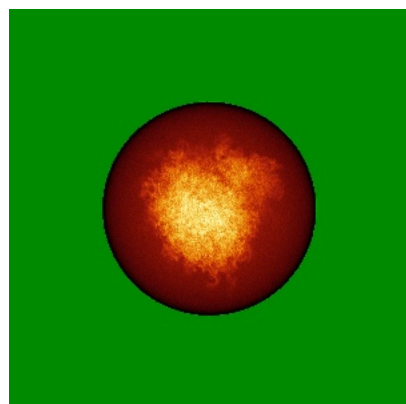


Y

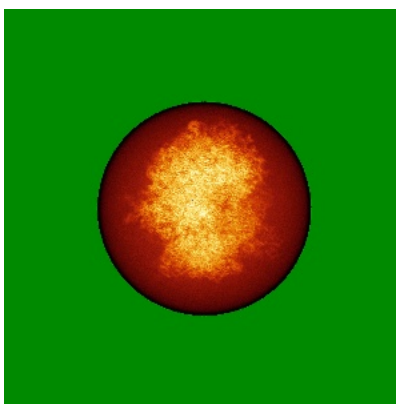


Z

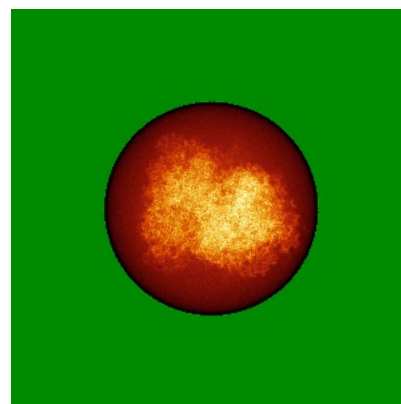
6.4.2 Raw map



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



X



Y



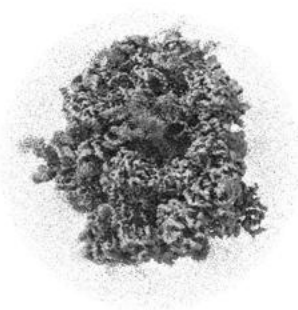
Z

The images above show the 3D surface view of the map at the recommended contour level 4.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

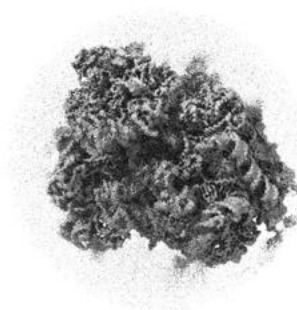
6.5.2 Raw map



X



Y



Z

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.

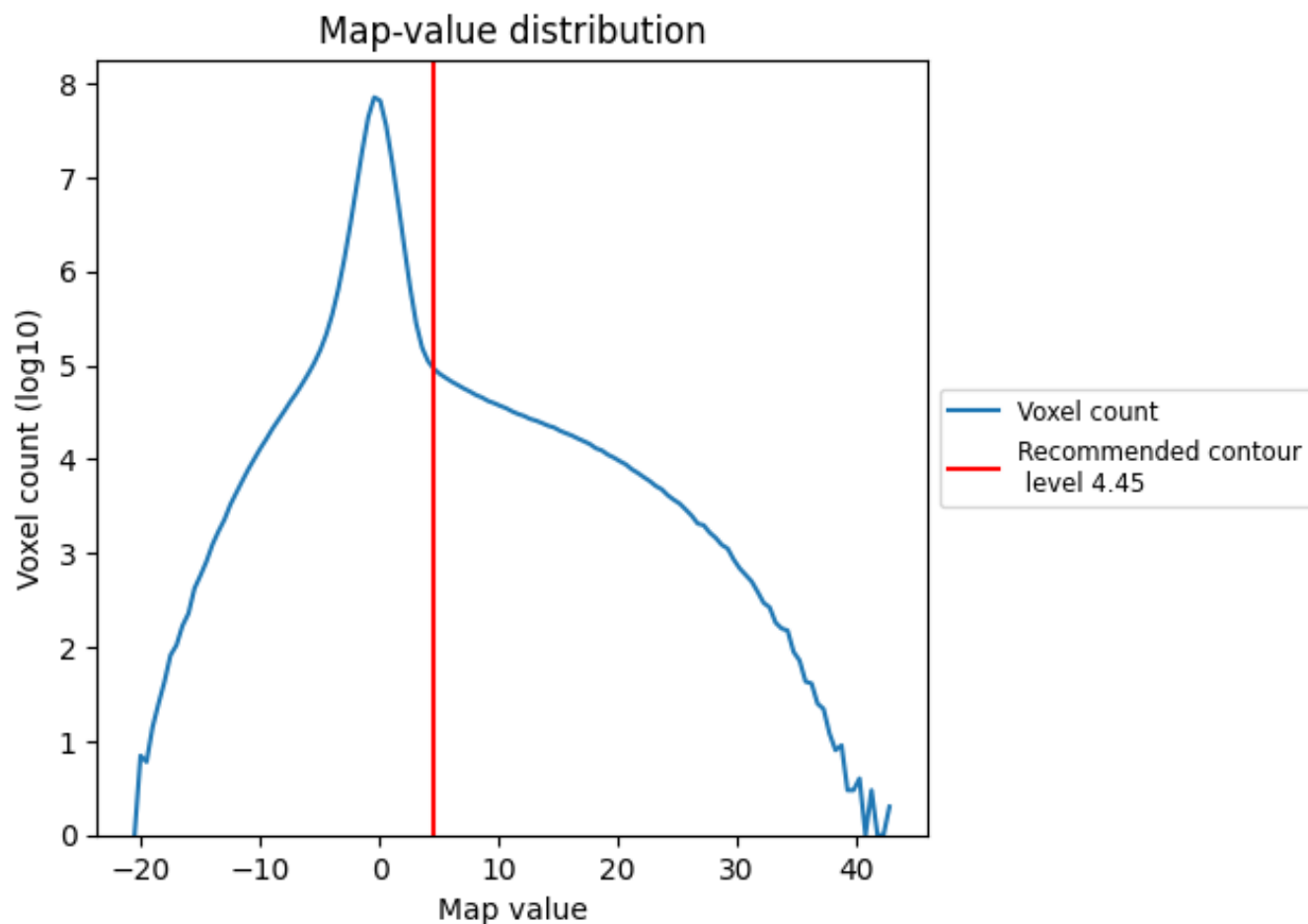
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

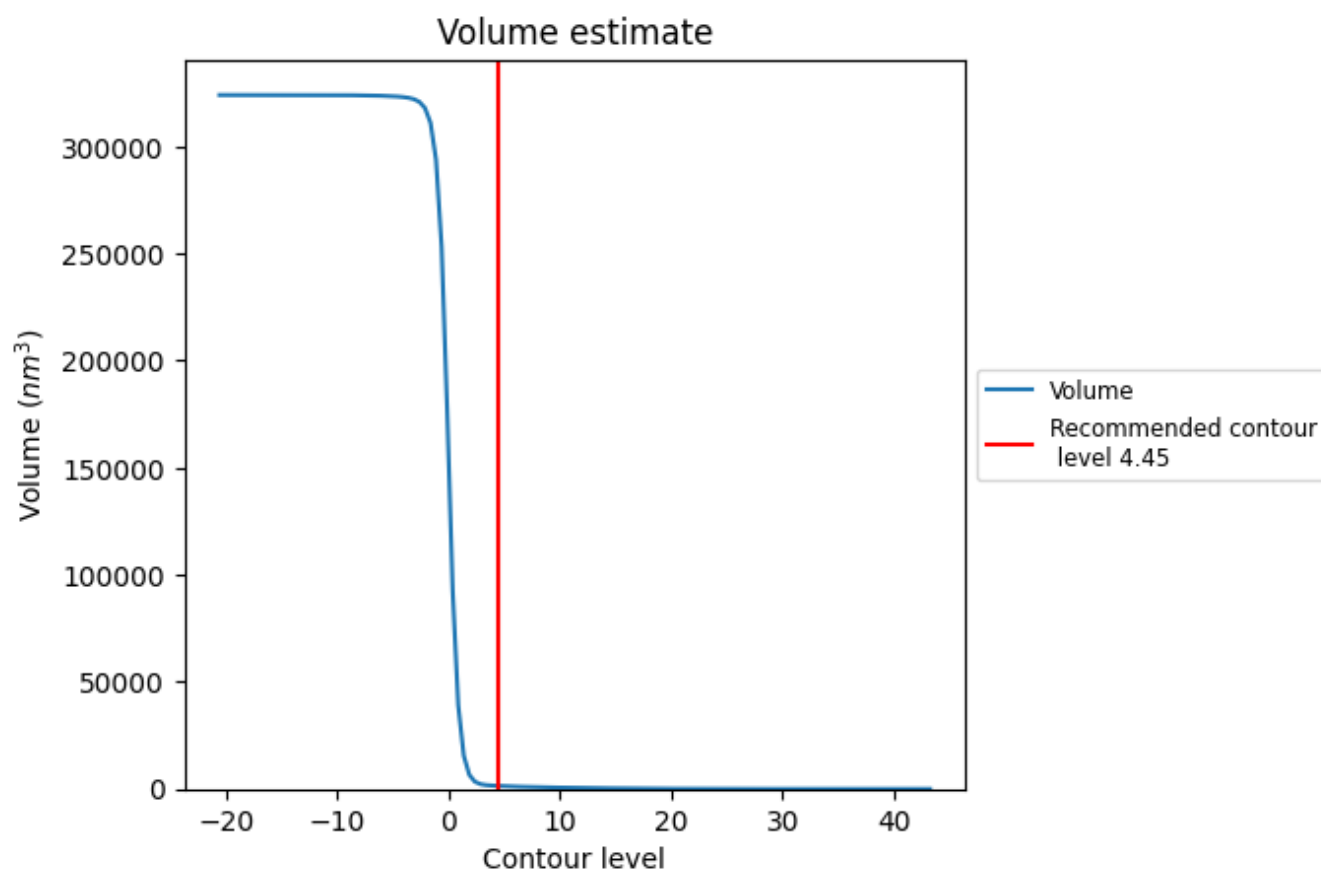
This section contains the results of statistical analysis of the map.

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.

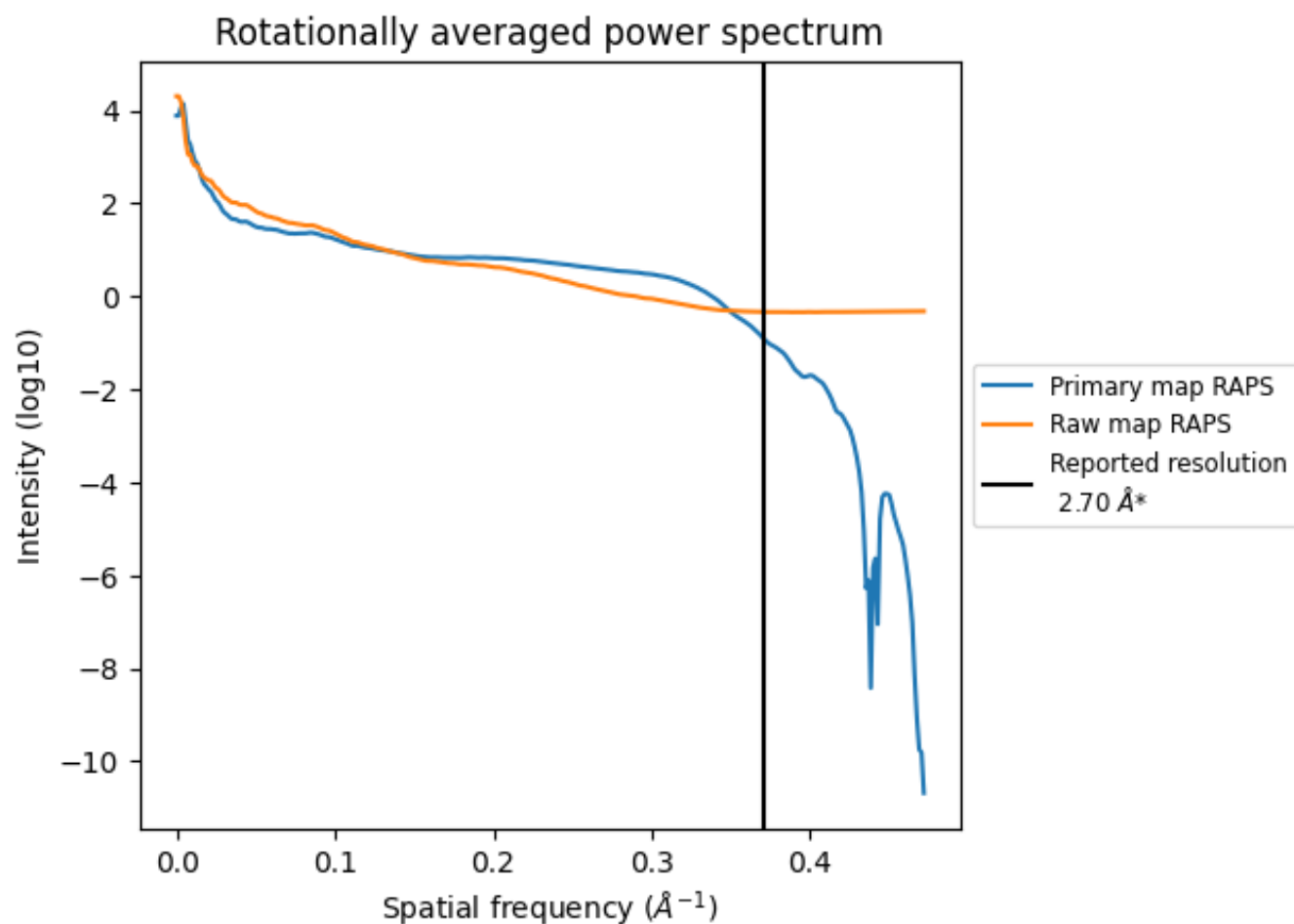
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1435 nm³; this corresponds to an approximate mass of 1296 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 ⓘ

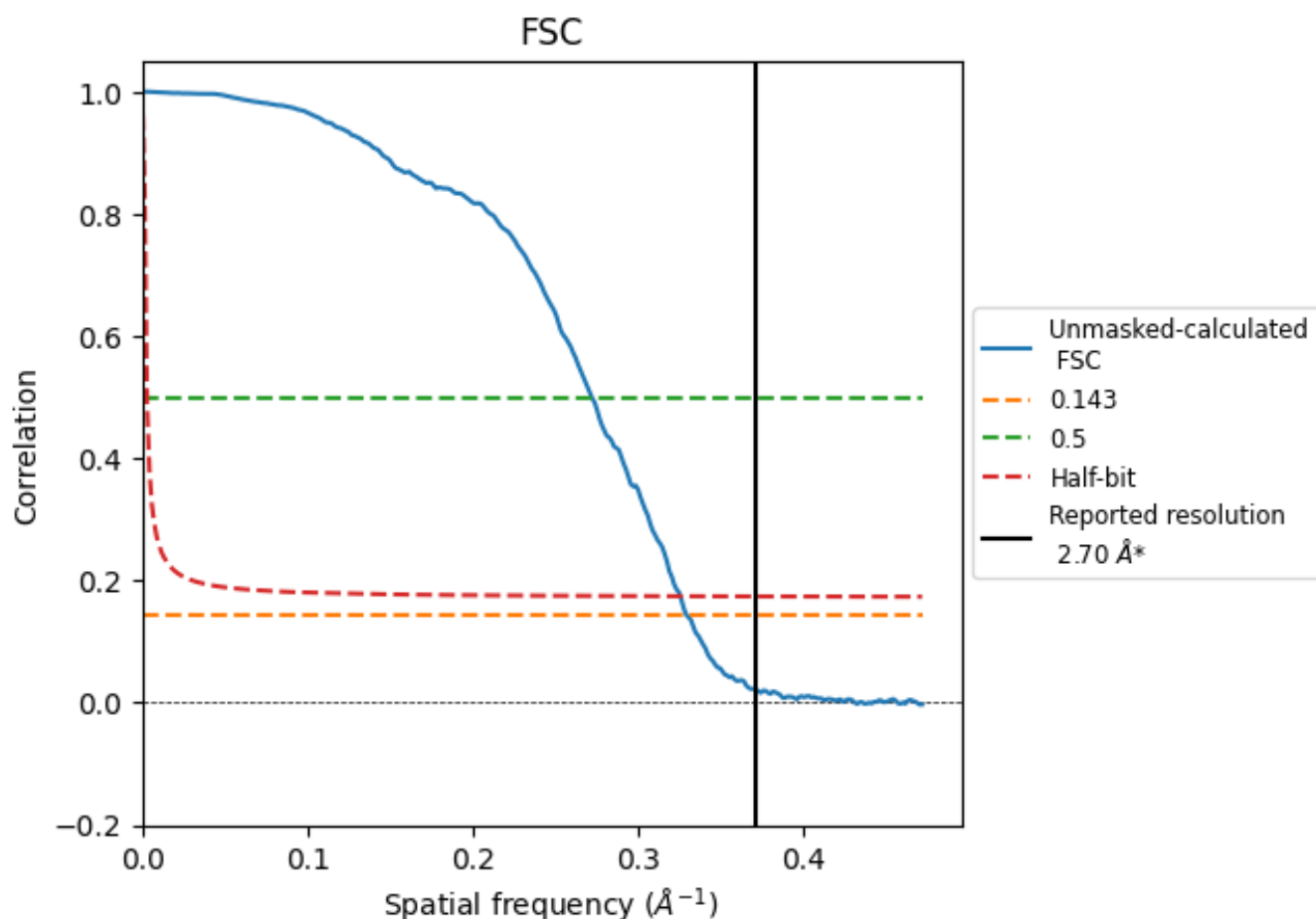


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

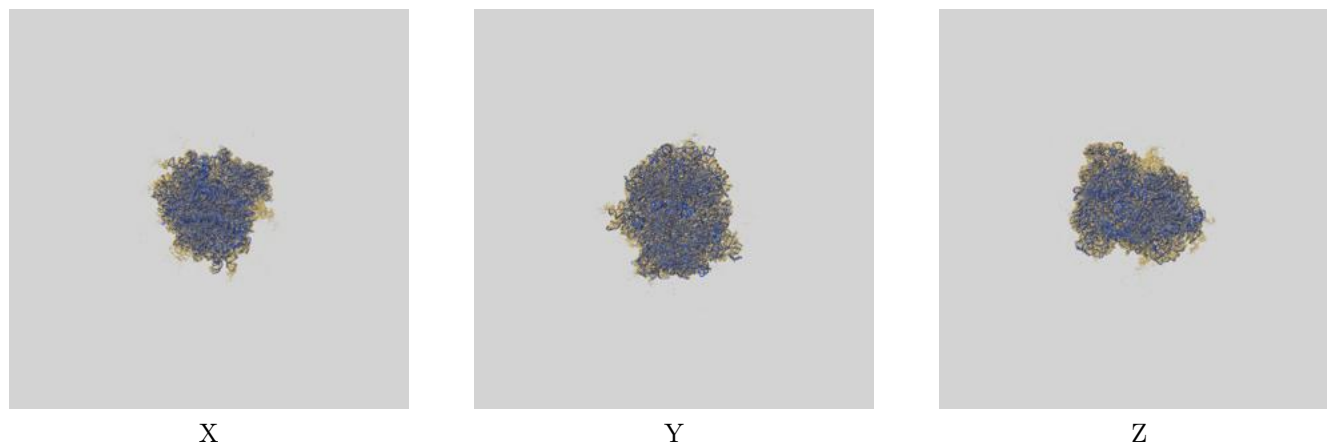
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.04	3.68	3.07

*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 3.04 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

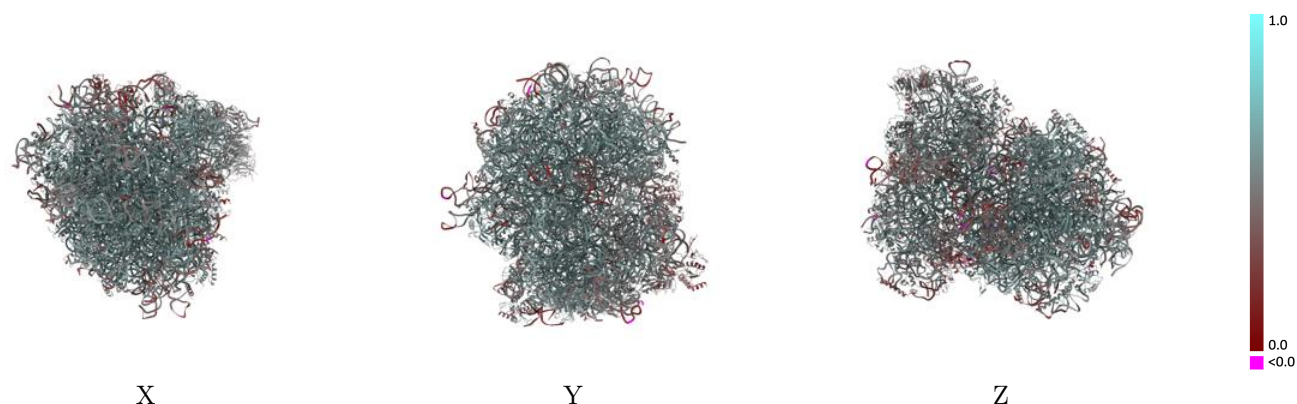
This section contains information regarding the fit between EMDB map EMD-43565 and PDB model 8VVQ. Per-residue inclusion information can be found in [section 3](#) on [page 27](#).

9.1 Map-model overlay [i](#)



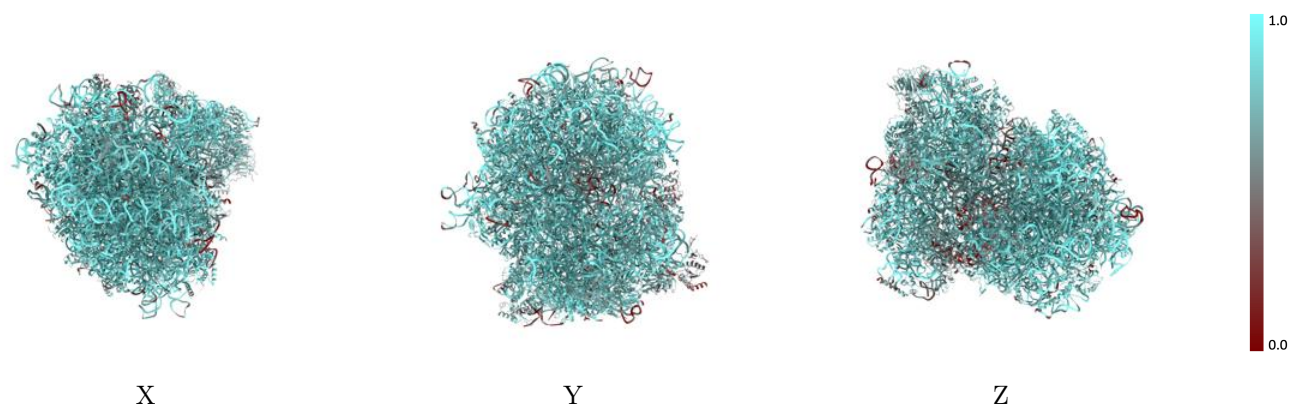
The images above show the 3D surface view of the map at the recommended contour level 4.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



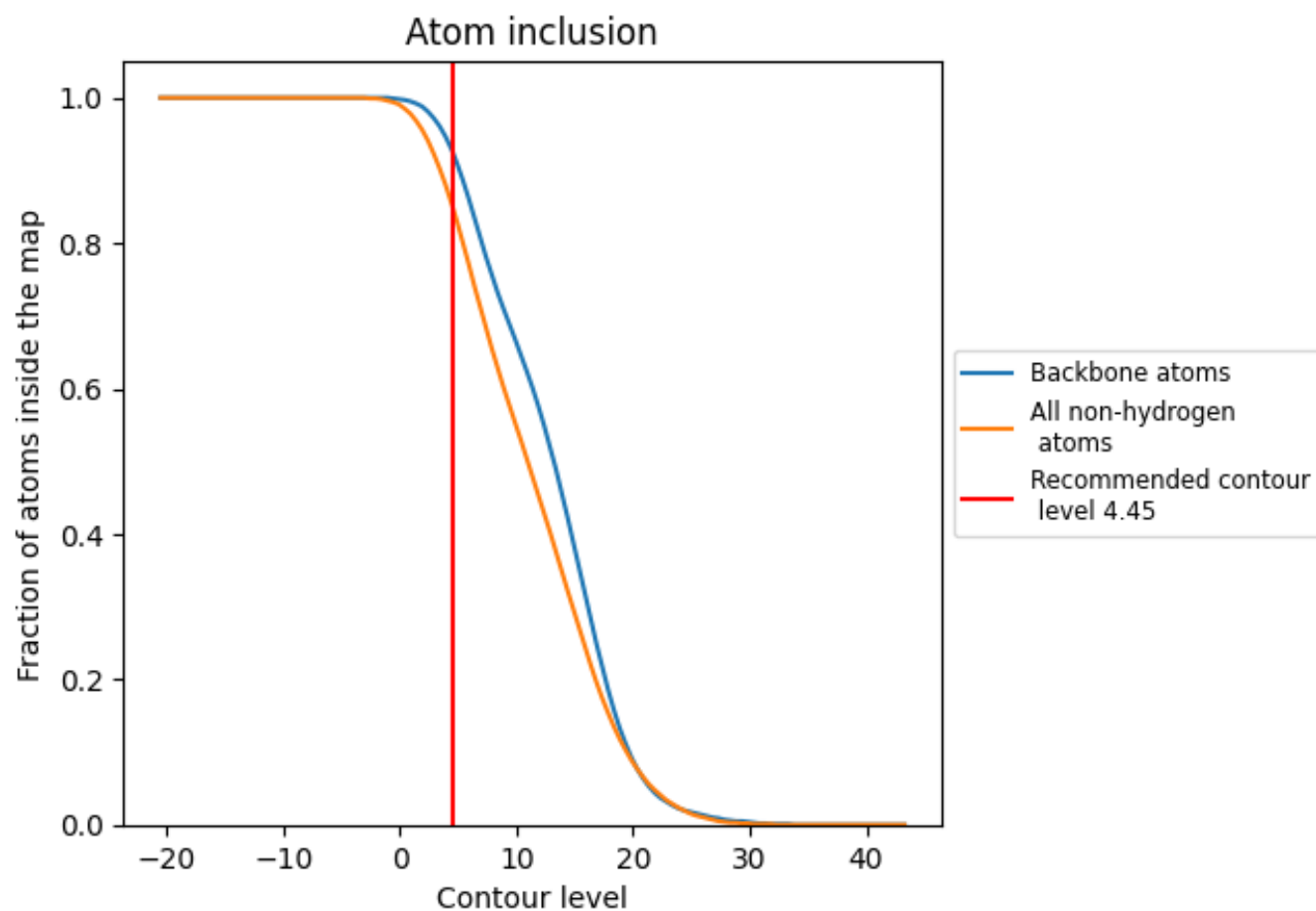
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.45).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 85% 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 (4.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8530	 0.5290
A	 0.8880	 0.5930
AA	 0.7620	 0.5140
AB	 0.8220	 0.5320
AC	 0.8260	 0.5500
B	 0.8820	 0.5730
BA	 0.8540	 0.5550
BB	 0.8130	 0.5430
BC	 0.7930	 0.5350
C	 0.8580	 0.5690
CA	 0.8500	 0.5620
CB	 0.8270	 0.5490
CC	 0.7150	 0.5110
D	 0.8600	 0.5410
DA	 0.8740	 0.5810
DB	 0.7200	 0.4900
DC	 0.8260	 0.5270
E	 0.8230	 0.5350
EA	 0.8860	 0.5920
EB	 0.8200	 0.5400
EC	 0.7020	 0.4920
F	 0.8550	 0.5720
FA	 0.8450	 0.5670
FB	 0.7740	 0.5110
FC	 0.4870	 0.3670
G	 0.8150	 0.5250
GA	 0.8310	 0.5460
GB	 0.7350	 0.4850
GC	 0.6700	 0.4450
H	 0.8280	 0.5520
HA	 0.8330	 0.5330
HB	 0.7220	 0.4850
HC	 0.5500	 0.4120
I	 0.8570	 0.5670
IA	 0.8960	 0.5760



























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Chain	Atom inclusion	Q-score
IB	 0.8060	 0.5340
IC	 0.6000	 0.5270
J	 0.8100	 0.5270
JA	 0.7680	 0.5090
JB	 0.8120	 0.5190
K	 0.8370	 0.5470
KA	 0.8690	 0.5610
KB	 0.7240	 0.4750
L	 0.8440	 0.5460
LA	 0.8750	 0.5650
LB	 0.8530	 0.5720
M	 0.9010	 0.5950
MA	 0.8620	 0.5710
MB	 0.4060	 0.2930
N	 0.8740	 0.5720
NA	 0.8720	 0.5840
NB	 0.8470	 0.5550
O	 0.8610	 0.5760
OA	 0.8550	 0.5850
OB	 0.8100	 0.5460
P	 0.8730	 0.5830
PA	 0.8760	 0.5640
PB	 0.6940	 0.4670
Q	 0.8450	 0.5470
QB	 0.7740	 0.5070
R	 0.8810	 0.5710
RA	 0.2760	 0.2790
RB	 0.7380	 0.4880
S	 0.8500	 0.5710
SA	 0.8180	 0.5140
SB	 0.7750	 0.4940
T	 0.7770	 0.4970
TA	 0.4320	 0.3360
TB	 0.7650	 0.4960
U	 0.8380	 0.5760
UA	 0.6010	 0.3440
UB	 0.6800	 0.4790
V	 0.7460	 0.4990
VA	 0.6670	 0.4600
VB	 0.8050	 0.5340
W	 0.8310	 0.5520
WA	 0.9200	 0.5420

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Chain	Atom inclusion	Q-score
WB	 0.8450	 0.5600
X	 0.8500	 0.5570
XA	 0.9740	 0.5740
XB	 0.8330	 0.5660
Y	 0.8670	 0.5560
YA	 0.9100	 0.5460
YB	 0.8050	 0.5120
Z	 0.8900	 0.5830
ZA	 0.8910	 0.5200
ZB	 0.6640	 0.4740
b	 0.3560	 0.2940
c	 0.0460	 0.3160