



Full wwPDB EM Validation Report ⓘ

Nov 9, 2024 – 11:55 PM EST

PDB ID : 6P5K
EMDB ID : EMD-20257
Title : Structure of a mammalian 80S ribosome in complex with the Israeli Acute Paralysis Virus IRES (Class 3)
Authors : Acosta-Reyes, F.J.; Neupane, R.; Frank, J.; Fernandez, I.S.
Deposited on : 2019-05-30
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

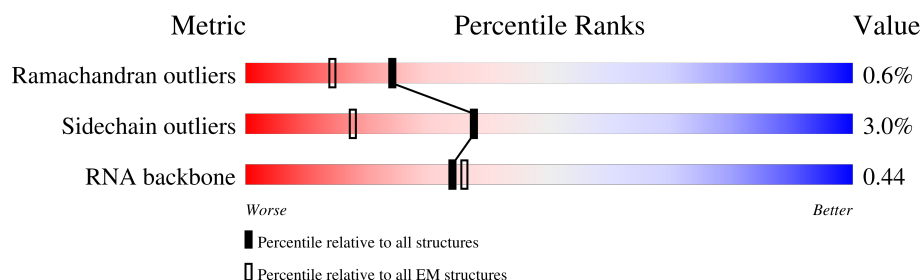
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 Å.

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





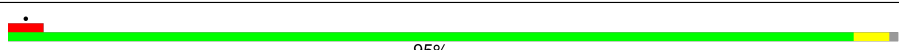
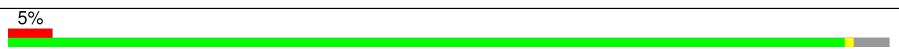
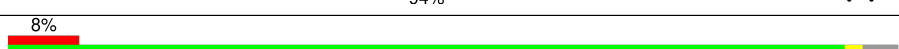
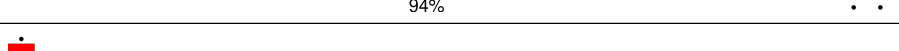
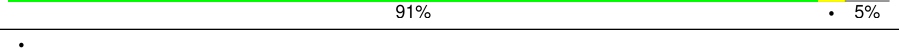

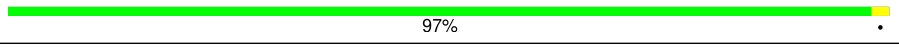
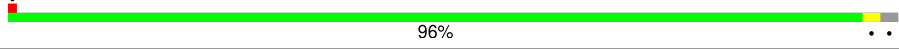


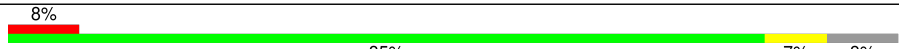


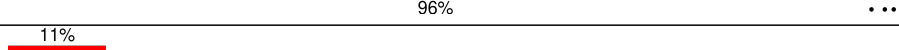





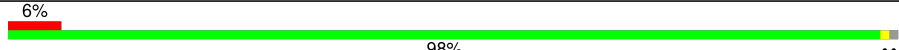

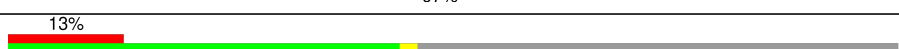
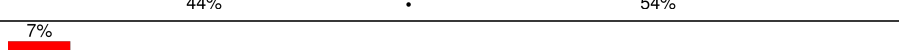
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	5	3594	
2	7	119	
3	8	156	
4	AA	257	
5	AB	403	
6	AC	392	
7	AD	297	
8	AE	291	

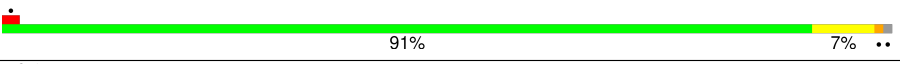
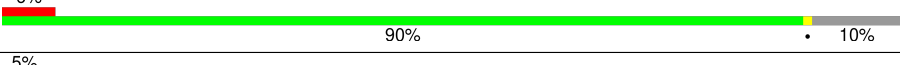
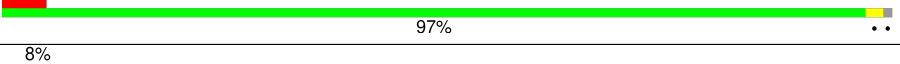
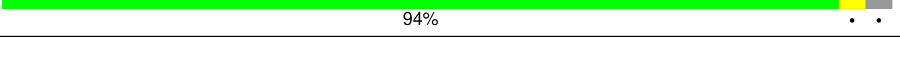

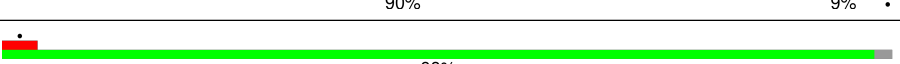
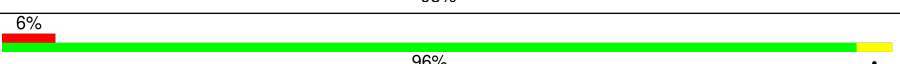
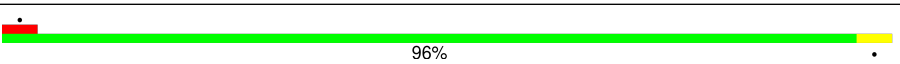
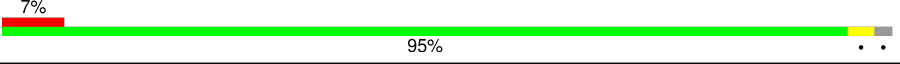
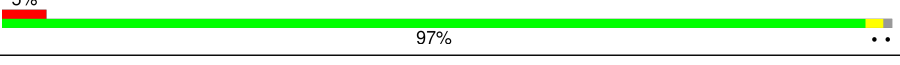
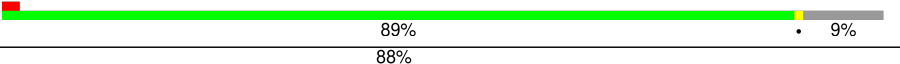
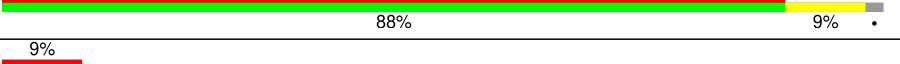

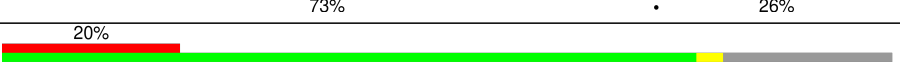
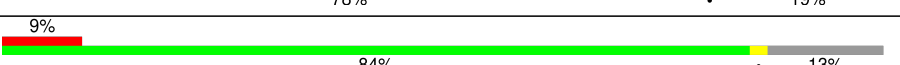

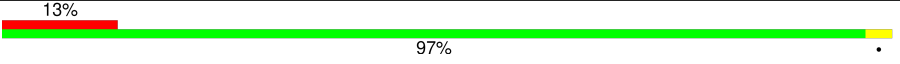

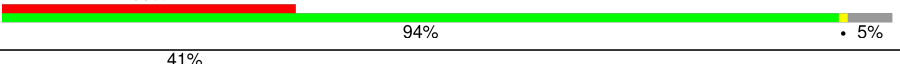
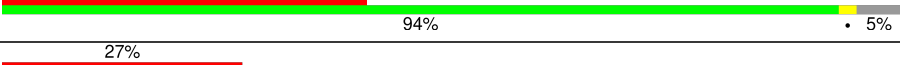
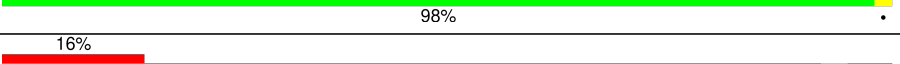
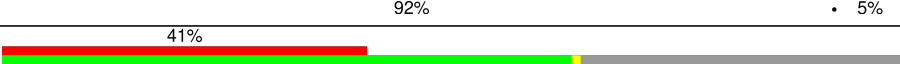



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Mol	Chain	Length	Quality of chain
9	AF	249	
10	AG	242	
11	AH	192	
12	AI	214	
13	AJ	178	
14	AL	211	
15	AM	198	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	
29	Aa	148	
30	Ab	226	
31	Ac	115	
32	Ad	125	
33	Ae	135	

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Mol	Chain	Length	Quality of chain
34	Af	110	
35	Ag	126	
36	Ah	123	
37	Ai	105	
38	Aj	97	
39	Ak	70	
40	Al	51	
41	Am	52	
42	An	25	
43	Ao	106	
44	Ap	92	
45	Ar	137	
46	AK	217	
47	2	1869	
48	B	295	
49	C	264	
50	D	255	
51	E	281	
52	F	263	
53	G	204	
54	H	249	
55	I	194	
56	J	207	
57	K	194	
58	L	149	

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Mol	Chain	Length	Quality of chain
59	M	158	
60	N	132	
61	O	151	
62	P	151	
63	Q	145	
64	R	172	
65	S	135	
66	T	152	
67	U	145	
68	V	119	
69	W	83	
70	X	130	
71	Y	143	
72	Z	134	
73	a	125	
74	b	115	
75	c	84	
76	d	69	
77	e	56	
78	f	133	
79	g	156	
80	h	317	
81	1	253	

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 215976 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3594	Total	C	N	O	P	0	0
			77074	34325	14116	25039	3594		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	248	Total	C	N	O	S	0	0
			1895	1186	389	314	6		

- Molecule 5 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 6 is a protein called uL4.

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

- Molecule 7 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 8 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 9 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 10 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	225	Total	C	N	O	S	0	0
			1819	1161	351	303	4		

- Molecule 11 is a protein called uL6.

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

- Molecule 12 is a protein called uL16.

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

- Molecule 13 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	201	Total	C	N	O	S	0	0
			1627	1020	341	262	4		

- Molecule 15 is a protein called L14e.

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

- Molecule 16 is a protein called eL15.

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

- Molecule 17 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	199	Total	C	N	O	S	0	0
			1631	1052	319	255	5		

- Molecule 18 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 19 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	187	Total	C	N	O	S	0	0
			1526	964	306	252	4		

- Molecule 20 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	180	Total	C	N	O	S	0	0
			1503	931	324	238	10		

- Molecule 21 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	176	Total	C	N	O	S	0	0
			1457	928	283	235	11		

- Molecule 22 is a protein called eL21.

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

- Molecule 23 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AU	99	Total	C	N	O	S	0	0
			818	520	146	150	2		

- Molecule 24 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 25 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AW	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called eL23.

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

- Molecule 27 is a protein called uL24.

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

- Molecule 28 is a protein called eL27.

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

- Molecule 29 is a protein called uL15.

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

- Molecule 30 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ab	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 32 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ad	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ae	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called eL33.

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

- Molecule 35 is a protein called eL34.

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

- Molecule 36 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ah	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 37 is a protein called eL36.

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

- Molecule 38 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Aj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ak	69	Total	C	N	O	S	0	0
			569	366	101	99	3		

- Molecule 40 is a protein called eL39.

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

- Molecule 41 is a protein called eL40.

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

- Molecule 42 is a protein called eL41.

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

- Molecule 43 is a protein called eL42.

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

- Molecule 44 is a protein called eL43.

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

- Molecule 45 is a protein called eL28.

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

- Molecule 46 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AK	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 48 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B	217	Total	C	N	O	S	0	0
			1706	1085	295	317	9		

- Molecule 49 is a protein called eS1.

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

- Molecule 50 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	D	221	Total	C	N	O	S	0	0
			1712	1107	296	299	10		

- Molecule 51 is a protein called uS3.

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

- Molecule 52 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F	262	Total	C	N	O	S	0	0
			2073	1323	384	357	9		

- Molecule 53 is a protein called uS7.

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

- Molecule 54 is a protein called eS6.

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

- Molecule 55 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 56 is a protein called eS8.

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

- Molecule 57 is a protein called uS4.

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

- Molecule 58 is a protein called eS10.

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

- Molecule 59 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	M	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 60 is a protein called eS12.

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

- Molecule 61 is a protein called uS15.

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

- Molecule 62 is a protein called uS11.

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

- Molecule 63 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Q	119	Total	C	N	O	S	0	0
			990	630	186	167	7		

- Molecule 64 is a protein called uS9.

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

- Molecule 65 is a protein called eS17.

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

- Molecule 66 is a protein called uS13.

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

- Molecule 67 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 68 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 69 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	W	83	Total	C	N	O	S	0	0
			630	387	118	120	5		

- Molecule 70 is a protein called uS8.

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

- Molecule 71 is a protein called uS12.

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

- Molecule 72 is a protein called eS24.

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

- Molecule 73 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	a	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 74 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	b	98	Total	C	N	O	S	0	0
			778	485	158	129	6		

- Molecule 75 is a protein called eS27.

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

- Molecule 76 is a protein called eS28.

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

- Molecule 77 is a protein called eS29.

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

- Molecule 78 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	f	56	Total	C	N	O	S	0	0
			447	276	98	72	1		

- Molecule 79 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 80 is a protein called RACK1.

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

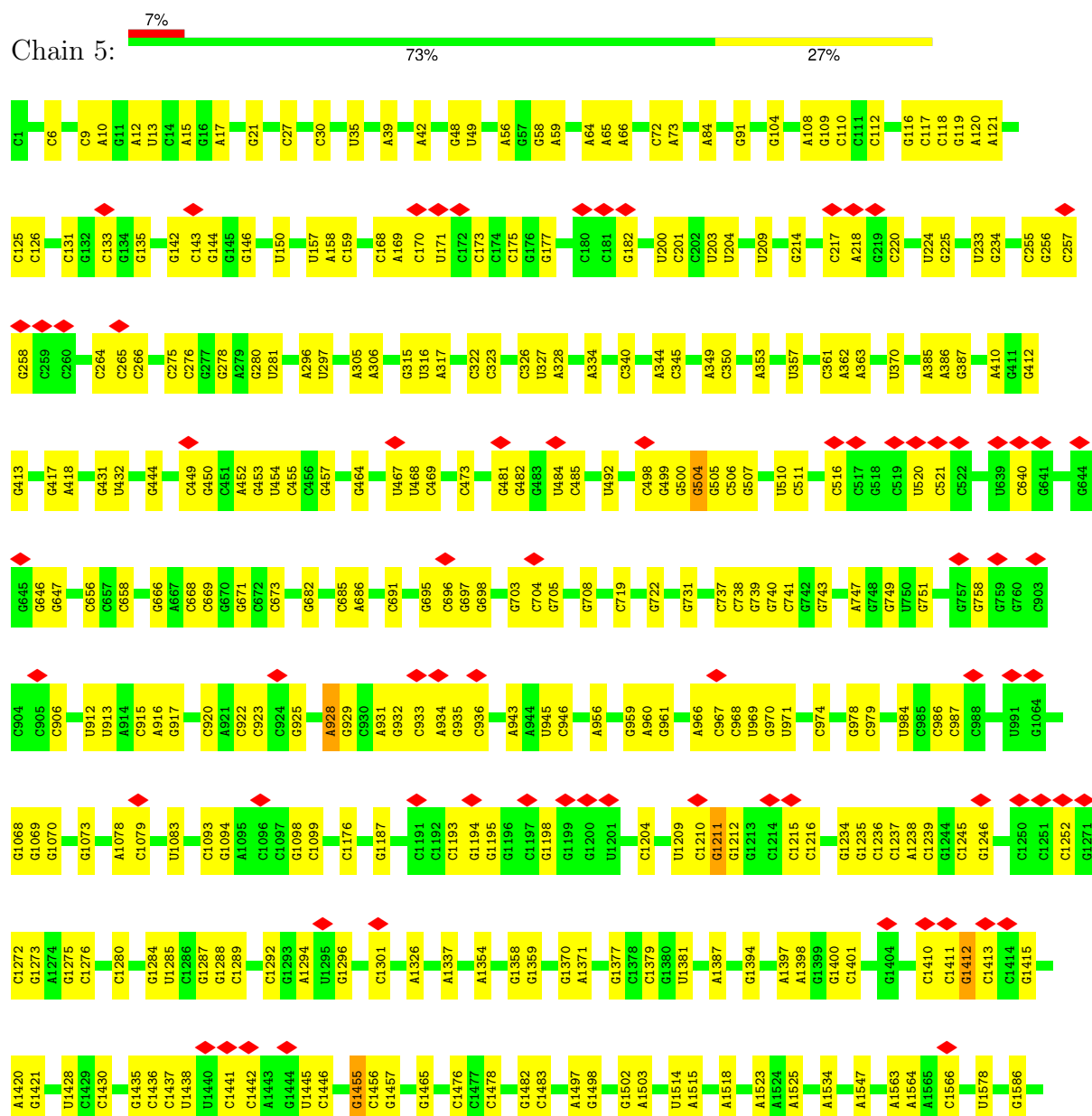
- Molecule 81 is a RNA chain called IAPV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	1	205	Total	C	N	O	P	0	0
			4366	1951	775	1435	205		

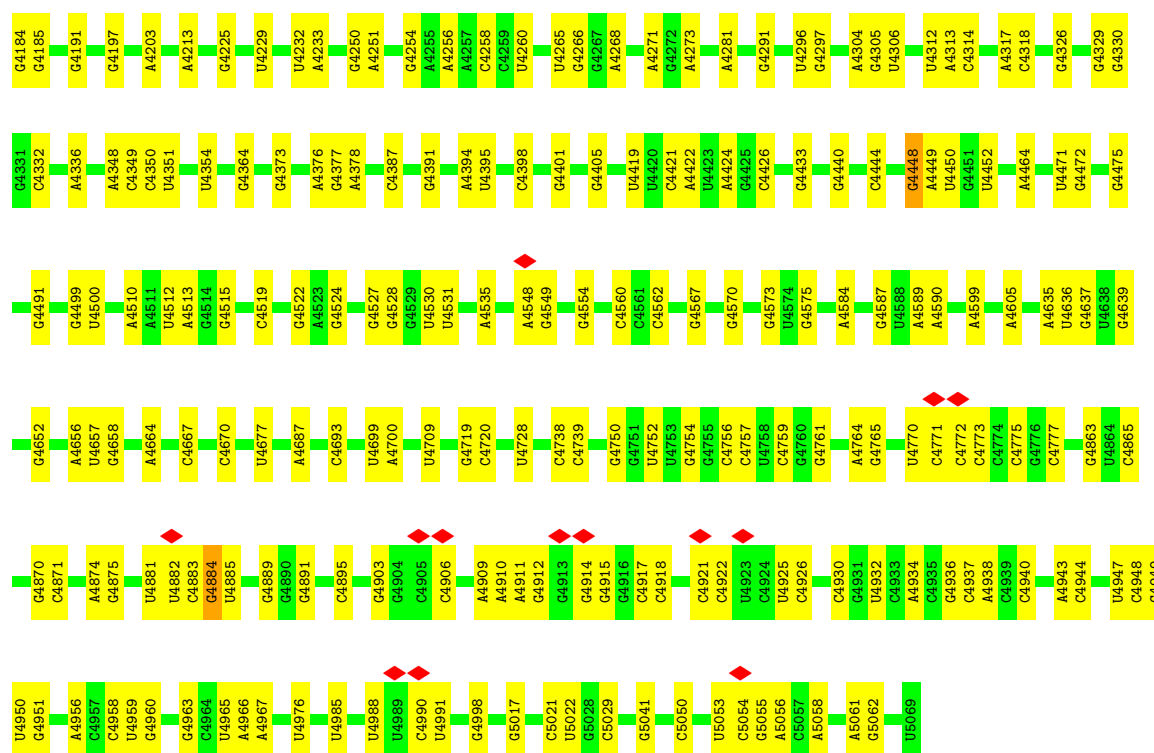
3 Residue-property plots

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: 28S rRNA

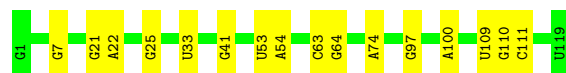






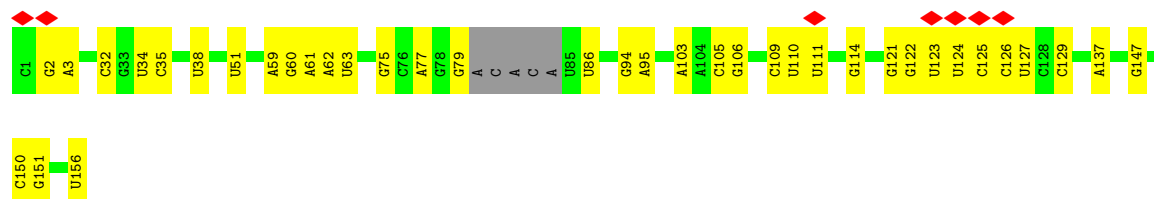
• Molecule 2: 5S rRNA

Chain 7: 87% 13%



• Molecule 3: 5.8S rRNA

Chain 8: 72% 24%



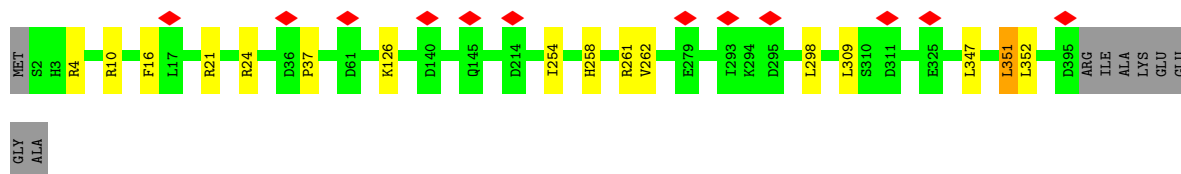
• Molecule 4: uL2

Chain AA: 88% 9%

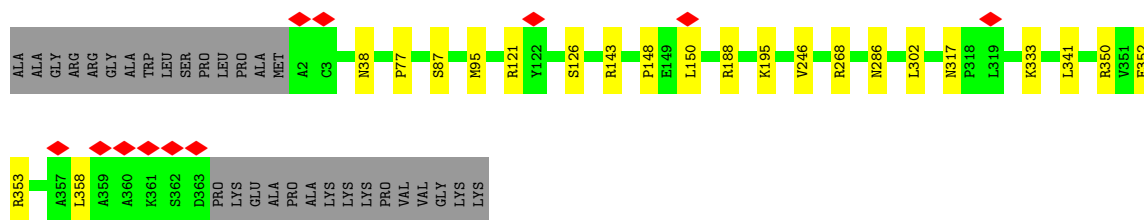


• Molecule 5: uL3

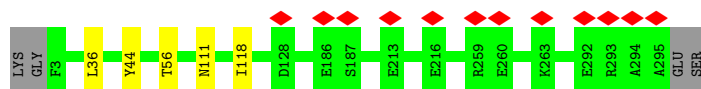
Chain AB: 94%



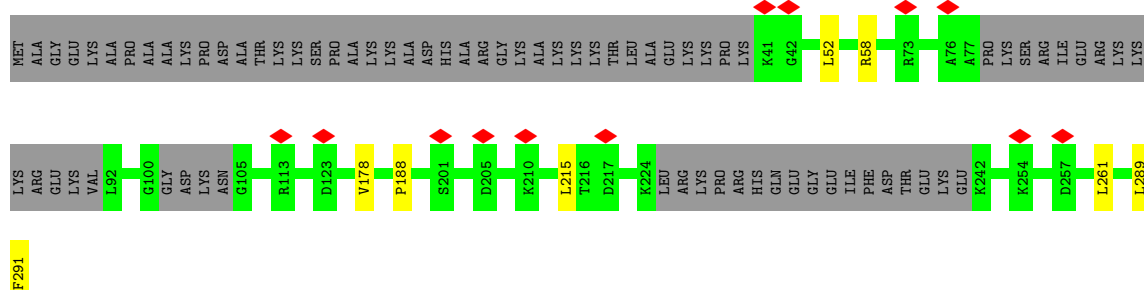
- Molecule 6: uL4



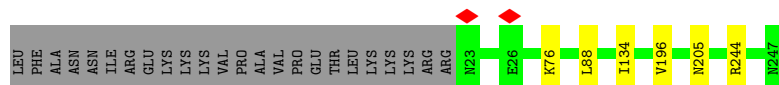
- Molecule 7: uL18



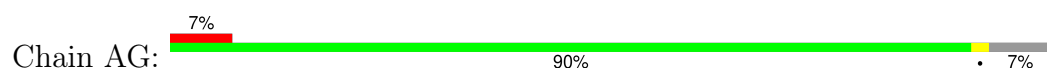
- Molecule 8: eL6



- Molecule 9: uL30




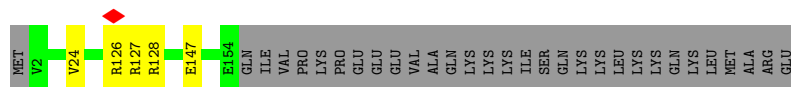
- Molecule 10: eL8




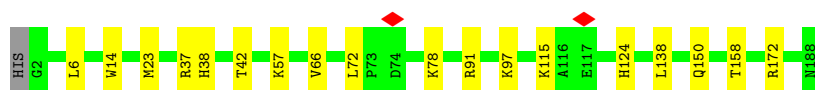
• Molecule 17: uL13

Chain AO:  96%


• Molecule 18: uL22

Chain AP:  80% 17%

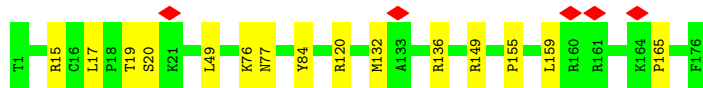
• Molecule 19: eL18

Chain AQ:  90% 10%

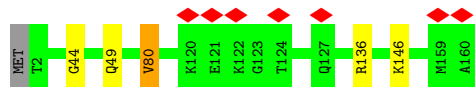
• Molecule 20: eL19

Chain AR:  8% 85% 7% 8%


• Molecule 21: eL20

Chain AS:  91% 9%

• Molecule 22: eL21

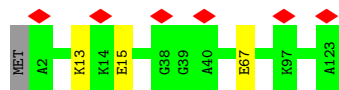
Chain AT:  96%

• Molecule 23: eL22

Chain AU:  11% 75% 23%

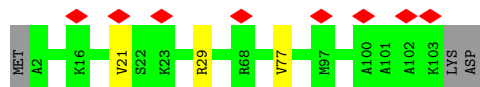
- Molecule 36: eL35

Chain Ah:  5% 97%




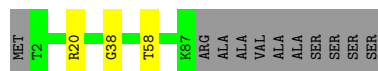
- Molecule 37: eL36

Chain Ai:  8% 94%



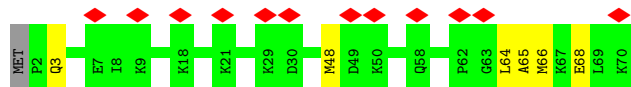
- Molecule 38: eL37

Chain Aj:  86% 11%



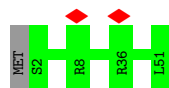
- Molecule 39: eL38

Chain Ak:  17% 90% 9%



- Molecule 40: eL39

Chain Al:  98%



- Molecule 41: eL40

Chain Am:  6% 96%

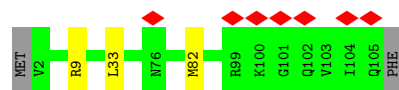


- Molecule 42: eL41

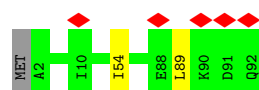
Chain An:  96%



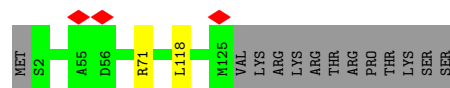
- Molecule 43: eL42



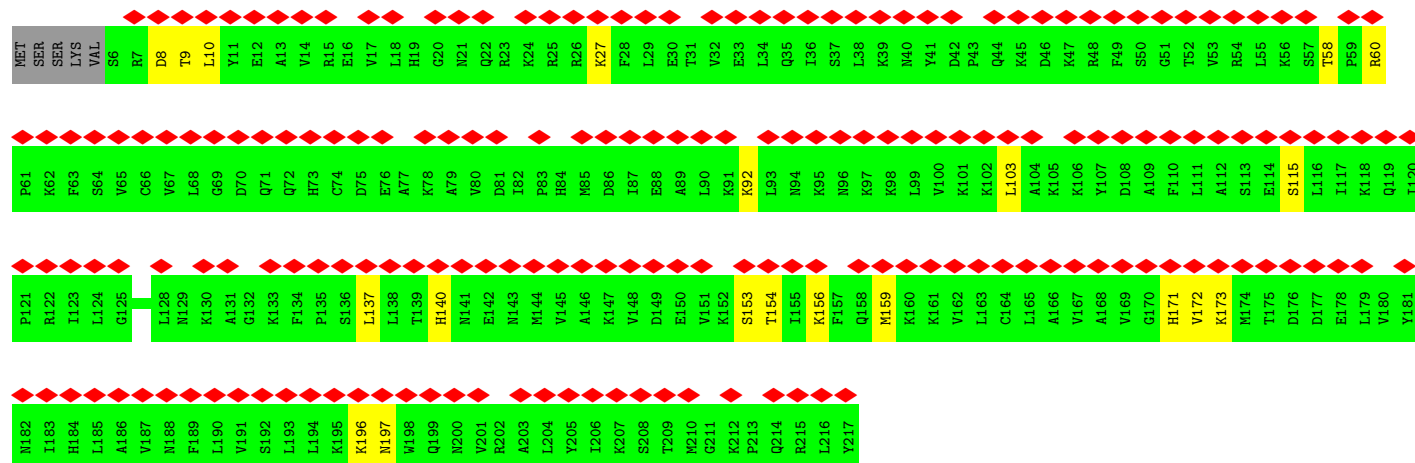
- Molecule 44: eL43



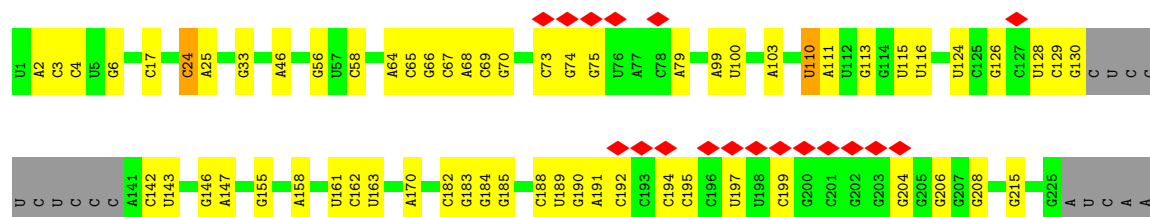
- Molecule 45: eL28



- Molecule 46: uL1

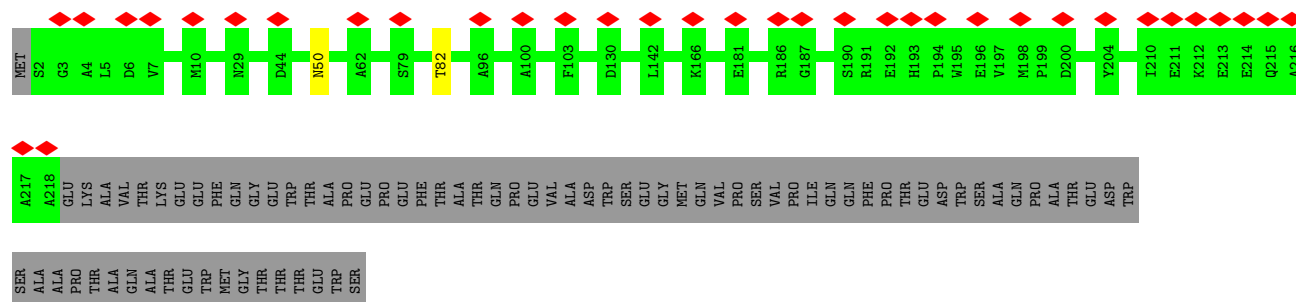
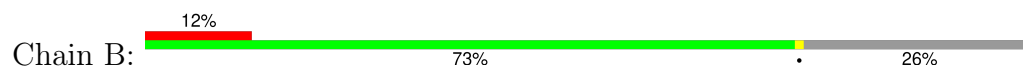


- Molecule 47: 18S rRNA

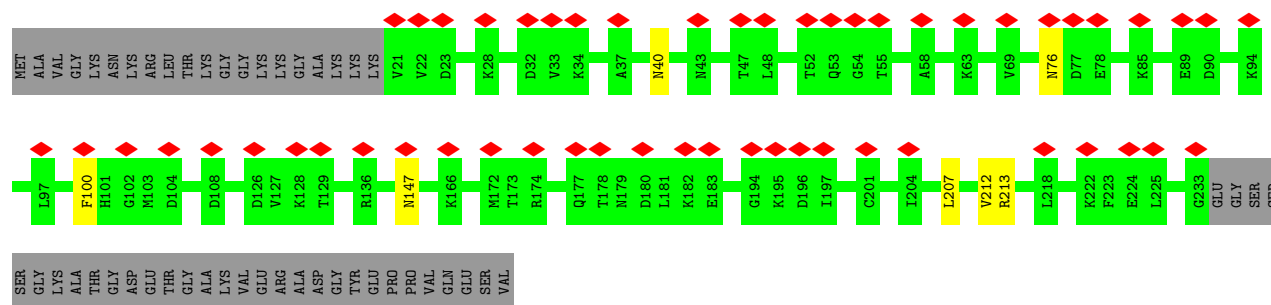
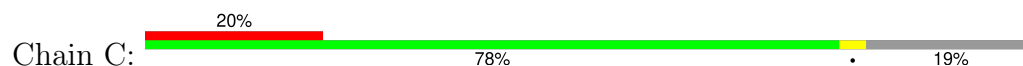




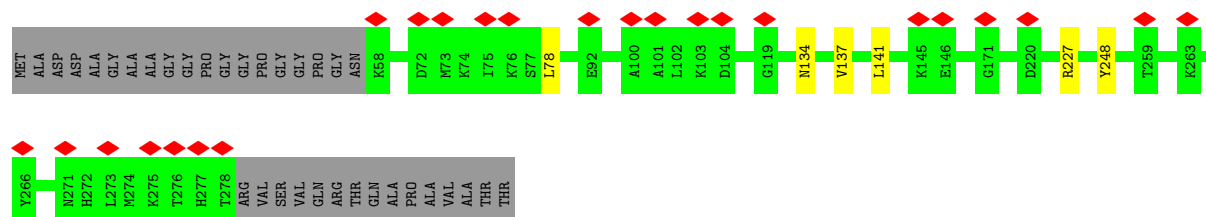
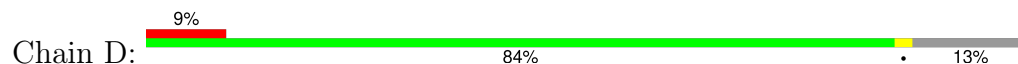
- Molecule 48: uS2



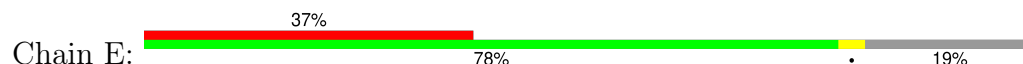
- Molecule 49: eS1

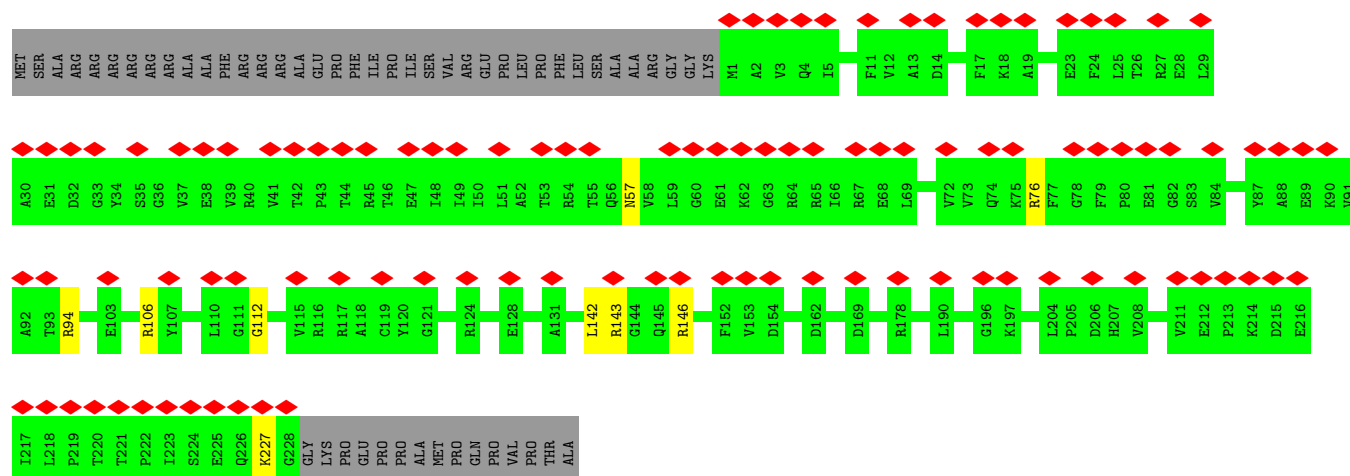


- Molecule 50: uS5

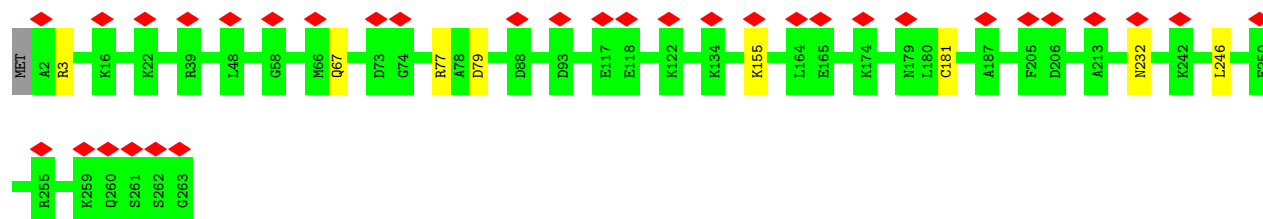


- Molecule 51: uS3

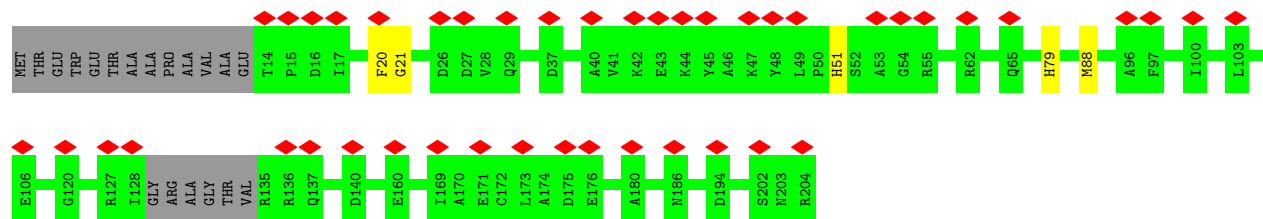
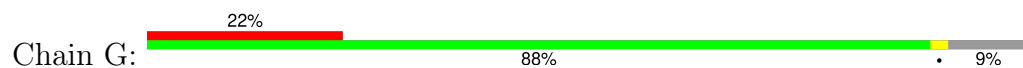




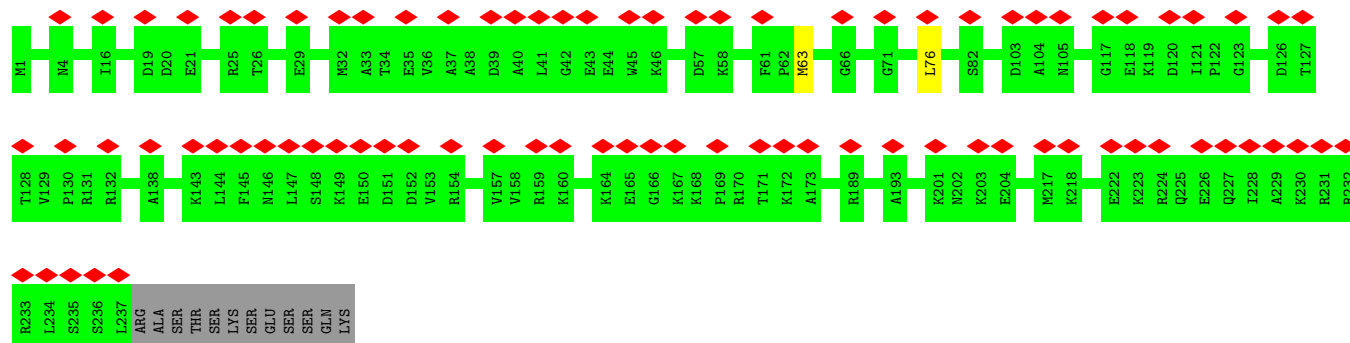
- Molecule 52: eS4



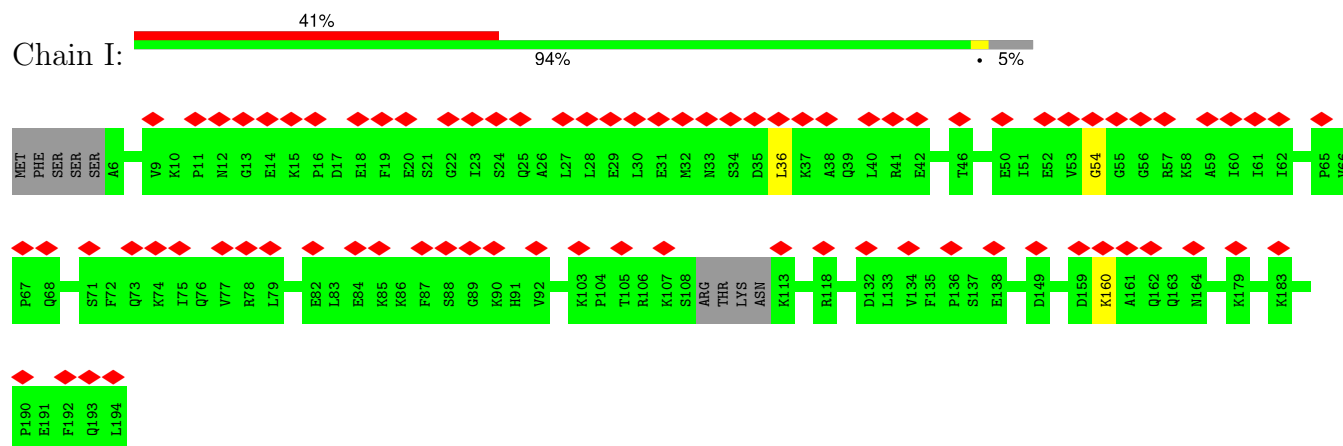
- Molecule 53: uS7



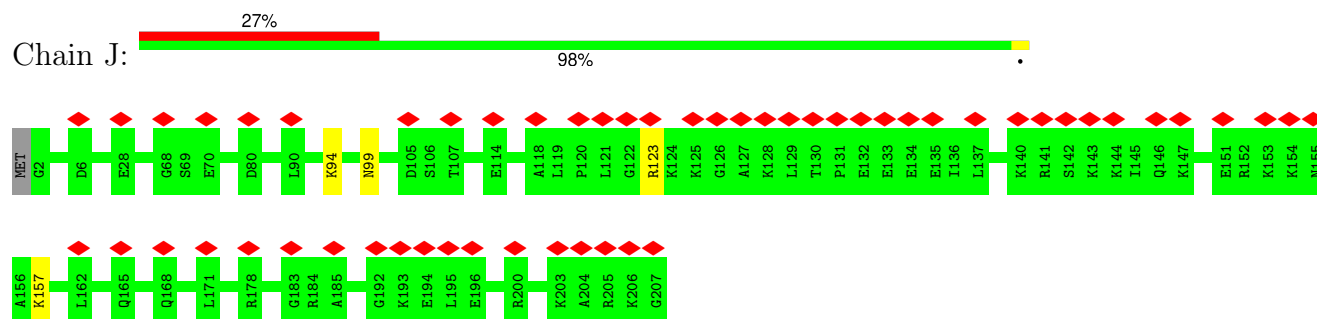
- Molecule 54: eS6



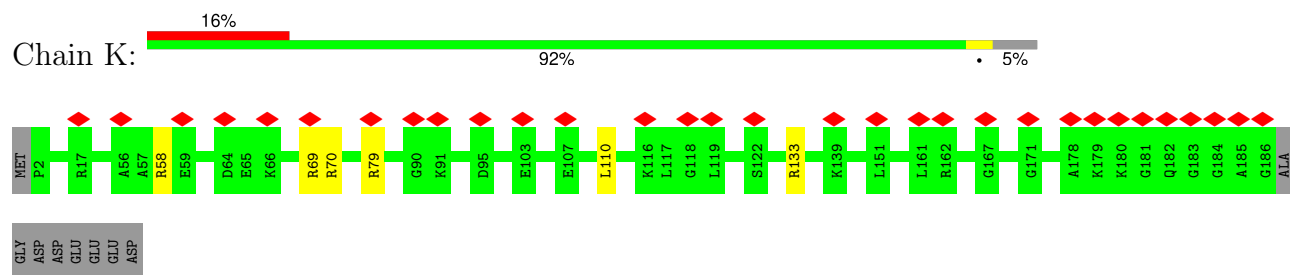
- Molecule 55: eS7



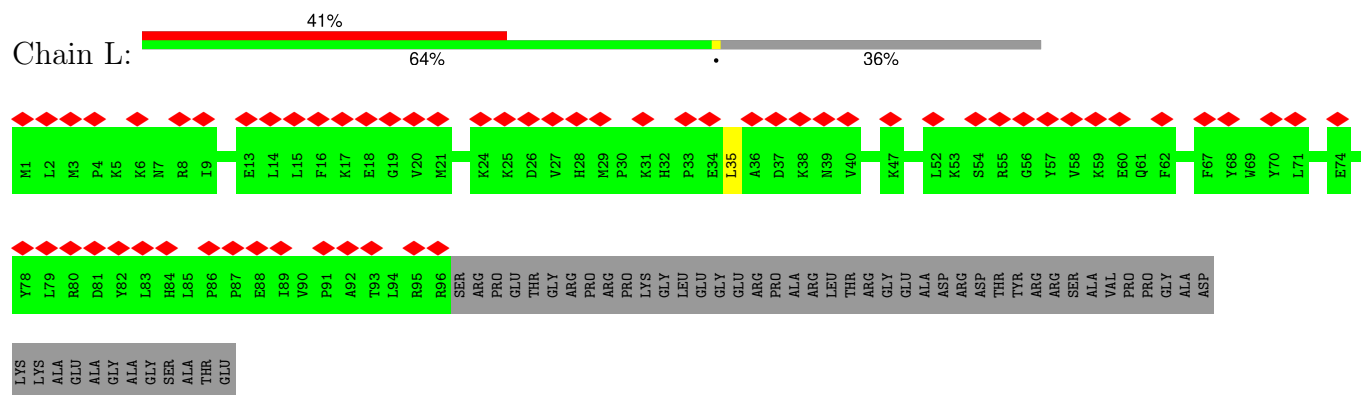
- Molecule 56: eS8



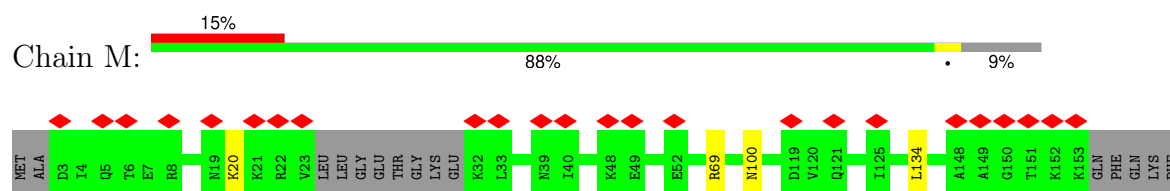
- Molecule 57: uS4



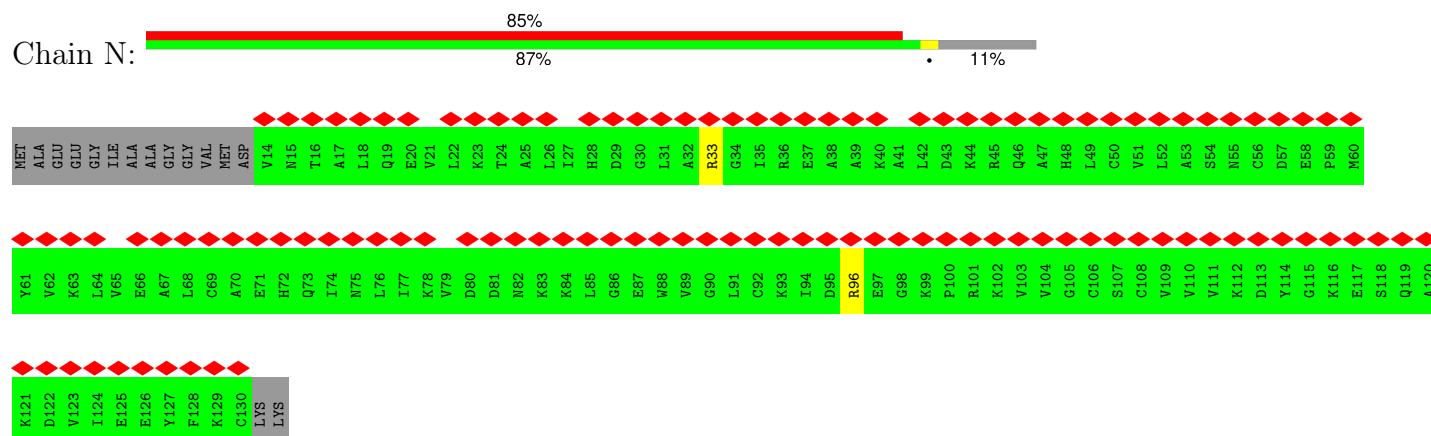
- Molecule 58: eS10



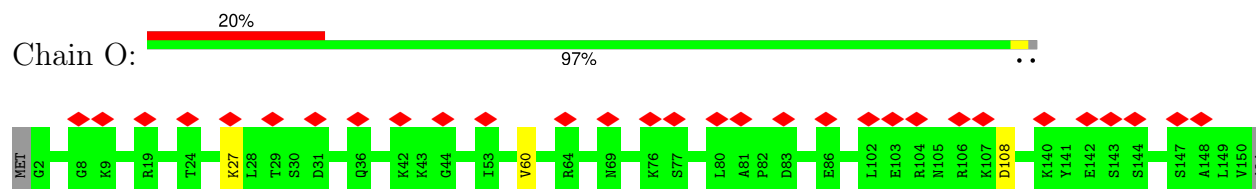
- Molecule 59: uS17



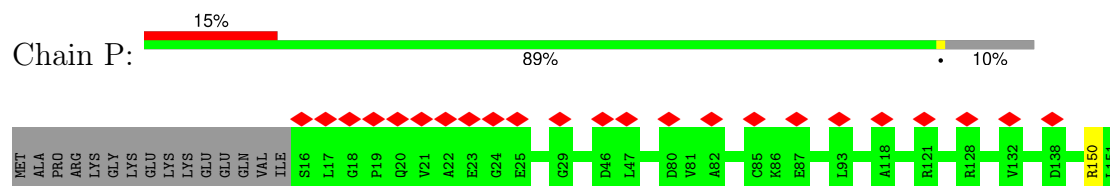
• Molecule 60: eS12



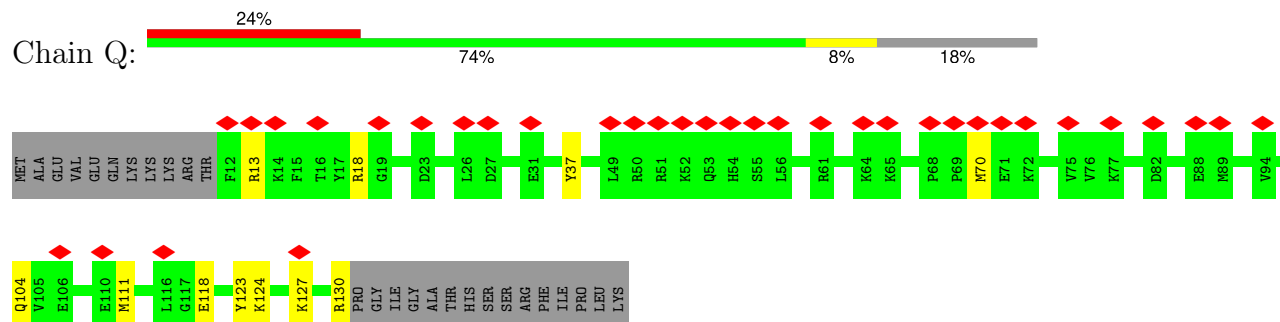
• Molecule 61: uS15



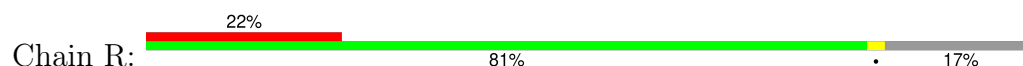
• Molecule 62: uS11

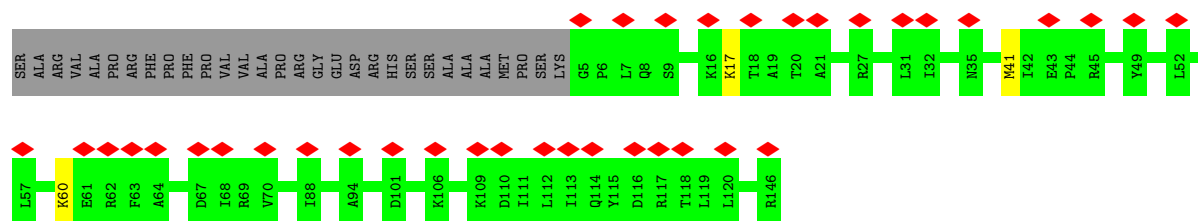


• Molecule 63: uS19

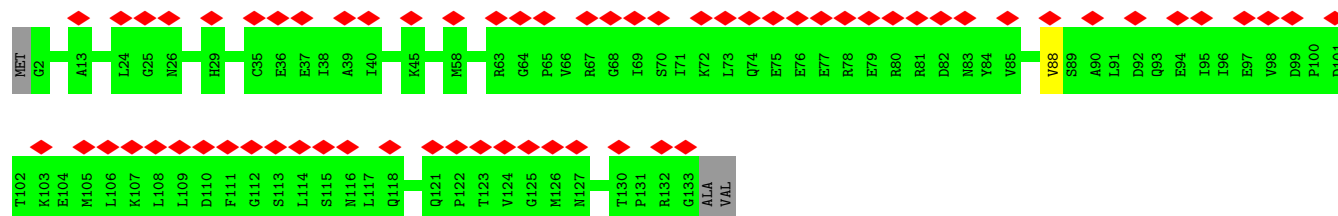


• Molecule 64: uS9

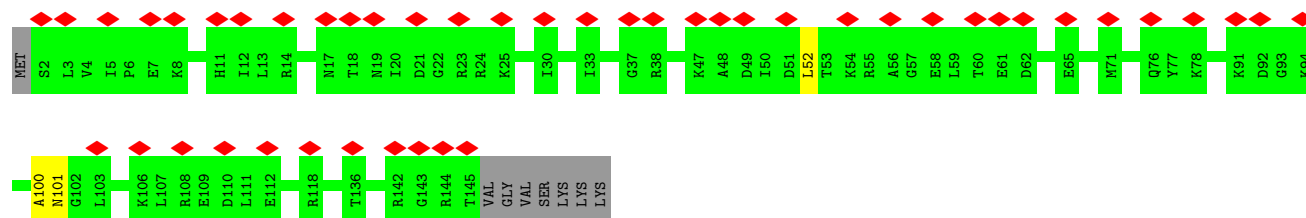




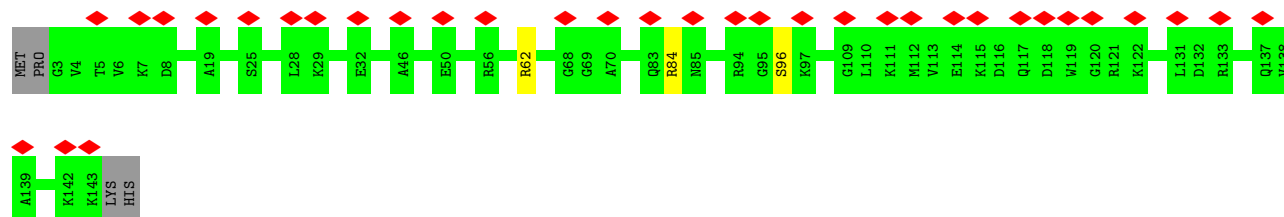
• Molecule 65: eS17



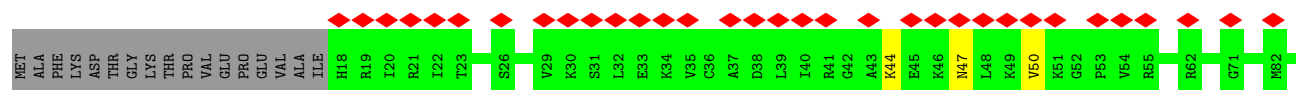
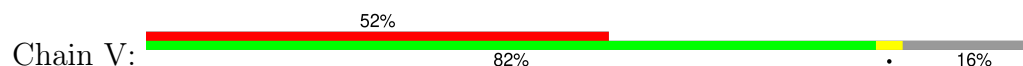
• Molecule 66: uS13

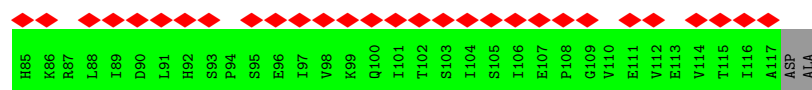


• Molecule 67: eS19

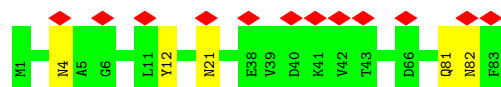


• Molecule 68: uS10

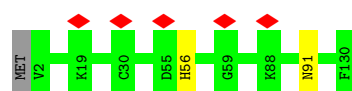




• Molecule 69: eS21



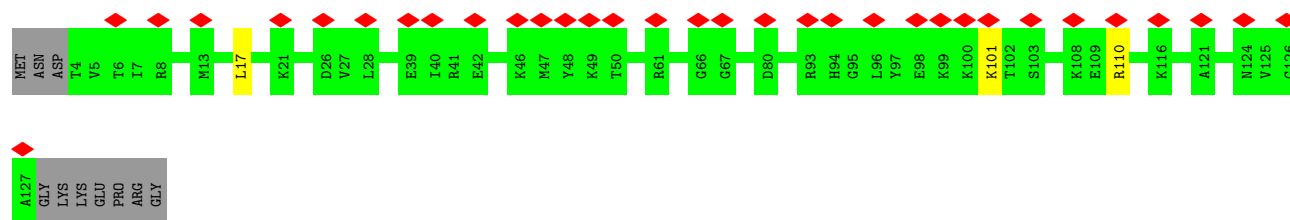
• Molecule 70: uS8



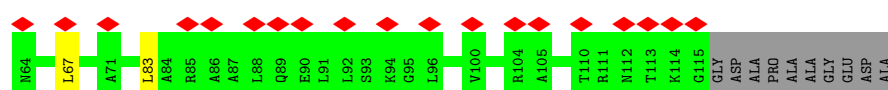
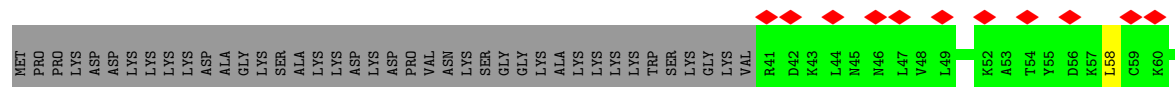
• Molecule 71: uS12



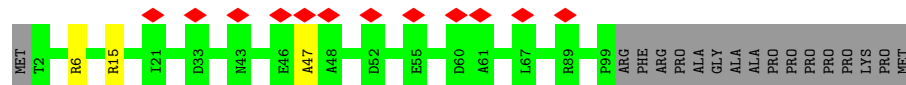
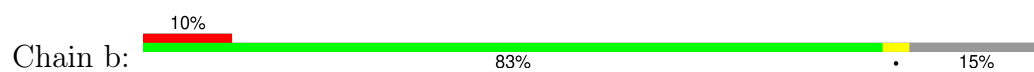
• Molecule 72: eS24



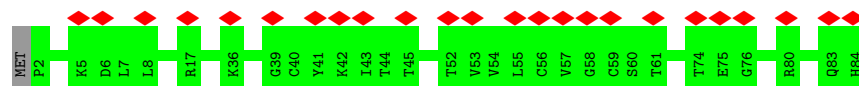
• Molecule 73: eS25



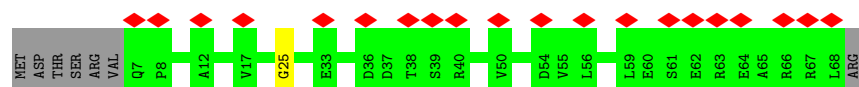
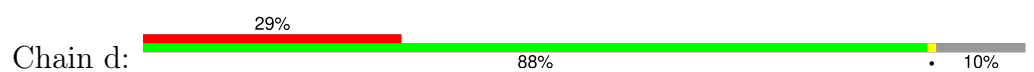
• Molecule 74: eS26



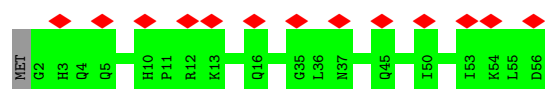
• Molecule 75: eS27



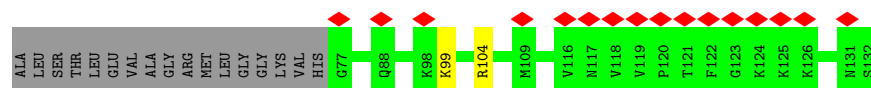
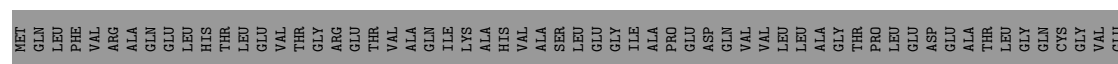
• Molecule 76: eS28



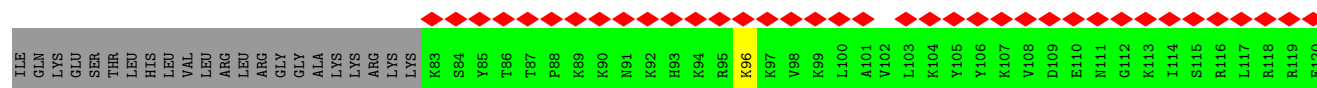
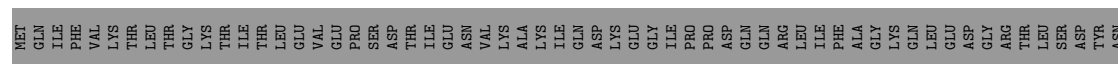
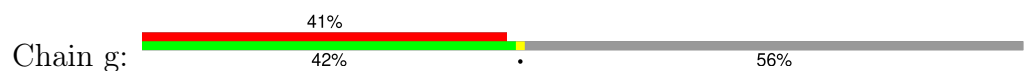
• Molecule 77: eS29



• Molecule 78: eS30

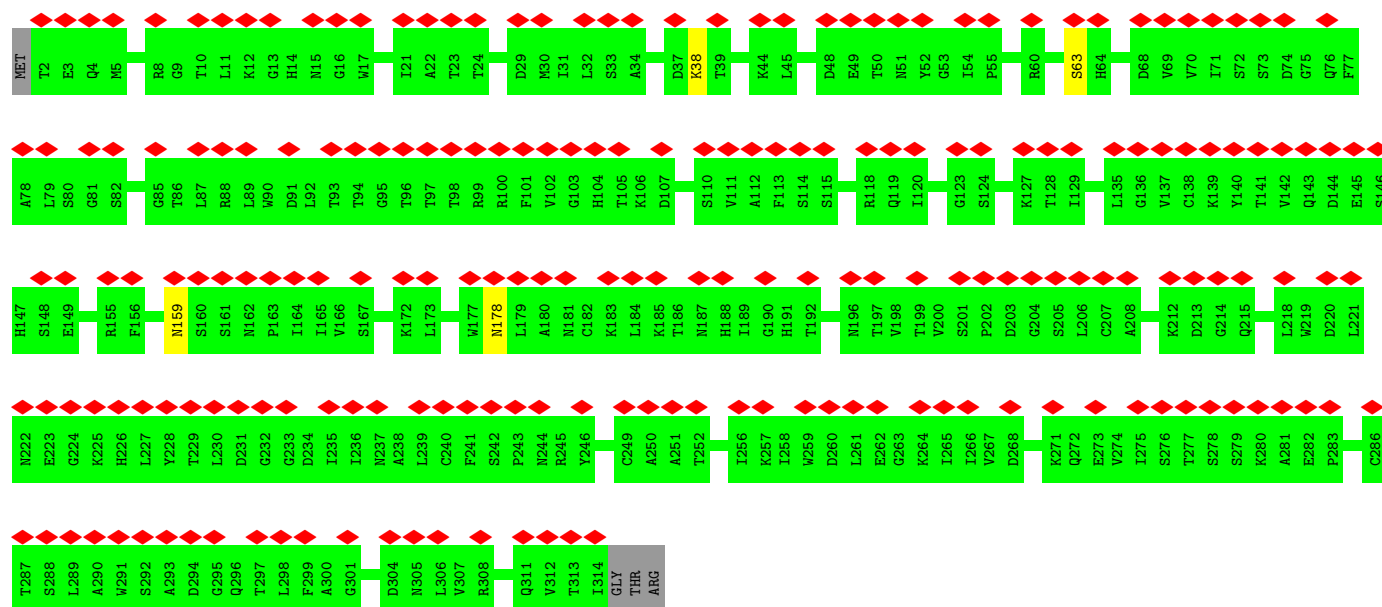


• Molecule 79: eS31

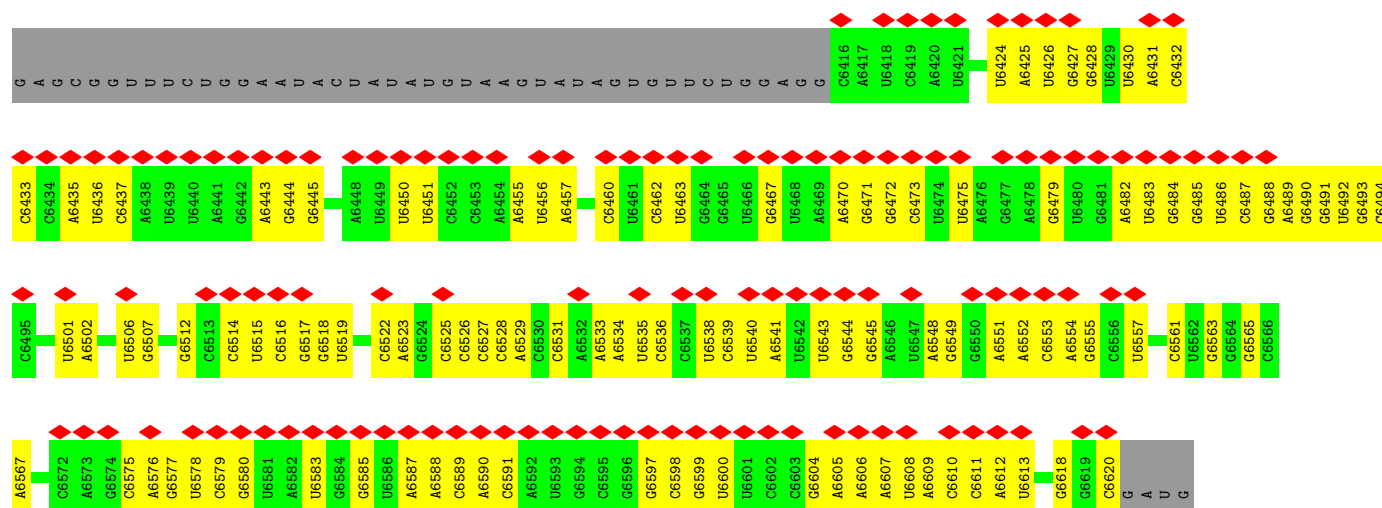




• Molecule 80: RACK1



• Molecule 81: IAPV-IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68697	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.09	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.283	Depositor
Minimum map value	-0.162	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	443.88, 443.88, 443.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.233, 1.233, 1.233	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	5	0.21	0/86215	0.69	11/134459 (0.0%)
2	7	0.19	0/2836	0.66	0/4421
3	8	0.21	0/3581	0.69	0/5577
4	AA	0.66	0/1933	0.83	0/2592
5	AB	0.66	0/3240	0.80	0/4339
6	AC	0.66	0/2937	0.80	0/3946
7	AD	0.66	0/2437	0.78	0/3264
8	AE	0.67	0/1762	0.81	0/2362
9	AF	0.66	0/1911	0.79	0/2549
10	AG	0.67	0/1850	0.81	0/2491
11	AH	0.69	0/1535	0.82	0/2063
12	AI	0.66	0/1702	0.79	0/2272
13	AJ	0.68	0/1385	0.81	0/1852
14	AL	0.66	0/1658	0.83	0/2219
15	AM	0.67	0/1158	0.80	0/1547
16	AN	0.65	0/1746	0.82	0/2338
17	AO	0.66	0/1663	0.80	0/2223
18	AP	0.66	0/1268	0.79	0/1700
19	AQ	0.65	0/1557	0.81	0/2086
20	AR	0.66	0/1519	0.79	0/2006
21	AS	0.65	0/1498	0.80	0/2012
22	AT	0.65	0/1326	0.80	0/1770
23	AU	0.68	0/832	0.79	0/1116
24	AV	0.69	0/983	0.82	0/1319
25	AW	0.66	0/541	0.77	0/720
26	AX	0.65	0/984	0.76	0/1323
27	AY	0.67	0/1132	0.81	0/1504
28	AZ	0.66	0/1130	0.82	0/1507
29	Aa	0.66	0/1191	0.80	0/1590
30	Ab	0.67	0/861	0.83	0/1138
31	Ac	0.69	0/771	0.79	0/1034
32	Ad	0.66	0/903	0.82	0/1216
33	Ae	0.66	0/1071	0.80	0/1429
34	Af	0.65	0/895	0.82	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ag	0.68	0/916	0.85	0/1220
36	Ah	0.67	0/1021	0.81	0/1348
37	Ai	0.68	0/841	0.82	0/1112
38	Aj	0.66	0/720	0.85	0/952
39	Ak	0.66	0/575	0.79	0/759
40	Al	0.64	0/459	0.81	0/608
41	Am	0.66	0/435	0.83	0/575
42	An	0.63	0/240	0.88	0/305
43	Ao	0.66	0/864	0.81	0/1140
44	Ap	0.69	0/718	0.81	0/953
45	Ar	0.68	0/1010	0.83	0/1354
46	AK	0.69	0/1733	0.81	0/2324
47	2	0.21	0/40509	0.69	7/63128 (0.0%)
48	B	0.67	0/1744	0.78	0/2371
49	C	0.68	0/1756	0.80	0/2350
50	D	0.68	0/1748	0.79	0/2362
51	E	0.69	0/1796	0.80	0/2417
52	F	0.67	0/2115	0.79	0/2843
53	G	0.69	0/1492	0.79	0/2005
54	H	0.68	0/1946	0.84	0/2590
55	I	0.69	0/1510	0.77	0/2022
56	J	0.67	0/1715	0.80	0/2287
57	K	0.68	0/1550	0.82	0/2069
58	L	0.66	0/834	0.77	0/1125
59	M	0.67	0/1195	0.81	0/1597
60	N	0.71	0/918	0.79	0/1233
61	O	0.68	0/1226	0.79	0/1649
62	P	0.69	0/1029	0.84	0/1380
63	Q	0.67	0/1009	0.81	0/1346
64	R	0.69	0/1146	0.83	0/1534
65	S	0.69	0/1082	0.78	0/1452
66	T	0.68	0/1208	0.82	0/1618
67	U	0.69	0/1115	0.82	0/1493
68	V	0.69	0/805	0.80	0/1081
69	W	0.71	0/638	0.82	0/855
70	X	0.68	0/1051	0.80	0/1406
71	Y	0.68	0/1116	0.83	0/1490
72	Z	0.68	0/1028	0.81	0/1366
73	a	0.69	0/604	0.79	0/810
74	b	0.68	0/791	0.81	0/1062
75	c	0.68	0/665	0.78	0/891
76	d	0.70	0/490	0.81	0/656
77	e	0.68	0/470	0.76	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	f	0.69	0/451	0.83	0/592
79	g	0.68	0/567	0.83	0/753
80	h	0.69	0/2493	0.80	0/3394
81	1	0.24	0/4881	0.73	1/7604 (0.0%)
All	All	0.46	0/232236	0.73	19/341286 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	AB	0	3
7	AD	0	1
8	AE	0	1
14	AL	0	1
18	AP	0	1
34	Af	0	2
46	AK	0	3
51	E	0	1
65	S	0	1
71	Y	0	1
All	All	0	15

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	928	A	C2'-C3'-O3'	6.33	123.82	113.70
1	5	1455	G	C2'-C3'-O3'	5.93	123.19	113.70
1	5	4884	G	C2'-C3'-O3'	5.90	123.14	113.70
1	5	4180	G	C2'-C3'-O3'	5.77	122.92	113.70
47	2	1137	U	C2'-C3'-O3'	5.46	122.44	113.70
1	5	2694	G	C2'-C3'-O3'	-5.46	97.49	109.50
47	2	24	C	C2'-C3'-O3'	5.43	122.39	113.70
1	5	1412	G	C2'-C3'-O3'	-5.41	97.61	109.50
47	2	1060	A	N9-C1'-C2'	5.32	120.91	114.00
81	1	6607	A	N9-C1'-C2'	5.31	120.90	114.00
1	5	2695	A	C2'-C3'-O3'	5.17	121.98	113.70
47	2	110	U	C2'-C3'-O3'	5.17	121.97	113.70
47	2	1664	A	C4'-C3'-O3'	5.16	123.33	113.00
47	2	1685	U	C2'-C3'-O3'	5.15	121.93	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	504	G	C2'-C3'-O3'	5.12	121.90	113.70
1	5	1211	G	C2'-C3'-O3'	5.09	121.85	113.70
47	2	688	U	C2'-C3'-O3'	5.09	121.84	113.70
1	5	3625	G	C2'-C3'-O3'	5.06	121.79	113.70
1	5	4448	G	C4'-C3'-O3'	5.04	123.08	113.00

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	AB	16	PHE	Peptide
5	AB	258	HIS	Peptide
5	AB	351	LEU	Peptide
7	AD	36	LEU	Peptide
8	AE	188	PRO	Peptide
46	AK	196	LYS	Peptide
46	AK	197	ASN	Peptide
46	AK	27	LYS	Peptide
14	AL	46	ILE	Peptide
18	AP	126	ARG	Peptide
34	Af	105	LEU	Peptide
34	Af	106	TYR	Peptide
51	E	142	LEU	Peptide
65	S	88	VAL	Peptide
71	Y	61	GLN	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AA	246/257 (96%)	223 (91%)	20 (8%)	3 (1%)	11	38
5	AB	392/403 (97%)	357 (91%)	33 (8%)	2 (0%)	25	58
6	AC	360/392 (92%)	334 (93%)	22 (6%)	4 (1%)	12	39
7	AD	291/297 (98%)	275 (94%)	15 (5%)	1 (0%)	37	68
8	AE	208/291 (72%)	188 (90%)	20 (10%)	0	100	100
9	AF	223/249 (90%)	209 (94%)	13 (6%)	1 (0%)	30	63
10	AG	221/242 (91%)	206 (93%)	14 (6%)	1 (0%)	25	58
11	AH	188/192 (98%)	175 (93%)	12 (6%)	1 (0%)	25	58
12	AI	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
13	AJ	168/178 (94%)	158 (94%)	8 (5%)	2 (1%)	11	38
14	AL	199/211 (94%)	190 (96%)	7 (4%)	2 (1%)	13	42
15	AM	136/198 (69%)	128 (94%)	7 (5%)	1 (1%)	19	51
16	AN	201/204 (98%)	183 (91%)	16 (8%)	2 (1%)	13	42
17	AO	197/203 (97%)	188 (95%)	9 (5%)	0	100	100
18	AP	151/184 (82%)	146 (97%)	5 (3%)	0	100	100
19	AQ	185/188 (98%)	172 (93%)	13 (7%)	0	100	100
20	AR	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
21	AS	174/176 (99%)	158 (91%)	14 (8%)	2 (1%)	12	39
22	AT	157/160 (98%)	144 (92%)	11 (7%)	2 (1%)	10	36
23	AU	97/128 (76%)	87 (90%)	10 (10%)	0	100	100
24	AV	127/140 (91%)	115 (91%)	11 (9%)	1 (1%)	16	48
25	AW	61/157 (39%)	59 (97%)	2 (3%)	0	100	100
26	AX	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
27	AY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	AZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
29	Aa	145/148 (98%)	129 (89%)	15 (10%)	1 (1%)	19	51
30	Ab	100/226 (44%)	92 (92%)	6 (6%)	2 (2%)	6	26
31	Ac	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
32	Ad	105/125 (84%)	98 (93%)	6 (6%)	1 (1%)	13	42
33	Ae	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
34	Af	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	6	27
35	Ag	112/126 (89%)	109 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Ah	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
37	Ai	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
38	Aj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	11	38
39	Ak	67/70 (96%)	61 (91%)	3 (4%)	3 (4%)	2	12
40	Al	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
41	Am	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
44	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Ar	122/137 (89%)	113 (93%)	9 (7%)	0	100	100
46	AK	210/217 (97%)	168 (80%)	36 (17%)	6 (3%)	3	20
48	B	215/295 (73%)	198 (92%)	17 (8%)	0	100	100
49	C	211/264 (80%)	193 (92%)	16 (8%)	2 (1%)	14	45
50	D	219/255 (86%)	204 (93%)	14 (6%)	1 (0%)	25	58
51	E	226/281 (80%)	203 (90%)	21 (9%)	2 (1%)	14	45
52	F	260/263 (99%)	233 (90%)	26 (10%)	1 (0%)	30	63
53	G	181/204 (89%)	164 (91%)	13 (7%)	4 (2%)	5	24
54	H	235/249 (94%)	213 (91%)	21 (9%)	1 (0%)	30	63
55	I	181/194 (93%)	166 (92%)	14 (8%)	1 (1%)	22	53
56	J	204/207 (99%)	185 (91%)	16 (8%)	3 (2%)	8	33
57	K	183/194 (94%)	167 (91%)	15 (8%)	1 (0%)	25	58
58	L	94/149 (63%)	84 (89%)	10 (11%)	0	100	100
59	M	139/158 (88%)	125 (90%)	13 (9%)	1 (1%)	19	51
60	N	115/132 (87%)	96 (84%)	19 (16%)	0	100	100
61	O	147/151 (97%)	134 (91%)	11 (8%)	2 (1%)	9	34
62	P	134/151 (89%)	123 (92%)	11 (8%)	0	100	100
63	Q	117/145 (81%)	98 (84%)	16 (14%)	3 (3%)	4	21
64	R	140/172 (81%)	126 (90%)	14 (10%)	0	100	100
65	S	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
66	T	142/152 (93%)	127 (89%)	14 (10%)	1 (1%)	19	51
67	U	139/145 (96%)	126 (91%)	12 (9%)	1 (1%)	19	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	V	98/119 (82%)	89 (91%)	9 (9%)	0	100	100
69	W	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
70	X	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	48
71	Y	139/143 (97%)	126 (91%)	10 (7%)	3 (2%)	5	24
72	Z	122/134 (91%)	110 (90%)	12 (10%)	0	100	100
73	a	73/125 (58%)	65 (89%)	8 (11%)	0	100	100
74	b	96/115 (84%)	82 (85%)	13 (14%)	1 (1%)	13	42
75	c	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
76	d	60/69 (87%)	57 (95%)	2 (3%)	1 (2%)	7	30
77	e	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
78	f	54/133 (41%)	49 (91%)	5 (9%)	0	100	100
79	g	66/156 (42%)	54 (82%)	11 (17%)	1 (2%)	8	33
80	h	311/317 (98%)	262 (84%)	49 (16%)	0	100	100
All	All	11321/12917 (88%)	10354 (92%)	895 (8%)	72 (1%)	24	53

All (72) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	AT	80	VAL
46	AK	140	HIS
6	AC	126	SER
9	AF	196	VAL
14	AL	6	ASN
22	AT	44	GLY
24	AV	17	SER
30	Ab	25	ARG
46	AK	10	LEU
49	C	76	ASN
51	E	143	ARG
52	F	79	ASP
53	G	51	HIS
55	I	54	GLY
56	J	94	LYS
63	Q	18	ARG
63	Q	70	MET
66	T	100	ALA
67	U	84	ARG

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Mol	Chain	Res	Type
70	X	56	HIS
71	Y	86	PRO
79	g	96	LYS
6	AC	148	PRO
13	AJ	146	ARG
38	Aj	38	GLY
46	AK	115	SER
71	Y	63	ASN
4	AA	77	ILE
4	AA	234	LYS
5	AB	4	ARG
6	AC	87	SER
10	AG	85	PHE
11	AH	108	ASN
13	AJ	91	GLU
29	Aa	14	HIS
32	Ad	58	GLY
39	Ak	64	LEU
39	Ak	65	ALA
39	Ak	68	GLU
46	AK	103	LEU
46	AK	154	THR
49	C	100	PHE
50	D	134	ASN
53	G	20	PHE
54	H	76	LEU
56	J	157	LYS
63	Q	104	GLN
71	Y	60	LYS
74	b	47	ALA
4	AA	179	ILE
14	AL	63	THR
15	AM	7	VAL
21	AS	155	PRO
30	Ab	29	TYR
46	AK	58	THR
53	G	21	GLY
56	J	123	ARG
59	M	100	ASN
61	O	108	ASP
5	AB	37	PRO
7	AD	44	TYR

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Mol	Chain	Res	Type
53	G	79	HIS
57	K	133	ARG
76	d	25	GLY
6	AC	77	PRO
34	Af	17	GLY
51	E	112	GLY
16	AN	84	PRO
16	AN	89	VAL
21	AS	165	PRO
34	Af	106	TYR
61	O	60	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	
4	AA	189/199 (95%)	169 (89%)	20 (11%)	5	21
5	AB	342/348 (98%)	330 (96%)	12 (4%)	31	61
6	AC	302/323 (94%)	284 (94%)	18 (6%)	16	44
7	AD	247/250 (99%)	244 (99%)	3 (1%)	67	83
8	AE	190/251 (76%)	183 (96%)	7 (4%)	29	59
9	AF	196/218 (90%)	191 (97%)	5 (3%)	41	68
10	AG	194/208 (93%)	189 (97%)	5 (3%)	41	68
11	AH	169/171 (99%)	162 (96%)	7 (4%)	26	57
12	AI	175/181 (97%)	172 (98%)	3 (2%)	56	78
13	AJ	143/149 (96%)	142 (99%)	1 (1%)	81	90
14	AL	167/176 (95%)	161 (96%)	6 (4%)	30	60
15	AM	117/151 (78%)	116 (99%)	1 (1%)	75	88
16	AN	171/172 (99%)	166 (97%)	5 (3%)	37	65
17	AO	171/173 (99%)	166 (97%)	5 (3%)	37	65
18	AP	134/163 (82%)	130 (97%)	4 (3%)	36	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AQ	166/167 (99%)	148 (89%)	18 (11%)	5	21
20	AR	159/175 (91%)	146 (92%)	13 (8%)	9	33
21	AS	155/155 (100%)	142 (92%)	13 (8%)	9	32
22	AT	139/140 (99%)	135 (97%)	4 (3%)	37	65
23	AU	91/116 (78%)	88 (97%)	3 (3%)	33	62
24	AV	100/107 (94%)	95 (95%)	5 (5%)	20	50
25	AW	55/126 (44%)	55 (100%)	0	100	100
26	AX	106/134 (79%)	105 (99%)	1 (1%)	75	88
27	AY	124/135 (92%)	119 (96%)	5 (4%)	27	58
28	AZ	117/118 (99%)	115 (98%)	2 (2%)	56	78
29	Aa	119/120 (99%)	116 (98%)	3 (2%)	42	69
30	Ab	84/172 (49%)	82 (98%)	2 (2%)	44	70
31	Ac	84/98 (86%)	82 (98%)	2 (2%)	44	70
32	Ad	98/110 (89%)	96 (98%)	2 (2%)	50	74
33	Ae	114/121 (94%)	111 (97%)	3 (3%)	41	68
34	Af	88/89 (99%)	82 (93%)	6 (7%)	13	40
35	Ag	98/106 (92%)	97 (99%)	1 (1%)	73	86
36	Ah	109/110 (99%)	106 (97%)	3 (3%)	38	66
37	Ai	86/89 (97%)	83 (96%)	3 (4%)	31	61
38	Aj	73/80 (91%)	71 (97%)	2 (3%)	40	67
39	Ak	64/65 (98%)	61 (95%)	3 (5%)	22	52
40	Al	47/48 (98%)	47 (100%)	0	100	100
41	Am	48/48 (100%)	46 (96%)	2 (4%)	25	56
42	An	24/24 (100%)	23 (96%)	1 (4%)	25	56
43	Ao	92/94 (98%)	89 (97%)	3 (3%)	33	62
44	Ap	74/75 (99%)	72 (97%)	2 (3%)	40	67
45	Ar	108/121 (89%)	106 (98%)	2 (2%)	52	75
46	AK	190/196 (97%)	179 (94%)	11 (6%)	17	45
48	B	180/245 (74%)	178 (99%)	2 (1%)	70	84
49	C	194/231 (84%)	189 (97%)	5 (3%)	41	68
50	D	186/205 (91%)	181 (97%)	5 (3%)	40	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	E	190/232 (82%)	184 (97%)	6 (3%)	34	63
52	F	223/225 (99%)	216 (97%)	7 (3%)	35	63
53	G	158/170 (93%)	157 (99%)	1 (1%)	84	91
54	H	207/218 (95%)	206 (100%)	1 (0%)	86	92
55	I	165/174 (95%)	163 (99%)	2 (1%)	67	83
56	J	178/179 (99%)	177 (99%)	1 (1%)	84	91
57	K	161/168 (96%)	156 (97%)	5 (3%)	35	63
58	L	87/125 (70%)	86 (99%)	1 (1%)	70	84
59	M	130/142 (92%)	127 (98%)	3 (2%)	45	70
60	N	99/108 (92%)	97 (98%)	2 (2%)	50	74
61	O	130/131 (99%)	129 (99%)	1 (1%)	79	89
62	P	106/119 (89%)	105 (99%)	1 (1%)	75	88
63	Q	108/130 (83%)	100 (93%)	8 (7%)	11	36
64	R	117/140 (84%)	114 (97%)	3 (3%)	41	68
65	S	119/121 (98%)	119 (100%)	0	100	100
66	T	125/132 (95%)	123 (98%)	2 (2%)	58	79
67	U	111/116 (96%)	109 (98%)	2 (2%)	54	76
68	V	92/107 (86%)	89 (97%)	3 (3%)	33	62
69	W	68/68 (100%)	63 (93%)	5 (7%)	11	36
70	X	112/113 (99%)	111 (99%)	1 (1%)	75	88
71	Y	113/114 (99%)	112 (99%)	1 (1%)	75	88
72	Z	107/115 (93%)	104 (97%)	3 (3%)	38	66
73	a	66/103 (64%)	63 (96%)	3 (4%)	23	53
74	b	86/99 (87%)	84 (98%)	2 (2%)	45	70
75	c	75/76 (99%)	75 (100%)	0	100	100
76	d	55/62 (89%)	55 (100%)	0	100	100
77	e	48/49 (98%)	48 (100%)	0	100	100
78	f	46/106 (43%)	44 (96%)	2 (4%)	25	55
79	g	61/140 (44%)	60 (98%)	1 (2%)	58	79
80	h	272/275 (99%)	268 (98%)	4 (2%)	60	80
All	All	9894/11010 (90%)	9594 (97%)	300 (3%)	37	64

All (300) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	AA	3	ARG
4	AA	24	LYS
4	AA	29	LEU
4	AA	64	ARG
4	AA	68	ARG
4	AA	80	GLU
4	AA	96	LEU
4	AA	101	VAL
4	AA	125	LYS
4	AA	128	ARG
4	AA	140	ASN
4	AA	155	LYS
4	AA	156	LYS
4	AA	159	SER
4	AA	165	VAL
4	AA	193	ARG
4	AA	194	ASN
4	AA	200	ARG
4	AA	207	VAL
4	AA	242	ARG
5	AB	10	ARG
5	AB	21	ARG
5	AB	24	ARG
5	AB	126	LYS
5	AB	254	ILE
5	AB	261	ARG
5	AB	262	VAL
5	AB	298	LEU
5	AB	309	LEU
5	AB	347	LEU
5	AB	351	LEU
5	AB	352	LEU
6	AC	38	ASN
6	AC	95	MET
6	AC	121	ARG
6	AC	143	ARG
6	AC	150	LEU
6	AC	188	ARG
6	AC	195	LYS
6	AC	246	VAL
6	AC	268	ARG
6	AC	286	ASN

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Mol	Chain	Res	Type
6	AC	302	LEU
6	AC	317	ASN
6	AC	333	LYS
6	AC	341	LEU
6	AC	350	ARG
6	AC	352	GLU
6	AC	353	ARG
6	AC	358	LEU
7	AD	56	THR
7	AD	111	ASN
7	AD	118	ILE
8	AE	52	LEU
8	AE	58	ARG
8	AE	178	VAL
8	AE	215	LEU
8	AE	261	LEU
8	AE	289	LEU
8	AE	291	PHE
9	AF	76	LYS
9	AF	88	LEU
9	AF	134	ILE
9	AF	205	ASN
9	AF	244	ARG
10	AG	159	THR
10	AG	242	ARG
10	AG	249	ARG
10	AG	282	ARG
10	AG	293	ASN
11	AH	1	MET
11	AH	15	ASN
11	AH	20	LEU
11	AH	23	ARG
11	AH	42	ASN
11	AH	84	VAL
11	AH	102	ASN
12	AI	3	ARG
12	AI	36	LEU
12	AI	100	ASN
13	AJ	16	ARG
14	AL	63	THR
14	AL	67	HIS
14	AL	130	LYS

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Mol	Chain	Res	Type
14	AL	159	ASN
14	AL	162	LYS
14	AL	194	ILE
15	AM	119	ARG
16	AN	50	ARG
16	AN	64	ILE
16	AN	80	THR
16	AN	89	VAL
16	AN	151	ILE
17	AO	36	VAL
17	AO	108	ILE
17	AO	113	ASP
17	AO	117	ARG
17	AO	194	GLU
18	AP	24	VAL
18	AP	127	ARG
18	AP	128	ARG
18	AP	147	GLU
19	AQ	6	LEU
19	AQ	14	TRP
19	AQ	23	MET
19	AQ	37	ARG
19	AQ	38	HIS
19	AQ	42	THR
19	AQ	57	LYS
19	AQ	66	VAL
19	AQ	72	LEU
19	AQ	78	LYS
19	AQ	91	ARG
19	AQ	97	LYS
19	AQ	115	LYS
19	AQ	124	HIS
19	AQ	138	LEU
19	AQ	150	GLN
19	AQ	158	THR
19	AQ	172	ARG
20	AR	36	ASN
20	AR	89	MET
20	AR	94	LYS
20	AR	151	ARG
20	AR	153	LYS
20	AR	162	ARG

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Mol	Chain	Res	Type
20	AR	163	ARG
20	AR	168	GLU
20	AR	171	LYS
20	AR	173	ARG
20	AR	174	GLU
20	AR	178	GLN
20	AR	181	LYS
21	AS	15	ARG
21	AS	17	LEU
21	AS	19	THR
21	AS	20	SER
21	AS	49	LEU
21	AS	76	LYS
21	AS	77	ASN
21	AS	84	TYR
21	AS	120	ARG
21	AS	132	MET
21	AS	136	ARG
21	AS	149	ARG
21	AS	159	LEU
22	AT	49	GLN
22	AT	80	VAL
22	AT	136	ARG
22	AT	146	LYS
23	AU	32	ARG
23	AU	36	GLU
23	AU	97	HIS
24	AV	15	ARG
24	AV	18	LEU
24	AV	25	VAL
24	AV	48	ARG
24	AV	60	MET
26	AX	95	THR
27	AY	2	LYS
27	AY	8	THR
27	AY	17	ARG
27	AY	79	VAL
27	AY	104	VAL
28	AZ	33	THR
28	AZ	42	LEU
29	Aa	4	ARG
29	Aa	44	ASN

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Mol	Chain	Res	Type
29	Aa	76	ASP
30	Ab	9	THR
30	Ab	60	ASN
31	Ac	90	ARG
31	Ac	91	VAL
32	Ad	18	ASN
32	Ad	31	LYS
33	Ae	48	ARG
33	Ae	78	LEU
33	Ae	89	LEU
34	Af	7	CYS
34	Af	16	ARG
34	Af	33	VAL
34	Af	80	ASN
34	Af	84	VAL
34	Af	101	ILE
35	Ag	15	THR
36	Ah	13	LYS
36	Ah	15	GLU
36	Ah	67	GLU
37	Ai	21	VAL
37	Ai	29	ARG
37	Ai	77	VAL
38	Aj	20	ARG
38	Aj	58	THR
39	Ak	3	GLN
39	Ak	48	MET
39	Ak	66	MET
41	Am	59	LEU
41	Am	96	ARG
42	An	13	LEU
43	Ao	9	ARG
43	Ao	33	LEU
43	Ao	82	MET
44	Ap	54	ILE
44	Ap	89	LEU
45	Ar	71	ARG
45	Ar	118	LEU
46	AK	8	ASP
46	AK	9	THR
46	AK	60	ARG
46	AK	92	LYS

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Mol	Chain	Res	Type
46	AK	137	LEU
46	AK	153	SER
46	AK	156	LYS
46	AK	159	MET
46	AK	171	HIS
46	AK	172	VAL
46	AK	173	LYS
48	B	50	ASN
48	B	82	THR
49	C	40	ASN
49	C	147	ASN
49	C	207	LEU
49	C	212	VAL
49	C	213	ARG
50	D	78	LEU
50	D	137	VAL
50	D	141	LEU
50	D	227	ARG
50	D	248	TYR
51	E	57	ASN
51	E	76	ARG
51	E	94	ARG
51	E	106	ARG
51	E	146	ARG
51	E	227	LYS
52	F	3	ARG
52	F	67	GLN
52	F	77	ARG
52	F	155	LYS
52	F	181	CYS
52	F	232	ASN
52	F	246	LEU
53	G	88	MET
54	H	63	MET
55	I	36	LEU
55	I	160	LYS
56	J	99	ASN
57	K	58	ARG
57	K	69	ARG
57	K	70	ARG
57	K	79	ARG
57	K	110	LEU

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Mol	Chain	Res	Type
58	L	35	LEU
59	M	20	LYS
59	M	69	ARG
59	M	134	LEU
60	N	33	ARG
60	N	96	ARG
61	O	27	LYS
62	P	150	ARG
63	Q	13	ARG
63	Q	37	TYR
63	Q	111	MET
63	Q	118	GLU
63	Q	123	TYR
63	Q	124	LYS
63	Q	127	LYS
63	Q	130	ARG
64	R	17	LYS
64	R	41	MET
64	R	60	LYS
66	T	52	LEU
66	T	101	ASN
67	U	62	ARG
67	U	96	SER
68	V	44	LYS
68	V	47	ASN
68	V	50	VAL
69	W	4	ASN
69	W	12	TYR
69	W	21	ASN
69	W	81	GLN
69	W	82	ASN
70	X	91	ASN
71	Y	7	LEU
72	Z	17	LEU
72	Z	101	LYS
72	Z	110	ARG
73	a	58	LEU
73	a	67	LEU
73	a	83	LEU
74	b	6	ARG
74	b	15	ARG
78	f	99	LYS

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Mol	Chain	Res	Type
78	f	104	ARG
79	g	138	ARG
80	h	38	LYS
80	h	63	SER
80	h	159	ASN
80	h	178	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (91) such sidechains are listed below:

Mol	Chain	Res	Type
4	AA	140	ASN
4	AA	162	ASN
5	AB	175	GLN
5	AB	271	GLN
6	AC	50	GLN
6	AC	119	GLN
6	AC	286	ASN
6	AC	310	HIS
6	AC	329	ASN
6	AC	343	GLN
7	AD	45	ASN
7	AD	111	ASN
7	AD	122	GLN
7	AD	229	ASN
10	AG	99	GLN
10	AG	293	ASN
11	AH	8	GLN
11	AH	42	ASN
11	AH	78	GLN
11	AH	79	ASN
11	AH	102	ASN
11	AH	116	ASN
12	AI	100	ASN
14	AL	19	GLN
14	AL	104	ASN
14	AL	188	ASN
15	AM	20	HIS
15	AM	83	ASN
16	AN	32	GLN
17	AO	5	GLN
17	AO	96	GLN
17	AO	184	ASN

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Mol	Chain	Res	Type
18	AP	80	GLN
19	AQ	38	HIS
19	AQ	150	GLN
21	AS	95	HIS
21	AS	146	HIS
22	AT	49	GLN
24	AV	27	ASN
26	AX	93	ASN
26	AX	111	GLN
26	AX	125	ASN
29	Aa	85	GLN
30	Ab	50	ASN
32	Ad	18	ASN
34	Af	24	HIS
38	Aj	13	ASN
43	Ao	45	GLN
44	Ap	33	GLN
46	AK	71	GLN
46	AK	94	ASN
46	AK	119	GLN
46	AK	171	HIS
48	B	128	GLN
48	B	180	GLN
49	C	40	ASN
49	C	147	ASN
52	F	232	ASN
53	G	31	ASN
53	G	114	ASN
54	H	65	GLN
54	H	202	ASN
55	I	44	ASN
55	I	165	ASN
56	J	84	ASN
56	J	99	ASN
56	J	168	GLN
59	M	18	GLN
59	M	100	ASN
61	O	36	GLN
63	Q	41	GLN
63	Q	53	GLN
64	R	48	GLN
64	R	86	GLN

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Mol	Chain	Res	Type
65	S	127	ASN
67	U	83	GLN
67	U	85	ASN
68	V	47	ASN
69	W	4	ASN
69	W	21	ASN
69	W	76	HIS
69	W	81	GLN
69	W	82	ASN
70	X	16	ASN
70	X	64	ASN
72	Z	15	ASN
75	c	26	GLN
80	h	119	GLN
80	h	159	ASN
80	h	162	ASN
80	h	178	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3569/3594 (99%)	960 (26%)	74 (2%)
2	7	118/119 (99%)	15 (12%)	1 (0%)
3	8	149/156 (95%)	36 (24%)	4 (2%)
47	2	1685/1869 (90%)	456 (27%)	31 (1%)
81	1	204/253 (80%)	110 (53%)	9 (4%)
All	All	5725/5991 (95%)	1577 (27%)	119 (2%)

All (1577) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	6	C
1	5	9	C
1	5	10	A
1	5	12	A
1	5	13	U
1	5	15	A
1	5	17	A
1	5	21	G
1	5	27	C
1	5	30	C

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Mol	Chain	Res	Type
1	5	35	U
1	5	39	A
1	5	42	A
1	5	48	G
1	5	49	U
1	5	56	A
1	5	58	G
1	5	59	A
1	5	64	A
1	5	65	A
1	5	66	A
1	5	72	C
1	5	73	A
1	5	84	A
1	5	91	G
1	5	104	G
1	5	108	A
1	5	109	G
1	5	110	C
1	5	112	C
1	5	116	G
1	5	117	C
1	5	118	C
1	5	119	G
1	5	120	A
1	5	121	A
1	5	126	C
1	5	131	C
1	5	133	C
1	5	135	G
1	5	142	G
1	5	143	C
1	5	144	G
1	5	146	G
1	5	150	U
1	5	157	U
1	5	158	A
1	5	159	C
1	5	168	C
1	5	169	A
1	5	170	C
1	5	171	U

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Mol	Chain	Res	Type
1	5	173	C
1	5	175	C
1	5	177	G
1	5	182	G
1	5	200	U
1	5	201	C
1	5	203	U
1	5	204	U
1	5	209	U
1	5	214	G
1	5	217	C
1	5	218	A
1	5	220	C
1	5	224	U
1	5	225	G
1	5	233	U
1	5	234	G
1	5	255	C
1	5	256	G
1	5	257	C
1	5	258	G
1	5	264	C
1	5	265	C
1	5	266	C
1	5	276	C
1	5	278	G
1	5	280	G
1	5	281	U
1	5	296	A
1	5	297	U
1	5	305	A
1	5	306	A
1	5	315	G
1	5	316	U
1	5	317	A
1	5	322	C
1	5	323	C
1	5	326	C
1	5	327	U
1	5	328	A
1	5	334	A
1	5	340	C

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Mol	Chain	Res	Type
1	5	344	A
1	5	345	C
1	5	349	A
1	5	350	C
1	5	353	A
1	5	357	U
1	5	361	C
1	5	362	A
1	5	363	A
1	5	370	U
1	5	386	A
1	5	387	G
1	5	410	A
1	5	412	G
1	5	413	G
1	5	418	A
1	5	431	G
1	5	432	U
1	5	444	G
1	5	449	C
1	5	450	G
1	5	452	A
1	5	453	G
1	5	454	U
1	5	455	C
1	5	457	G
1	5	464	G
1	5	467	U
1	5	468	U
1	5	469	C
1	5	473	C
1	5	481	G
1	5	482	G
1	5	484	U
1	5	485	C
1	5	492	U
1	5	498	C
1	5	499	G
1	5	500	G
1	5	505	G
1	5	506	C
1	5	507	G

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Mol	Chain	Res	Type
1	5	510	U
1	5	511	C
1	5	516	C
1	5	520	U
1	5	521	C
1	5	640	C
1	5	646	G
1	5	647	G
1	5	656	C
1	5	658	C
1	5	666	G
1	5	668	C
1	5	669	C
1	5	671	G
1	5	673	C
1	5	682	G
1	5	685	C
1	5	686	A
1	5	691	C
1	5	695	G
1	5	696	C
1	5	697	G
1	5	698	G
1	5	703	G
1	5	704	C
1	5	705	G
1	5	708	G
1	5	719	C
1	5	722	G
1	5	731	G
1	5	737	C
1	5	738	C
1	5	739	G
1	5	740	G
1	5	741	C
1	5	743	G
1	5	747	A
1	5	749	G
1	5	751	G
1	5	758	G
1	5	906	C
1	5	912	U

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Mol	Chain	Res	Type
1	5	913	U
1	5	915	C
1	5	916	A
1	5	917	G
1	5	920	C
1	5	922	C
1	5	923	C
1	5	925	G
1	5	928	A
1	5	929	G
1	5	931	A
1	5	932	G
1	5	933	C
1	5	934	A
1	5	935	G
1	5	936	C
1	5	943	A
1	5	945	U
1	5	946	C
1	5	956	A
1	5	959	G
1	5	960	A
1	5	961	G
1	5	966	A
1	5	967	C
1	5	968	C
1	5	969	U
1	5	970	G
1	5	971	U
1	5	974	C
1	5	978	G
1	5	979	C
1	5	984	U
1	5	986	C
1	5	987	C
1	5	1068	G
1	5	1069	G
1	5	1070	G
1	5	1073	G
1	5	1078	A
1	5	1079	C
1	5	1083	U

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Mol	Chain	Res	Type
1	5	1093	C
1	5	1094	G
1	5	1098	G
1	5	1099	C
1	5	1176	C
1	5	1187	G
1	5	1193	C
1	5	1194	G
1	5	1195	G
1	5	1198	G
1	5	1204	C
1	5	1209	U
1	5	1210	C
1	5	1211	G
1	5	1212	G
1	5	1215	C
1	5	1216	C
1	5	1234	G
1	5	1235	G
1	5	1236	C
1	5	1237	C
1	5	1238	A
1	5	1239	C
1	5	1245	C
1	5	1246	G
1	5	1252	C
1	5	1272	C
1	5	1273	G
1	5	1275	G
1	5	1276	C
1	5	1280	C
1	5	1284	G
1	5	1285	U
1	5	1287	G
1	5	1288	G
1	5	1289	C
1	5	1292	C
1	5	1294	A
1	5	1296	G
1	5	1301	C
1	5	1326	A
1	5	1337	A

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Mol	Chain	Res	Type
1	5	1354	A
1	5	1358	G
1	5	1359	G
1	5	1370	G
1	5	1371	A
1	5	1377	G
1	5	1379	C
1	5	1381	U
1	5	1387	A
1	5	1394	G
1	5	1397	A
1	5	1398	A
1	5	1400	G
1	5	1401	C
1	5	1410	C
1	5	1411	C
1	5	1412	G
1	5	1413	C
1	5	1415	G
1	5	1420	A
1	5	1421	G
1	5	1428	U
1	5	1430	C
1	5	1435	G
1	5	1436	C
1	5	1437	C
1	5	1438	U
1	5	1441	C
1	5	1442	C
1	5	1445	U
1	5	1446	C
1	5	1456	C
1	5	1457	G
1	5	1465	G
1	5	1476	C
1	5	1478	C
1	5	1482	G
1	5	1483	C
1	5	1497	A
1	5	1498	G
1	5	1502	G
1	5	1503	A

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Mol	Chain	Res	Type
1	5	1514	U
1	5	1515	A
1	5	1518	A
1	5	1523	A
1	5	1525	A
1	5	1534	A
1	5	1547	A
1	5	1563	A
1	5	1564	A
1	5	1566	C
1	5	1578	U
1	5	1586	G
1	5	1591	U
1	5	1596	U
1	5	1597	G
1	5	1601	A
1	5	1612	G
1	5	1613	A
1	5	1614	C
1	5	1624	G
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1634	A
1	5	1637	A
1	5	1640	C
1	5	1641	G
1	5	1642	A
1	5	1651	G
1	5	1654	G
1	5	1660	U
1	5	1661	C
1	5	1676	C
1	5	1677	U
1	5	1684	A
1	5	1694	C
1	5	1724	G
1	5	1732	C
1	5	1734	G
1	5	1741	G
1	5	1742	A
1	5	1750	G

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Mol	Chain	Res	Type
1	5	1754	U
1	5	1756	U
1	5	1757	U
1	5	1758	G
1	5	1761	G
1	5	1763	C
1	5	1764	G
1	5	1767	A
1	5	1768	C
1	5	1769	G
1	5	1772	C
1	5	1773	U
1	5	1775	A
1	5	1781	U
1	5	1787	A
1	5	1797	G
1	5	1804	A
1	5	1806	G
1	5	1809	C
1	5	1812	C
1	5	1818	G
1	5	1820	U
1	5	1821	G
1	5	1822	U
1	5	1828	C
1	5	1830	G
1	5	1831	G
1	5	1836	G
1	5	1837	A
1	5	1842	G
1	5	1855	G
1	5	1869	G
1	5	1881	C
1	5	1882	U
1	5	1890	G
1	5	1891	A
1	5	1893	C
1	5	1897	A
1	5	1910	G
1	5	1918	U
1	5	1920	C
1	5	1921	C

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Mol	Chain	Res	Type
1	5	1922	G
1	5	1930	U
1	5	1931	C
1	5	1932	A
1	5	1935	C
1	5	1940	G
1	5	1948	G
1	5	1952	G
1	5	1957	U
1	5	1958	A
1	5	1959	U
1	5	1961	G
1	5	1962	A
1	5	1968	G
1	5	1969	G
1	5	1972	G
1	5	1975	G
1	5	1976	G
1	5	1977	C
1	5	1983	A
1	5	1984	A
1	5	1986	U
1	5	1987	C
1	5	1990	A
1	5	1991	A
1	5	1992	U
1	5	1993	C
1	5	1994	C
1	5	1996	C
1	5	1998	A
1	5	2001	G
1	5	2002	A
1	5	2003	G
1	5	2004	U
1	5	2008	U
1	5	2011	C
1	5	2017	A
1	5	2018	C
1	5	2020	U
1	5	2021	G
1	5	2024	G
1	5	2025	A

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Mol	Chain	Res	Type
1	5	2026	A
1	5	2027	U
1	5	2031	C
1	5	2033	A
1	5	2046	G
1	5	2047	A
1	5	2048	U
1	5	2052	G
1	5	2055	G
1	5	2056	G
1	5	2062	C
1	5	2069	A
1	5	2070	U
1	5	2084	U
1	5	2085	G
1	5	2088	A
1	5	2089	G
1	5	2090	U
1	5	2092	G
1	5	2093	G
1	5	2096	G
1	5	2097	A
1	5	2098	G
1	5	2100	G
1	5	2101	A
1	5	2102	G
1	5	2104	A
1	5	2105	A
1	5	2106	G
1	5	2108	G
1	5	2112	G
1	5	2113	G
1	5	2259	G
1	5	2260	C
1	5	2263	A
1	5	2267	U
1	5	2268	A
1	5	2275	G
1	5	2280	G
1	5	2289	C
1	5	2297	G
1	5	2300	A

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Mol	Chain	Res	Type
1	5	2301	G
1	5	2306	G
1	5	2313	A
1	5	2314	G
1	5	2316	G
1	5	2331	G
1	5	2332	A
1	5	2333	G
1	5	2345	G
1	5	2346	C
1	5	2348	G
1	5	2351	C
1	5	2357	G
1	5	2395	A
1	5	2396	A
1	5	2402	G
1	5	2409	U
1	5	2417	A
1	5	2421	G
1	5	2422	C
1	5	2425	U
1	5	2428	A
1	5	2433	G
1	5	2441	C
1	5	2447	U
1	5	2450	G
1	5	2470	C
1	5	2475	G
1	5	2476	G
1	5	2477	A
1	5	2481	G
1	5	2482	C
1	5	2483	G
1	5	2485	U
1	5	2486	G
1	5	2488	C
1	5	2489	C
1	5	2490	U
1	5	2491	C
1	5	2492	C
1	5	2496	G
1	5	2498	C

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Mol	Chain	Res	Type
1	5	2500	U
1	5	2503	G
1	5	2504	C
1	5	2505	C
1	5	2506	G
1	5	2513	A
1	5	2514	G
1	5	2520	C
1	5	2529	A
1	5	2530	U
1	5	2537	A
1	5	2544	G
1	5	2546	G
1	5	2549	G
1	5	2553	A
1	5	2554	U
1	5	2555	G
1	5	2557	G
1	5	2562	G
1	5	2564	G
1	5	2565	A
1	5	2566	G
1	5	2569	G
1	5	2572	C
1	5	2575	U
1	5	2583	C
1	5	2586	G
1	5	2587	A
1	5	2588	C
1	5	2589	C
1	5	2601	A
1	5	2602	G
1	5	2618	G
1	5	2627	C
1	5	2630	U
1	5	2638	G
1	5	2643	G
1	5	2647	A
1	5	2653	C
1	5	2655	C
1	5	2656	U
1	5	2657	G

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Mol	Chain	Res	Type
1	5	2658	G
1	5	2659	A
1	5	2661	U
1	5	2662	G
1	5	2669	C
1	5	2670	C
1	5	2673	G
1	5	2675	G
1	5	2686	G
1	5	2687	U
1	5	2694	G
1	5	2695	A
1	5	2696	A
1	5	2701	U
1	5	2706	G
1	5	2707	U
1	5	2708	U
1	5	2709	C
1	5	2710	C
1	5	2711	G
1	5	2714	G
1	5	2716	C
1	5	2721	G
1	5	2724	G
1	5	2725	A
1	5	2732	G
1	5	2735	G
1	5	2740	U
1	5	2743	A
1	5	2744	A
1	5	2754	G
1	5	2755	A
1	5	2756	G
1	5	2760	G
1	5	2761	U
1	5	2763	U
1	5	2764	A
1	5	2769	U
1	5	2770	C
1	5	2787	A
1	5	2788	U
1	5	2789	A

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Mol	Chain	Res	Type
1	5	2790	U
1	5	2794	C
1	5	2796	G
1	5	2798	A
1	5	2806	A
1	5	2814	C
1	5	2815	A
1	5	2827	G
1	5	2830	G
1	5	2835	A
1	5	2839	U
1	5	2842	G
1	5	2845	A
1	5	2848	G
1	5	2849	A
1	5	2850	A
1	5	2855	G
1	5	2856	C
1	5	2867	C
1	5	2874	U
1	5	2875	C
1	5	2879	A
1	5	2884	G
1	5	2892	C
1	5	2898	G
1	5	2900	U
1	5	3598	C
1	5	3603	G
1	5	3604	A
1	5	3606	U
1	5	3615	G
1	5	3616	U
1	5	3618	C
1	5	3619	G
1	5	3625	G
1	5	3626	G
1	5	3630	A
1	5	3635	A
1	5	3643	A
1	5	3644	U
1	5	3646	A
1	5	3648	A

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Mol	Chain	Res	Type
1	5	3653	A
1	5	3662	A
1	5	3670	C
1	5	3673	C
1	5	3696	C
1	5	3710	G
1	5	3711	A
1	5	3712	A
1	5	3713	U
1	5	3725	G
1	5	3729	U
1	5	3740	G
1	5	3748	A
1	5	3753	G
1	5	3754	G
1	5	3755	G
1	5	3760	A
1	5	3761	C
1	5	3763	A
1	5	3777	G
1	5	3778	U
1	5	3780	G
1	5	3784	A
1	5	3799	A
1	5	3802	U
1	5	3809	G
1	5	3810	C
1	5	3811	G
1	5	3812	C
1	5	3814	U
1	5	3817	A
1	5	3819	G
1	5	3824	A
1	5	3838	U
1	5	3839	G
1	5	3840	U
1	5	3877	A
1	5	3878	C
1	5	3879	G
1	5	3887	C
1	5	3889	G
1	5	3897	G

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Mol	Chain	Res	Type
1	5	3898	G
1	5	3901	A
1	5	3905	A
1	5	3906	A
1	5	3907	G
1	5	3908	A
1	5	3915	U
1	5	3916	G
1	5	3917	A
1	5	3922	G
1	5	3938	G
1	5	3939	G
1	5	3949	A
1	5	3951	G
1	5	3953	G
1	5	3954	A
1	5	3956	G
1	5	3957	U
1	5	3958	G
1	5	3964	U
1	5	3965	A
1	5	3966	A
1	5	3968	U
1	5	3969	G
1	5	3970	G
1	5	3972	A
1	5	3973	G
1	5	3974	G
1	5	3975	C
1	5	4046	A
1	5	4047	A
1	5	4049	U
1	5	4050	A
1	5	4053	A
1	5	4054	C
1	5	4055	U
1	5	4058	U
1	5	4064	C
1	5	4065	G
1	5	4072	C
1	5	4074	C
1	5	4076	G

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Mol	Chain	Res	Type
1	5	4084	G
1	5	4085	A
1	5	4086	G
1	5	4087	G
1	5	4088	C
1	5	4090	G
1	5	4096	C
1	5	4097	G
1	5	4100	C
1	5	4101	C
1	5	4115	G
1	5	4116	C
1	5	4119	C
1	5	4120	U
1	5	4122	G
1	5	4124	G
1	5	4125	C
1	5	4127	A
1	5	4133	C
1	5	4135	G
1	5	4136	G
1	5	4148	C
1	5	4149	C
1	5	4150	G
1	5	4154	G
1	5	4156	G
1	5	4162	C
1	5	4163	U
1	5	4168	G
1	5	4170	A
1	5	4171	C
1	5	4172	A
1	5	4181	U
1	5	4183	G
1	5	4184	G
1	5	4185	G
1	5	4191	G
1	5	4197	G
1	5	4203	A
1	5	4213	A
1	5	4225	G
1	5	4229	U

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Mol	Chain	Res	Type
1	5	4233	A
1	5	4250	G
1	5	4251	A
1	5	4254	G
1	5	4256	A
1	5	4258	C
1	5	4260	U
1	5	4265	U
1	5	4266	G
1	5	4268	A
1	5	4271	A
1	5	4273	A
1	5	4281	A
1	5	4291	G
1	5	4296	U
1	5	4297	G
1	5	4304	A
1	5	4305	G
1	5	4306	U
1	5	4312	U
1	5	4313	A
1	5	4314	C
1	5	4317	A
1	5	4318	C
1	5	4326	G
1	5	4329	G
1	5	4330	G
1	5	4332	C
1	5	4336	A
1	5	4348	A
1	5	4349	C
1	5	4350	C
1	5	4351	U
1	5	4354	U
1	5	4364	G
1	5	4373	G
1	5	4376	A
1	5	4377	G
1	5	4378	A
1	5	4387	C
1	5	4391	G
1	5	4394	A

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Mol	Chain	Res	Type
1	5	4395	U
1	5	4398	C
1	5	4401	G
1	5	4405	G
1	5	4419	U
1	5	4421	C
1	5	4422	A
1	5	4424	A
1	5	4426	C
1	5	4433	G
1	5	4440	G
1	5	4444	C
1	5	4448	G
1	5	4449	A
1	5	4450	U
1	5	4452	U
1	5	4464	A
1	5	4471	U
1	5	4472	G
1	5	4475	G
1	5	4491	G
1	5	4499	G
1	5	4500	U
1	5	4510	A
1	5	4512	U
1	5	4513	A
1	5	4515	G
1	5	4519	C
1	5	4522	G
1	5	4524	G
1	5	4528	G
1	5	4530	U
1	5	4531	U
1	5	4535	A
1	5	4548	A
1	5	4549	G
1	5	4554	G
1	5	4560	C
1	5	4562	C
1	5	4567	G
1	5	4570	G
1	5	4573	G

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Mol	Chain	Res	Type
1	5	4575	G
1	5	4584	A
1	5	4587	G
1	5	4589	A
1	5	4590	A
1	5	4599	A
1	5	4605	A
1	5	4635	A
1	5	4636	U
1	5	4637	G
1	5	4639	G
1	5	4652	G
1	5	4656	A
1	5	4657	U
1	5	4658	G
1	5	4664	A
1	5	4667	C
1	5	4670	C
1	5	4677	U
1	5	4687	A
1	5	4693	C
1	5	4700	A
1	5	4709	U
1	5	4719	G
1	5	4720	C
1	5	4728	U
1	5	4738	C
1	5	4739	C
1	5	4750	G
1	5	4752	U
1	5	4754	G
1	5	4756	C
1	5	4757	C
1	5	4759	C
1	5	4761	G
1	5	4764	A
1	5	4765	G
1	5	4770	U
1	5	4771	C
1	5	4772	C
1	5	4773	C
1	5	4775	C

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Mol	Chain	Res	Type
1	5	4777	C
1	5	4863	G
1	5	4865	C
1	5	4870	G
1	5	4871	C
1	5	4874	A
1	5	4875	G
1	5	4881	U
1	5	4882	U
1	5	4883	C
1	5	4885	U
1	5	4889	G
1	5	4891	G
1	5	4895	C
1	5	4903	G
1	5	4906	C
1	5	4909	A
1	5	4910	A
1	5	4911	A
1	5	4912	G
1	5	4914	G
1	5	4915	G
1	5	4917	C
1	5	4918	C
1	5	4921	C
1	5	4922	C
1	5	4925	U
1	5	4926	C
1	5	4930	C
1	5	4932	U
1	5	4934	A
1	5	4937	C
1	5	4938	A
1	5	4940	C
1	5	4943	A
1	5	4944	C
1	5	4947	U
1	5	4948	C
1	5	4949	G
1	5	4950	U
1	5	4951	G
1	5	4956	A

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Mol	Chain	Res	Type
1	5	4958	C
1	5	4959	U
1	5	4960	G
1	5	4963	G
1	5	4965	U
1	5	4966	A
1	5	4967	A
1	5	4976	U
1	5	4985	U
1	5	4988	U
1	5	4990	C
1	5	4991	U
1	5	4998	G
1	5	5017	G
1	5	5021	C
1	5	5022	U
1	5	5029	C
1	5	5041	G
1	5	5050	C
1	5	5053	U
1	5	5054	C
1	5	5055	G
1	5	5056	A
1	5	5058	A
1	5	5061	A
1	5	5062	G
2	7	7	G
2	7	21	G
2	7	22	A
2	7	25	G
2	7	33	U
2	7	41	G
2	7	53	U
2	7	54	A
2	7	63	C
2	7	64	G
2	7	74	A
2	7	97	G
2	7	100	A
2	7	110	G
2	7	111	C
3	8	2	G

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Mol	Chain	Res	Type
3	8	3	A
3	8	32	C
3	8	34	U
3	8	35	C
3	8	38	U
3	8	59	A
3	8	60	G
3	8	61	A
3	8	62	A
3	8	63	U
3	8	75	G
3	8	77	A
3	8	79	G
3	8	86	U
3	8	94	G
3	8	95	A
3	8	103	A
3	8	105	C
3	8	106	G
3	8	109	C
3	8	110	U
3	8	111	U
3	8	114	G
3	8	121	G
3	8	122	G
3	8	123	U
3	8	125	C
3	8	126	C
3	8	127	U
3	8	129	C
3	8	137	A
3	8	147	G
3	8	150	C
3	8	151	G
3	8	156	U
47	2	2	A
47	2	3	C
47	2	4	C
47	2	6	G
47	2	17	C
47	2	25	A
47	2	33	G

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Mol	Chain	Res	Type
47	2	46	A
47	2	56	G
47	2	58	C
47	2	64	A
47	2	65	C
47	2	66	G
47	2	67	C
47	2	68	A
47	2	69	C
47	2	70	G
47	2	73	C
47	2	74	G
47	2	75	G
47	2	79	A
47	2	99	A
47	2	100	U
47	2	103	A
47	2	110	U
47	2	111	A
47	2	113	G
47	2	115	U
47	2	116	U
47	2	124	U
47	2	126	G
47	2	128	U
47	2	129	C
47	2	130	G
47	2	142	C
47	2	143	U
47	2	146	G
47	2	147	A
47	2	155	G
47	2	158	A
47	2	161	U
47	2	162	C
47	2	163	U
47	2	170	A
47	2	182	C
47	2	183	G
47	2	184	G
47	2	185	G
47	2	188	C

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Mol	Chain	Res	Type
47	2	189	U
47	2	190	G
47	2	191	A
47	2	192	C
47	2	194	C
47	2	195	C
47	2	197	U
47	2	199	C
47	2	204	G
47	2	206	G
47	2	208	G
47	2	215	G
47	2	294	U
47	2	297	A
47	2	302	A
47	2	304	C
47	2	306	C
47	2	307	G
47	2	308	G
47	2	309	G
47	2	312	G
47	2	313	A
47	2	314	U
47	2	317	C
47	2	318	A
47	2	319	C
47	2	320	G
47	2	322	C
47	2	323	C
47	2	330	G
47	2	333	G
47	2	347	G
47	2	351	G
47	2	362	C
47	2	364	A
47	2	367	U
47	2	368	U
47	2	369	C
47	2	370	G
47	2	371	A
47	2	377	G
47	2	381	C

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Mol	Chain	Res	Type
47	2	383	G
47	2	384	U
47	2	385	G
47	2	386	C
47	2	388	U
47	2	400	C
47	2	408	A
47	2	409	C
47	2	418	A
47	2	429	C
47	2	436	G
47	2	438	G
47	2	441	C
47	2	447	A
47	2	448	A
47	2	449	A
47	2	450	C
47	2	465	A
47	2	466	G
47	2	467	G
47	2	471	G
47	2	472	C
47	2	473	A
47	2	474	G
47	2	478	G
47	2	479	C
47	2	482	G
47	2	487	U
47	2	489	A
47	2	492	C
47	2	493	A
47	2	496	C
47	2	500	A
47	2	502	C
47	2	507	G
47	2	508	A
47	2	509	G
47	2	517	C
47	2	518	G
47	2	530	U
47	2	532	C
47	2	533	A

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Mol	Chain	Res	Type
47	2	536	A
47	2	537	C
47	2	543	C
47	2	544	G
47	2	547	G
47	2	548	C
47	2	550	C
47	2	551	U
47	2	554	A
47	2	555	A
47	2	556	U
47	2	558	G
47	2	559	G
47	2	561	A
47	2	562	U
47	2	567	C
47	2	568	C
47	2	569	A
47	2	570	C
47	2	574	A
47	2	576	A
47	2	583	A
47	2	584	A
47	2	588	G
47	2	589	G
47	2	590	A
47	2	591	U
47	2	593	C
47	2	597	G
47	2	600	G
47	2	604	A
47	2	606	G
47	2	608	C
47	2	614	C
47	2	623	G
47	2	627	U
47	2	628	A
47	2	629	A
47	2	631	U
47	2	632	C
47	2	643	A
47	2	644	G

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Mol	Chain	Res	Type
47	2	646	G
47	2	660	C
47	2	666	U
47	2	668	A
47	2	669	A
47	2	671	A
47	2	672	A
47	2	673	G
47	2	683	G
47	2	687	C
47	2	688	U
47	2	689	U
47	2	691	G
47	2	692	G
47	2	734	C
47	2	736	C
47	2	751	G
47	2	752	G
47	2	753	C
47	2	754	G
47	2	756	C
47	2	790	C
47	2	793	G
47	2	794	A
47	2	799	U
47	2	800	U
47	2	810	A
47	2	811	A
47	2	821	G
47	2	822	U
47	2	830	A
47	2	834	C
47	2	845	G
47	2	847	A
47	2	868	G
47	2	870	A
47	2	871	U
47	2	872	A
47	2	873	G
47	2	875	A
47	2	877	C
47	2	878	G

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Mol	Chain	Res	Type
47	2	884	C
47	2	885	U
47	2	886	A
47	2	887	U
47	2	888	U
47	2	890	U
47	2	892	U
47	2	894	G
47	2	898	U
47	2	901	G
47	2	905	C
47	2	906	U
47	2	908	A
47	2	909	G
47	2	910	G
47	2	913	A
47	2	914	U
47	2	919	A
47	2	920	A
47	2	933	G
47	2	949	G
47	2	952	G
47	2	955	A
47	2	958	G
47	2	961	G
47	2	963	A
47	2	971	G
47	2	978	G
47	2	988	C
47	2	990	A
47	2	992	A
47	2	999	G
47	2	1008	A
47	2	1016	U
47	2	1017	U
47	2	1023	A
47	2	1030	A
47	2	1060	A
47	2	1077	A
47	2	1083	A
47	2	1085	C
47	2	1100	A

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Mol	Chain	Res	Type
47	2	1110	G
47	2	1115	U
47	2	1116	C
47	2	1117	C
47	2	1118	C
47	2	1121	G
47	2	1123	C
47	2	1126	G
47	2	1133	A
47	2	1138	C
47	2	1140	G
47	2	1148	A
47	2	1149	A
47	2	1150	A
47	2	1153	C
47	2	1154	U
47	2	1155	U
47	2	1168	G
47	2	1176	G
47	2	1195	A
47	2	1203	G
47	2	1207	G
47	2	1210	G
47	2	1212	G
47	2	1215	C
47	2	1221	G
47	2	1224	G
47	2	1230	C
47	2	1235	G
47	2	1240	A
47	2	1242	U
47	2	1243	U
47	2	1251	A
47	2	1253	A
47	2	1256	G
47	2	1257	G
47	2	1259	A
47	2	1266	C
47	2	1274	G
47	2	1275	G
47	2	1280	G
47	2	1284	A

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Mol	Chain	Res	Type
47	2	1285	G
47	2	1286	G
47	2	1287	A
47	2	1290	G
47	2	1292	C
47	2	1293	A
47	2	1294	G
47	2	1295	A
47	2	1298	G
47	2	1299	A
47	2	1301	A
47	2	1302	G
47	2	1306	U
47	2	1307	U
47	2	1308	U
47	2	1311	C
47	2	1312	G
47	2	1313	A
47	2	1314	U
47	2	1318	G
47	2	1322	G
47	2	1330	G
47	2	1342	U
47	2	1351	G
47	2	1354	G
47	2	1371	U
47	2	1372	U
47	2	1373	C
47	2	1378	A
47	2	1379	A
47	2	1395	C
47	2	1396	A
47	2	1397	U
47	2	1402	A
47	2	1403	C
47	2	1404	U
47	2	1409	A
47	2	1425	G
47	2	1428	G
47	2	1429	G
47	2	1432	U
47	2	1441	U

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Mol	Chain	Res	Type
47	2	1444	U
47	2	1449	G
47	2	1453	C
47	2	1454	A
47	2	1462	U
47	2	1463	U
47	2	1466	G
47	2	1473	G
47	2	1475	G
47	2	1476	A
47	2	1478	U
47	2	1480	A
47	2	1490	G
47	2	1493	C
47	2	1495	G
47	2	1497	G
47	2	1498	A
47	2	1503	C
47	2	1506	A
47	2	1507	G
47	2	1509	U
47	2	1514	G
47	2	1518	C
47	2	1519	U
47	2	1520	G
47	2	1521	C
47	2	1522	A
47	2	1523	C
47	2	1525	C
47	2	1533	A
47	2	1535	U
47	2	1547	C
47	2	1548	G
47	2	1552	G
47	2	1553	C
47	2	1554	C
47	2	1555	U
47	2	1556	A
47	2	1557	C
47	2	1558	C
47	2	1568	C
47	2	1575	G

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Mol	Chain	Res	Type
47	2	1580	A
47	2	1584	G
47	2	1585	U
47	2	1586	U
47	2	1588	A
47	2	1601	A
47	2	1604	G
47	2	1606	G
47	2	1619	A
47	2	1621	U
47	2	1622	U
47	2	1623	A
47	2	1624	U
47	2	1637	A
47	2	1638	G
47	2	1641	A
47	2	1646	C
47	2	1648	G
47	2	1654	G
47	2	1664	A
47	2	1665	G
47	2	1667	U
47	2	1671	G
47	2	1683	C
47	2	1686	G
47	2	1689	C
47	2	1698	C
47	2	1699	A
47	2	1702	G
47	2	1706	G
47	2	1715	A
47	2	1721	U
47	2	1722	G
47	2	1725	U
47	2	1726	G
47	2	1744	G
47	2	1745	A
47	2	1746	U
47	2	1748	G
47	2	1750	C
47	2	1756	C
47	2	1758	G

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Mol	Chain	Res	Type
47	2	1759	G
47	2	1773	C
47	2	1774	C
47	2	1776	G
47	2	1777	G
47	2	1779	G
47	2	1780	G
47	2	1781	A
47	2	1782	G
47	2	1783	C
47	2	1784	G
47	2	1807	C
47	2	1823	A
47	2	1824	A
47	2	1825	A
47	2	1831	A
47	2	1836	G
47	2	1838	U
47	2	1839	U
47	2	1849	G
47	2	1851	A
47	2	1852	C
47	2	1861	G
47	2	1862	G
47	2	1863	A
47	2	1864	U
47	2	1865	C
47	2	1867	U
47	2	1869	A
81	1	6424	U
81	1	6425	A
81	1	6426	U
81	1	6427	G
81	1	6428	G
81	1	6430	U
81	1	6431	A
81	1	6432	C
81	1	6433	C
81	1	6435	A
81	1	6436	U
81	1	6437	C
81	1	6443	A

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Mol	Chain	Res	Type
81	1	6444	G
81	1	6445	G
81	1	6450	U
81	1	6451	U
81	1	6455	A
81	1	6457	A
81	1	6460	C
81	1	6462	C
81	1	6463	U
81	1	6467	G
81	1	6470	A
81	1	6471	G
81	1	6472	G
81	1	6473	C
81	1	6475	U
81	1	6479	G
81	1	6482	A
81	1	6483	U
81	1	6484	G
81	1	6485	G
81	1	6486	U
81	1	6487	C
81	1	6488	G
81	1	6489	A
81	1	6490	G
81	1	6491	G
81	1	6492	U
81	1	6493	G
81	1	6494	C
81	1	6501	U
81	1	6502	A
81	1	6506	U
81	1	6507	G
81	1	6512	G
81	1	6514	C
81	1	6515	U
81	1	6516	C
81	1	6517	G
81	1	6518	G
81	1	6519	U
81	1	6522	C
81	1	6523	A

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Mol	Chain	Res	Type
81	1	6525	C
81	1	6526	C
81	1	6527	C
81	1	6528	C
81	1	6529	A
81	1	6531	C
81	1	6533	A
81	1	6534	A
81	1	6535	U
81	1	6536	C
81	1	6539	C
81	1	6540	U
81	1	6541	A
81	1	6543	U
81	1	6544	G
81	1	6545	G
81	1	6548	A
81	1	6549	G
81	1	6552	A
81	1	6553	C
81	1	6554	A
81	1	6555	G
81	1	6557	U
81	1	6561	C
81	1	6563	G
81	1	6565	G
81	1	6567	A
81	1	6575	C
81	1	6576	A
81	1	6577	G
81	1	6578	U
81	1	6579	C
81	1	6580	G
81	1	6583	U
81	1	6585	G
81	1	6587	A
81	1	6588	A
81	1	6589	C
81	1	6590	A
81	1	6591	C
81	1	6597	G
81	1	6598	C

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Mol	Chain	Res	Type
81	1	6599	G
81	1	6600	U
81	1	6604	G
81	1	6605	A
81	1	6606	A
81	1	6608	U
81	1	6609	A
81	1	6610	C
81	1	6611	C
81	1	6612	A
81	1	6613	U
81	1	6618	G
81	1	6620	C

All (119) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	12	A
1	5	48	G
1	5	125	C
1	5	170	C
1	5	217	C
1	5	265	C
1	5	266	C
1	5	275	C
1	5	315	G
1	5	385	A
1	5	417	G
1	5	449	C
1	5	504	G
1	5	912	U
1	5	928	A
1	5	933	C
1	5	935	G
1	5	969	U
1	5	978	G
1	5	1209	U
1	5	1211	G
1	5	1236	C
1	5	1237	C
1	5	1370	G
1	5	1411	C

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Mol	Chain	Res	Type
1	5	1412	G
1	5	1445	U
1	5	1455	G
1	5	1633	G
1	5	1676	C
1	5	1733	G
1	5	1974	U
1	5	2046	G
1	5	2089	G
1	5	2259	G
1	5	2467	U
1	5	2502	A
1	5	2513	A
1	5	2529	A
1	5	2530	U
1	5	2587	A
1	5	2601	A
1	5	2661	U
1	5	2695	A
1	5	2709	C
1	5	2724	G
1	5	2754	G
1	5	2806	A
1	5	3603	G
1	5	3625	G
1	5	3681	G
1	5	3752	C
1	5	3753	G
1	5	3765	G
1	5	3876	A
1	5	3888	G
1	5	3904	G
1	5	3938	G
1	5	4054	C
1	5	4119	C
1	5	4155	C
1	5	4170	A
1	5	4180	G
1	5	4232	U
1	5	4448	G
1	5	4527	G
1	5	4635	A

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Mol	Chain	Res	Type
1	5	4699	U
1	5	4719	G
1	5	4882	U
1	5	4884	G
1	5	4925	U
1	5	4936	G
1	5	5041	G
2	7	109	U
3	8	51	U
3	8	60	G
3	8	94	G
3	8	124	U
47	2	24	C
47	2	110	U
47	2	370	G
47	2	464	A
47	2	465	A
47	2	532	C
47	2	553	U
47	2	561	A
47	2	606	G
47	2	627	U
47	2	668	A
47	2	688	U
47	2	752	G
47	2	870	A
47	2	874	G
47	2	885	U
47	2	908	A
47	2	1016	U
47	2	1137	U
47	2	1165	G
47	2	1395	C
47	2	1462	U
47	2	1519	U
47	2	1556	A
47	2	1623	A
47	2	1637	A
47	2	1664	A
47	2	1685	U
47	2	1698	C
47	2	1743	G

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Mol	Chain	Res	Type
47	2	1744	G
81	1	6456	U
81	1	6484	G
81	1	6493	G
81	1	6506	U
81	1	6538	U
81	1	6551	A
81	1	6589	C
81	1	6605	A
81	1	6609	A

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	25

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.49
1	5	1252:C	O3'	1271:G	P	36.06

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1219:G	O3'	1233:G	P	21.64
1	5	1405:C	O3'	1409:G	P	19.72
1	5	1696:C	O3'	1720:C	P	19.06
1	5	4138:C	O3'	4146:G	P	18.68
1	5	523:C	O3'	638:G	P	17.16
1	5	3977:C	O3'	4034:G	P	16.71
1	5	991:U	O3'	1064:G	P	16.26
1	5	4101:C	O3'	4107:G	P	14.73
1	5	4777:C	O3'	4859:C	P	14.69
1	5	760:G	O3'	903:C	P	14.64
1	5	5022:U	O3'	5028:G	P	14.23
1	5	1364:U	O3'	1368:A	P	13.82
1	5	2901:G	O3'	3597:G	P	11.65
1	5	512:U	O3'	515:C	P	9.66
1	5	1180:C	O3'	1183:C	P	9.24
1	5	182:G	O3'	189:G	P	8.24
1	5	4729:A	O3'	4735:G	P	7.17
1	5	500:G	O3'	504:G	P	6.59
1	5	4740:G	O3'	4743:G	P	5.53
1	5	1438:U	O3'	1440:U	P	4.46
1	5	1239:C	O3'	1244:G	P	3.87
1	5	4899:G	O3'	4902:C	P	3.52
1	5	1100:U	O3'	1168:G	P	3.40

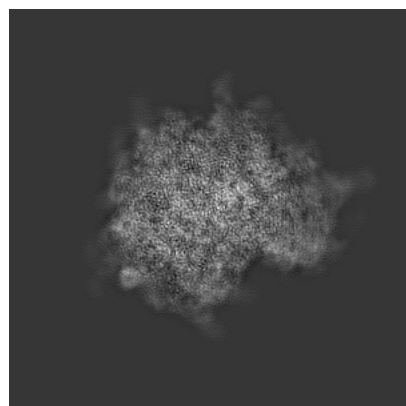
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20257. These allow visual inspection of the internal detail of the map and identification of artifacts.

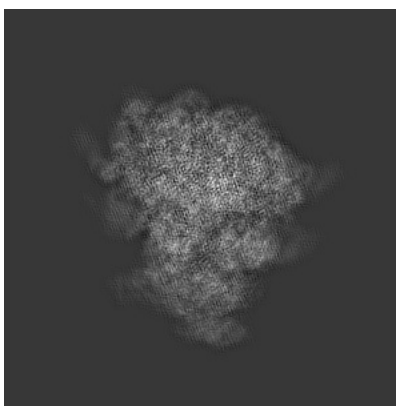
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

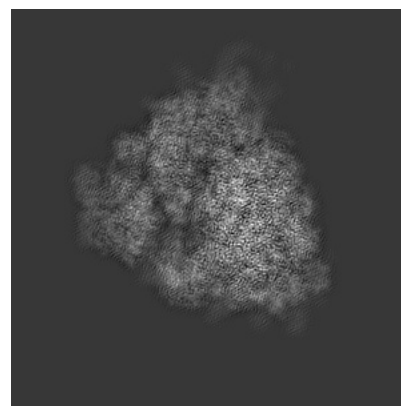
6.1.1 Primary map



X

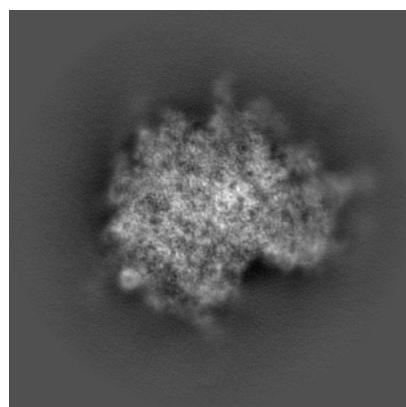


Y

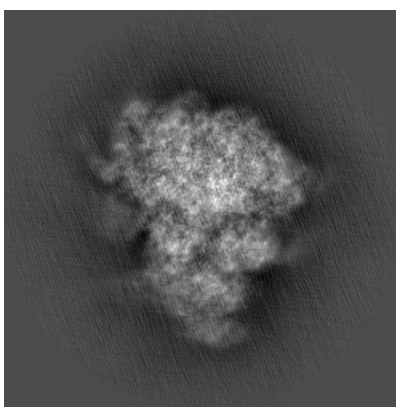


Z

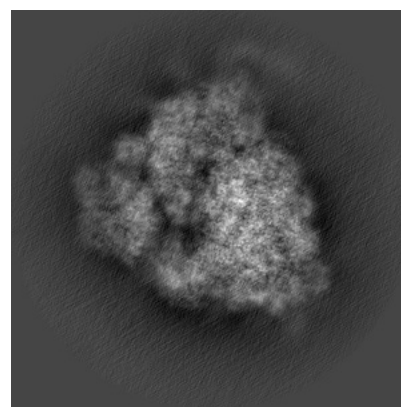
6.1.2 Raw map



X



Y

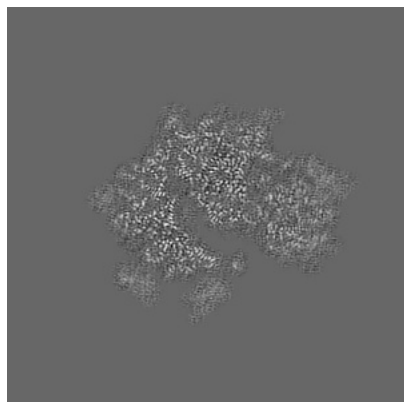


Z

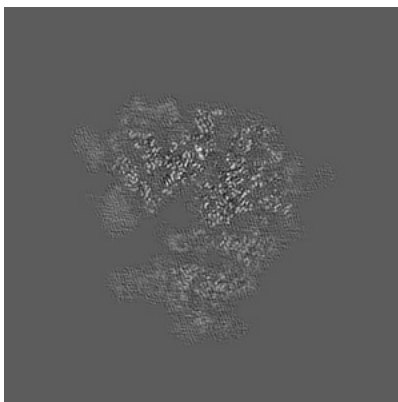
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

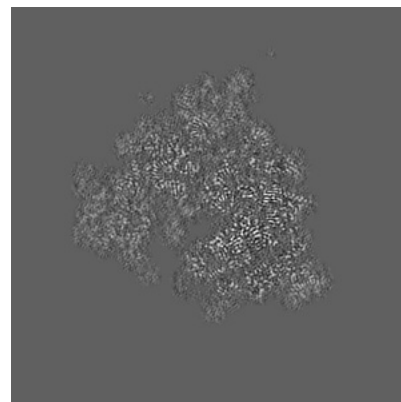
6.2.1 Primary map



X Index: 180

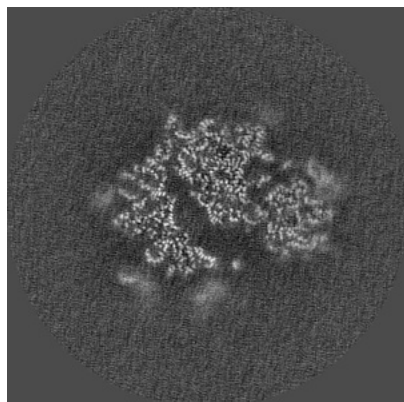


Y Index: 180

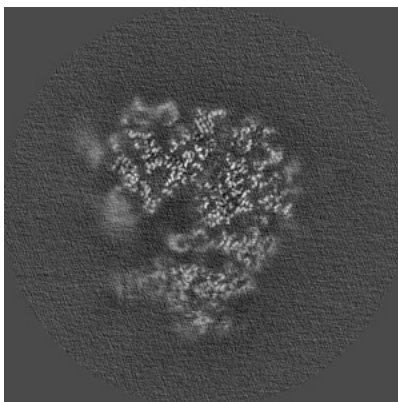


Z Index: 180

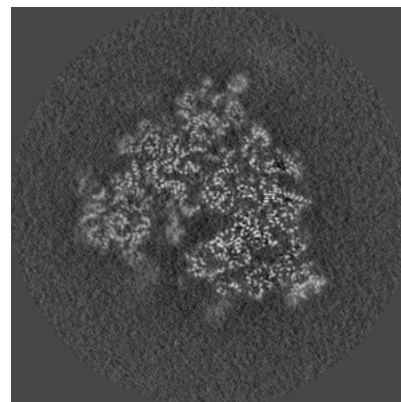
6.2.2 Raw map



X Index: 180



Y Index: 180

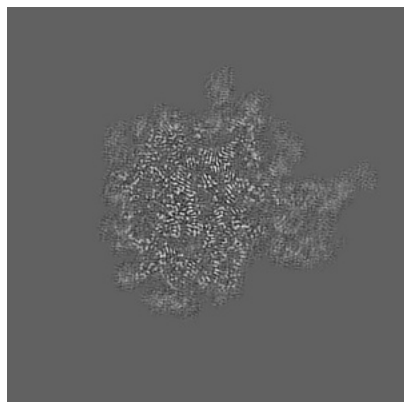


Z Index: 180

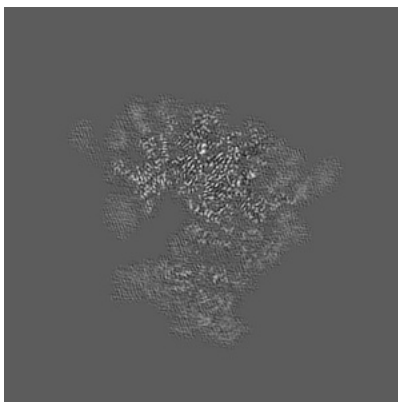
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

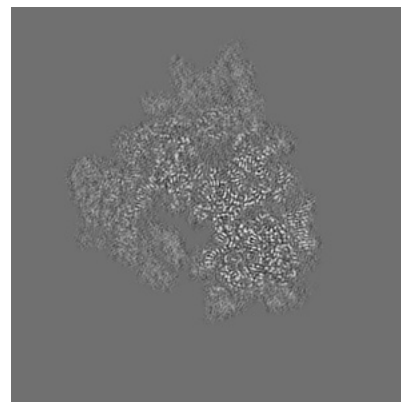
6.3.1 Primary map



X Index: 206

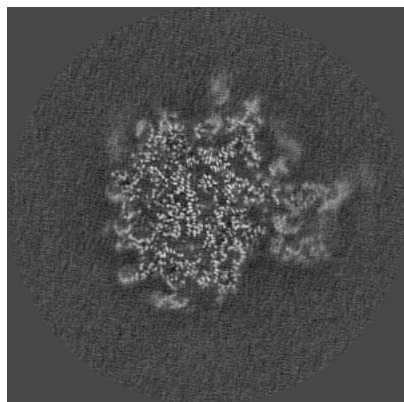


Y Index: 188

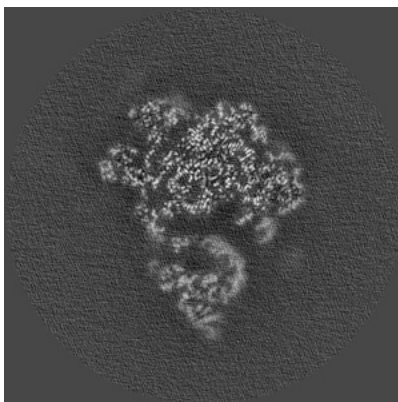


Z Index: 195

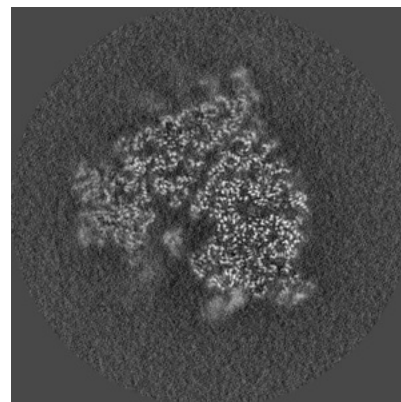
6.3.2 Raw map



X Index: 206



Y Index: 148

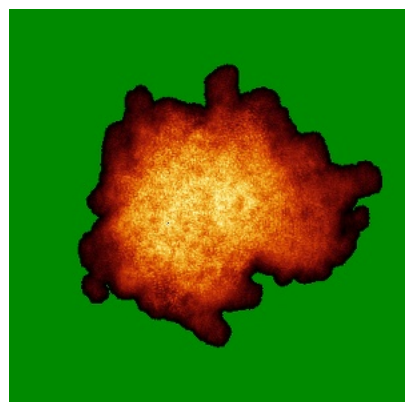


Z Index: 188

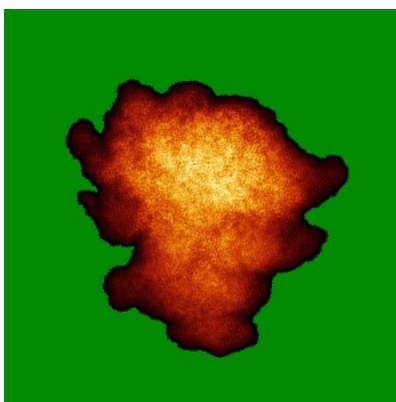
The images above show the largest variance slices of the map in three orthogonal directions.

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

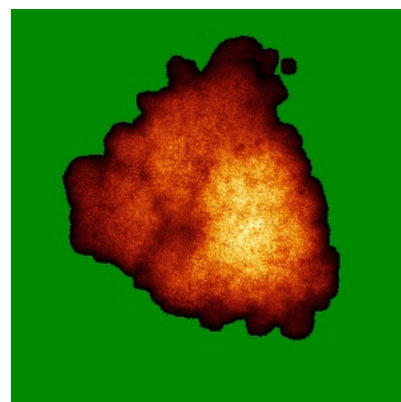
6.4.1 Primary map



X

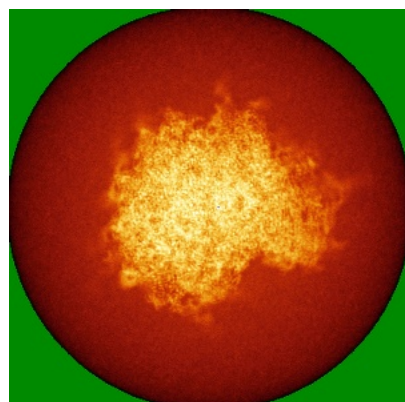


Y

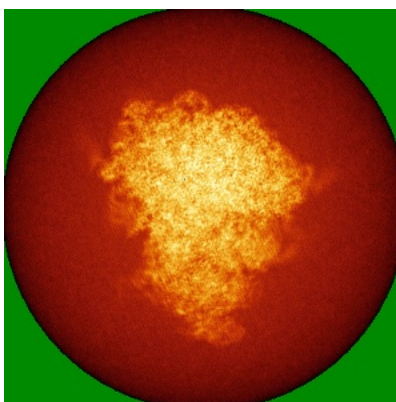


Z

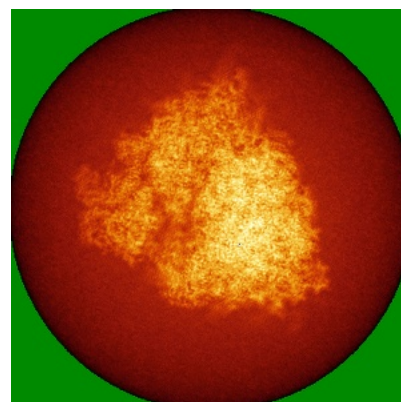
6.4.2 Raw map



X



Y

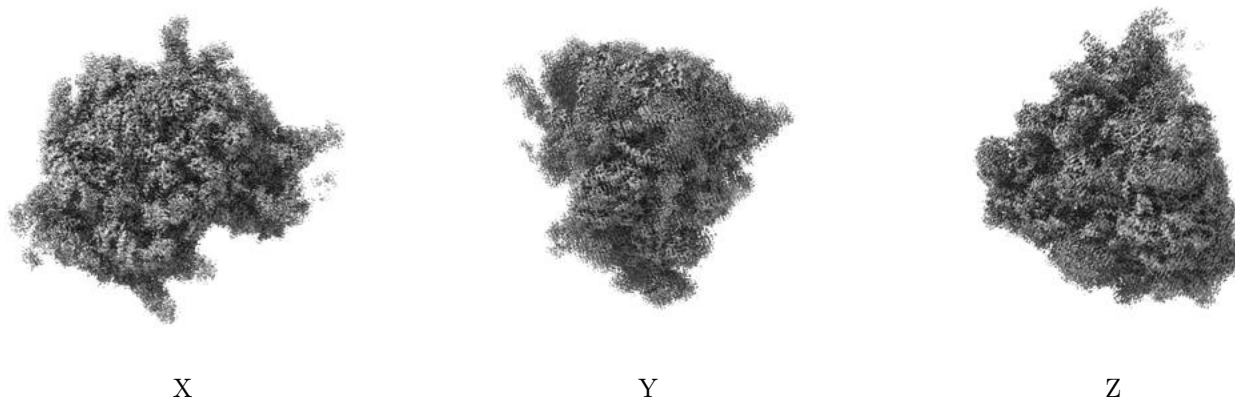


Z

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

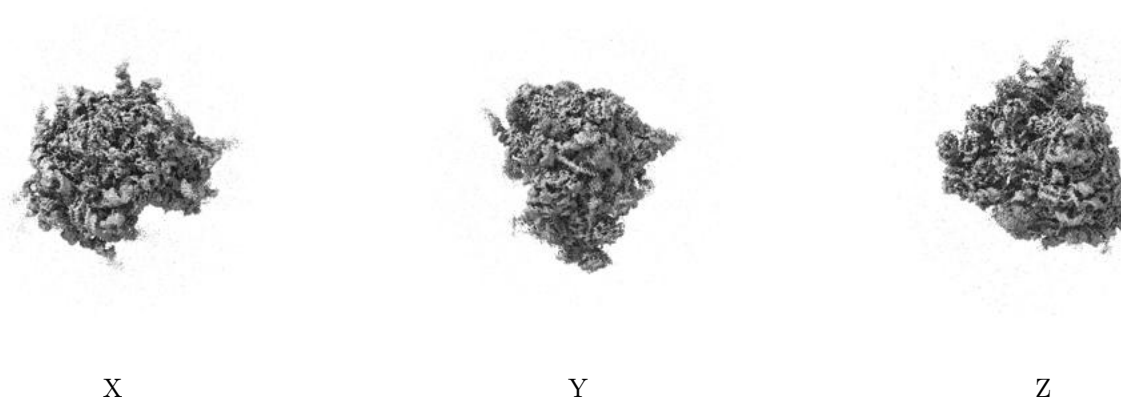
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.028. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

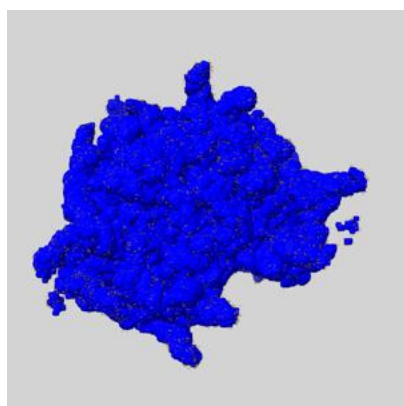
6.6 Mask visualisation [i](#)

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

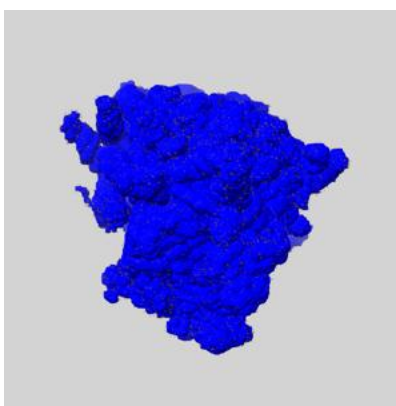
A mask typically either:

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

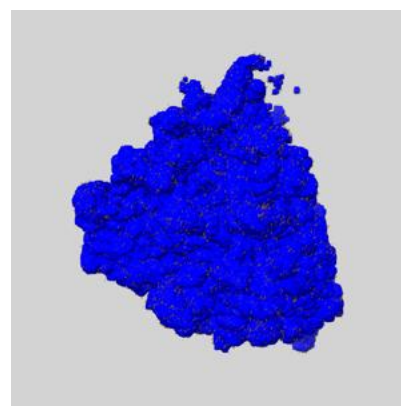
6.6.1 emd_20257_msk_1.map [i](#)



X



Y

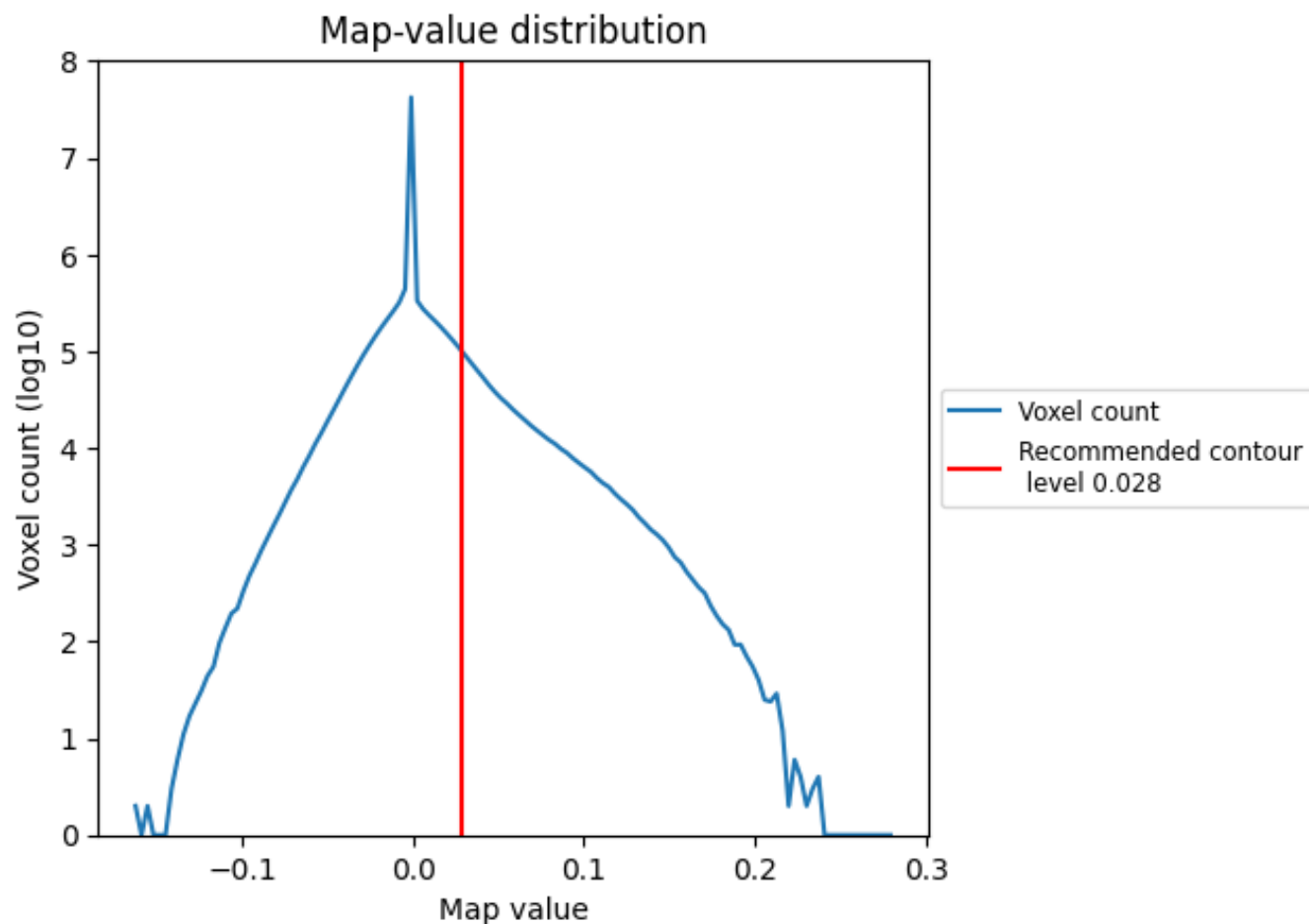


Z

7 Map analysis [i](#)

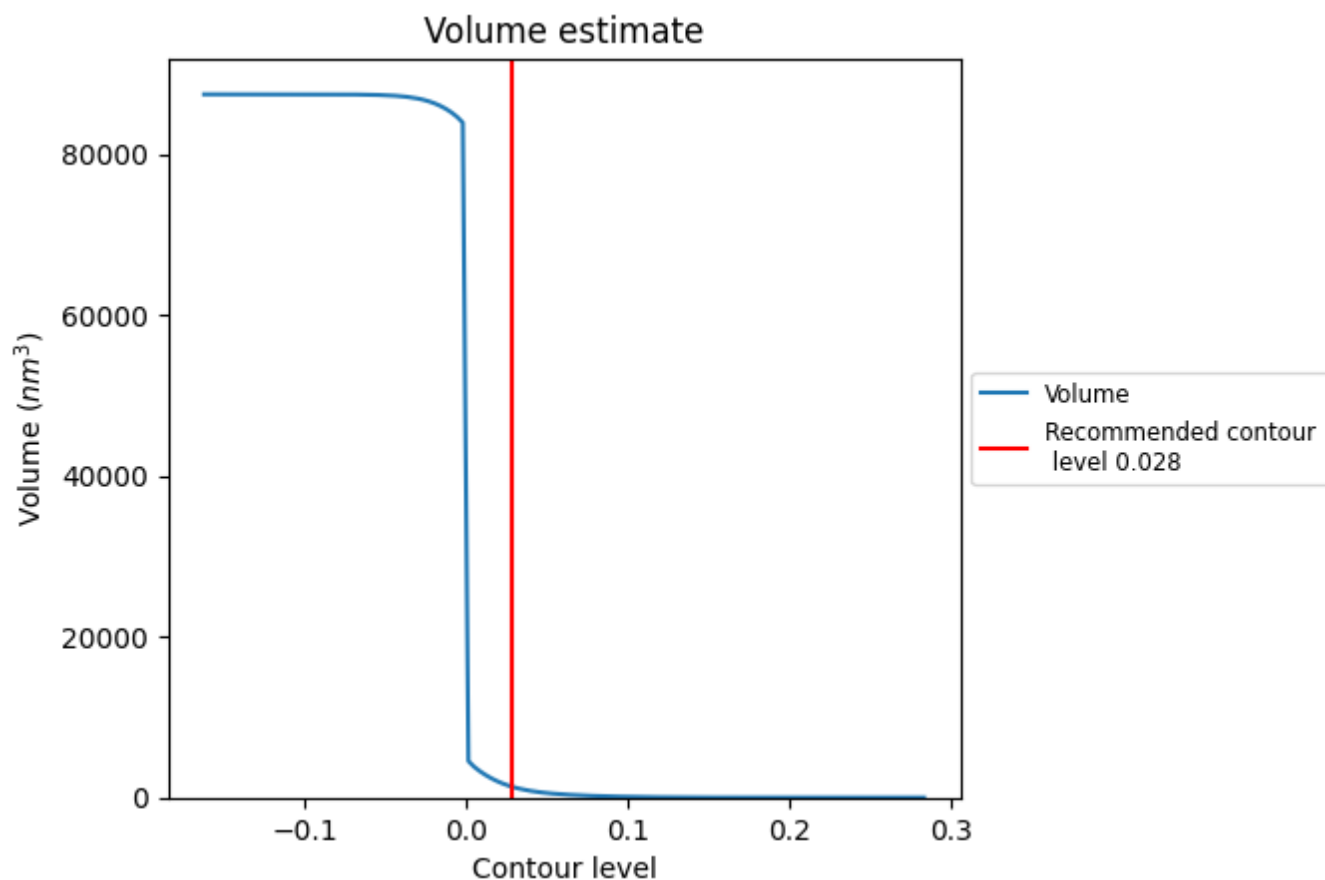
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

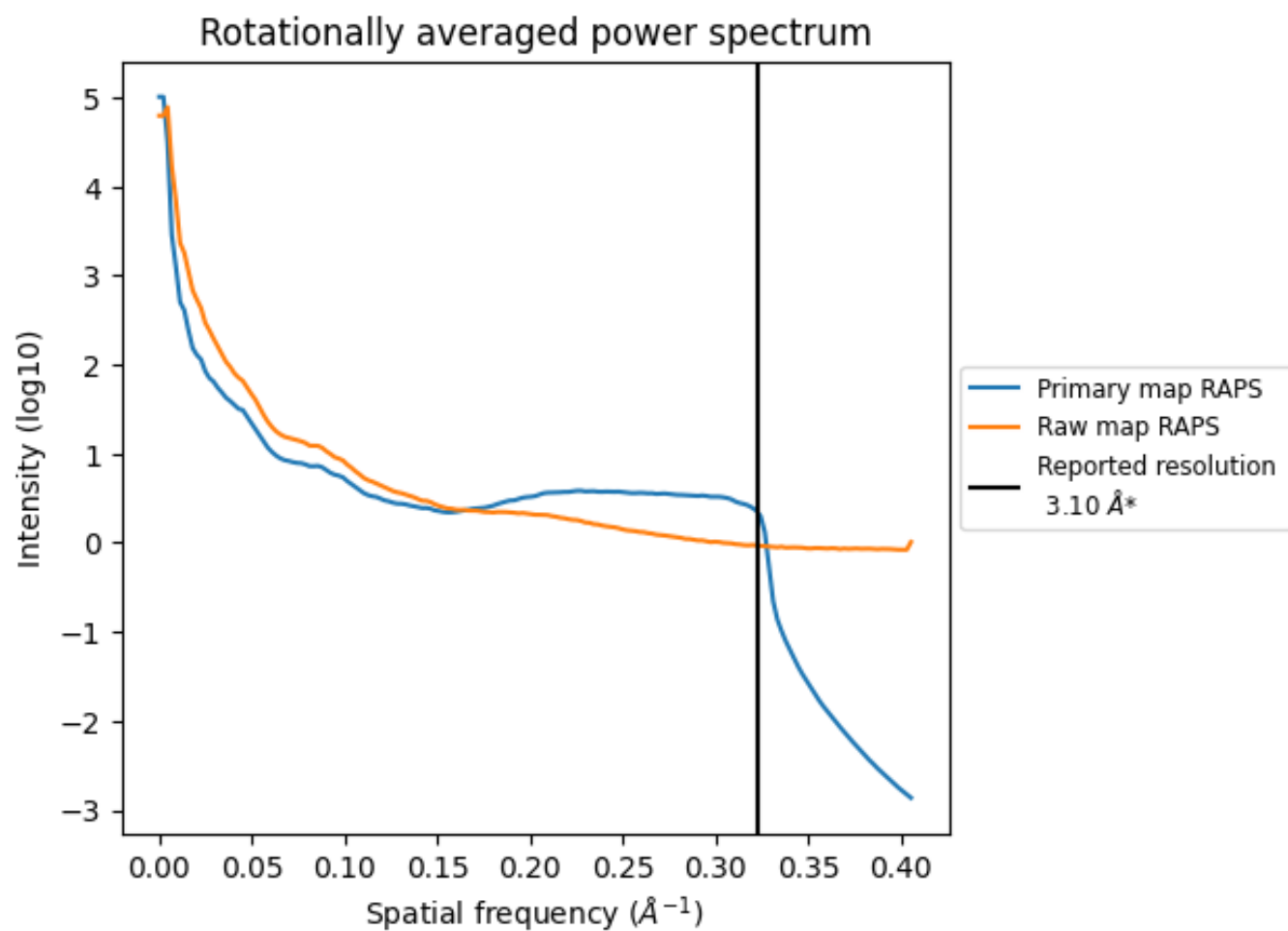
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1368 nm³; this corresponds to an approximate mass of 1236 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 ⓘ

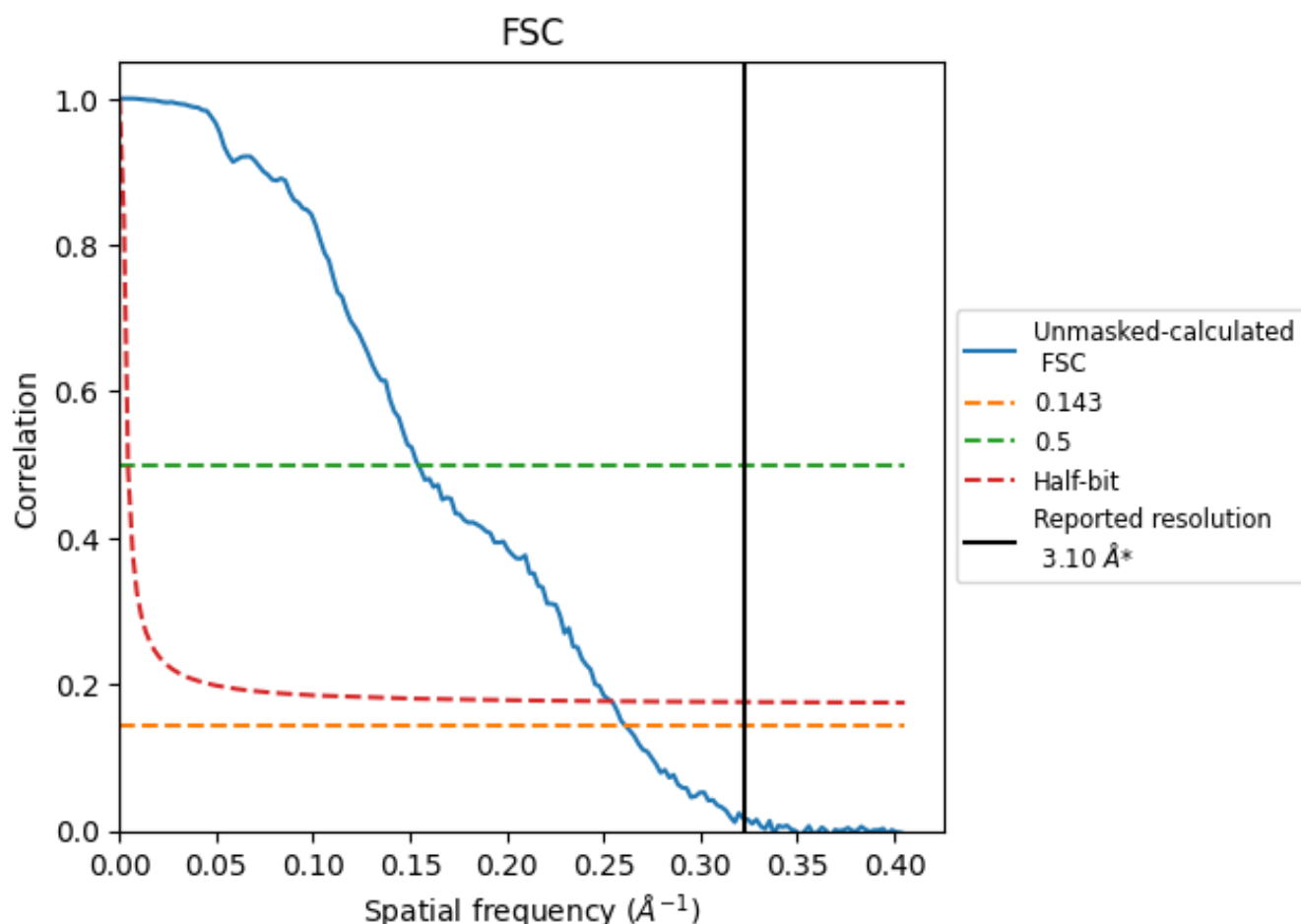


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

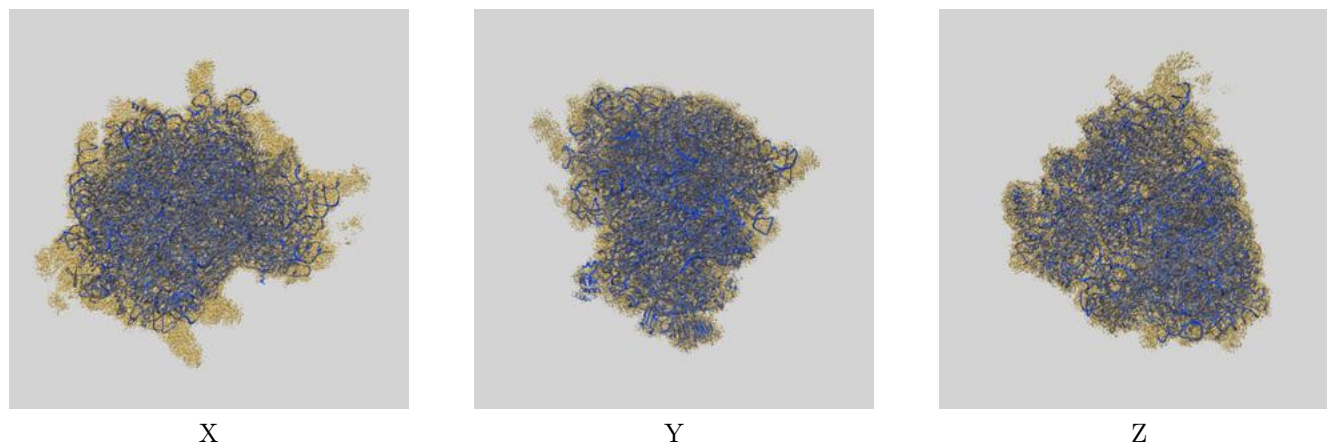
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	6.49	3.94

*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 3.82 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

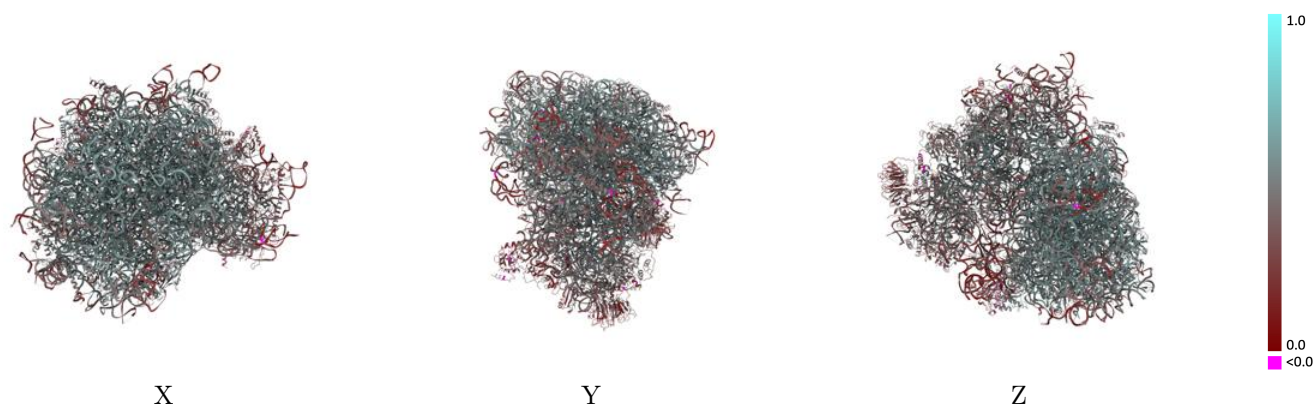
This section contains information regarding the fit between EMDB map EMD-20257 and PDB model 6P5K. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



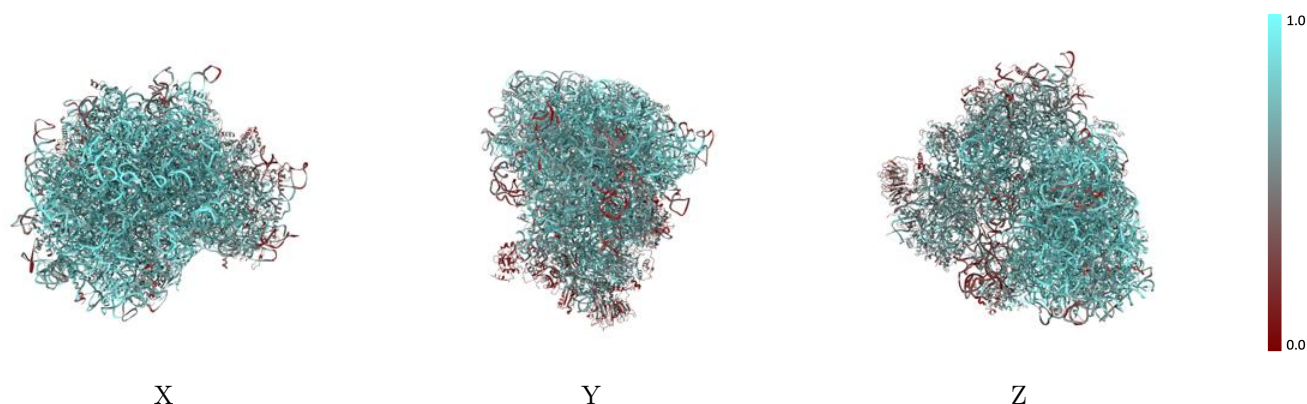
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



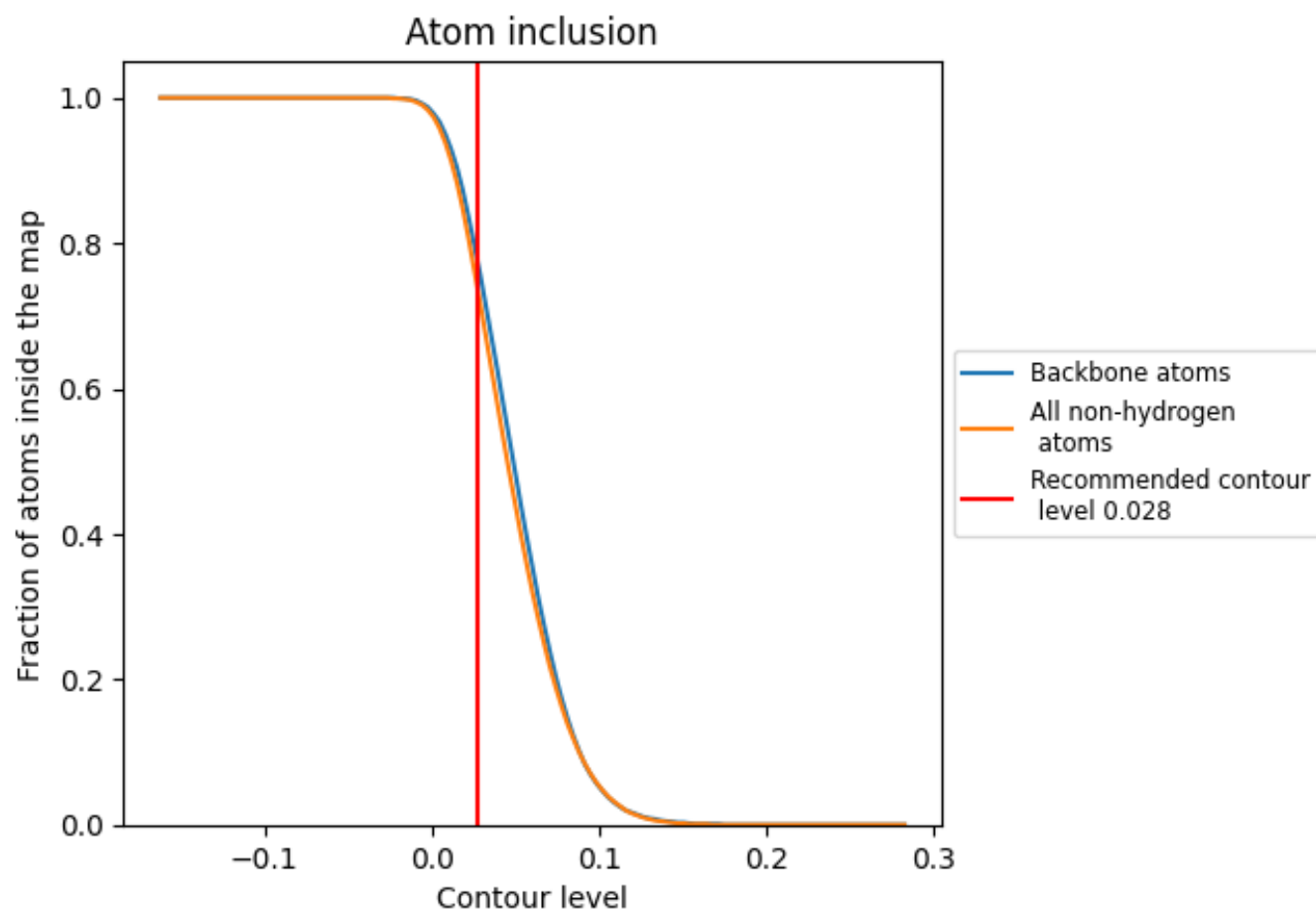
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.028).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 77% of all backbone atoms, 73% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7320	 0.4740
1	 0.3670	 0.2380
2	 0.7500	 0.4560
5	 0.8290	 0.5090
7	 0.9160	 0.5580
8	 0.8670	 0.5390
AA	 0.8020	 0.5400
AB	 0.7870	 0.5290
AC	 0.7980	 0.5300
AD	 0.7470	 0.4940
AE	 0.7410	 0.4970
AF	 0.8020	 0.5370
AG	 0.7150	 0.4770
AH	 0.7330	 0.5080
AI	 0.7670	 0.5140
AJ	 0.6900	 0.4700
AK	 0.1930	 0.2040
AL	 0.7590	 0.5140
AM	 0.7670	 0.5110
AN	 0.8430	 0.5600
AO	 0.8000	 0.5380
AP	 0.8070	 0.5400
AQ	 0.7930	 0.5350
AR	 0.7000	 0.4780
AS	 0.8160	 0.5390
AT	 0.7470	 0.5100
AU	 0.6250	 0.4340
AV	 0.7630	 0.5370
AW	 0.7520	 0.5140
AX	 0.7720	 0.5130
AY	 0.7800	 0.5230
AZ	 0.7340	 0.4830
Aa	 0.8340	 0.5530
Ab	 0.6210	 0.4590
Ac	 0.6760	 0.4740













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Chain	Atom inclusion	Q-score
Ad	 0.7190	 0.4950
Ae	 0.7990	 0.5520
Af	 0.8470	 0.5560
Ag	 0.7430	 0.5190
Ah	 0.7380	 0.5030
Ai	 0.7170	 0.4900
Aj	 0.8140	 0.5400
Ak	 0.6400	 0.4510
Al	 0.7590	 0.5140
Am	 0.7850	 0.5140
An	 0.6790	 0.4940
Ao	 0.7460	 0.5180
Ap	 0.7430	 0.5240
Ar	 0.8020	 0.5360
B	 0.5930	 0.4180
C	 0.5580	 0.4120
D	 0.6540	 0.4600
E	 0.4220	 0.3500
F	 0.6100	 0.4340
G	 0.5540	 0.4030
H	 0.4730	 0.3650
I	 0.4530	 0.3670
J	 0.5500	 0.4000
K	 0.5990	 0.4060
L	 0.3330	 0.2990
M	 0.6180	 0.4660
N	 0.0870	 0.2100
O	 0.5950	 0.4430
P	 0.6000	 0.4500
Q	 0.5090	 0.3410
R	 0.5330	 0.3880
S	 0.4390	 0.3670
T	 0.5420	 0.4020
U	 0.5570	 0.4000
V	 0.3400	 0.3450
W	 0.5890	 0.4140
X	 0.6880	 0.4770
Y	 0.6990	 0.4890
Z	 0.5410	 0.3860
a	 0.4700	 0.3400
b	 0.6700	 0.4720
c	 0.5350	 0.4090

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Chain	Atom inclusion	Q-score
d	 0.5020	 0.3770
e	 0.5810	 0.4220
f	 0.5070	 0.3720
g	 0.1180	 0.2190
h	 0.3400	 0.2780