



## wwPDB EM Validation Summary Report ⓘ

Aug 26, 2021 – 10:27 pm BST

PDB ID : 7O80  
EMDB ID : EMD-12758  
Title : Rabbit 80S ribosome in complex with eRF1 and ABCE1 stalled at the STOP codon in the mutated SARS-CoV-2 slippery site  
Authors : Bhatt, P.R.; Scaiola, A.; Leibundgut, M.A.; Atkins, J.F.; Ban, N.  
Deposited on : 2021-04-14  
Resolution : 2.90 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

EMDB validation analysis : 0.0.0.dev97  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.1

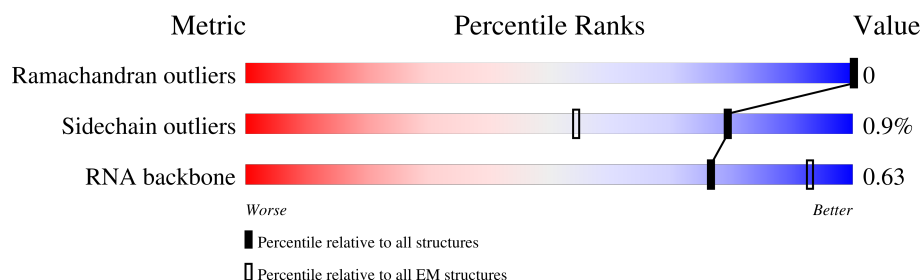
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A2	1870	
2	AA	84	
3	AB	69	
4	AC	156	
5	AD	133	
6	AE	115	
7	AF	317	
8	AG	56	

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Mol	Chain	Length	Quality of chain
9	AH	217	
10	AI	76	
11	AT	86	
12	AZ	295	
13	Aa	264	
14	Ab	293	
15	Ac	281	
16	Ad	263	
17	Ae	204	
18	Af	249	
19	Ag	194	
20	Ah	208	
21	Ai	194	
22	Aj	165	
23	Ak	158	
24	Al	132	
25	Am	151	
26	An	151	
27	Ao	145	
28	Ap	146	
29	Aq	135	
30	Ar	152	
31	As	145	
32	At	119	
33	Au	83	

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Mol	Chain	Length	Quality of chain
34	Av	130	
35	Aw	143	
36	Ax	130	
37	Ay	124	
38	Az	25	
39	B5	4808	
40	B7	119	
41	B8	158	
42	BA	257	
43	BB	403	
44	BC	413	
45	BD	297	
46	BE	291	
47	BF	247	
48	BG	266	
49	BH	192	
50	BI	214	
51	BJ	178	
52	BK	1071	
53	BL	211	
54	BM	218	
55	BN	204	
56	BO	203	
57	BP	184	
58	BQ	188	

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Mol	Chain	Length	Quality of chain
59	BR	196	
60	BS	176	
61	BT	160	
62	BU	128	
63	BV	140	
64	BW	157	
65	BX	156	
66	BY	145	
67	BZ	136	
68	Ba	148	
69	Bb	245	
70	Bc	115	
71	Bd	125	
72	Be	135	
73	Bf	110	
74	Bg	117	
75	Bh	123	
76	Bi	105	
77	Bj	97	
78	Bk	70	
79	Bl	51	
80	Bm	128	
81	Bo	106	
82	Bp	92	
83	Br	137	

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Mol	Chain	Length	Quality of chain
84	Bs	318	
85	Bt	165	
86	Bv	217	
87	By	437	
88	Bz	599	

## 2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 235677 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A2	1770	Total	C	N	O	P	0	0
			37833	16911	6781	12371	1770		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	1249	B8N	C	conflict	GB GBCT01000564.1
A2	1338	4AC	C	conflict	GB GBCT01000564.1
A2	1843	4AC	C	conflict	GB GBCT01000564.1

- Molecule 2 is a protein called 40S ribosomal protein S27.

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

- Molecule 3 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	63	Total	C	N	O	S	0	0
			495	302	98	93	2		

- Molecule 4 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	73	Total	C	N	O	S	0	0
			601	379	115	100	7		

- Molecule 5 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AD	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 6 is a protein called Ribosomal protein eS26.

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

- Molecule 7 is a protein called RACK1.

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

- Molecule 8 is a protein called uS14.

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

- Molecule 9 is a RNA chain called mRNA containing SARS-CoV-2 sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	24	Total	C	N	O	P	0	0
			508	227	84	173	24		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AH	3466	U	A	conflict	GB NC_045512.2
AH	3468	A	C	conflict	GB NC_045512.2

- Molecule 10 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	76	Total	C	N	O	P	0	0
			939	393	11	459	76		

- Molecule 11 is a RNA chain called P-site Leu-tRNA(Leu).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AT	86	Total	C	N	O	P	0	0
			1840	820	330	604	86		

- Molecule 12 is a protein called 40S ribosomal protein SA.



Mol	Chain	Residues	Atoms					AltConf	Trace
12	AZ	221	Total	C	N	O	S	0	0
			1743	1107	305	323	8		

- Molecule 13 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Aa	224	Total	C	N	O	S	0	0
			1815	1152	328	321	14		

- Molecule 14 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Ab	220	Total	C	N	O	S	0	0
			1706	1105	292	300	9		

- Molecule 15 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ac	225	Total	C	N	O	S	0	0
			1751	1116	315	313	7		

- Molecule 16 is a protein called Ribosomal protein eS4.

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

- Molecule 17 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ae	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 18 is a protein called 40S ribosomal protein S6.

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

- Molecule 19 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ag	190	Total	C	N	O	S	0	0
			1529	975	281	272	1		

- Molecule 20 is a protein called 40S ribosomal protein S8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 21 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 22 is a protein called Ribosomal protein eS10.

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

- Molecule 23 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Ak	154	Total	C	N	O	S	0	0
			1262	804	236	216	6		

- Molecule 24 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Al	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 25 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Am	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 26 is a protein called 40S ribosomal protein uS11.

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

- Molecule 27 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ao	133	Total	C	N	O	S	0	0
			1091	694	205	185	7		

- Molecule 28 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ap	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 29 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Aq	134	Total	C	N	O	S	0	0
			1080	678	201	197	4		

- Molecule 30 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ar	145	Total	C	N	O	S	0	0
			1200	753	242	204	1		

- Molecule 31 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	As	143	Total	C	N	O	S	0	0
			1113	698	214	198	3		

- Molecule 32 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	At	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 33 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Au	83	Total	C	N	O	S	0	0
			640	394	117	124	5		

- Molecule 34 is a protein called Ribosomal protein S15a.

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

- Molecule 35 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Aw	141	Total	C	N	O	S	0	0
			1099	693	219	184	3		

- Molecule 36 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ax	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 37 is a protein called 40S ribosomal protein S25.

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

- Molecule 38 is a protein called 60s ribosomal protein l41.

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

- Molecule 39 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B5	3764	Total	C	N	O	P	0	0
			80772	36003	14762	26243	3764		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	3550	UY1	U	conflict	GB GBCN01009604.1

- Molecule 40 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	B7	119	Total	C	N	O	P	0	0
			2538	1131	451	837	119		

- Molecule 41 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	B8	156	Total	C	N	O	P	0	0
			3319	1481	585	1097	156		

- Molecule 42 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BA	253	Total	C	N	O	S	0	0
			1940	1214	396	324	6		

- Molecule 43 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BB	398	Total	C	N	O	S	0	0
			3206	2042	605	546	13		

- Molecule 44 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BC	362	Total	C	N	O	S	0	0
			2886	1814	577	481	14		

- Molecule 45 is a protein called Ribosomal\_L18\_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BD	294	Total	C	N	O	S	0	0
			2398	1516	439	429	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BD	2	AAC	GLY	conflict	UNP G1SYJ6

- Molecule 46 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BE	243	Total	C	N	O	S	0	0
			1960	1258	378	321	3		

- Molecule 47 is a protein called Ribosomal Protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BF	226	Total	C	N	O	S	0	0
			1886	1211	362	304	9		

- Molecule 48 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BG	233	Total	C	N	O	S	0	0
			1877	1197	361	315	4		

- Molecule 49 is a protein called 60S ribosomal protein L9.

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

- Molecule 50 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BI	213	Total	C	N	O	S	0	0
			1717	1086	332	285	14		

- Molecule 51 is a protein called Ribosomal protein L11.

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

- Molecule 52 is a protein called Replicase polyprotein 1ab.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BK	36	Total	C	N	O	S	0	0
			273	169	46	52	6		

- Molecule 53 is a protein called Ribosomal protein eL13.

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

- Molecule 54 is a protein called Ribosomal protein L14.

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

- Molecule 55 is a protein called Ribosomal protein L15.

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

- Molecule 56 is a protein called Ribosomal protein L13a.

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

- Molecule 57 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BP	159	Total	C	N	O	S	0	0
			1289	809	249	222	9		

- Molecule 58 is a protein called Ribosomal protein L18.

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

- Molecule 59 is a protein called 60S ribosomal protein L19.

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

- Molecule 60 is a protein called Ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BS	176	Total	C	N	O	S	0	0
			1457	924	288	234	11		

- Molecule 61 is a protein called eL21.

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

- Molecule 62 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BU	99	Total	C	N	O	S	0	0
			806	516	141	147	2		

- Molecule 63 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BV	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 64 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BW	121	Total	C	N	O	S	0	0
			991	619	202	166	4		

- Molecule 65 is a protein called uL23.



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

- Molecule 66 is a protein called Ribosomal protein L26.

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

- Molecule 67 is a protein called 60S ribosomal protein L27.

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

- Molecule 68 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ba	147	Total	C	N	O	S	0	0
			1163	734	239	186	4		

- Molecule 69 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bb	108	Total	C	N	O	S	0	0
			881	548	196	134	3		

- Molecule 70 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bc	108	Total	C	N	O	S	0	0
			836	530	148	151	7		

- Molecule 71 is a protein called eL31.

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

- Molecule 72 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Be	130	Total	C	N	O	S	0	0
			1070	676	221	168	5		

- Molecule 73 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bf	110	Total	C	N	O	S	0	0
			884	560	175	144	5		

- Molecule 74 is a protein called 60S ribosomal protein L34.

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

- Molecule 75 is a protein called uL29.

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

- Molecule 76 is a protein called 60S ribosomal protein L36.

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

- Molecule 77 is a protein called Ribosomal protein L37.

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

- Molecule 78 is a protein called eL38.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 79 is a protein called eL39.

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

- Molecule 80 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Bm	52	Total	C	N	O	S	0	0
			432	269	90	67	6		

- Molecule 81 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bo	105	Total	C	N	O	S	0	0
			863	543	175	139	6		

- Molecule 82 is a protein called eL43.

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

- Molecule 83 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Br	126	Total	C	N	O	S	0	0
			1014	629	209	170	6		

- Molecule 84 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bs	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 85 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Bt	156	Total	C	N	O	S	0	0
			1178	733	221	220	4		

- Molecule 86 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Bv	212	Total	C	N	O	S	0	0
			1707	1092	308	299	8		

- Molecule 87 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	By	416	Total	C	N	O	S	0	0
			3280	2087	559	623	11		

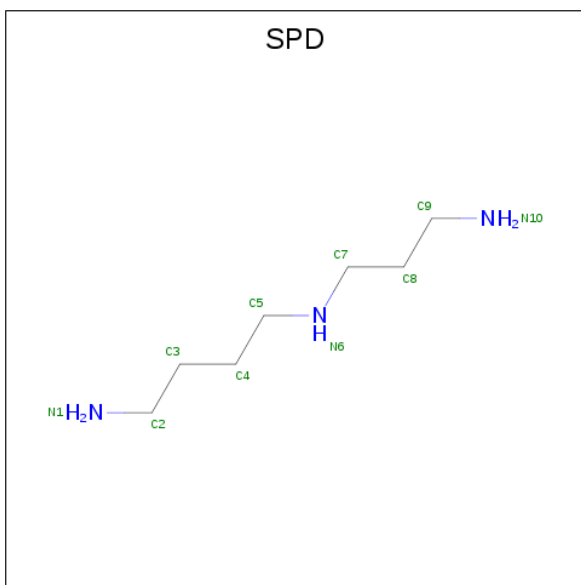
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
By	183	ALA	GLY	engineered mutation	UNP P62497
By	184	ALA	GLY	engineered mutation	UNP P62497

- Molecule 88 is a protein called ATP binding cassette subfamily E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	Bz	595	Total	C	N	O	S	0	0
			4668	2982	801	854	31		

- Molecule 89 is SPERMIDINE (three-letter code: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).



Mol	Chain	Residues	Atoms			AltConf
89	A2	1	Total	C	N	0
			10	7	3	

- Molecule 90 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
90	A2	102	Total	Mg	0
			102	102	
90	AH	1	Total	Mg	0
			1	1	
90	AT	2	Total	Mg	0
			2	2	
90	B5	235	Total	Mg	0
			235	235	
90	B7	4	Total	Mg	0
			4	4	
90	B8	6	Total	Mg	0
			6	6	
90	BI	1	Total	Mg	0
			1	1	
90	BP	1	Total	Mg	0
			1	1	
90	BR	1	Total	Mg	0
			1	1	
90	BV	1	Total	Mg	0
			1	1	
90	Ba	1	Total	Mg	0
			1	1	

- Molecule 91 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		AltConf
91	A2	76	Total 76	X 76	0
91	AT	4	Total 4	X 4	0
91	Ab	1	Total 1	X 1	0
91	Ak	1	Total 1	X 1	0
91	Ar	1	Total 1	X 1	0
91	B5	244	Total 244	X 244	0
91	B7	10	Total 10	X 10	0
91	B8	16	Total 16	X 16	0
91	BA	2	Total 2	X 2	0
91	BB	3	Total 3	X 3	0
91	BC	1	Total 1	X 1	0
91	BH	1	Total 1	X 1	0
91	BI	1	Total 1	X 1	0
91	BL	1	Total 1	X 1	0
91	BN	2	Total 2	X 2	0
91	BP	1	Total 1	X 1	0
91	BQ	2	Total 2	X 2	0
91	BT	1	Total 1	X 1	0
91	Bb	1	Total 1	X 1	0
91	Be	2	Total 2	X 2	0
91	Bf	1	Total 1	X 1	0

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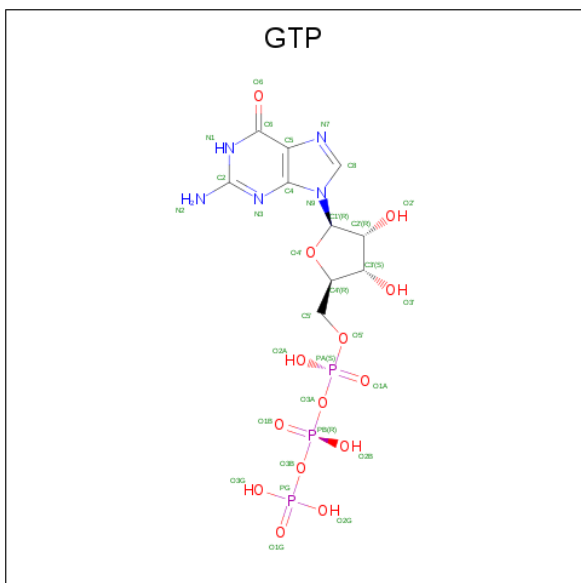
*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
91	Bg	1	Total 1	X 1	0
91	Bo	1	Total 1	X 1	0

- Molecule 92 is ZINC ION (three-letter code: ZN) (formula: Zn).

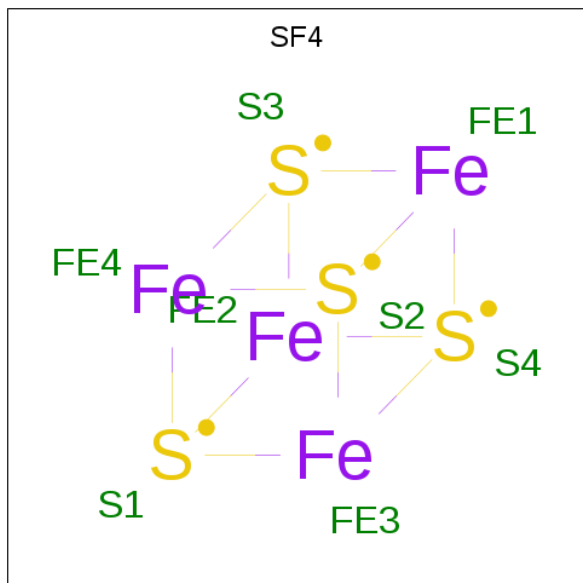
Mol	Chain	Residues	Atoms		AltConf
92	AC	1	Total 1	Zn 1	0
92	AE	1	Total 1	Zn 1	0
92	AG	1	Total 1	Zn 1	0
92	Bg	1	Total 1	Zn 1	0
92	Bj	1	Total 1	Zn 1	0
92	Bm	1	Total 1	Zn 1	0
92	Bo	1	Total 1	Zn 1	0
92	Bp	1	Total 1	Zn 1	0

- Molecule 93 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					AltConf
93	B7	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 94 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms			AltConf
94	Bz	1	Total	Fe	S	0
			16	8	8	
94	Bz	1	Total	Fe	S	0
			16	8	8	

- Molecule 95 is water.

Mol	Chain	Residues	Atoms		AltConf
95	A2	473	Total	O	0
			473	473	
95	AH	10	Total	O	0
			10	10	
95	AT	12	Total	O	0
			12	12	
95	Aa	2	Total	O	0
			2	2	
95	Ab	1	Total	O	0
			1	1	
95	Ad	1	Total	O	0
			1	1	
95	Af	2	Total	O	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
95	Ak	1	Total 1	O 1	0
95	Am	1	Total 1	O 1	0
95	An	2	Total 2	O 2	0
95	Ap	4	Total 4	O 4	0
95	Ar	1	Total 1	O 1	0
95	As	4	Total 4	O 4	0
95	Aw	4	Total 4	O 4	0
95	B5	1117	Total 1117	O 1117	0
95	B7	17	Total 17	O 17	0
95	B8	31	Total 31	O 31	0
95	BA	5	Total 5	O 5	0
95	BB	7	Total 7	O 7	0
95	BC	3	Total 3	O 3	0
95	BD	1	Total 1	O 1	0
95	BF	1	Total 1	O 1	0
95	BH	1	Total 1	O 1	0
95	BI	1	Total 1	O 1	0
95	BL	1	Total 1	O 1	0
95	BN	2	Total 2	O 2	0
95	BO	3	Total 3	O 3	0
95	BP	3	Total 3	O 3	0

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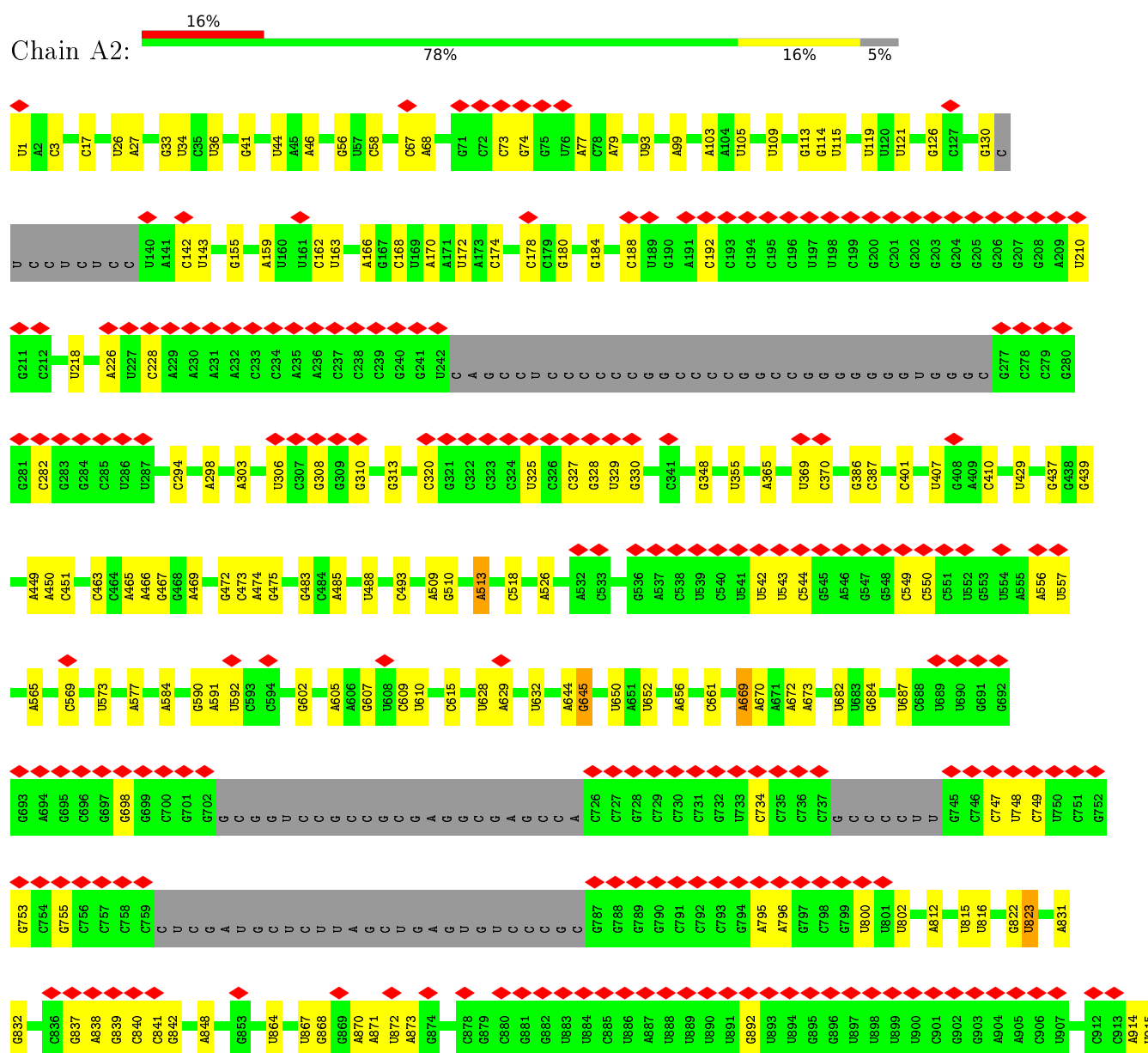
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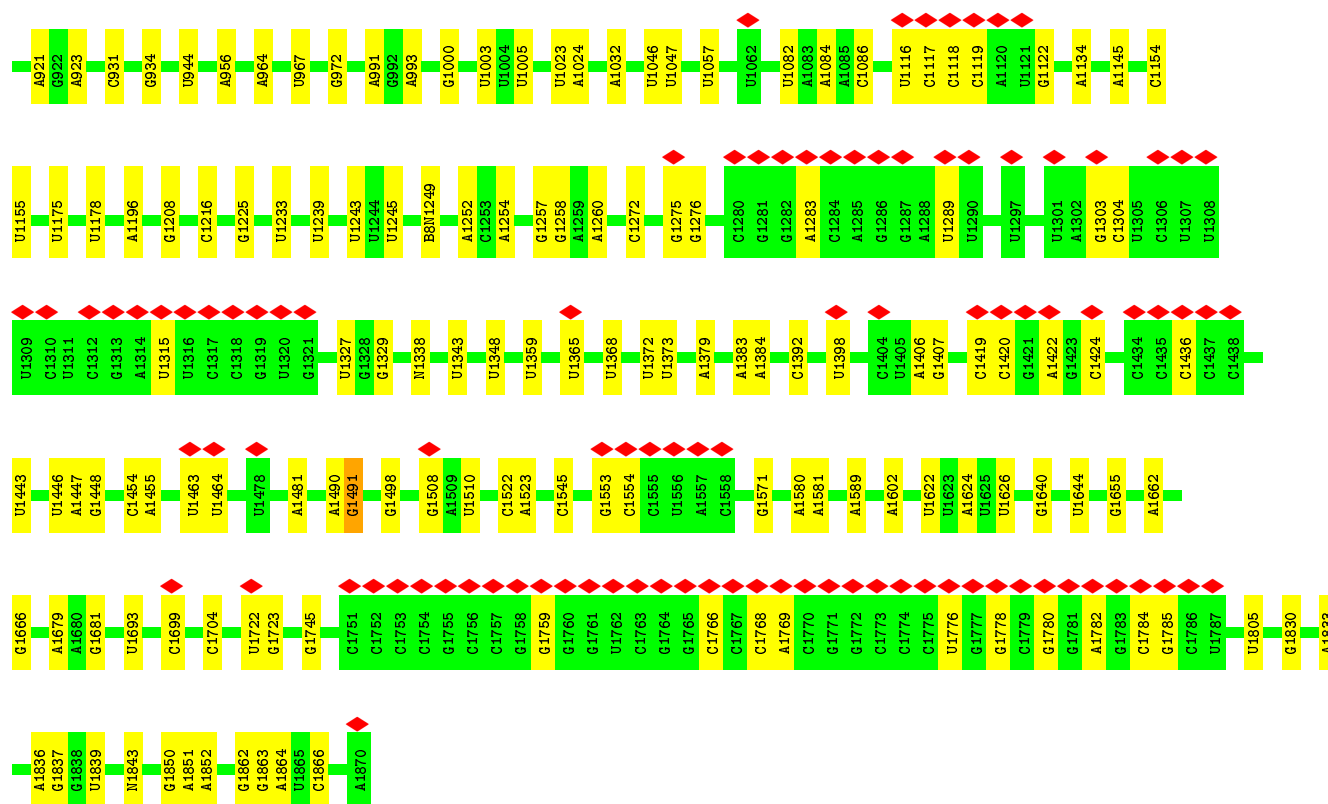
Mol	Chain	Residues	Atoms		AltConf
95	BR	5	Total 5	O 5	0
95	BV	4	Total 4	O 4	0
95	BX	1	Total 1	O 1	0
95	BY	1	Total 1	O 1	0
95	Ba	7	Total 7	O 7	0
95	Bb	1	Total 1	O 1	0
95	Bd	1	Total 1	O 1	0
95	Be	4	Total 4	O 4	0
95	Bf	1	Total 1	O 1	0
95	By	1	Total 1	O 1	0

### 3 Residue-property plots

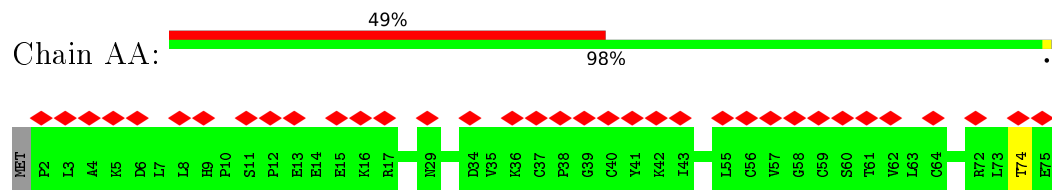
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

#### • Molecule 1: 18S rRNA

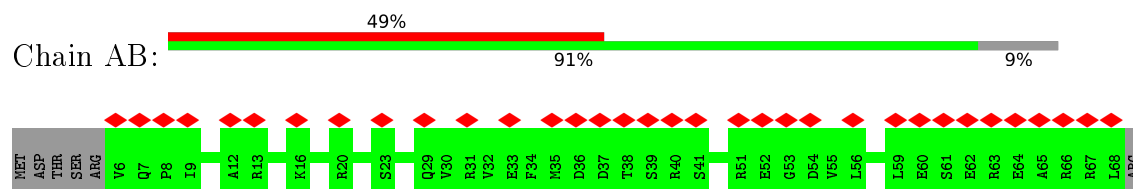




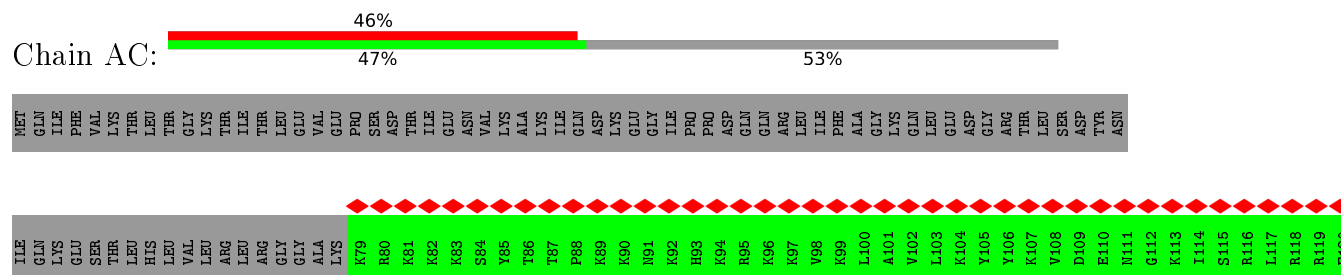
- Molecule 2: 40S ribosomal protein S27

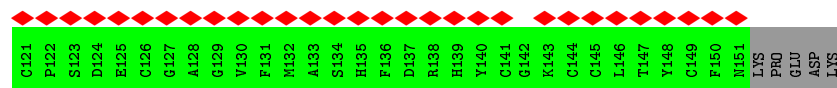


- Molecule 3: Ribosomal protein S28

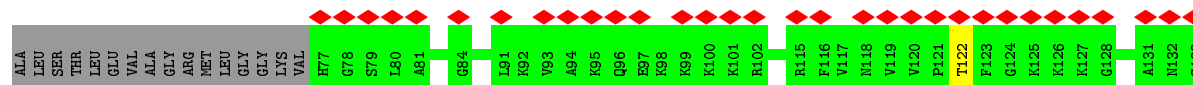
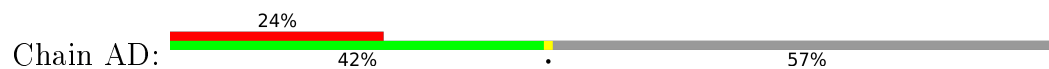


- Molecule 4: Ribosomal protein S27a

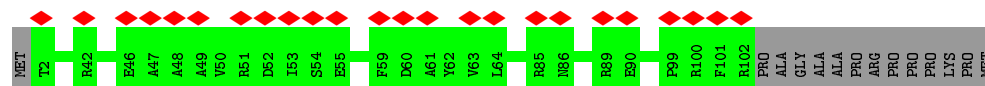
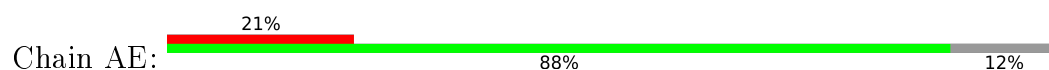




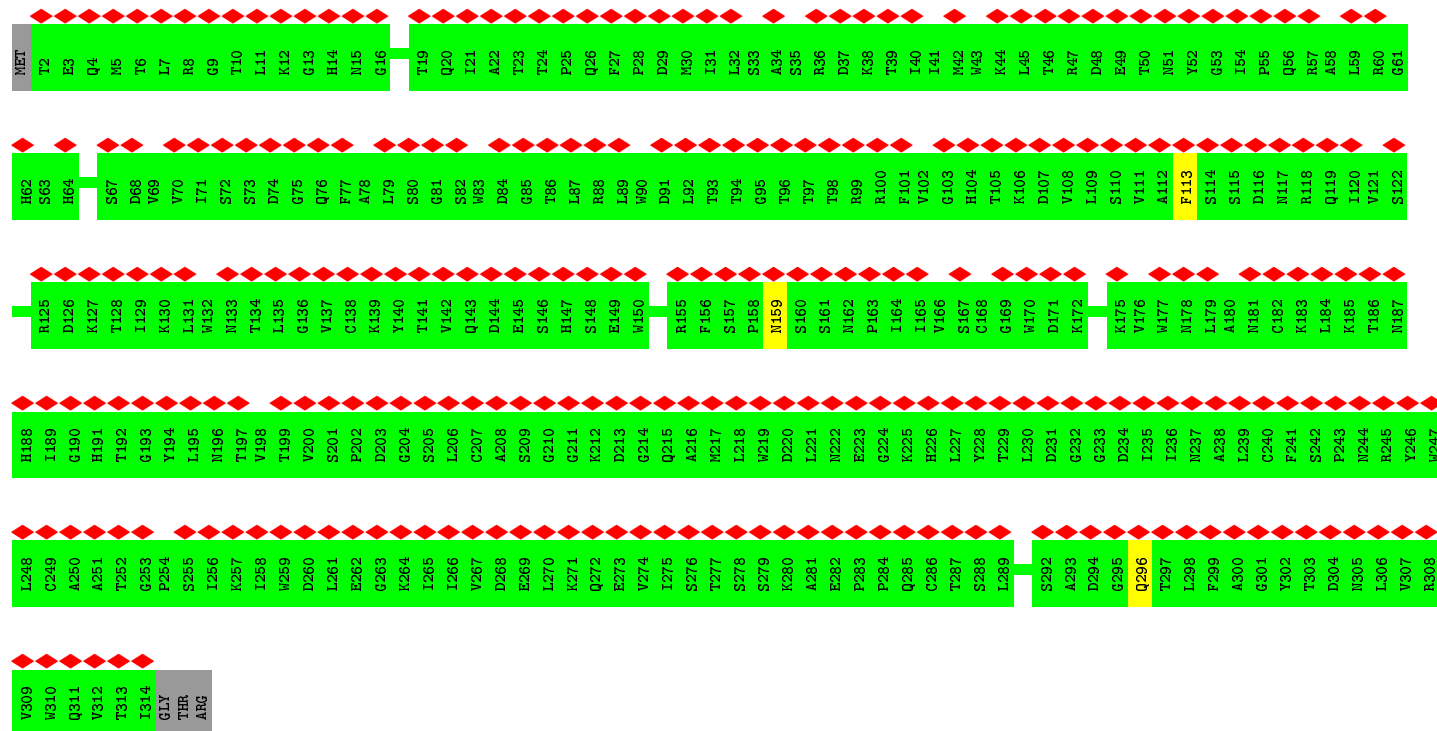
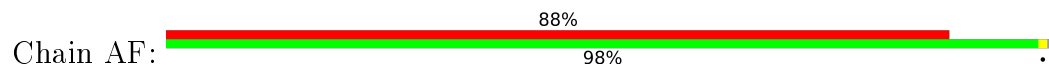
- Molecule 5: 40S ribosomal protein S30



- Molecule 6: Ribosomal protein eS26



- Molecule 7: RACK1



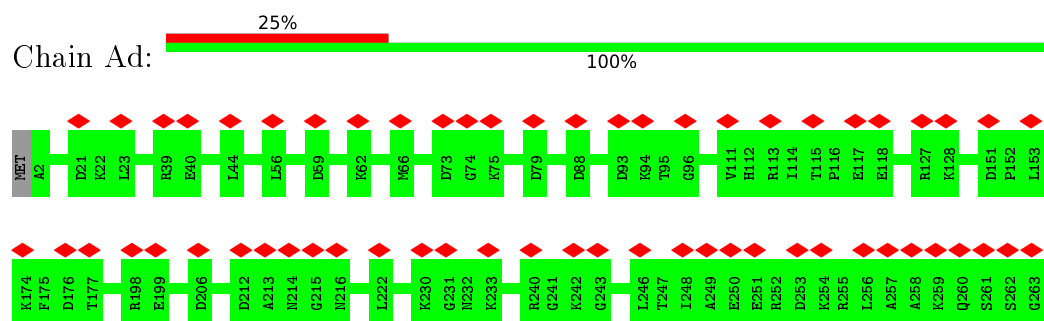
- Molecule 8: uS14



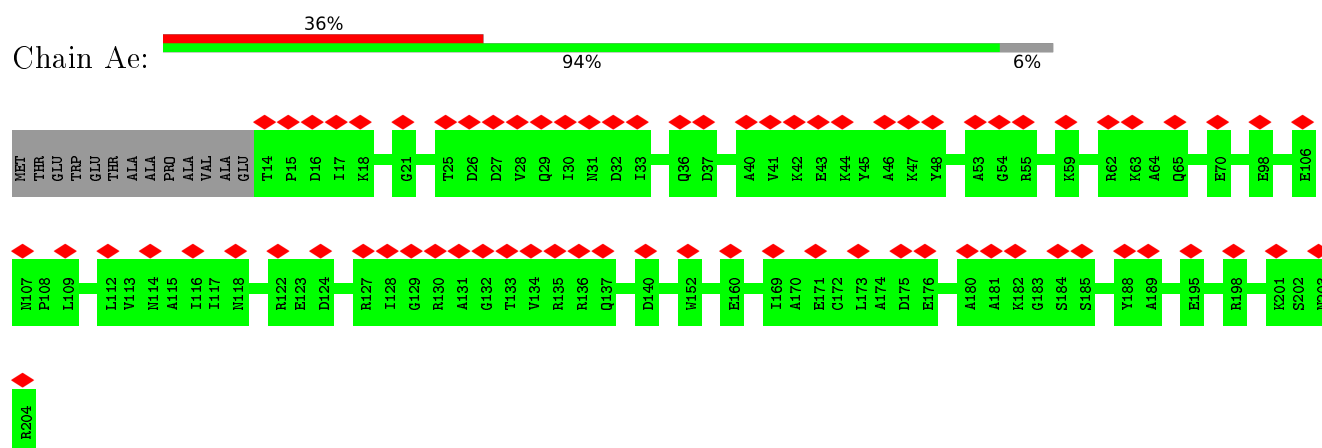




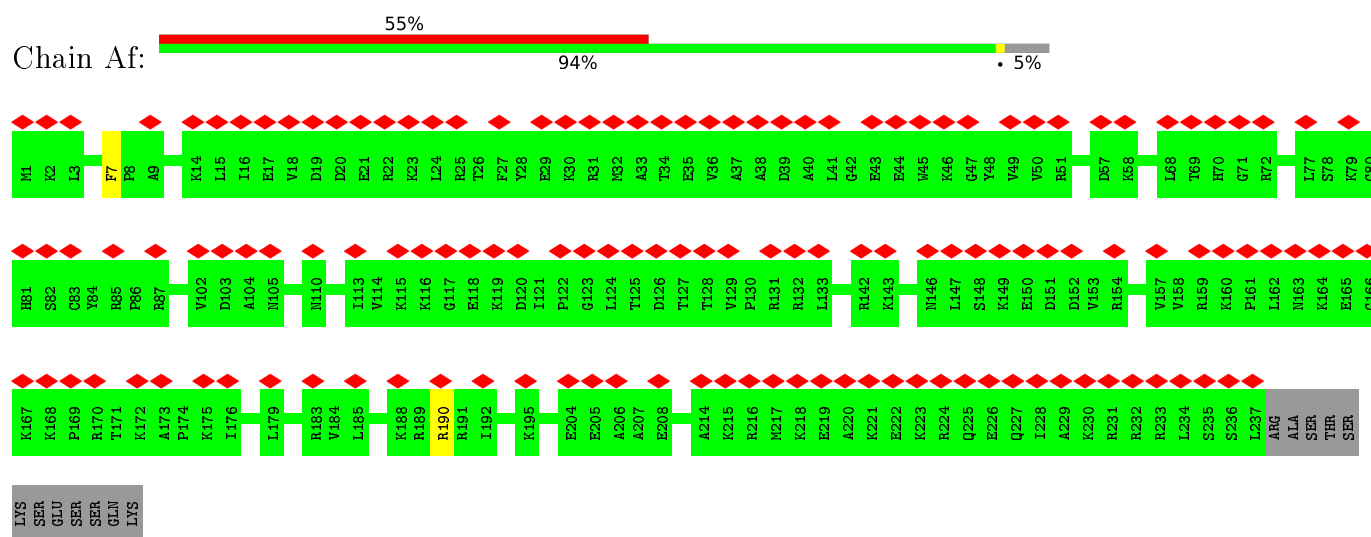
- Molecule 16: Ribosomal protein eS4



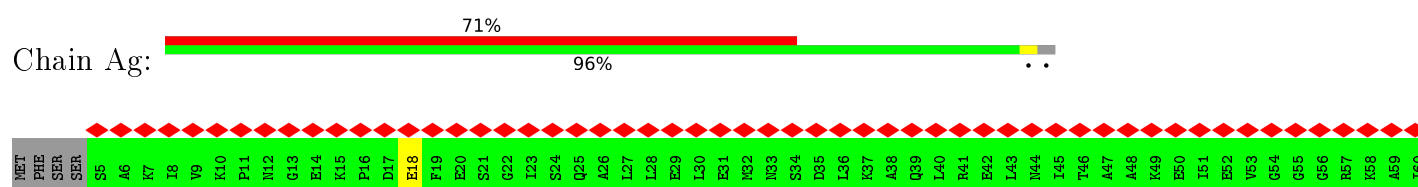
- Molecule 17: Ribosomal protein S5



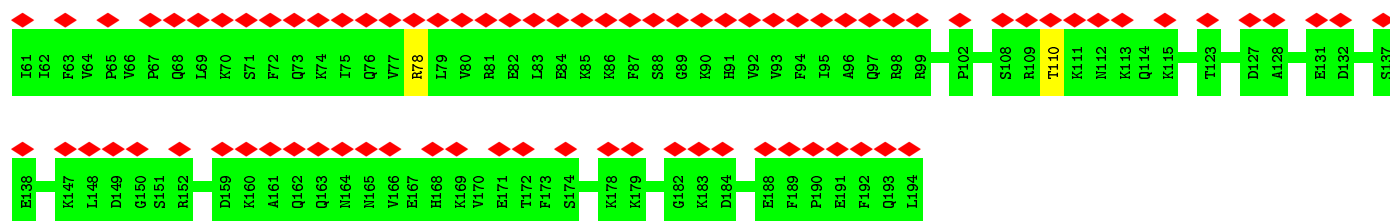
- Molecule 18: 40S ribosomal protein S6



- Molecule 19: 40S ribosomal protein S7

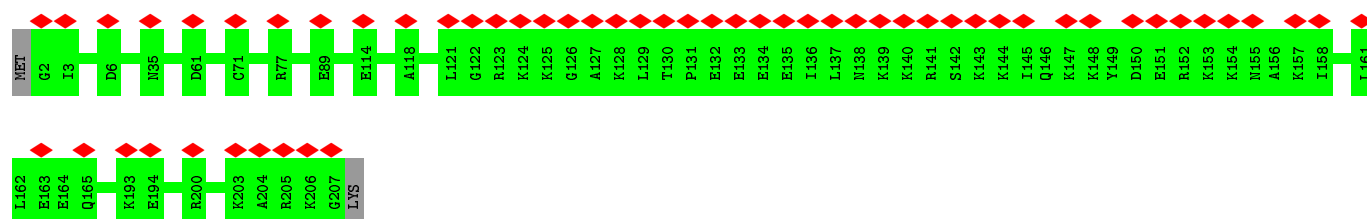






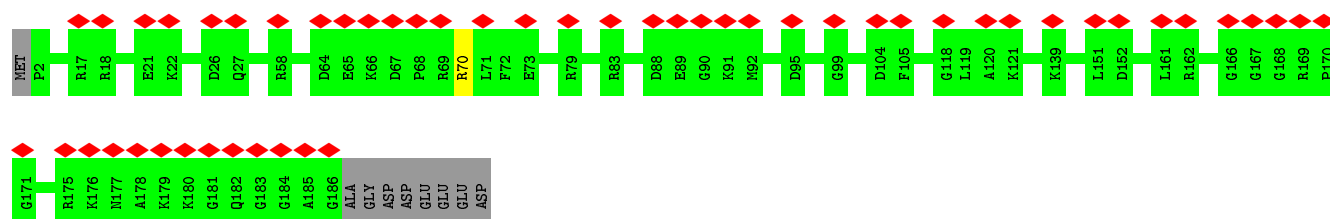
- Molecule 20: 40S ribosomal protein S8

Chain Ah: 27% 99%



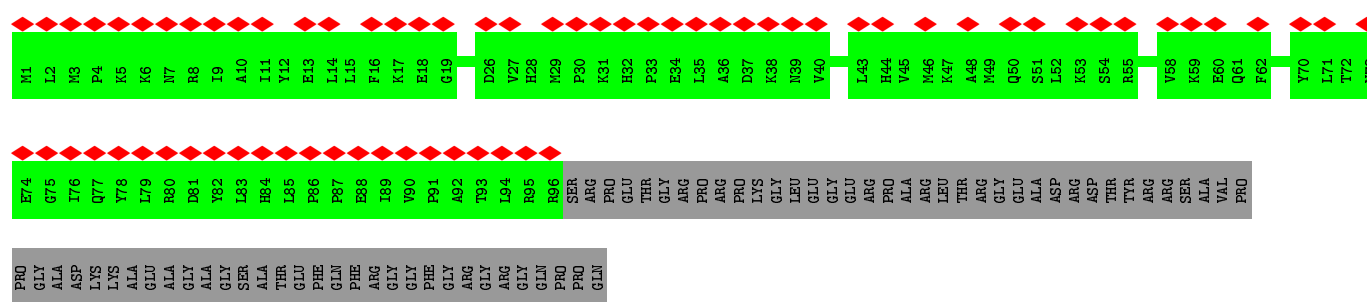
- Molecule 21: Ribosomal protein S9 (Predicted)

Chain Ai: 27% 95% 5%



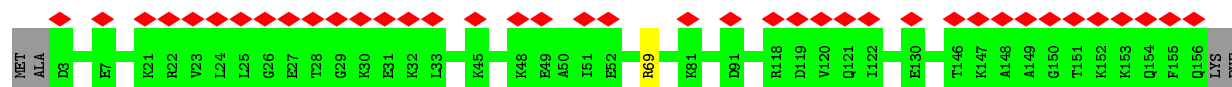
- Molecule 22: Ribosomal protein eS10

Chain Aj: 42% 58% 42%



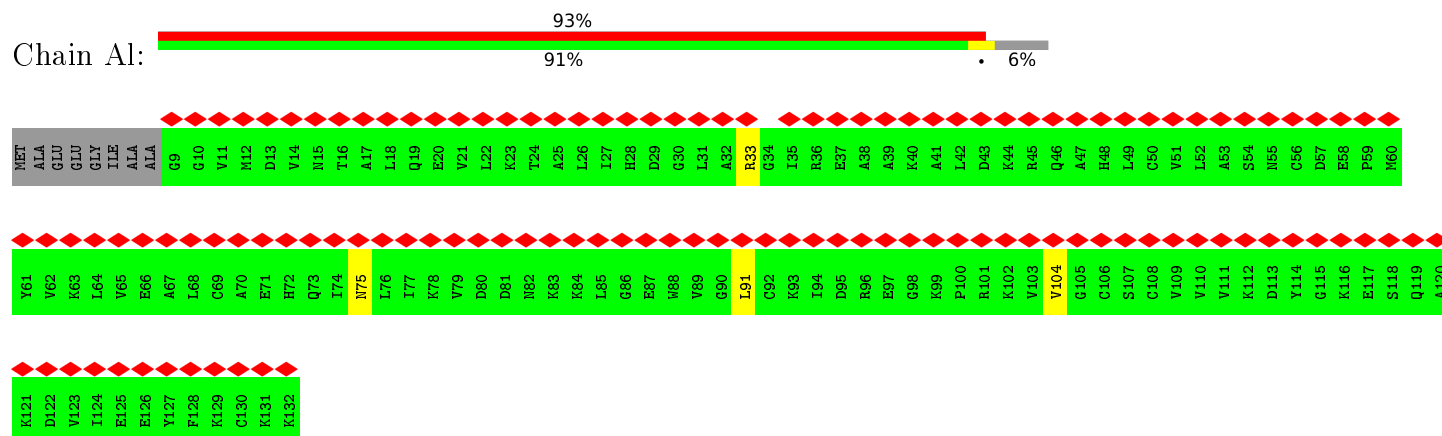
- Molecule 23: 40S ribosomal protein S11

Chain Ak: 25% 97%



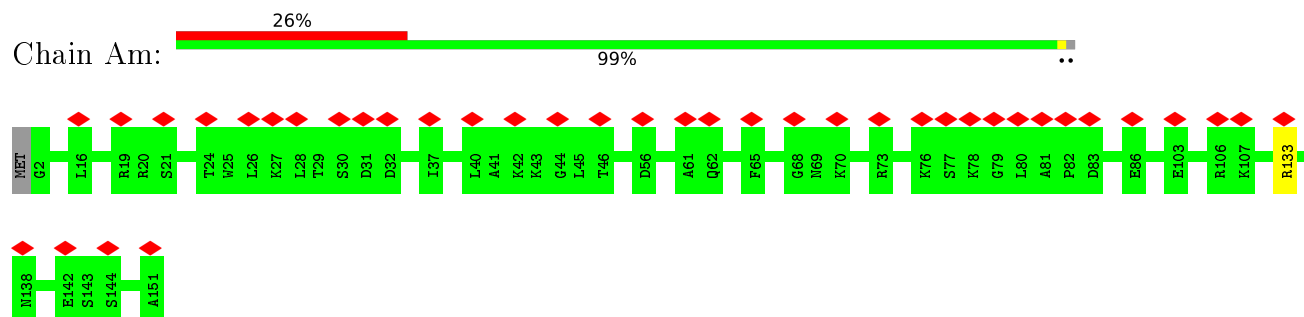
- Molecule 24: 40S ribosomal protein S12

Chain A1:



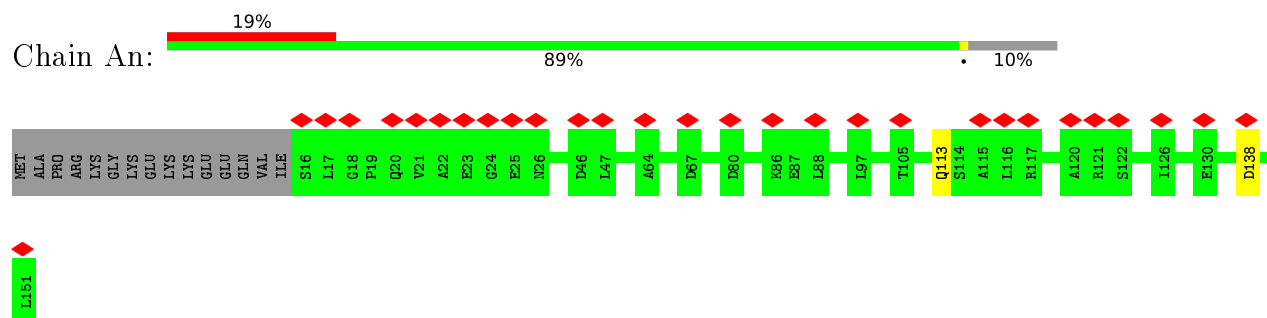
- Molecule 25: uS15

Chain Am:



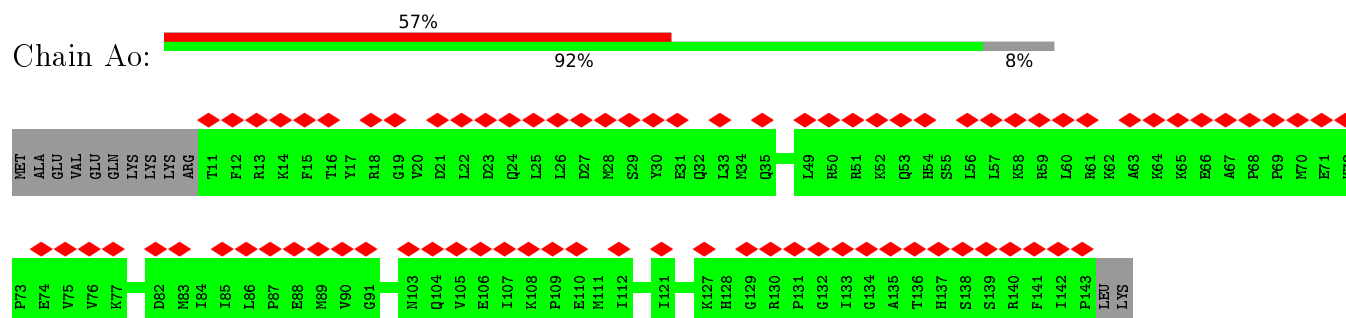
- Molecule 26: 40S ribosomal protein uS11

Chain An:



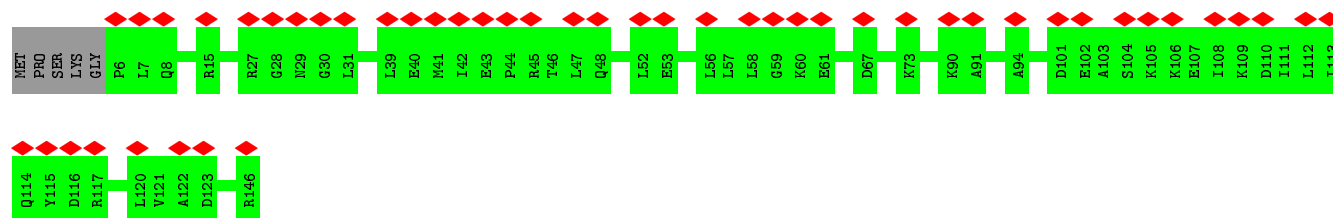
- Molecule 27: 40S ribosomal protein uS19

Chain Ao:



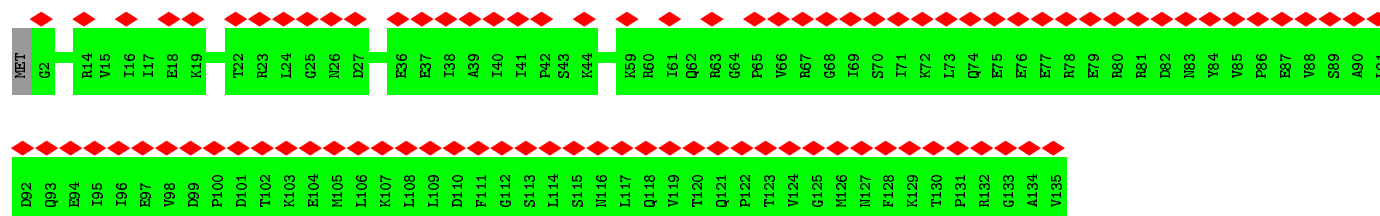
- Molecule 28: Ribosomal protein S16

Chain Ap: 



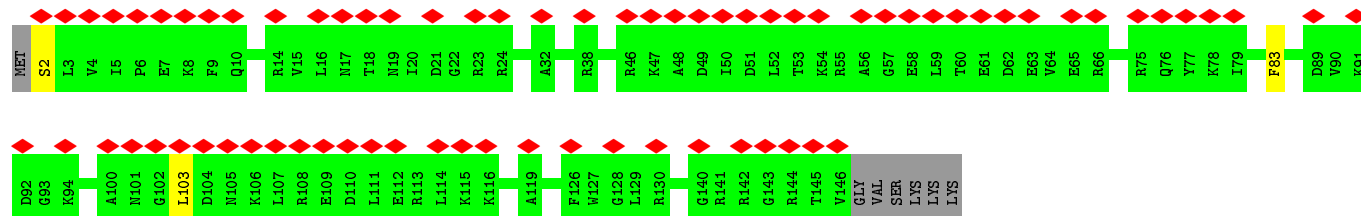
- Molecule 29: 40S ribosomal protein eS17

Chain Aq: 

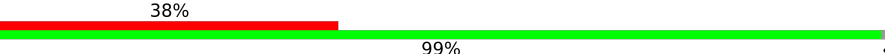


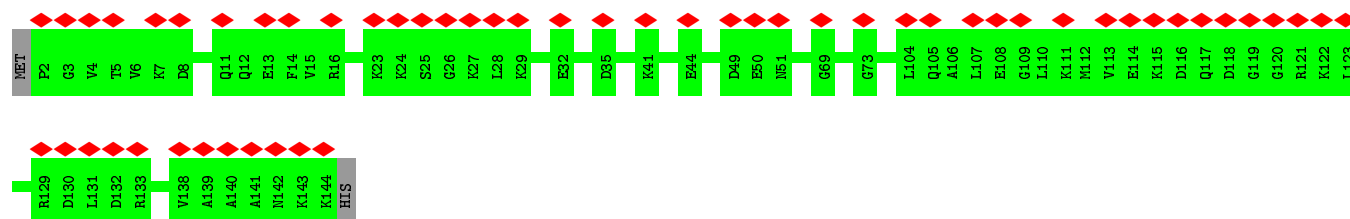
- Molecule 30: 40S ribosomal protein S18

Chain Ar: 




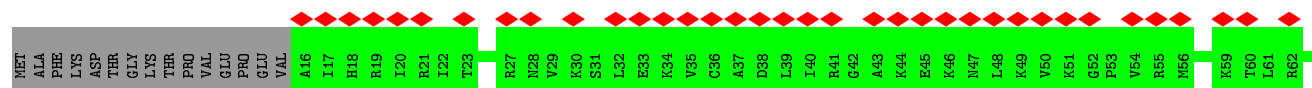
- Molecule 31: Ribosomal protein eS19

Chain As: 



- Molecule 32: 40S ribosomal protein uS10

Chain At: 



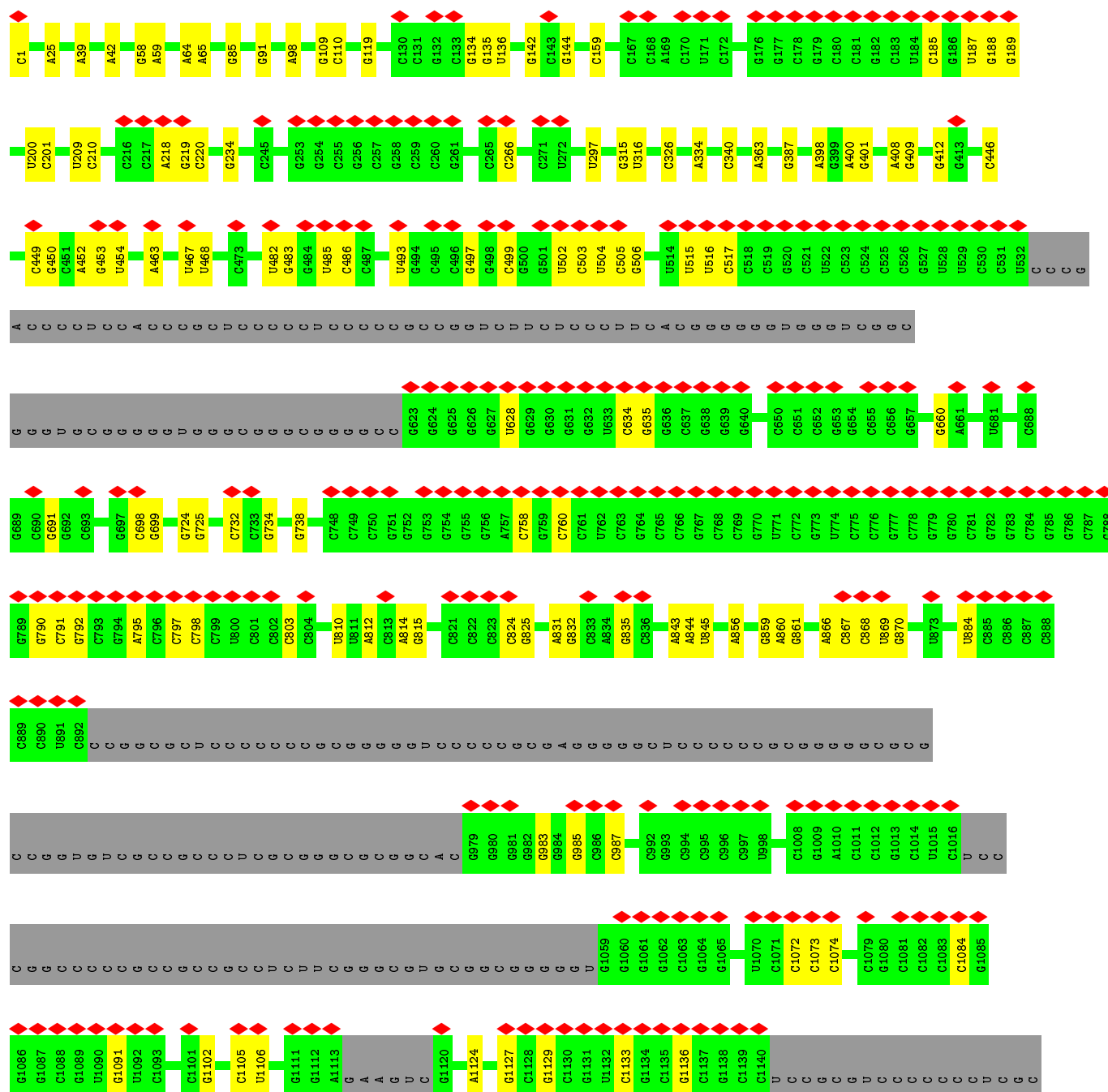


Chain Az:  100%



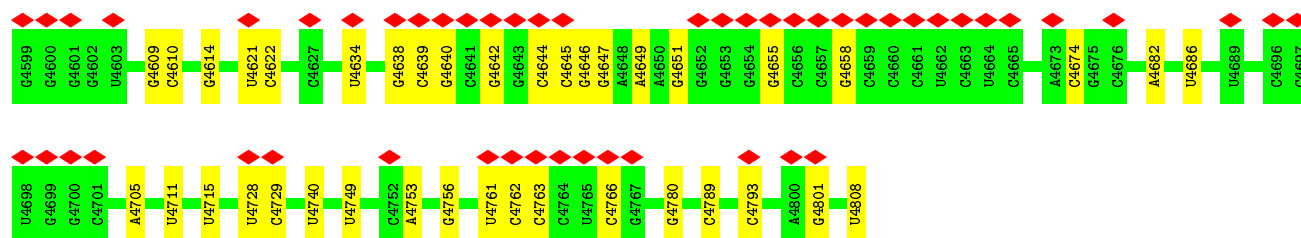
• Molecule 39: 28S rRNA

Chain B5:  14% 66% 12% 22%

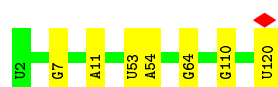




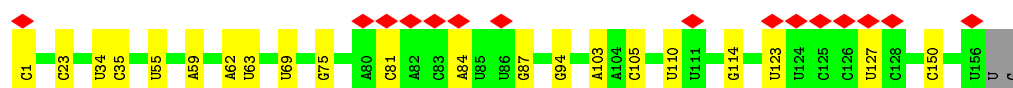
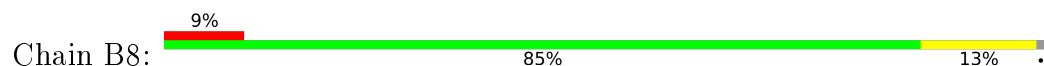




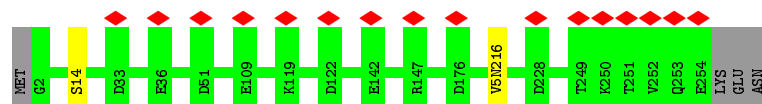
• Molecule 40: 5S rRNA



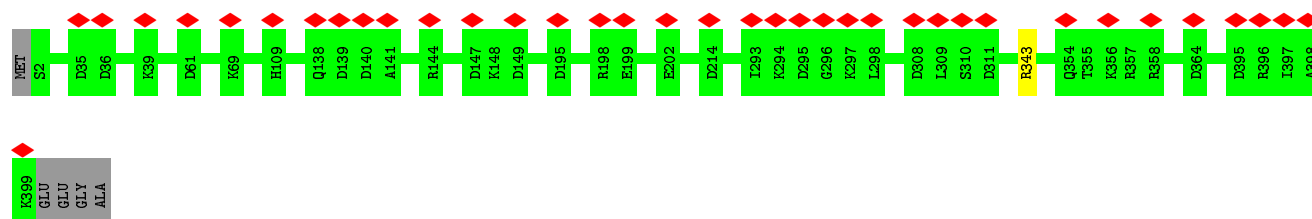
• Molecule 41: 5.8S rRNA



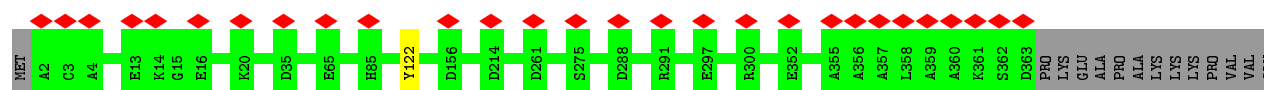
• Molecule 42: Ribosomal protein uL2



• Molecule 43: Ribosomal protein L3



• Molecule 44: 60S ribosomal protein L4

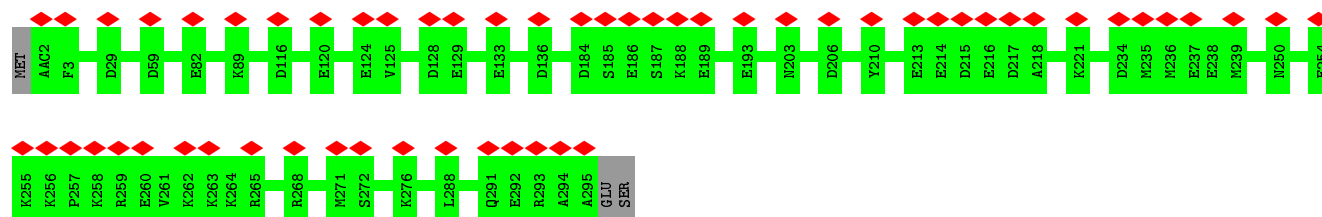




LYS  
LYS  
LYS  
LYS  
PRO  
VAL  
VAL  
GLY  
ARG  
LYS  
LYS  
ALA  
ALA  
ALA  
LYS  
LYS  
LYS  
PRO  
ALA  
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ASP  
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ALA

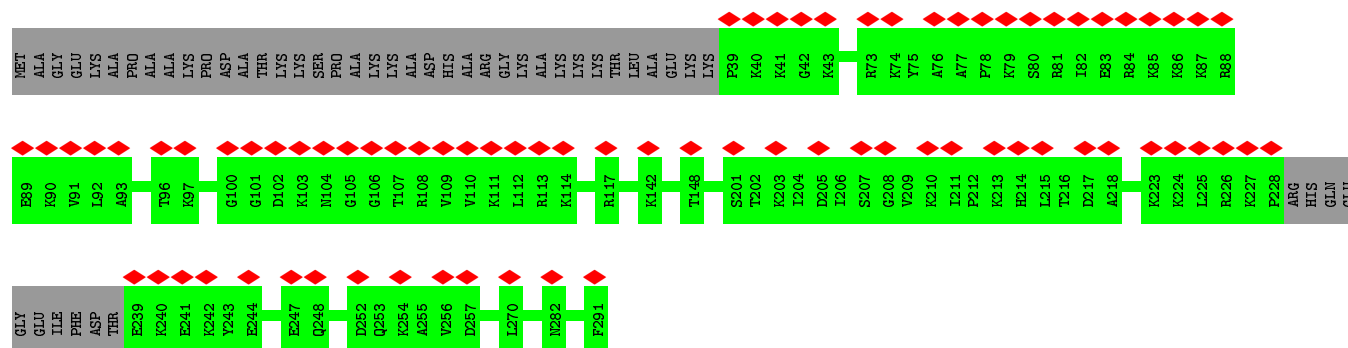
- Molecule 45: Ribosomal\_L18\_c domain-containing protein

Chain BD: 19% 99%



- Molecule 46: 60S ribosomal protein L6

Chain BE: 26% 84% 16%



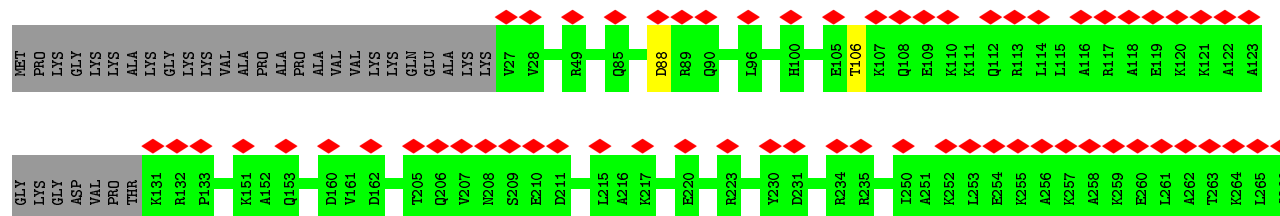
- Molecule 47: Ribosomal Protein uL30

Chain BF: 6% 91% 9%



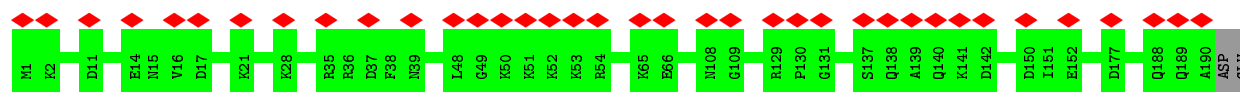
- Molecule 48: Ribosomal protein eL8

Chain BG: 24% 87% 12%

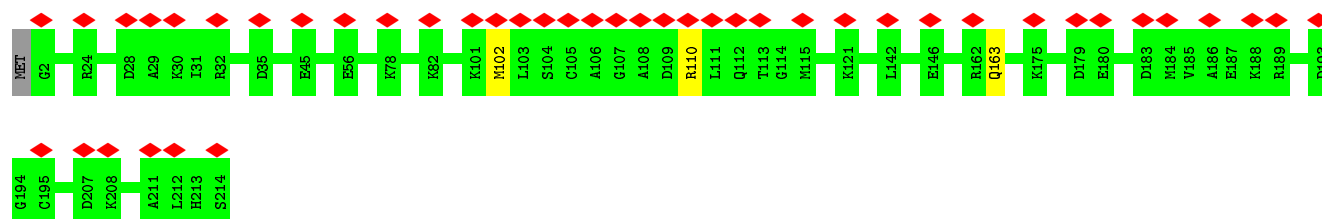


- Molecule 49: 60S ribosomal protein L9

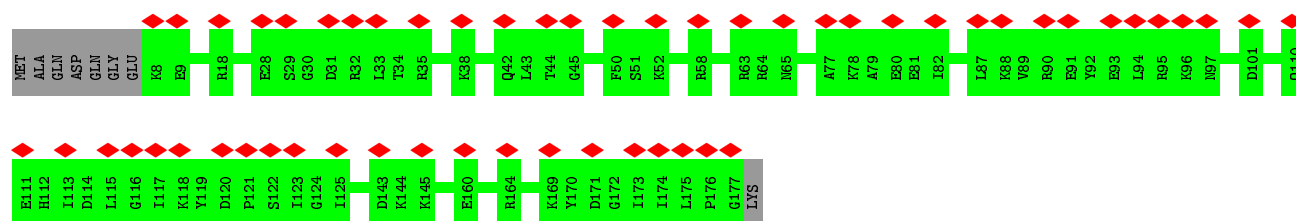
Chain BH: 19% 99%



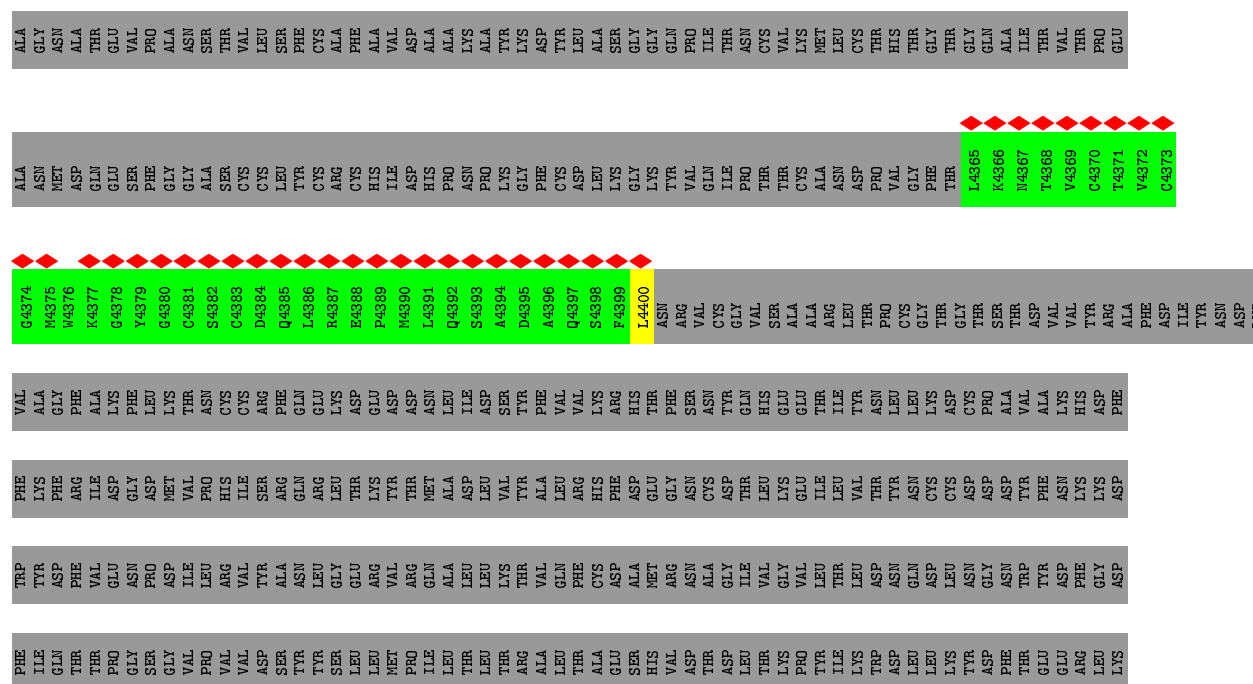
- Molecule 50: 60S ribosomal protein L10



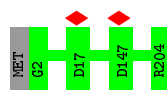
- Molecule 51: Ribosomal protein L11



- Molecule 52: Replicase polypeptide 1ab



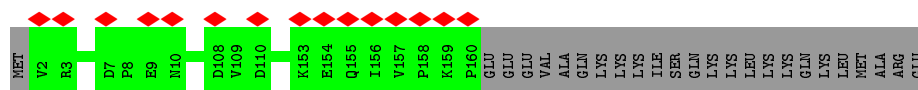




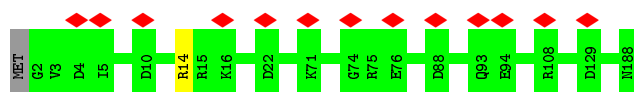
- Molecule 56: Ribosomal protein L13a



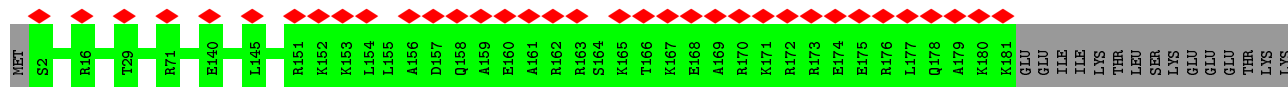
- Molecule 57: uL22



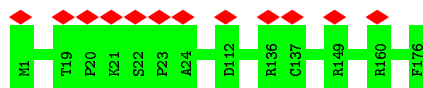
- Molecule 58: Ribosomal protein L18



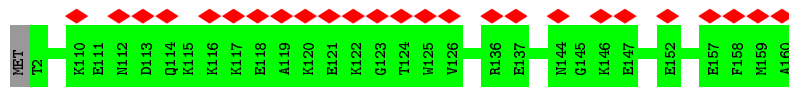
- Molecule 59: 60S ribosomal protein L19



- Molecule 60: Ribosomal protein L18a



- Molecule 61: eL21

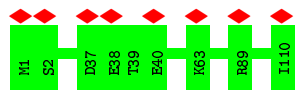


- Molecule 62: Ribosomal protein eL22

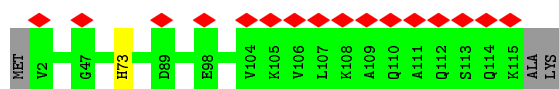




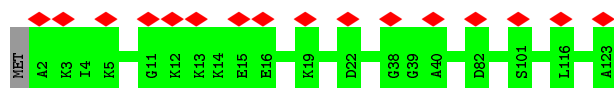
## • Molecule 73: eL33



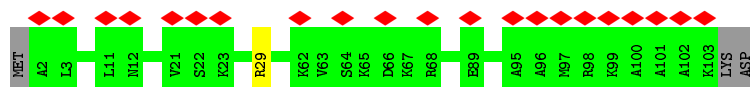
## • Molecule 74: 60S ribosomal protein L34



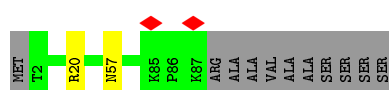
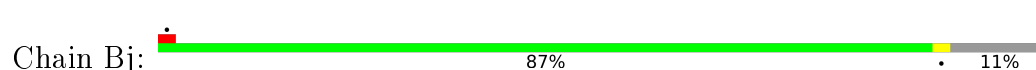
## • Molecule 75: uL29



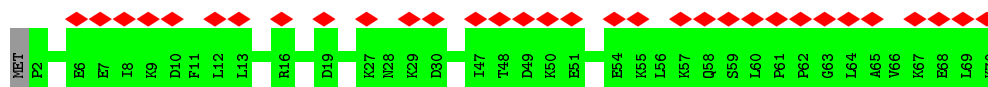
## • Molecule 76: 60S ribosomal protein L36



## • Molecule 77: Ribosomal protein L37

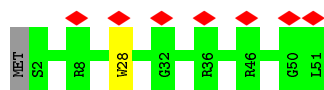


## • Molecule 78: eL38

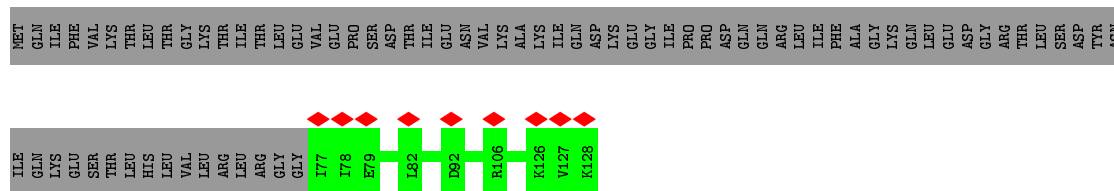


## • Molecule 79: eL39

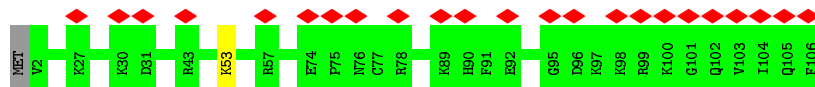




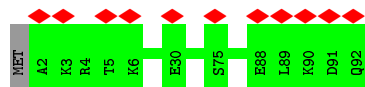
- Molecule 80: 60S ribosomal protein L40



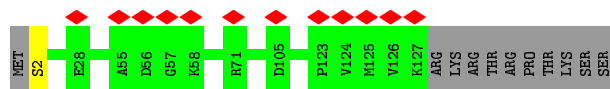
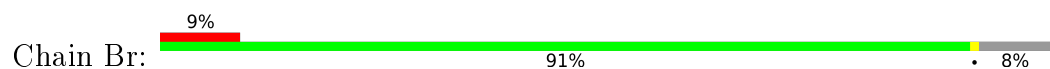
- Molecule 81: eL42



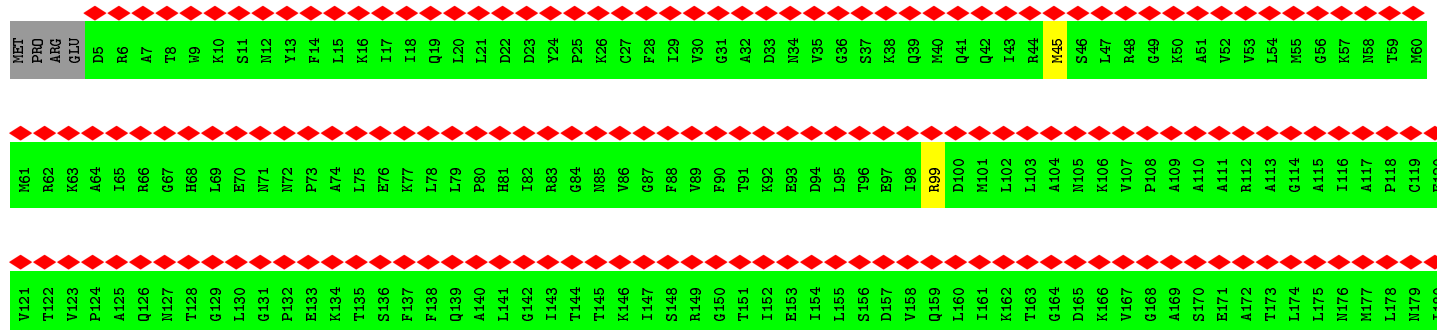
- Molecule 82: eL43



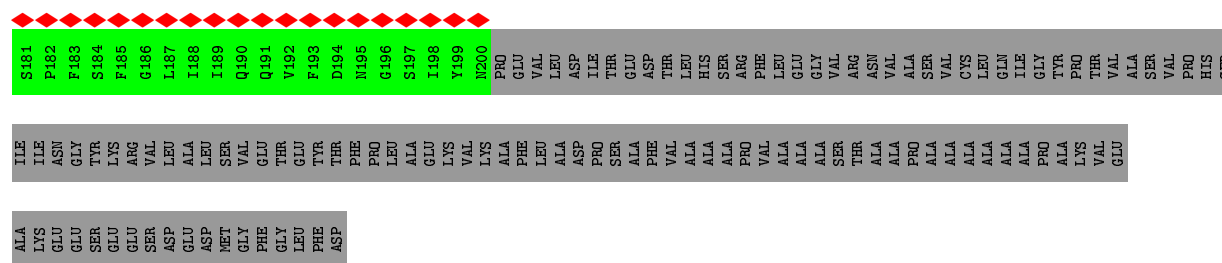
- Molecule 83: Ribosomal protein eL28



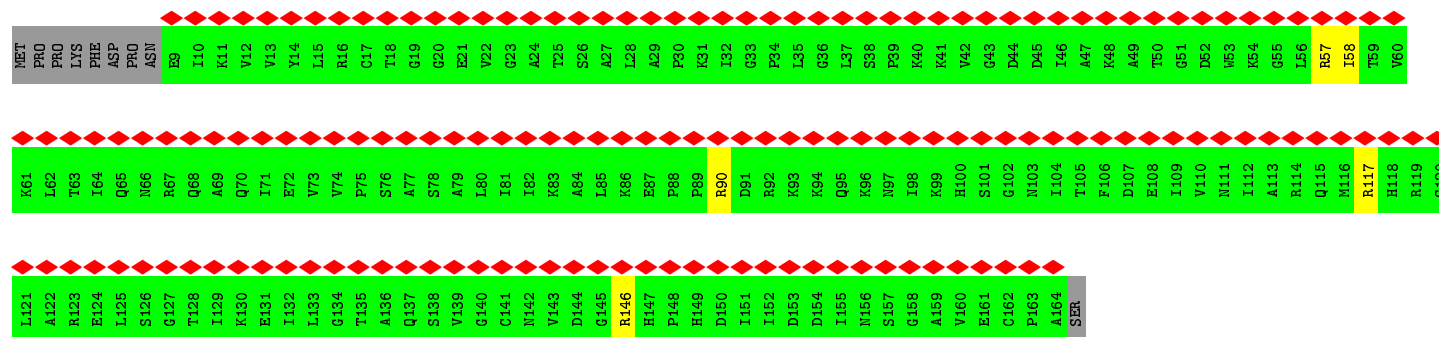
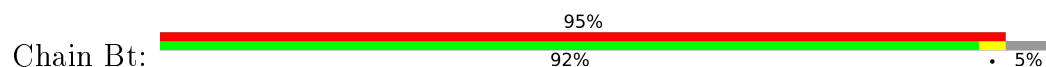
- Molecule 84: 60S acidic ribosomal protein P0



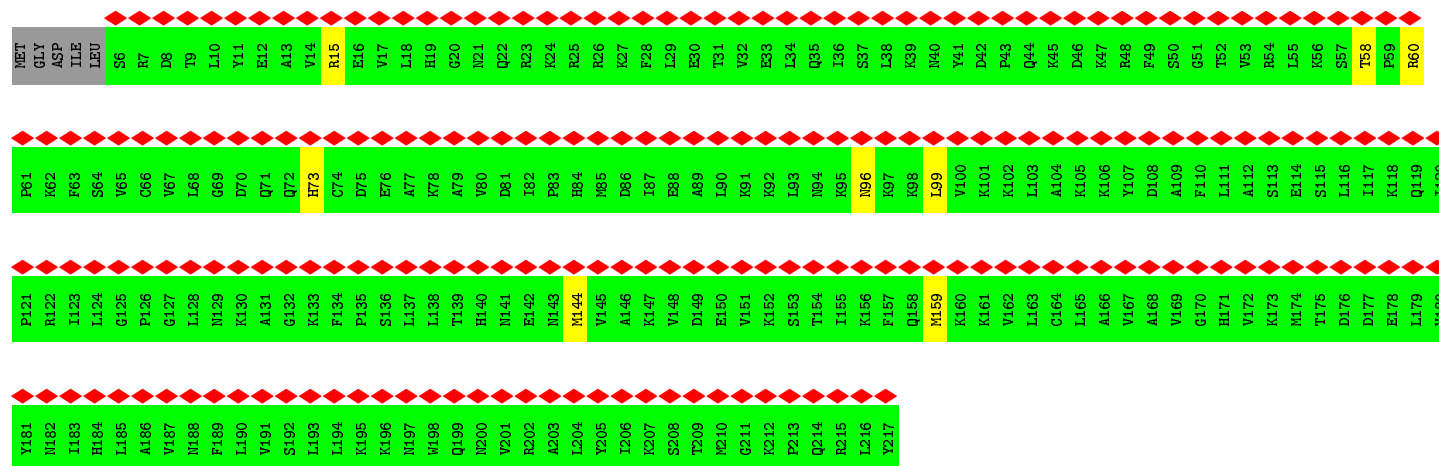




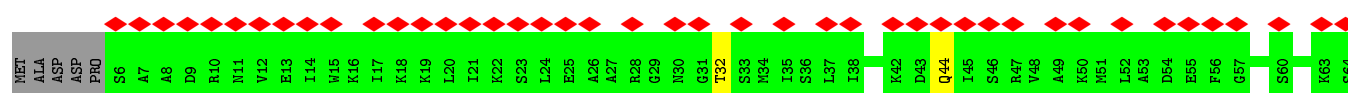
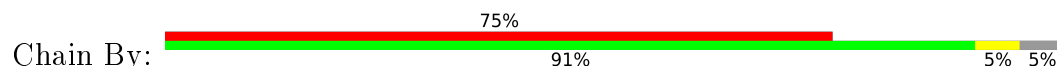
• Molecule 85: Ribosomal protein L12

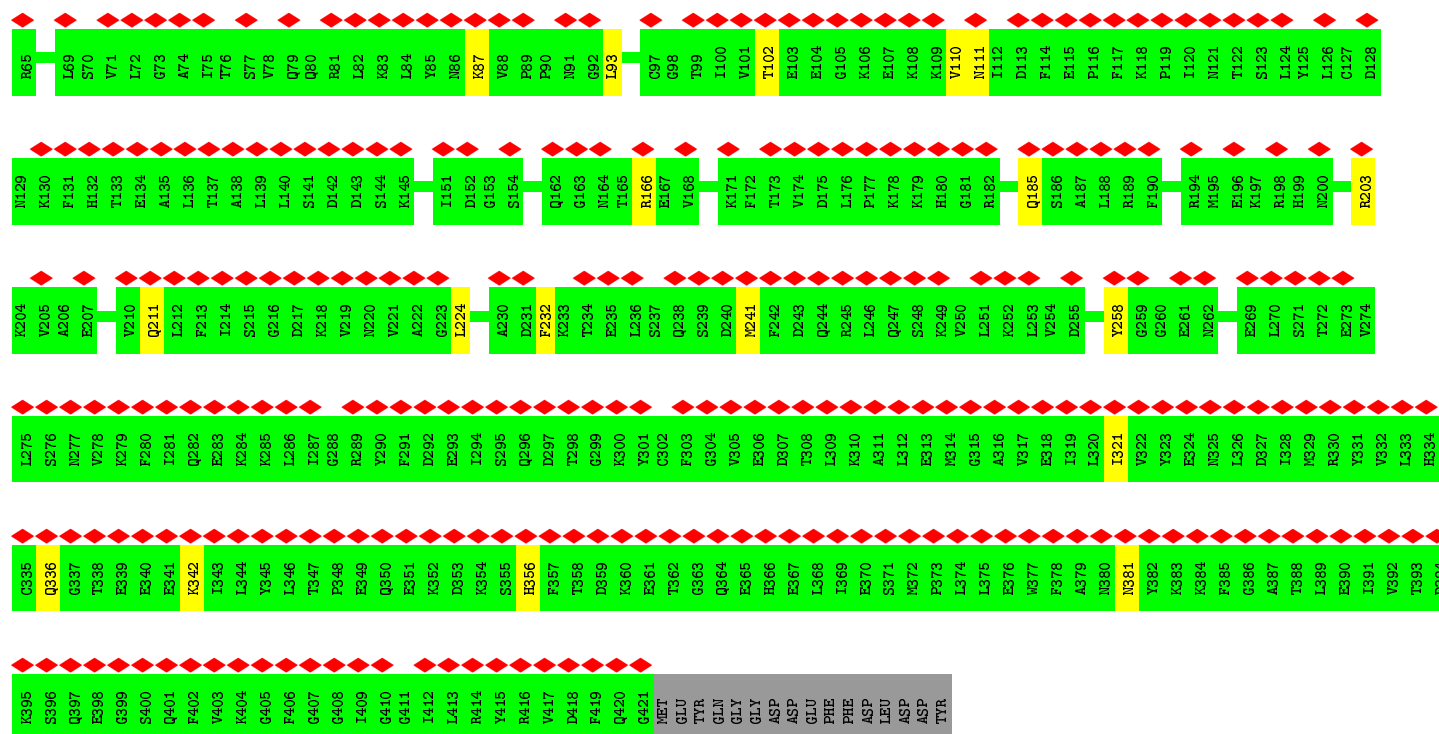


• Molecule 86: Ribosomal protein

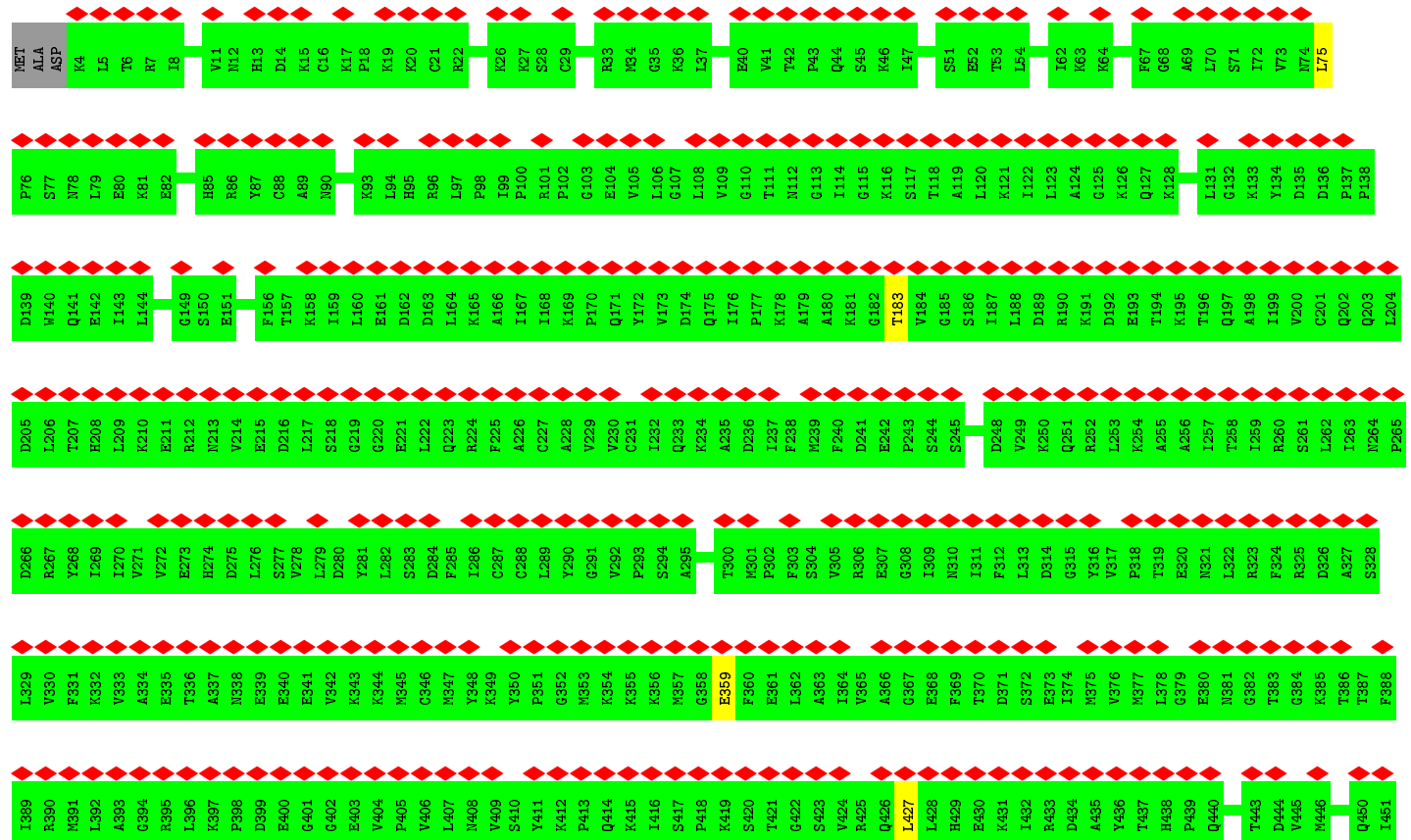
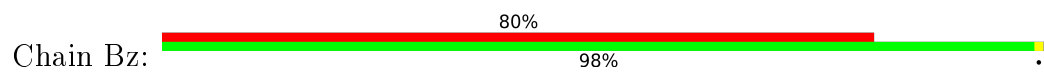


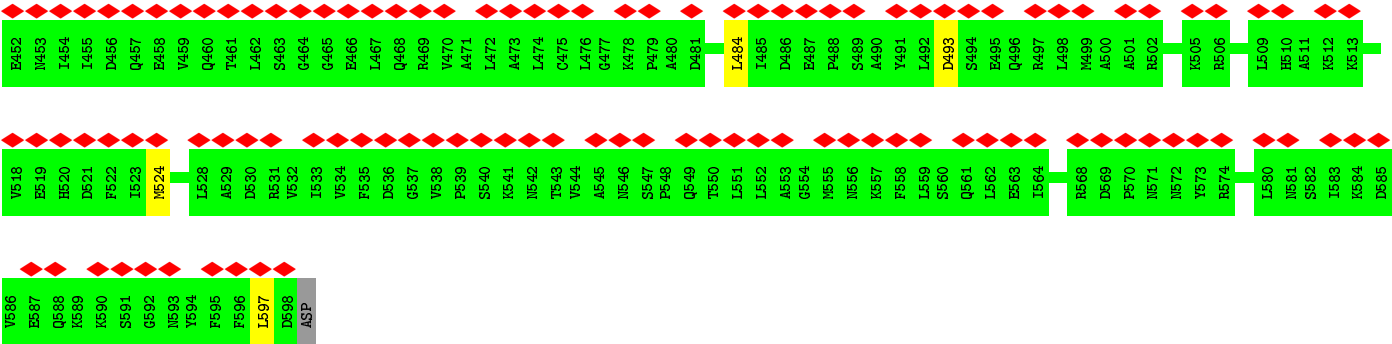
• Molecule 87: Eukaryotic peptide chain release factor subunit 1





• Molecule 88: ATP binding cassette subfamily E member 1





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55057	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	56604	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.379	Depositor
Minimum map value	-1.818	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.131	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	593.6, 593.6, 593.6	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, OMC, A2M, MA6, M3L, 1MA, AME, GTP, B8N, SF4, AAC, 4AC, V5N, MLZ, HIC, 5MC, 6MZ, SAC, UR3, PSU, UY1, OMG, AYA, OMU, G7M, 5MU, UNX, NMM, HY3, SPD

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	A2	0.18	1/40342 (0.0%)	0.68	10/62877 (0.0%)
2	AA	0.24	0/665	0.46	0/891
3	AB	0.24	0/497	0.57	0/666
4	AC	0.24	0/613	0.50	0/811
5	AD	0.24	0/462	0.53	0/607
6	AE	0.24	0/828	0.53	0/1109
7	AF	0.23	0/2493	0.46	0/3394
8	AG	0.24	0/470	0.51	0/623
9	AH	0.13	0/566	0.66	0/879
10	AI	0.18	0/68	0.68	0/103
11	AT	0.28	1/2011 (0.0%)	0.68	0/3133
12	AZ	0.23	0/1771	0.46	0/2406
13	Aa	0.23	0/1841	0.46	0/2459
14	Ab	0.24	0/1742	0.45	0/2354
15	Ac	0.24	0/1779	0.48	0/2395
16	Ad	0.24	0/2118	0.50	0/2849
17	Ae	0.23	0/1531	0.48	0/2059
18	Af	0.24	0/1946	0.52	0/2590
19	Ag	0.24	0/1552	0.46	0/2079
20	Ah	0.24	0/1715	0.51	0/2287
21	Ai	0.23	0/1550	0.52	0/2069
22	Aj	0.24	0/834	0.42	0/1125
23	Ak	0.25	0/1284	0.51	0/1717
24	Al	0.23	0/968	0.41	0/1296
25	Am	0.23	0/1232	0.47	0/1656
26	An	0.24	0/1029	0.53	0/1380
27	Ao	0.25	0/1114	0.48	0/1490
28	Ap	0.24	0/1142	0.50	0/1528
29	Aq	0.23	0/1094	0.48	0/1469
30	Ar	0.23	0/1209	0.52	0/1620
31	As	0.23	0/1119	0.46	0/1498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	At	0.23	0/831	0.52	0/1115
33	Au	0.24	0/636	0.48	0/852
34	Av	0.24	0/1051	0.48	0/1406
35	Aw	0.24	0/1107	0.50	0/1475
36	Ax	0.24	0/1032	0.50	0/1371
37	Ay	0.23	0/691	0.46	0/922
38	Az	0.22	0/240	0.66	0/305
39	B5	0.21	3/87403 (0.0%)	0.68	16/136359 (0.0%)
40	B7	0.18	0/2835	0.67	0/4418
41	B8	0.26	1/3635 (0.0%)	0.68	0/5661
42	BA	0.25	0/1965	0.54	0/2633
43	BB	0.25	0/3261	0.50	0/4364
44	BC	0.24	0/2932	0.50	0/3939
45	BD	0.25	0/2437	0.47	0/3264
46	BE	0.24	0/1998	0.50	0/2673
47	BF	0.25	0/1922	0.49	0/2563
48	BG	0.23	0/1908	0.48	0/2566
49	BH	0.24	0/1535	0.49	0/2063
50	BI	0.25	0/1756	0.50	0/2346
51	BJ	0.24	0/1385	0.51	0/1852
52	BK	0.25	0/277	0.46	0/372
53	BL	0.24	0/1733	0.53	0/2316
54	BM	0.24	0/1158	0.49	0/1547
55	BN	0.24	0/1746	0.54	0/2338
56	BO	0.24	0/1662	0.49	0/2222
57	BP	0.24	0/1317	0.48	0/1768
58	BQ	0.25	0/1539	0.56	0/2054
59	BR	0.23	0/1524	0.53	0/2013
60	BS	0.25	0/1497	0.53	0/2008
61	BT	0.25	0/1326	0.49	0/1770
62	BU	0.24	0/820	0.47	0/1100
63	BV	0.26	0/1048	0.51	0/1402
64	BW	0.24	0/1006	0.50	0/1334
65	BX	0.24	0/984	0.49	0/1323
66	BY	0.24	0/1132	0.52	0/1504
67	BZ	0.25	0/1130	0.49	0/1507
68	Ba	0.24	0/1179	0.50	0/1572
69	Bb	0.23	0/884	0.50	0/1169
70	Bc	0.24	0/847	0.43	0/1134
71	Bd	0.24	0/903	0.52	0/1216
72	Be	0.24	0/1088	0.52	0/1451
73	Bf	0.26	0/903	0.53	0/1208
74	Bg	0.24	0/916	0.54	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
75	Bh	0.23	0/1021	0.50	0/1348
76	Bi	0.23	0/841	0.52	0/1112
77	Bj	0.25	0/720	0.57	0/952
78	Bk	0.24	0/575	0.45	0/761
79	Bl	0.23	0/459	0.51	0/608
80	Bm	0.23	0/426	0.50	0/564
81	Bo	0.25	0/866	0.51	0/1141
82	Bp	0.24	0/718	0.49	0/953
83	Br	0.23	0/1020	0.53	0/1366
84	Bs	0.24	0/1530	0.46	0/2064
85	Bt	0.23	0/1193	0.47	0/1609
86	Bv	0.23	0/1735	0.44	0/2328
87	By	0.24	0/3333	0.44	0/4483
88	Bz	0.24	0/4755	0.45	0/6421
All	All	0.22	6/243956 (0.0%)	0.61	26/356824 (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
81	Bo	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	4761	U	C4-O4	12.82	1.33	1.23
11	AT	1	A	OP3-P	-10.68	1.48	1.61
41	B8	1	C	OP3-P	-10.62	1.48	1.61
1	A2	1	U	OP3-P	-10.59	1.48	1.61
39	B5	1	C	OP3-P	-10.52	1.48	1.61

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	4761	U	N3-C4-C5	12.16	121.89	114.60
39	B5	4761	U	C2-N3-C4	-11.63	120.02	127.00
39	B5	4761	U	C5-C4-O4	-9.76	120.04	125.90
1	A2	1454	C	C2-N1-C1'	7.92	127.52	118.80
1	A2	1454	C	N1-C2-O2	7.83	123.60	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
81	Bo	53	MLZ	Mainchain

## 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	
2	AA	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
3	AB	61/69 (88%)	61 (100%)	0	0	100	100
4	AC	71/156 (46%)	69 (97%)	2 (3%)	0	100	100
5	AD	55/133 (41%)	55 (100%)	0	0	100	100
6	AE	99/115 (86%)	99 (100%)	0	0	100	100
7	AF	311/317 (98%)	300 (96%)	11 (4%)	0	100	100
8	AG	53/56 (95%)	53 (100%)	0	0	100	100
12	AZ	219/295 (74%)	215 (98%)	4 (2%)	0	100	100
13	Aa	220/264 (83%)	218 (99%)	2 (1%)	0	100	100
14	Ab	218/293 (74%)	218 (100%)	0	0	100	100
15	Ac	223/281 (79%)	222 (100%)	1 (0%)	0	100	100
16	Ad	260/263 (99%)	256 (98%)	4 (2%)	0	100	100
17	Ae	189/204 (93%)	184 (97%)	5 (3%)	0	100	100
18	Af	235/249 (94%)	235 (100%)	0	0	100	100
19	Ag	188/194 (97%)	184 (98%)	4 (2%)	0	100	100
20	Ah	204/208 (98%)	203 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	Ai	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
22	Aj	94/165 (57%)	93 (99%)	1 (1%)	0	100	100
23	Ak	152/158 (96%)	149 (98%)	3 (2%)	0	100	100
24	Al	122/132 (92%)	119 (98%)	3 (2%)	0	100	100
25	Am	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
26	An	134/151 (89%)	133 (99%)	1 (1%)	0	100	100
27	Ao	131/145 (90%)	130 (99%)	1 (1%)	0	100	100
28	Ap	139/146 (95%)	133 (96%)	6 (4%)	0	100	100
29	Aq	132/135 (98%)	132 (100%)	0	0	100	100
30	Ar	143/152 (94%)	141 (99%)	2 (1%)	0	100	100
31	As	140/145 (97%)	139 (99%)	1 (1%)	0	100	100
32	At	102/119 (86%)	101 (99%)	1 (1%)	0	100	100
33	Au	81/83 (98%)	81 (100%)	0	0	100	100
34	Av	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
35	Aw	136/143 (95%)	135 (99%)	1 (1%)	0	100	100
36	Ax	123/130 (95%)	121 (98%)	2 (2%)	0	100	100
37	Ay	83/124 (67%)	83 (100%)	0	0	100	100
38	Az	23/25 (92%)	23 (100%)	0	0	100	100
42	BA	250/257 (97%)	244 (98%)	6 (2%)	0	100	100
43	BB	395/403 (98%)	392 (99%)	3 (1%)	0	100	100
44	BC	360/413 (87%)	357 (99%)	3 (1%)	0	100	100
45	BD	291/297 (98%)	289 (99%)	2 (1%)	0	100	100
46	BE	239/291 (82%)	235 (98%)	4 (2%)	0	100	100
47	BF	224/247 (91%)	219 (98%)	5 (2%)	0	100	100
48	BG	229/266 (86%)	228 (100%)	1 (0%)	0	100	100
49	BH	188/192 (98%)	188 (100%)	0	0	100	100
50	BI	211/214 (99%)	208 (99%)	3 (1%)	0	100	100
51	BJ	168/178 (94%)	167 (99%)	1 (1%)	0	100	100
52	BK	34/1071 (3%)	34 (100%)	0	0	100	100
53	BL	208/211 (99%)	204 (98%)	4 (2%)	0	100	100
54	BM	136/218 (62%)	133 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	BN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
56	BO	197/203 (97%)	197 (100%)	0	0	100	100
57	BP	157/184 (85%)	156 (99%)	1 (1%)	0	100	100
58	BQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
59	BR	178/196 (91%)	178 (100%)	0	0	100	100
60	BS	174/176 (99%)	174 (100%)	0	0	100	100
61	BT	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
62	BU	97/128 (76%)	95 (98%)	2 (2%)	0	100	100
63	BV	137/140 (98%)	137 (100%)	0	0	100	100
64	BW	119/157 (76%)	119 (100%)	0	0	100	100
65	BX	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
66	BY	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
67	BZ	133/136 (98%)	133 (100%)	0	0	100	100
68	Ba	144/148 (97%)	139 (96%)	5 (4%)	0	100	100
69	Bb	103/245 (42%)	97 (94%)	6 (6%)	0	100	100
70	Bc	106/115 (92%)	106 (100%)	0	0	100	100
71	Bd	105/125 (84%)	105 (100%)	0	0	100	100
72	Be	128/135 (95%)	128 (100%)	0	0	100	100
73	Bf	108/110 (98%)	108 (100%)	0	0	100	100
74	Bg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
75	Bh	120/123 (98%)	120 (100%)	0	0	100	100
76	Bi	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
77	Bj	84/97 (87%)	84 (100%)	0	0	100	100
78	Bk	67/70 (96%)	67 (100%)	0	0	100	100
79	Bl	48/51 (94%)	48 (100%)	0	0	100	100
80	Bm	49/128 (38%)	49 (100%)	0	0	100	100
81	Bo	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
82	Bp	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
83	Br	124/137 (90%)	122 (98%)	2 (2%)	0	100	100
84	Bs	194/318 (61%)	190 (98%)	4 (2%)	0	100	100
85	Bt	154/165 (93%)	153 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
86	Bv	210/217 (97%)	203 (97%)	7 (3%)	0	100	100
87	By	414/437 (95%)	406 (98%)	8 (2%)	0	100	100
88	Bz	593/599 (99%)	582 (98%)	11 (2%)	0	100	100
All	All	12950/15680 (83%)	12787 (99%)	163 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AA	75/76 (99%)	74 (99%)	1 (1%)	69	90
3	AB	56/62 (90%)	56 (100%)	0	100	100
4	AC	66/140 (47%)	66 (100%)	0	100	100
5	AD	47/106 (44%)	46 (98%)	1 (2%)	53	81
6	AE	88/98 (90%)	88 (100%)	0	100	100
7	AF	272/275 (99%)	269 (99%)	3 (1%)	73	92
8	AG	48/49 (98%)	48 (100%)	0	100	100
12	AZ	182/243 (75%)	180 (99%)	2 (1%)	73	92
13	Aa	203/231 (88%)	201 (99%)	2 (1%)	76	92
14	Ab	185/223 (83%)	182 (98%)	3 (2%)	62	86
15	Ac	189/232 (82%)	188 (100%)	1 (0%)	88	96
16	Ad	224/225 (100%)	224 (100%)	0	100	100
17	Ae	161/170 (95%)	161 (100%)	0	100	100
18	Af	207/218 (95%)	205 (99%)	2 (1%)	76	92
19	Ag	170/174 (98%)	167 (98%)	3 (2%)	59	85
20	Ah	178/180 (99%)	178 (100%)	0	100	100
21	Ai	161/168 (96%)	160 (99%)	1 (1%)	86	96
22	Aj	87/136 (64%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	Ak	139/142 (98%)	138 (99%)	1 (1%)	84	95
24	Al	104/108 (96%)	100 (96%)	4 (4%)	33	67
25	Am	130/131 (99%)	129 (99%)	1 (1%)	81	94
26	An	106/119 (89%)	104 (98%)	2 (2%)	57	84
27	Ao	119/130 (92%)	119 (100%)	0	100	100
28	Ap	117/121 (97%)	117 (100%)	0	100	100
29	Aq	120/121 (99%)	120 (100%)	0	100	100
30	Ar	125/131 (95%)	123 (98%)	2 (2%)	62	86
31	As	112/114 (98%)	112 (100%)	0	100	100
32	At	94/107 (88%)	93 (99%)	1 (1%)	73	92
33	Au	67/67 (100%)	66 (98%)	1 (2%)	65	87
34	Av	112/113 (99%)	112 (100%)	0	100	100
35	Aw	112/114 (98%)	110 (98%)	2 (2%)	59	85
36	Ax	107/112 (96%)	106 (99%)	1 (1%)	78	93
37	Ay	75/102 (74%)	75 (100%)	0	100	100
38	Az	24/24 (100%)	24 (100%)	0	100	100
42	BA	194/198 (98%)	193 (100%)	1 (0%)	88	96
43	BB	344/347 (99%)	343 (100%)	1 (0%)	92	98
44	BC	302/337 (90%)	301 (100%)	1 (0%)	92	98
45	BD	247/250 (99%)	247 (100%)	0	100	100
46	BE	216/251 (86%)	216 (100%)	0	100	100
47	BF	197/215 (92%)	196 (100%)	1 (0%)	88	96
48	BG	199/223 (89%)	197 (99%)	2 (1%)	76	92
49	BH	169/171 (99%)	169 (100%)	0	100	100
50	BI	180/181 (99%)	177 (98%)	3 (2%)	60	86
51	BJ	143/149 (96%)	143 (100%)	0	100	100
52	BK	31/936 (3%)	30 (97%)	1 (3%)	39	73
53	BL	175/176 (99%)	171 (98%)	4 (2%)	50	80
54	BM	117/161 (73%)	116 (99%)	1 (1%)	78	93
55	BN	171/172 (99%)	171 (100%)	0	100	100
56	BO	171/173 (99%)	170 (99%)	1 (1%)	86	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BP	140/163 (86%)	140 (100%)	0	100	100
58	BQ	164/165 (99%)	163 (99%)	1 (1%)	86	96
59	BR	159/175 (91%)	159 (100%)	0	100	100
60	BS	154/154 (100%)	154 (100%)	0	100	100
61	BT	139/140 (99%)	139 (100%)	0	100	100
62	BU	88/113 (78%)	88 (100%)	0	100	100
63	BV	106/107 (99%)	104 (98%)	2 (2%)	57	84
64	BW	100/126 (79%)	99 (99%)	1 (1%)	76	92
65	BX	106/134 (79%)	106 (100%)	0	100	100
66	BY	124/135 (92%)	122 (98%)	2 (2%)	62	86
67	BZ	117/118 (99%)	117 (100%)	0	100	100
68	Ba	118/119 (99%)	118 (100%)	0	100	100
69	Bb	87/183 (48%)	87 (100%)	0	100	100
70	Bc	92/98 (94%)	92 (100%)	0	100	100
71	Bd	98/110 (89%)	98 (100%)	0	100	100
72	Be	116/121 (96%)	116 (100%)	0	100	100
73	Bf	89/89 (100%)	89 (100%)	0	100	100
74	Bg	98/100 (98%)	97 (99%)	1 (1%)	76	92
75	Bh	109/110 (99%)	109 (100%)	0	100	100
76	Bi	86/89 (97%)	85 (99%)	1 (1%)	71	91
77	Bj	73/80 (91%)	71 (97%)	2 (3%)	44	77
78	Bk	64/65 (98%)	64 (100%)	0	100	100
79	Bl	47/48 (98%)	46 (98%)	1 (2%)	53	81
80	Bm	47/115 (41%)	47 (100%)	0	100	100
81	Bo	92/93 (99%)	92 (100%)	0	100	100
82	Bp	74/75 (99%)	74 (100%)	0	100	100
83	Br	109/120 (91%)	109 (100%)	0	100	100
84	Bs	164/258 (64%)	162 (99%)	2 (1%)	71	91
85	Bt	128/137 (93%)	123 (96%)	5 (4%)	32	66
86	Bv	191/195 (98%)	183 (96%)	8 (4%)	30	63
87	By	358/376 (95%)	338 (94%)	20 (6%)	21	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
88	Bz	516/526 (98%)	508 (98%)	8 (2%)	62	86
All	All	11271/13339 (84%)	11167 (99%)	104 (1%)	79	93

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
76	Bi	29	ARG
86	Bv	73	HIS
88	Bz	427	LEU
77	Bj	57	ASN
85	Bt	90	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
53	BL	188	ASN
66	BY	14	ASN
88	Bz	549	GLN
87	By	381	ASN
56	BO	180	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	1758/1870 (94%)	231 (13%)	1 (0%)
10	AI	2/76 (2%)	1 (50%)	0
11	AT	85/86 (98%)	15 (17%)	0
39	B5	3750/4808 (77%)	469 (12%)	1 (0%)
40	B7	118/119 (99%)	7 (5%)	0
41	B8	155/158 (98%)	17 (10%)	0
9	AH	23/217 (10%)	8 (34%)	0
All	All	5891/7334 (80%)	748 (12%)	2 (0%)

5 of 748 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	3	C
1	A2	17	C
1	A2	26	U

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Mol	Chain	Res	Type
1	A2	33	G
1	A2	41	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A2	549	C
39	B5	4445	U

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

224 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	A2M	A2	1384	1	18,25,26	1.02	1 (5%)	18,36,39	1.20	2 (11%)
1	MA6	A2	1852	1	19,26,27	0.95	1 (5%)	18,38,41	1.46	3 (16%)
39	A2M	B5	3456	39	18,25,26	1.03	1 (5%)	18,36,39	1.22	2 (11%)
1	PSU	A2	1368	1	17,21,22	1.58	2 (11%)	20,30,33	3.06	6 (30%)
39	5MC	B5	4193	39	15,22,23	1.28	1 (6%)	19,32,35	1.47	4 (21%)
39	OMG	B5	1580	39	18,26,27	1.19	2 (11%)	20,38,41	2.15	6 (30%)
1	PSU	A2	967	1	17,21,22	1.57	3 (17%)	20,30,33	3.07	6 (30%)
39	OMC	B5	2208	39,90	15,22,23	0.71	0	17,31,34	1.31	2 (11%)
39	UR3	B5	4276	39	14,22,23	0.72	0	15,32,35	0.67	0
39	OMC	B5	2667	39	15,22,23	0.68	0	17,31,34	1.33	2 (11%)
1	PSU	A2	652	1	17,21,22	1.61	2 (11%)	20,30,33	3.11	6 (30%)
1	PSU	A2	109	1	17,21,22	1.58	2 (11%)	20,30,33	3.08	6 (30%)
12	SAC	AZ	2	12	7,8,9	0.53	0	8,9,11	0.86	1 (12%)
39	A2M	B5	4336	39	18,25,26	1.02	1 (5%)	18,36,39	1.20	2 (11%)
39	OMC	B5	2647	39	15,22,23	0.69	0	17,31,34	1.33	2 (11%)
1	PSU	A2	1348	1	17,21,22	1.58	2 (11%)	20,30,33	3.07	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
39	PSU	B5	4188	39	17,21,22	1.61	3 (17%)	20,30,33	3.04	6 (30%)
39	OMU	B5	2680	39	14,22,23	0.83	1 (7%)	14,31,34	0.83	0
39	PSU	B5	4740	39	17,21,22	1.58	2 (11%)	20,30,33	3.08	6 (30%)
39	PSU	B5	3427	39	17,21,22	1.58	3 (17%)	20,30,33	3.07	6 (30%)
39	PSU	B5	4169	39	17,21,22	1.60	2 (11%)	20,30,33	3.11	6 (30%)
39	OMG	B5	4369	39	18,26,27	1.20	2 (11%)	20,38,41	2.18	6 (30%)
30	SAC	Ar	2	30	7,8,9	0.54	0	8,9,11	0.92	1 (12%)
11	5MU	AT	64	11	15,22,23	1.05	1 (6%)	16,32,35	1.87	2 (12%)
1	PSU	A2	1233	1	17,21,22	1.59	2 (11%)	20,30,33	3.15	6 (30%)
39	PSU	B5	1801	39	17,21,22	1.60	2 (11%)	20,30,33	3.11	6 (30%)
1	A2M	A2	1679	1	18,25,26	1.02	1 (5%)	18,36,39	1.24	2 (11%)
1	PSU	A2	407	1	17,21,22	1.59	2 (11%)	20,30,33	3.12	6 (30%)
1	OMG	A2	437	1	18,26,27	1.21	2 (11%)	20,38,41	2.16	6 (30%)
31	NMM	As	67	31	9,11,12	0.59	0	6,12,14	0.39	0
39	OMG	B5	4116	39	18,26,27	1.20	2 (11%)	20,38,41	2.17	6 (30%)
39	PSU	B5	4203	39	17,21,22	1.58	2 (11%)	20,30,33	3.07	6 (30%)
39	OMC	B5	2704	39	15,22,23	0.68	0	17,31,34	1.28	2 (11%)
1	OMU	A2	1327	1,90	14,22,23	0.79	1 (7%)	14,31,34	0.81	0
39	OMG	B5	2207	39	18,26,27	1.20	2 (11%)	20,38,41	2.20	6 (30%)
39	PSU	B5	3616	39	17,21,22	1.61	3 (17%)	20,30,33	3.06	6 (30%)
1	PSU	A2	1178	1	17,21,22	1.58	3 (17%)	20,30,33	3.08	6 (30%)
39	OMG	B5	3942	11,39	18,26,27	1.16	2 (11%)	20,38,41	2.16	6 (30%)
39	PSU	B5	4419	39	17,21,22	1.59	2 (11%)	20,30,33	3.09	6 (30%)
1	PSU	A2	1057	1	17,21,22	1.61	3 (17%)	20,30,33	3.06	6 (30%)
39	A2M	B5	1489	39,90	18,25,26	1.00	1 (5%)	18,36,39	1.33	2 (11%)
1	PSU	A2	1446	1	17,21,22	1.57	2 (11%)	20,30,33	3.05	6 (30%)
39	5MC	B5	3514	39,90	15,22,23	1.28	1 (6%)	19,32,35	1.33	3 (15%)
39	PSU	B5	3490	39	17,21,22	1.59	2 (11%)	20,30,33	3.08	6 (30%)
35	HY3	Aw	62	35	6,8,9	2.13	1 (16%)	5,10,12	1.12	1 (20%)
1	MA6	A2	1851	1	19,26,27	0.95	1 (5%)	18,38,41	1.61	3 (16%)
39	OMC	B5	4202	39	15,22,23	0.70	0	17,31,34	1.32	2 (11%)
39	OMU	B5	4366	39	14,22,23	0.82	1 (7%)	14,31,34	0.88	0
39	OMG	B5	4364	39	18,26,27	1.20	2 (11%)	20,38,41	2.17	6 (30%)
39	PSU	B5	1721	39	17,21,22	1.60	2 (11%)	20,30,33	3.09	6 (30%)
39	PSU	B5	4374	39	17,21,22	1.59	3 (17%)	20,30,33	3.05	6 (30%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
39	PSU	B5	4217	39	17,21,22	1.59	2 (11%)	20,30,33	3.10	6 (30%)
1	PSU	A2	1245	1	17,21,22	1.59	2 (11%)	20,30,33	3.06	6 (30%)
39	PSU	B5	4325	39	17,21,22	1.61	2 (11%)	20,30,33	3.11	6 (30%)
39	PSU	B5	4058	39	17,21,22	1.61	2 (11%)	20,30,33	3.07	6 (30%)
39	A2M	B5	3492	39	18,25,26	1.03	1 (5%)	18,36,39	1.33	2 (11%)
39	A2M	B5	3599	39	18,25,26	0.99	1 (5%)	18,36,39	1.22	2 (11%)
1	OMU	A2	1805	1	14,22,23	0.80	1 (7%)	14,31,34	0.84	0
1	PSU	A2	1046	1	17,21,22	1.57	2 (11%)	20,30,33	3.07	6 (30%)
39	OMC	B5	2194	39,90	15,22,23	0.68	0	17,31,34	1.39	2 (11%)
39	PSU	B5	1632	39	17,21,22	1.69	2 (11%)	20,30,33	2.99	6 (30%)
39	OMU	B5	3657	39	14,22,23	0.83	1 (7%)	14,31,34	0.80	0
39	OMU	B5	2258	39	14,22,23	0.78	1 (7%)	14,31,34	0.71	0
1	PSU	A2	1626	1	17,21,22	1.58	2 (11%)	20,30,33	3.08	6 (30%)
39	PSU	B5	1731	39	17,21,22	1.57	2 (11%)	20,30,33	3.06	6 (30%)
39	OMG	B5	1260	39	18,26,27	1.17	2 (11%)	20,38,41	2.16	6 (30%)
39	OMC	B5	3573	39	15,22,23	0.69	0	17,31,34	1.30	2 (11%)
39	PSU	B5	3371	39	17,21,22	1.59	2 (11%)	20,30,33	3.04	6 (30%)
1	A2M	A2	577	1	18,25,26	1.01	1 (5%)	18,36,39	1.22	2 (11%)
39	OMG	B5	3676	39	18,26,27	1.23	2 (11%)	20,38,41	2.18	6 (30%)
39	OMU	B5	4052	39	14,22,23	0.80	1 (7%)	14,31,34	0.81	0
1	PSU	A2	93	1	17,21,22	1.59	3 (17%)	20,30,33	3.10	6 (30%)
39	PSU	B5	4298	39	17,21,22	1.59	3 (17%)	20,30,33	3.07	6 (30%)
1	B8N	A2	1249	1	17,29,30	1.66	2 (11%)	21,42,45	1.08	1 (4%)
1	OMU	A2	355	1	14,22,23	0.81	1 (7%)	14,31,34	0.86	0
39	PSU	B5	3494	39	17,21,22	1.60	2 (11%)	20,30,33	3.08	6 (30%)
39	OMC	B5	3619	39	15,22,23	0.67	0	17,31,34	1.34	2 (11%)
1	A2M	A2	27	1,90	18,25,26	1.02	1 (5%)	18,36,39	1.23	2 (11%)
39	OMC	B5	3540	39	15,22,23	0.71	0	17,31,34	1.30	2 (11%)
1	OMC	A2	518	1	15,22,23	0.66	0	17,31,34	1.34	2 (11%)
39	PSU	B5	4382	39	17,21,22	1.54	2 (11%)	20,30,33	3.13	8 (40%)
1	PSU	A2	1239	1	17,21,22	1.60	2 (11%)	20,30,33	3.08	6 (30%)
39	PSU	B5	1683	39	17,21,22	1.59	2 (11%)	20,30,33	3.12	6 (30%)
1	OMC	A2	1392	1	15,22,23	0.68	0	17,31,34	1.35	2 (11%)
39	OMU	B5	4244	39	14,22,23	0.79	1 (7%)	14,31,34	0.76	0
39	A2M	B5	2206	39,90	18,25,26	1.00	1 (5%)	18,36,39	1.22	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	A2M	A2	591	1	18,25,26	1.05	1 (5%)	18,36,39	1.21	2 (11%)
39	PSU	B5	4042	39	17,21,22	1.58	2 (11%)	20,30,33	3.13	6 (30%)
39	PSU	B5	3583	39	17,21,22	1.59	3 (17%)	20,30,33	3.03	6 (30%)
39	PSU	B5	1537	39	17,21,22	1.62	2 (11%)	20,30,33	3.07	6 (30%)
39	PSU	B5	4039	39	17,21,22	1.58	2 (11%)	20,30,33	3.10	6 (30%)
39	PSU	B5	4267	39,90	17,21,22	1.61	3 (17%)	20,30,33	3.06	6 (30%)
39	PSU	B5	3496	39	17,21,22	1.57	2 (11%)	20,30,33	3.03	6 (30%)
1	OMU	A2	116	1	14,22,23	0.78	0	14,31,34	0.77	0
39	A2M	B5	1479	39	18,25,26	1.02	1 (5%)	18,36,39	1.26	2 (11%)
1	PSU	A2	34	1	17,21,22	1.60	2 (11%)	20,30,33	3.09	6 (30%)
39	PSU	B5	2351	39	17,21,22	1.59	2 (11%)	20,30,33	3.11	6 (30%)
39	PSU	B5	4322	39	17,21,22	1.59	2 (11%)	20,30,33	3.08	6 (30%)
68	V5N	Ba	39	68	4,11,12	0.77	0	5,14,16	1.54	1 (20%)
39	PSU	B5	4435	39	17,21,22	1.60	2 (11%)	20,30,33	3.08	6 (30%)
1	PSU	A2	867	1	17,21,22	1.59	2 (11%)	20,30,33	3.09	6 (30%)
39	A2M	B5	398	39	18,25,26	1.01	1 (5%)	18,36,39	1.25	2 (11%)
1	PSU	A2	1644	1,90	17,21,22	1.57	3 (17%)	20,30,33	3.08	6 (30%)
39	OMG	B5	2719	39	18,26,27	1.20	2 (11%)	20,38,41	2.15	6 (30%)
39	A2M	B5	3557	39	18,25,26	1.01	1 (5%)	18,36,39	1.20	2 (11%)
1	PSU	A2	802	1	17,21,22	1.58	2 (11%)	20,30,33	3.07	6 (30%)
39	PSU	B5	4099	39	17,21,22	1.58	3 (17%)	20,30,33	3.03	6 (30%)
1	PSU	A2	864	1	17,21,22	1.57	3 (17%)	20,30,33	3.07	6 (30%)
39	OMG	B5	1477	39	18,26,27	1.21	2 (11%)	20,38,41	2.19	6 (30%)
39	PSU	B5	3502	39	17,21,22	1.57	2 (11%)	20,30,33	3.08	6 (30%)
39	PSU	B5	3500	39	17,21,22	1.57	2 (11%)	20,30,33	3.12	6 (30%)
39	OMG	B5	4240	39	18,26,27	1.20	2 (11%)	20,38,41	2.13	6 (30%)
1	OMG	A2	1448	1	18,26,27	1.23	2 (11%)	20,38,41	2.16	6 (30%)
39	OMG	B5	3524	39	18,26,27	1.17	2 (11%)	20,38,41	2.14	6 (30%)
39	PSU	B5	4045	39	17,21,22	1.59	2 (11%)	20,30,33	3.08	6 (30%)
1	OMU	A2	1289	1	14,22,23	0.79	1 (7%)	14,31,34	0.75	0
39	PSU	B5	4749	39	17,21,22	1.60	2 (11%)	20,30,33	3.06	6 (30%)
39	1MA	B5	1266	39,90	15,25,26	1.51	3 (20%)	15,37,40	1.33	2 (13%)
1	PSU	A2	1693	1	17,21,22	1.62	2 (11%)	20,30,33	3.11	6 (30%)
1	OMU	A2	628	1	14,22,23	0.79	1 (7%)	14,31,34	0.80	0
81	MLZ	Bo	53	81	8,9,10	0.48	0	4,9,11	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
39	PSU	B5	1718	39	17,21,22	1.60	2 (11%)	20,30,33	3.11	6 (30%)
1	OMC	A2	174	1,90	15,22,23	0.68	0	17,31,34	1.32	2 (11%)
39	PSU	B5	4166	39	17,21,22	1.51	2 (11%)	20,30,33	3.15	5 (25%)
42	V5N	BA	216	42	4,11,12	0.77	0	5,14,16	1.54	1 (20%)
39	OMG	B5	2267	39	18,26,27	1.16	2 (11%)	20,38,41	2.13	6 (30%)
43	HIC	BB	245	43	8,11,12	0.88	0	6,14,16	0.84	0
39	UY1	B5	3550	39	18,22,23	1.19	1 (5%)	20,31,34	3.07	7 (35%)
1	PSU	A2	1005	1	17,21,22	1.57	2 (11%)	20,30,33	3.10	6 (30%)
39	PSU	B5	4246	39	17,21,22	1.61	3 (17%)	20,30,33	3.01	6 (30%)
1	PSU	A2	1047	1	17,21,22	1.60	3 (17%)	20,30,33	3.06	6 (30%)
1	PSU	A2	687	1	17,21,22	1.59	2 (11%)	20,30,33	3.06	6 (30%)
39	A2M	B5	3517	39	18,25,26	0.92	1 (5%)	18,36,39	1.38	2 (11%)
39	A2M	B5	400	39	18,25,26	1.00	1 (5%)	18,36,39	1.22	2 (11%)
1	OMG	A2	1329	1	18,26,27	1.22	2 (11%)	20,38,41	2.16	6 (30%)
39	A2M	B5	2630	39,90	18,25,26	0.96	1 (5%)	18,36,39	1.34	2 (11%)
1	OMC	A2	1704	1	15,22,23	0.70	0	17,31,34	1.39	2 (11%)
39	PSU	B5	3585	39,90	17,21,22	1.59	2 (11%)	20,30,33	3.10	6 (30%)
39	A2M	B5	3450	39	18,25,26	1.02	1 (5%)	18,36,39	1.21	2 (11%)
1	PSU	A2	105	1	17,21,22	1.60	2 (11%)	20,30,33	3.12	6 (30%)
39	OMG	B5	3476	39	18,26,27	1.22	2 (11%)	20,38,41	2.19	6 (30%)
1	PSU	A2	119	1	17,21,22	1.57	3 (17%)	20,30,33	3.06	6 (30%)
1	PSU	A2	36	1	17,21,22	1.58	2 (11%)	20,30,33	3.09	6 (30%)
39	PSU	B5	1799	39	17,21,22	1.61	2 (11%)	20,30,33	3.10	6 (30%)
1	A2M	A2	166	1	18,25,26	1.05	1 (5%)	18,36,39	1.28	2 (11%)
1	A2M	A2	1032	1	18,25,26	1.01	1 (5%)	18,36,39	1.26	2 (11%)
1	PSU	A2	816	1	17,21,22	1.60	2 (11%)	20,30,33	3.09	6 (30%)
39	A2M	B5	4317	39	18,25,26	1.01	1 (5%)	18,36,39	1.27	2 (11%)
39	OMC	B5	3433	39	15,22,23	0.69	0	17,31,34	1.32	2 (11%)
39	PSU	B5	4278	39	17,21,22	1.58	2 (11%)	20,30,33	3.09	6 (30%)
83	SAC	Br	2	83	7,8,9	0.53	0	8,9,11	0.82	1 (12%)
39	OMG	B5	4383	39	18,26,27	1.21	2 (11%)	20,38,41	2.17	6 (30%)
1	A2M	A2	669	1,90	18,25,26	0.97	1 (5%)	18,36,39	1.32	2 (11%)
39	PSU	B5	4177	39	17,21,22	1.61	3 (17%)	20,30,33	3.11	6 (30%)
39	OMG	B5	3974	39	18,26,27	1.19	2 (11%)	20,38,41	2.22	6 (30%)
39	PSU	B5	3369	39	17,21,22	1.58	3 (17%)	20,30,33	3.10	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
39	OMC	B5	1820	39,90	15,22,23	0.69	0	17,31,34	1.29	2 (11%)
1	OMG	A2	868	1	18,26,27	1.24	2 (11%)	20,38,41	2.14	6 (30%)
39	PSU	B5	3447	39	17,21,22	1.61	3 (17%)	20,30,33	3.05	6 (30%)
39	A2M	B5	4269	39,90	18,25,26	1.01	1 (5%)	18,36,39	1.25	2 (11%)
69	MLZ	Bb	5	69	8,9,10	0.49	0	4,9,11	0.24	0
1	PSU	A2	573	1	17,21,22	1.59	3 (17%)	20,30,33	3.06	6 (30%)
1	OMU	A2	1443	1,90	14,22,23	0.81	1 (7%)	14,31,34	0.75	0
1	PSU	A2	682	1	17,21,22	1.59	2 (11%)	20,30,33	3.07	6 (30%)
1	PSU	A2	1082	1	17,21,22	1.53	3 (17%)	20,30,33	3.06	5 (25%)
1	OMU	A2	429	1	14,22,23	0.78	1 (7%)	14,31,34	0.76	0
39	OMG	B5	3359	39	18,26,27	1.21	2 (11%)	20,38,41	2.20	6 (30%)
39	PSU	B5	3652	39,90	17,21,22	1.56	3 (17%)	20,30,33	3.06	6 (30%)
39	PSU	B5	1491	39	17,21,22	1.60	2 (11%)	20,30,33	3.08	6 (30%)
1	PSU	A2	1175	1	17,21,22	1.59	2 (11%)	20,30,33	3.06	6 (30%)
1	OMU	A2	172	1	14,22,23	0.78	1 (7%)	14,31,34	0.84	0
1	PSU	A2	650	1	17,21,22	1.63	2 (11%)	20,30,33	3.12	6 (30%)
41	PSU	B8	69	41	17,21,22	1.59	2 (11%)	20,30,33	3.00	6 (30%)
1	A2M	A2	513	1	18,25,26	1.01	1 (5%)	18,36,39	1.19	2 (11%)
44	AYA	BC	2	44	6,7,8	0.76	0	5,8,10	0.28	0
39	PSU	B5	2475	39	17,21,22	1.60	3 (17%)	20,30,33	3.07	7 (35%)
39	PSU	B5	1638	39	17,21,22	1.62	2 (11%)	20,30,33	3.05	6 (30%)
39	A2M	B5	2658	39	18,25,26	1.01	1 (5%)	18,36,39	1.23	2 (11%)
1	OMG	A2	510	1,90	18,26,27	1.19	2 (11%)	20,38,41	2.16	6 (30%)
1	A2M	A2	485	1	18,25,26	1.02	1 (5%)	18,36,39	1.22	2 (11%)
39	A2M	B5	1810	39,90	18,25,26	1.01	1 (5%)	18,36,39	1.24	2 (11%)
39	OMU	B5	3973	39	14,22,23	0.82	1 (7%)	14,31,34	0.79	0
41	OMG	B8	75	41	18,26,27	1.22	2 (11%)	20,38,41	2.18	6 (30%)
80	M3L	Bm	98	80	10,11,12	0.82	0	9,14,16	0.47	0
1	PSU	A2	815	1	17,21,22	1.55	2 (11%)	20,30,33	3.12	6 (30%)
33	AME	Au	1	33	9,10,11	0.48	0	9,11,13	0.85	1 (11%)
39	PSU	B5	3466	39	17,21,22	1.58	2 (11%)	20,30,33	3.09	6 (30%)
39	PSU	B5	3462	39	17,21,22	1.58	2 (11%)	20,30,33	3.08	6 (30%)
39	PSU	B5	3576	39	17,21,22	1.60	2 (11%)	20,30,33	3.12	6 (30%)
39	OMC	B5	2265	39,90	15,22,23	0.69	0	17,31,34	1.33	2 (11%)
39	A2M	B5	2244	39,90	18,25,26	1.01	1 (5%)	18,36,39	1.22	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
39	OMG	B5	4245	39	18,26,27	1.22	2 (11%)	20,38,41	2.18	6 (30%)
1	OMC	A2	463	1	15,22,23	0.67	0	17,31,34	1.33	2 (11%)
1	4AC	A2	1338	1	18,24,25	0.85	1 (5%)	20,34,37	1.60	3 (15%)
1	OMG	A2	602	1	18,26,27	1.20	2 (11%)	20,38,41	2.15	6 (30%)
39	PSU	B5	4711	39	17,21,22	1.59	2 (11%)	20,30,33	3.11	6 (30%)
41	PSU	B8	55	41	17,21,22	1.62	2 (11%)	20,30,33	3.09	6 (30%)
11	PSU	AT	65	11	17,21,22	1.60	2 (11%)	20,30,33	3.12	6 (30%)
1	PSU	A2	610	1	17,21,22	1.58	2 (11%)	20,30,33	3.14	6 (30%)
39	OMG	B5	3631	39	18,26,27	1.20	2 (11%)	20,38,41	2.21	6 (30%)
39	PSU	B5	1720	39	17,21,22	1.61	2 (11%)	20,30,33	3.09	6 (30%)
1	PSU	A2	823	1	17,21,22	1.55	3 (17%)	20,30,33	3.00	6 (30%)
39	PSU	B5	3554	39	17,21,22	1.58	3 (17%)	20,30,33	3.06	6 (30%)
39	6MZ	B5	3966	39	18,25,26	0.86	1 (5%)	16,36,39	2.19	4 (25%)
1	OMG	A2	684	1	18,26,27	1.23	2 (11%)	20,38,41	2.23	6 (30%)
1	PSU	A2	218	1	17,21,22	1.56	2 (11%)	20,30,33	3.08	6 (30%)
39	A2M	B5	3562	39	18,25,26	1.01	1 (5%)	18,36,39	1.24	2 (11%)
1	G7M	A2	1640	1,11	20,26,27	2.81	4 (20%)	20,39,42	2.10	5 (25%)
39	PSU	B5	4149	39	17,21,22	1.62	2 (11%)	20,30,33	3.02	6 (30%)
1	A2M	A2	99	1,90	18,25,26	1.04	1 (5%)	18,36,39	1.25	2 (11%)
1	4AC	A2	1843	1	18,24,25	0.90	1 (5%)	20,34,37	1.54	3 (15%)
39	PSU	B5	4107	39	17,21,22	1.59	2 (11%)	20,30,33	3.08	6 (30%)
1	PSU	A2	210	1	17,21,22	1.55	2 (11%)	20,30,33	3.10	6 (30%)
39	OMC	B5	4282	39	15,22,23	0.71	0	17,31,34	1.33	2 (11%)
39	OMG	B5	4138	39	18,26,27	1.17	2 (11%)	20,38,41	2.15	6 (30%)
1	A2M	A2	159	1	18,25,26	1.02	1 (5%)	18,36,39	1.39	2 (11%)
39	OMC	B5	1284	39	15,22,23	0.72	0	17,31,34	1.34	2 (11%)
1	OMG	A2	1491	1,90	18,26,27	1.19	2 (11%)	20,38,41	2.13	6 (30%)
1	OMG	A2	645	1	18,26,27	1.21	2 (11%)	20,38,41	2.17	6 (30%)
39	OMC	B5	3601	39	15,22,23	0.68	0	17,31,34	1.33	2 (11%)
39	A2M	B5	1270	39	18,25,26	0.95	1 (5%)	18,36,39	1.26	2 (11%)
1	6MZ	A2	1833	1,90	18,25,26	0.92	1 (5%)	16,36,39	1.77	4 (25%)
1	OMU	A2	121	1	14,22,23	0.82	1 (7%)	14,31,34	0.78	0
1	A2M	A2	469	1	18,25,26	1.02	1 (5%)	18,36,39	1.24	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	A2	1384	1	-	0/5/27/28	0/3/3/3
1	MA6	A2	1852	1	-	1/7/29/30	0/3/3/3
39	A2M	B5	3456	39	-	0/5/27/28	0/3/3/3
1	PSU	A2	1368	1	-	0/7/25/26	0/2/2/2
39	5MC	B5	4193	39	-	2/5/25/26	0/2/2/2
39	OMG	B5	1580	39	-	0/5/27/28	0/3/3/3
1	PSU	A2	967	1	-	0/7/25/26	0/2/2/2
39	OMC	B5	2208	39,90	-	0/7/27/28	0/2/2/2
39	UR3	B5	4276	39	-	0/5/25/26	0/2/2/2
39	OMC	B5	2667	39	-	1/7/27/28	0/2/2/2
1	PSU	A2	652	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	109	1	-	0/7/25/26	0/2/2/2
12	SAC	AZ	2	12	-	1/7/8/10	-
39	A2M	B5	4336	39	-	1/5/27/28	0/3/3/3
39	OMC	B5	2647	39	-	0/7/27/28	0/2/2/2
1	PSU	A2	1348	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4188	39	-	0/7/25/26	0/2/2/2
39	OMU	B5	2680	39	-	1/7/27/28	0/2/2/2
39	PSU	B5	4740	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	3427	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4169	39	-	0/7/25/26	0/2/2/2
39	OMG	B5	4369	39	-	1/5/27/28	0/3/3/3
30	SAC	Ar	2	30	-	0/7/8/10	-
11	5MU	AT	64	11	-	0/5/25/26	0/2/2/2
1	PSU	A2	1233	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	1801	39	-	0/7/25/26	0/2/2/2
1	A2M	A2	1679	1	-	0/5/27/28	0/3/3/3
1	PSU	A2	407	1	-	0/7/25/26	0/2/2/2
1	OMG	A2	437	1	-	0/5/27/28	0/3/3/3
31	NMM	As	67	31	-	0/9/11/13	-
39	OMG	B5	4116	39	-	0/5/27/28	0/3/3/3
39	PSU	B5	4203	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	2704	39	-	0/7/27/28	0/2/2/2
1	OMU	A2	1327	1,90	-	0/7/27/28	0/2/2/2
39	OMG	B5	2207	39	-	2/5/27/28	0/3/3/3
39	PSU	B5	3616	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	1178	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	3942	11,39	-	0/5/27/28	0/3/3/3
39	PSU	B5	4419	39	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A2	1057	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	1489	39,90	-	1/5/27/28	0/3/3/3
1	PSU	A2	1446	1	-	0/7/25/26	0/2/2/2
39	5MC	B5	3514	39,90	-	0/5/25/26	0/2/2/2
39	PSU	B5	3490	39	-	0/7/25/26	0/2/2/2
35	HY3	Aw	62	35	-	1/1/12/14	0/1/1/1
1	MA6	A2	1851	1	-	0/7/29/30	0/3/3/3
39	OMC	B5	4202	39	-	0/7/27/28	0/2/2/2
39	OMU	B5	4366	39	-	0/7/27/28	0/2/2/2
39	OMG	B5	4364	39	-	0/5/27/28	0/3/3/3
39	PSU	B5	1721	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4374	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4217	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	1245	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4325	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4058	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	3492	39	-	0/5/27/28	0/3/3/3
39	A2M	B5	3599	39	-	2/5/27/28	0/3/3/3
1	OMU	A2	1805	1	-	0/7/27/28	0/2/2/2
1	PSU	A2	1046	1	-	0/7/25/26	0/2/2/2
39	OMC	B5	2194	39,90	-	2/7/27/28	0/2/2/2
39	PSU	B5	1632	39	-	5/7/25/26	0/2/2/2
39	OMU	B5	3657	39	-	0/7/27/28	0/2/2/2
39	OMU	B5	2258	39	-	0/7/27/28	0/2/2/2
1	PSU	A2	1626	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	1731	39	-	0/7/25/26	0/2/2/2
39	OMG	B5	1260	39	-	1/5/27/28	0/3/3/3
39	OMC	B5	3573	39	-	0/7/27/28	0/2/2/2
39	PSU	B5	3371	39	-	0/7/25/26	0/2/2/2
1	A2M	A2	577	1	-	2/5/27/28	0/3/3/3
39	OMG	B5	3676	39	-	0/5/27/28	0/3/3/3
39	OMU	B5	4052	39	-	0/7/27/28	0/2/2/2
1	PSU	A2	93	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4298	39	-	0/7/25/26	0/2/2/2
1	B8N	A2	1249	1	-	0/12/34/35	0/2/2/2
1	OMU	A2	355	1	-	0/7/27/28	0/2/2/2
39	PSU	B5	3494	39	-	3/7/25/26	0/2/2/2
39	OMC	B5	3619	39	-	2/7/27/28	0/2/2/2
1	A2M	A2	27	1,90	-	0/5/27/28	0/3/3/3
39	OMC	B5	3540	39	-	1/7/27/28	0/2/2/2
1	OMC	A2	518	1	-	0/7/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	PSU	B5	4382	39	-	4/7/25/26	0/2/2/2
1	PSU	A2	1239	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	1683	39	-	0/7/25/26	0/2/2/2
1	OMC	A2	1392	1	-	0/7/27/28	0/2/2/2
39	OMU	B5	4244	39	-	0/7/27/28	0/2/2/2
39	A2M	B5	2206	39,90	-	0/5/27/28	0/3/3/3
1	A2M	A2	591	1	-	0/5/27/28	0/3/3/3
39	PSU	B5	4042	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	3583	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	1537	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4039	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4267	39,90	-	0/7/25/26	0/2/2/2
39	PSU	B5	3496	39	-	0/7/25/26	0/2/2/2
1	OMU	A2	116	1	-	1/7/27/28	0/2/2/2
39	A2M	B5	1479	39	-	0/5/27/28	0/3/3/3
1	PSU	A2	34	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	2351	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4322	39	-	0/7/25/26	0/2/2/2
68	V5N	Ba	39	68	-	0/5/10/12	0/1/1/1
39	PSU	B5	4435	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	867	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	398	39	-	2/5/27/28	0/3/3/3
1	PSU	A2	1644	1,90	-	0/7/25/26	0/2/2/2
39	OMG	B5	2719	39	-	0/5/27/28	0/3/3/3
39	A2M	B5	3557	39	-	1/5/27/28	0/3/3/3
1	PSU	A2	802	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4099	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	864	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	1477	39	-	0/5/27/28	0/3/3/3
39	PSU	B5	3502	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	3500	39	-	0/7/25/26	0/2/2/2
39	OMG	B5	4240	39	-	0/5/27/28	0/3/3/3
1	OMG	A2	1448	1	-	3/5/27/28	0/3/3/3
39	OMG	B5	3524	39	-	0/5/27/28	0/3/3/3
39	PSU	B5	4045	39	-	0/7/25/26	0/2/2/2
1	OMU	A2	1289	1	-	2/7/27/28	0/2/2/2
39	PSU	B5	4749	39	-	0/7/25/26	0/2/2/2
39	1MA	B5	1266	39,90	-	0/3/25/26	0/3/3/3
1	PSU	A2	1693	1	-	0/7/25/26	0/2/2/2
1	OMU	A2	628	1	-	2/7/27/28	0/2/2/2
81	MLZ	Bo	53	81	-	0/7/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	PSU	B5	1718	39	-	0/7/25/26	0/2/2/2
1	OMC	A2	174	1,90	-	0/7/27/28	0/2/2/2
39	PSU	B5	4166	39	-	1/7/25/26	0/2/2/2
42	V5N	BA	216	42	-	1/5/10/12	0/1/1/1
39	OMG	B5	2267	39	-	0/5/27/28	0/3/3/3
43	HIC	BB	245	43	-	1/5/6/8	0/1/1/1
39	UY1	B5	3550	39	-	1/9/27/28	0/2/2/2
1	PSU	A2	1005	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4246	39	-	1/7/25/26	0/2/2/2
1	PSU	A2	1047	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	687	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	3517	39	-	1/5/27/28	0/3/3/3
39	A2M	B5	400	39	-	0/5/27/28	0/3/3/3
1	OMG	A2	1329	1	-	0/5/27/28	0/3/3/3
39	A2M	B5	2630	39,90	-	0/5/27/28	0/3/3/3
1	OMC	A2	1704	1	-	2/7/27/28	0/2/2/2
39	PSU	B5	3585	39,90	-	0/7/25/26	0/2/2/2
39	A2M	B5	3450	39	-	1/5/27/28	0/3/3/3
1	PSU	A2	105	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	3476	39	-	1/5/27/28	0/3/3/3
1	PSU	A2	119	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	36	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	1799	39	-	0/7/25/26	0/2/2/2
1	A2M	A2	166	1	-	0/5/27/28	0/3/3/3
1	A2M	A2	1032	1	-	0/5/27/28	0/3/3/3
1	PSU	A2	816	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	4317	39	-	0/5/27/28	0/3/3/3
39	OMC	B5	3433	39	-	1/7/27/28	0/2/2/2
39	PSU	B5	4278	39	-	2/7/25/26	0/2/2/2
83	SAC	Br	2	83	-	0/7/8/10	-
39	OMG	B5	4383	39	-	1/5/27/28	0/3/3/3
1	A2M	A2	669	1,90	-	2/5/27/28	0/3/3/3
39	PSU	B5	4177	39	-	0/7/25/26	0/2/2/2
39	OMG	B5	3974	39	-	0/5/27/28	0/3/3/3
39	PSU	B5	3369	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	1820	39,90	-	1/7/27/28	0/2/2/2
1	OMG	A2	868	1	-	0/5/27/28	0/3/3/3
39	PSU	B5	3447	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	4269	39,90	-	2/5/27/28	0/3/3/3
69	MLZ	Bb	5	69	-	2/7/8/10	-
1	PSU	A2	573	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	A2	1443	1,90	-	2/7/27/28	0/2/2/2
1	PSU	A2	682	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	1082	1	-	1/7/25/26	0/2/2/2
1	OMU	A2	429	1	-	2/7/27/28	0/2/2/2
39	OMG	B5	3359	39	-	0/5/27/28	0/3/3/3
39	PSU	B5	3652	39,90	-	0/7/25/26	0/2/2/2
39	PSU	B5	1491	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	1175	1	-	0/7/25/26	0/2/2/2
1	OMU	A2	172	1	-	0/7/27/28	0/2/2/2
1	PSU	A2	650	1	-	0/7/25/26	0/2/2/2
41	PSU	B8	69	41	-	0/7/25/26	0/2/2/2
1	A2M	A2	513	1	-	2/5/27/28	0/3/3/3
44	AYA	BC	2	44	-	3/4/6/8	-
39	PSU	B5	2475	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	1638	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	2658	39	-	2/5/27/28	0/3/3/3
1	OMG	A2	510	1,90	-	1/5/27/28	0/3/3/3
1	A2M	A2	485	1	-	0/5/27/28	0/3/3/3
39	A2M	B5	1810	39,90	-	2/5/27/28	0/3/3/3
39	OMU	B5	3973	39	-	1/7/27/28	0/2/2/2
41	OMG	B8	75	41	-	1/5/27/28	0/3/3/3
80	M3L	Bm	98	80	-	0/9/10/12	-
1	PSU	A2	815	1	-	0/7/25/26	0/2/2/2
33	AME	Au	1	33	-	2/9/10/12	-
39	PSU	B5	3466	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	3462	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	3576	39	-	1/7/25/26	0/2/2/2
39	OMC	B5	2265	39,90	-	1/7/27/28	0/2/2/2
39	A2M	B5	2244	39,90	-	0/5/27/28	0/3/3/3
39	OMG	B5	4245	39	-	0/5/27/28	0/3/3/3
1	OMC	A2	463	1	-	0/7/27/28	0/2/2/2
1	4AC	A2	1338	1	-	4/9/29/30	0/2/2/2
1	OMG	A2	602	1	-	0/5/27/28	0/3/3/3
39	PSU	B5	4711	39	-	0/7/25/26	0/2/2/2
41	PSU	B8	55	41	-	0/7/25/26	0/2/2/2
11	PSU	AT	65	11	-	0/7/25/26	0/2/2/2
1	PSU	A2	610	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	3631	39	-	1/5/27/28	0/3/3/3
39	PSU	B5	1720	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	823	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	PSU	B5	3554	39	-	0/7/25/26	0/2/2/2
39	6MZ	B5	3966	39	-	0/5/27/28	0/3/3/3
1	OMG	A2	684	1	-	3/5/27/28	0/3/3/3
1	PSU	A2	218	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	3562	39	-	0/5/27/28	0/3/3/3
1	G7M	A2	1640	1,11	-	0/3/25/26	0/3/3/3
39	PSU	B5	4149	39	-	0/7/25/26	0/2/2/2
1	A2M	A2	99	1,90	-	2/5/27/28	0/3/3/3
1	4AC	A2	1843	1	-	2/9/29/30	0/2/2/2
39	PSU	B5	4107	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	210	1	-	0/7/25/26	0/2/2/2
39	OMC	B5	4282	39	-	0/7/27/28	0/2/2/2
39	OMG	B5	4138	39	-	0/5/27/28	0/3/3/3
1	A2M	A2	159	1	-	1/5/27/28	0/3/3/3
39	OMC	B5	1284	39	-	2/7/27/28	0/2/2/2
1	OMG	A2	1491	1,90	-	1/5/27/28	0/3/3/3
1	OMG	A2	645	1	-	3/5/27/28	0/3/3/3
39	OMC	B5	3601	39	-	0/7/27/28	0/2/2/2
39	A2M	B5	1270	39	-	0/5/27/28	0/3/3/3
1	6MZ	A2	1833	1,90	-	1/5/27/28	0/3/3/3
1	OMU	A2	121	1	-	0/7/27/28	0/2/2/2
1	A2M	A2	469	1	-	1/5/27/28	0/3/3/3

The worst 5 of 349 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	1640	G7M	C8-N9	7.36	1.46	1.33
1	A2	1640	G7M	C8-N7	7.11	1.46	1.33
1	A2	1640	G7M	C5-C4	5.86	1.47	1.39
1	A2	1249	B8N	C6-N1	5.47	1.39	1.33
35	Aw	62	HY3	C3-C2	-4.91	1.50	1.55

The worst 5 of 920 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	3550	UY1	N1-C2-N3	-10.39	120.17	128.43
39	B5	4166	PSU	N1-C2-N3	-8.58	121.61	128.43
1	A2	610	PSU	N1-C2-N3	-8.35	121.80	128.43
1	A2	218	PSU	N1-C2-N3	-8.33	121.81	128.43
1	A2	210	PSU	N1-C2-N3	-8.32	121.82	128.43

There are no chirality outliers.

5 of 108 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A2	159	A2M	C1'-C2'-O2'-CM'
1	A2	513	A2M	O4'-C4'-C5'-O5'
1	A2	628	OMU	C2'-C1'-N1-C6
1	A2	628	OMU	O4'-C1'-N1-C6
1	A2	645	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 741 ligands modelled in this entry, 363 are monoatomic and 374 are unknown - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
93	GTP	B7	201	40	26,34,34	1.05	1 (3%)	33,54,54	2.10	4 (12%)
94	SF4	Bz	1000	88	0,12,12	0.00	-	-		
94	SF4	Bz	1001	88	0,12,12	0.00	-	-		
89	SPD	A2	1901	-	9,9,9	0.16	0	8,8,8	0.16	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
93	GTP	B7	201	40	-	0/18/38/38	0/3/3/3
94	SF4	Bz	1000	88	-	-	0/6/5/5
94	SF4	Bz	1001	88	-	-	0/6/5/5
89	SPD	A2	1901	-	-	0/7/7/7	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
93	B7	201	GTP	C6-N1	4.00	1.40	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
93	B7	201	GTP	C5-C6-N1	-8.79	111.41	123.43
93	B7	201	GTP	C6-N1-C2	5.87	125.26	115.93
93	B7	201	GTP	C2-N3-C4	-2.83	112.12	115.36
93	B7	201	GTP	N3-C2-N1	-2.72	123.60	127.22

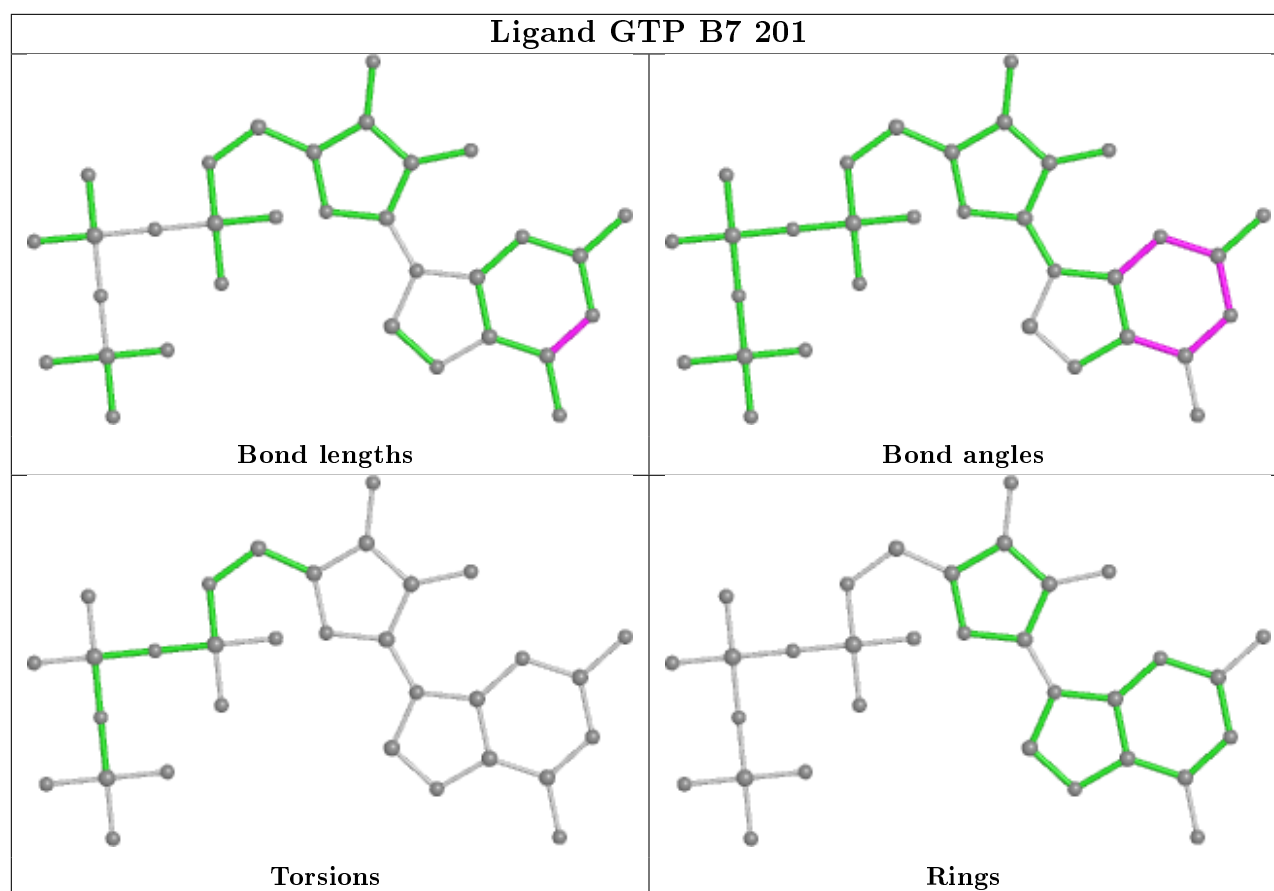
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

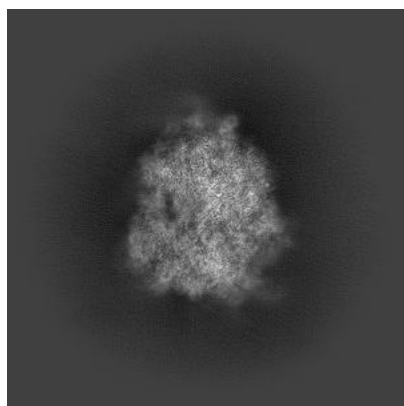
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12758. These allow visual inspection of the internal detail of the map and identification of artifacts.

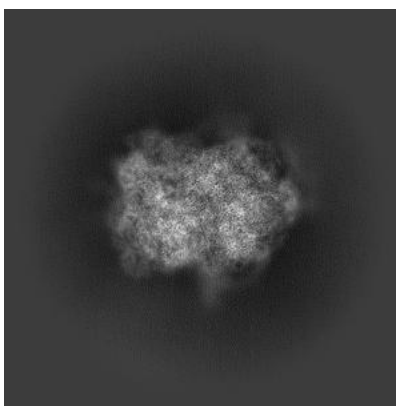
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

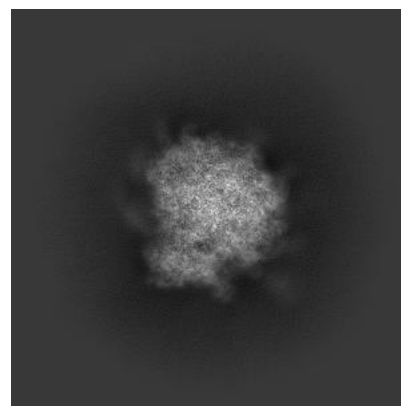
#### 6.1.1 Primary map



X

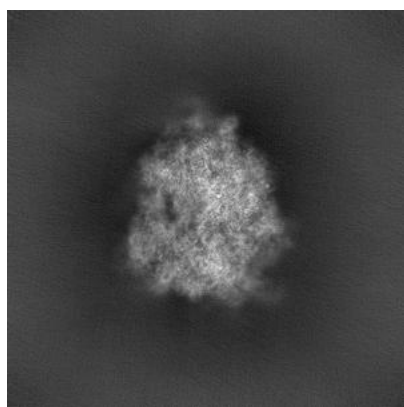


Y

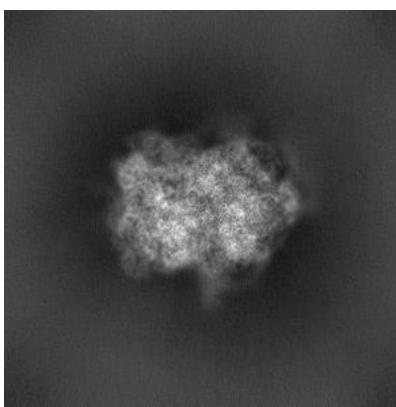


Z

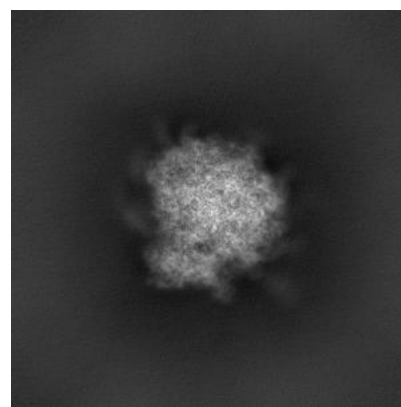
#### 6.1.2 Raw map



X



Y

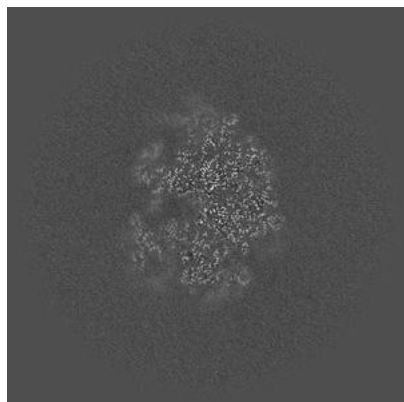


Z

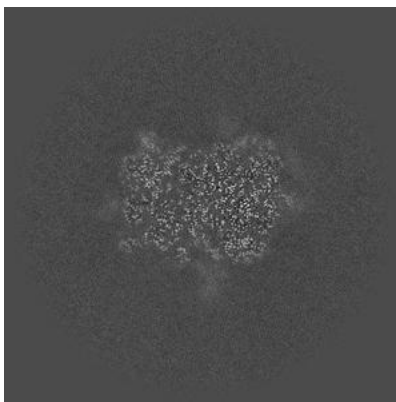
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

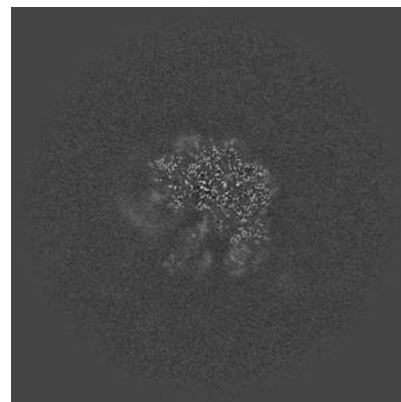
### 6.2.1 Primary map



X Index: 280

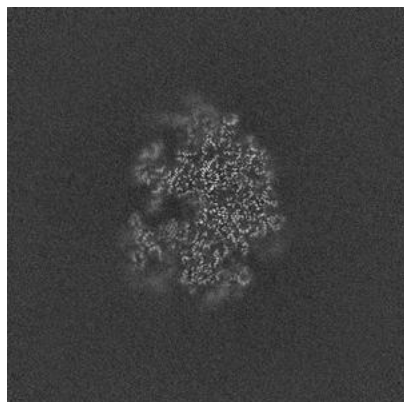


Y Index: 280

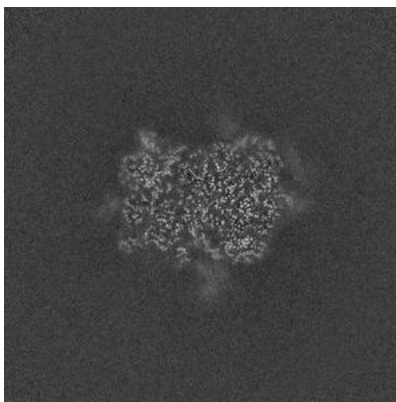


Z Index: 280

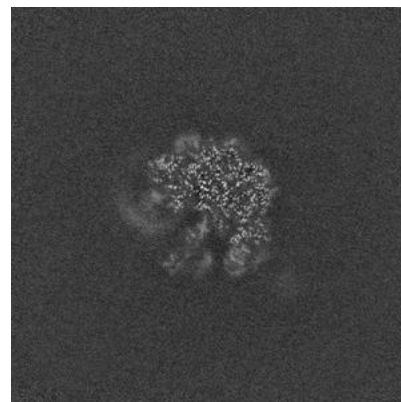
### 6.2.2 Raw map



X Index: 280



Y Index: 280



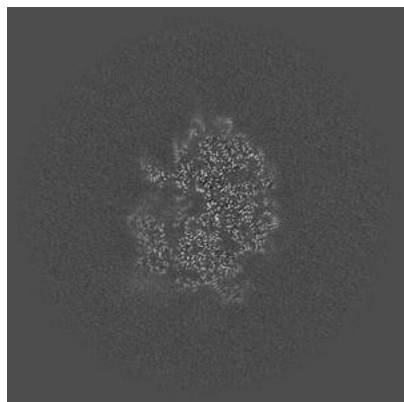
Z Index: 280

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

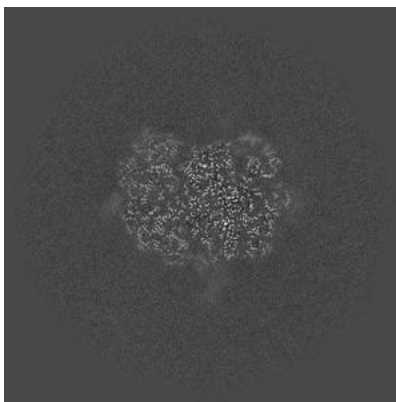


## 6.3 Largest variance slices [i](#)

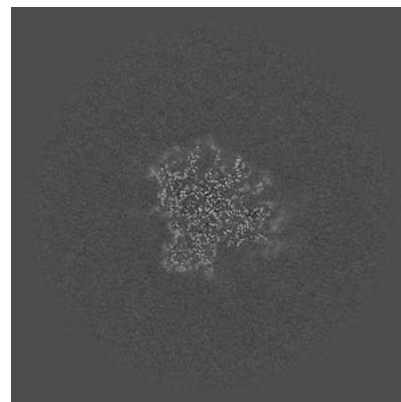
### 6.3.1 Primary map



X Index: 263

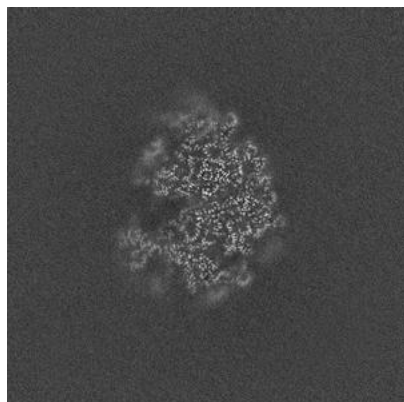


Y Index: 289

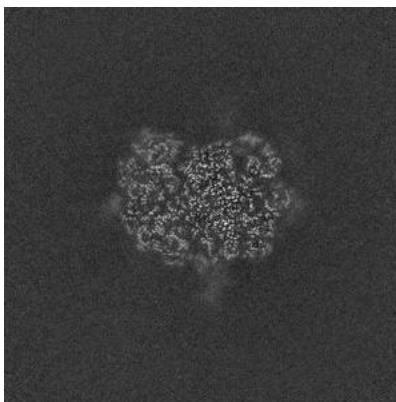


Z Index: 323

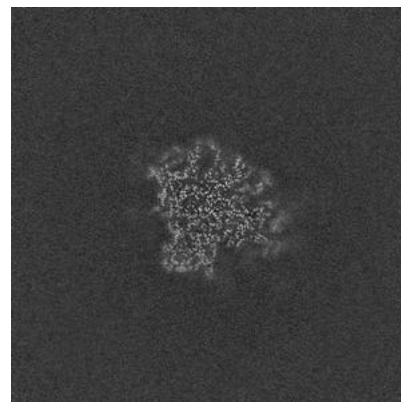
### 6.3.2 Raw map



X Index: 285



Y Index: 289

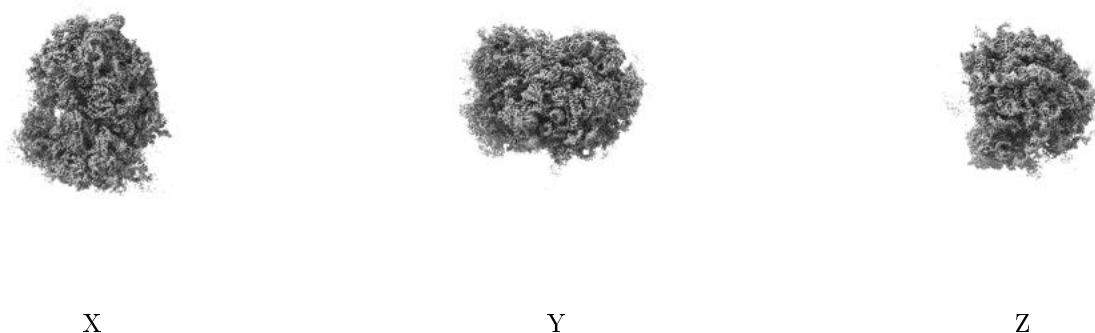


Z Index: 323

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

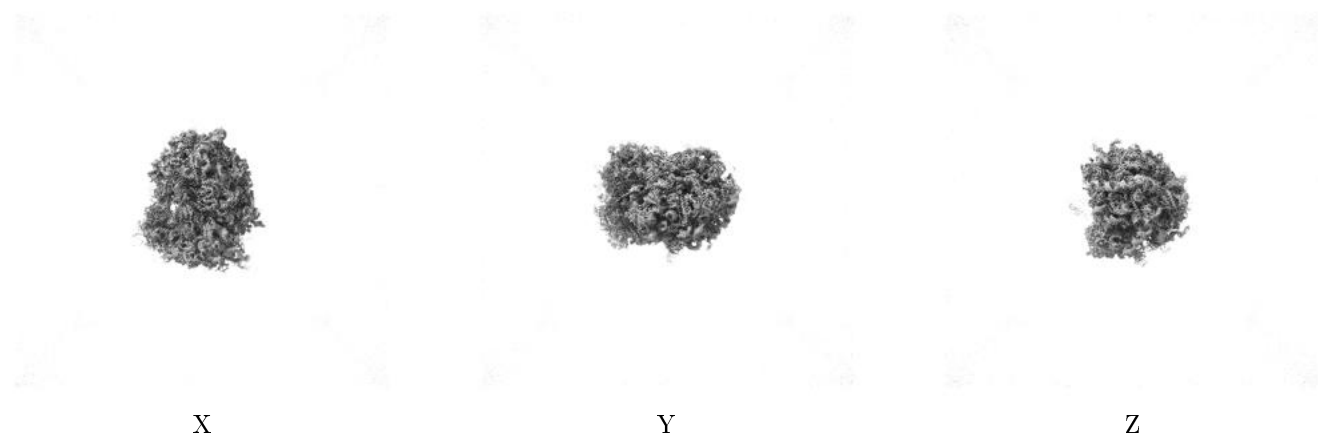
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



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

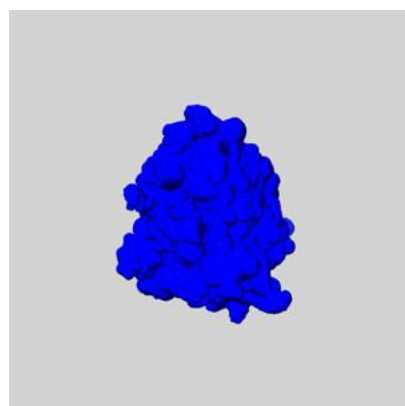
## 6.5 Mask visualisation [i](#)

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

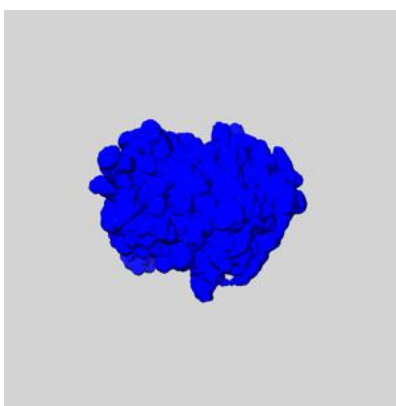
A mask typically either:

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

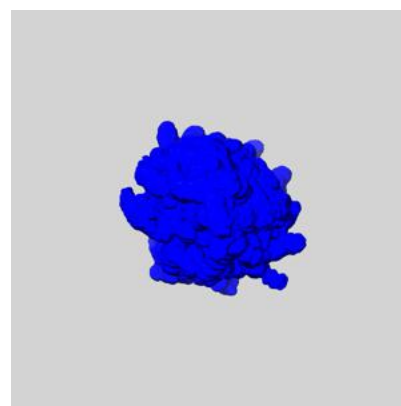
### 6.5.1 emd\_12758\_msk\_1.map [i](#)



X

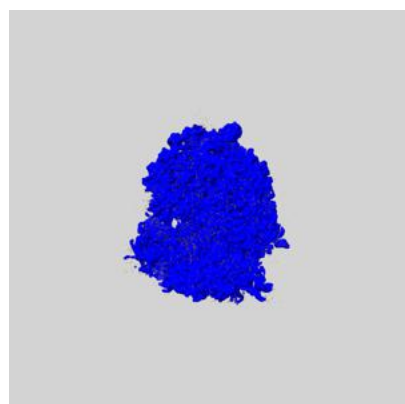


Y

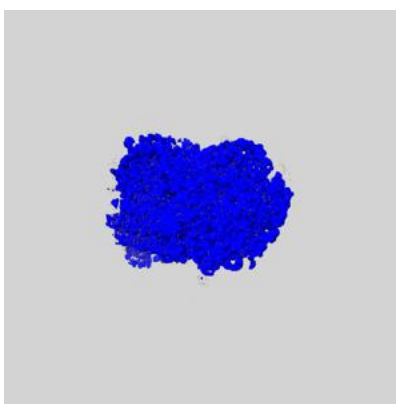


Z

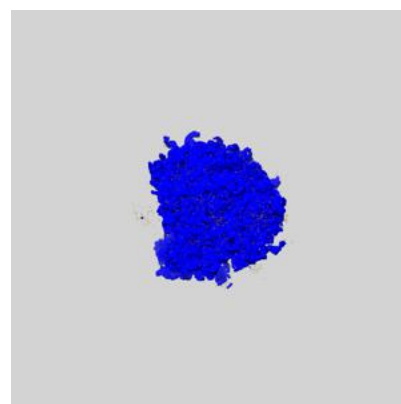
### 6.5.2 emd\_12758\_msk\_2.map [i](#)



X



Y

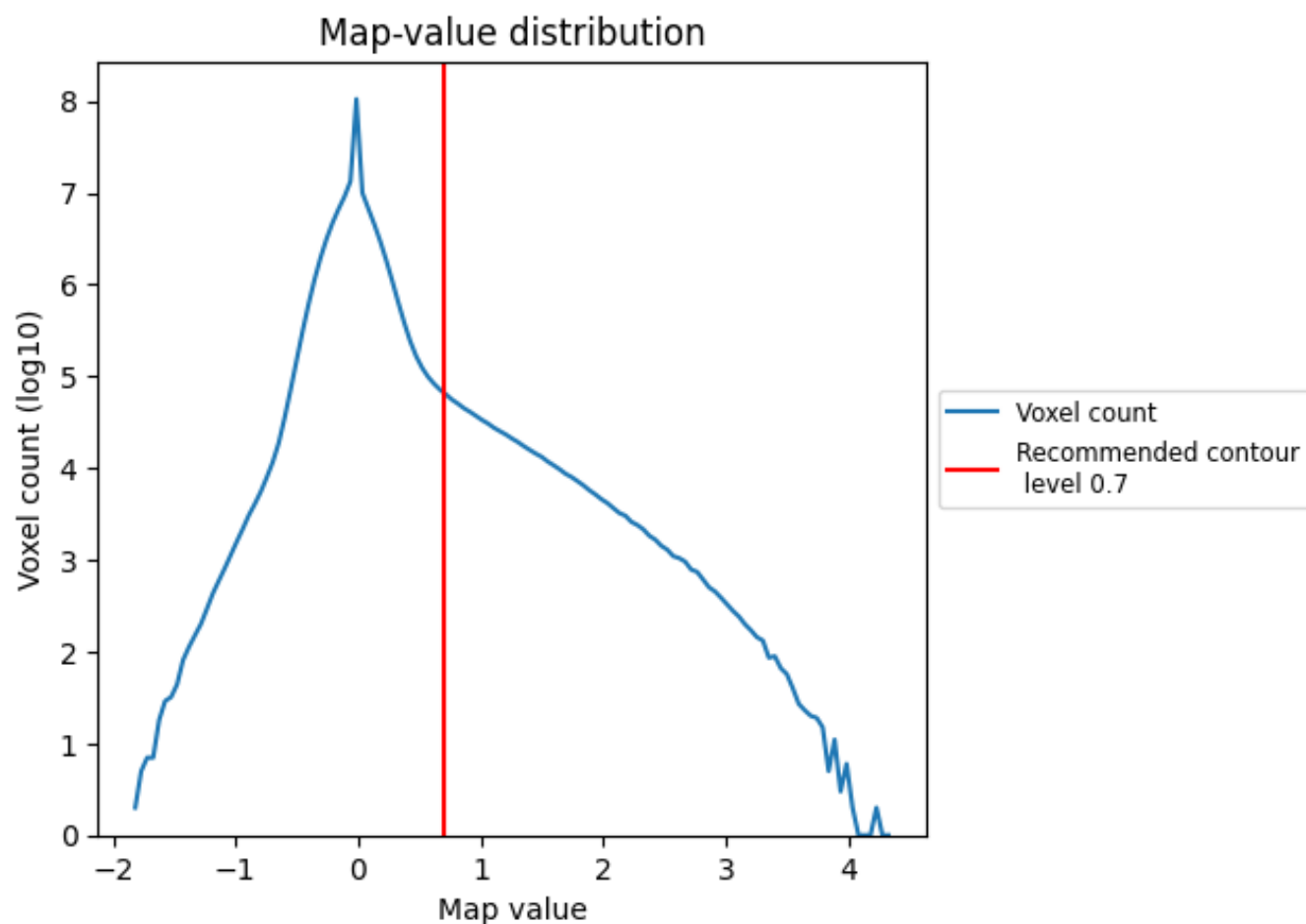


Z

## 7 Map analysis [i](#)

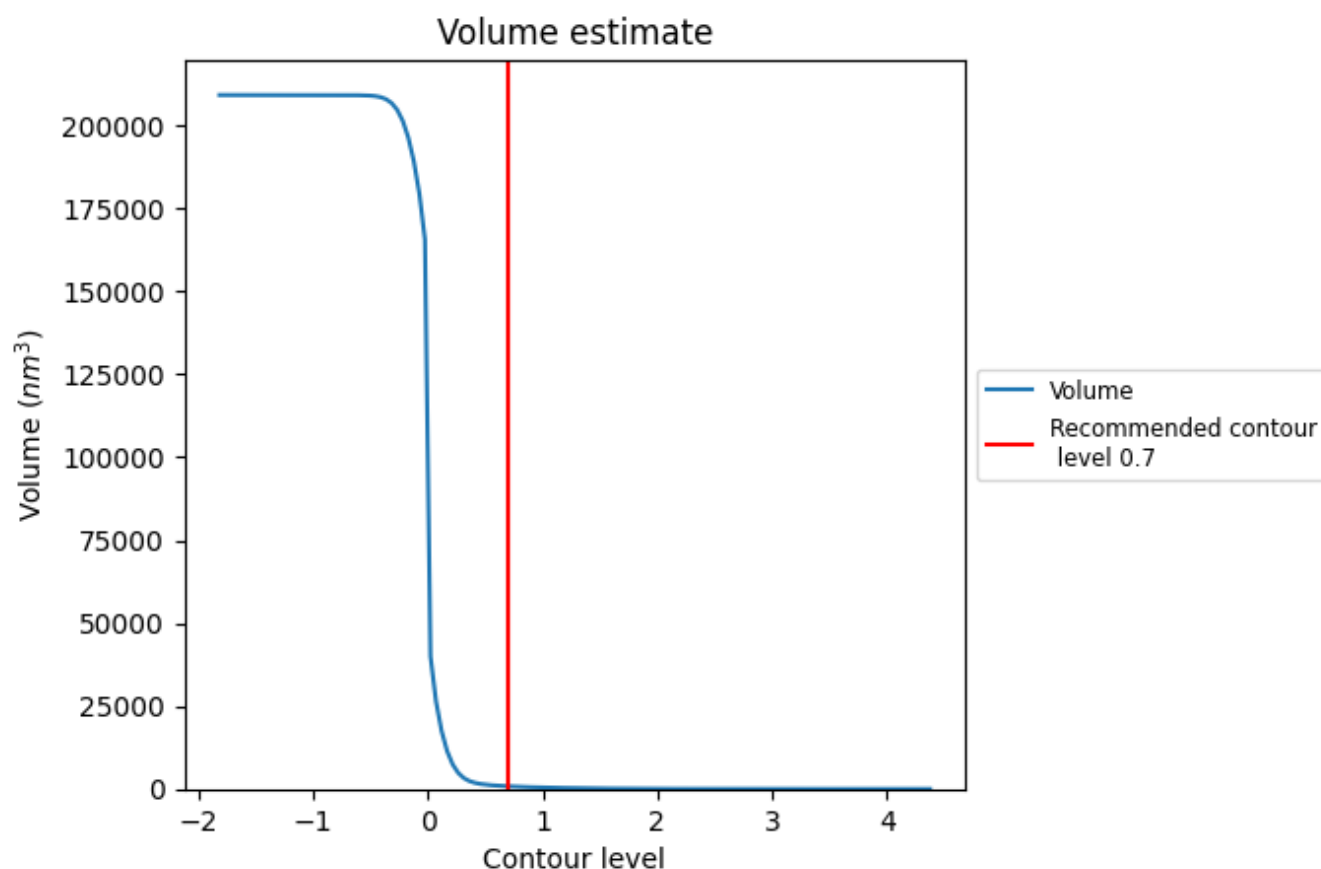
This section contains the results of statistical analysis of the map.

### 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.

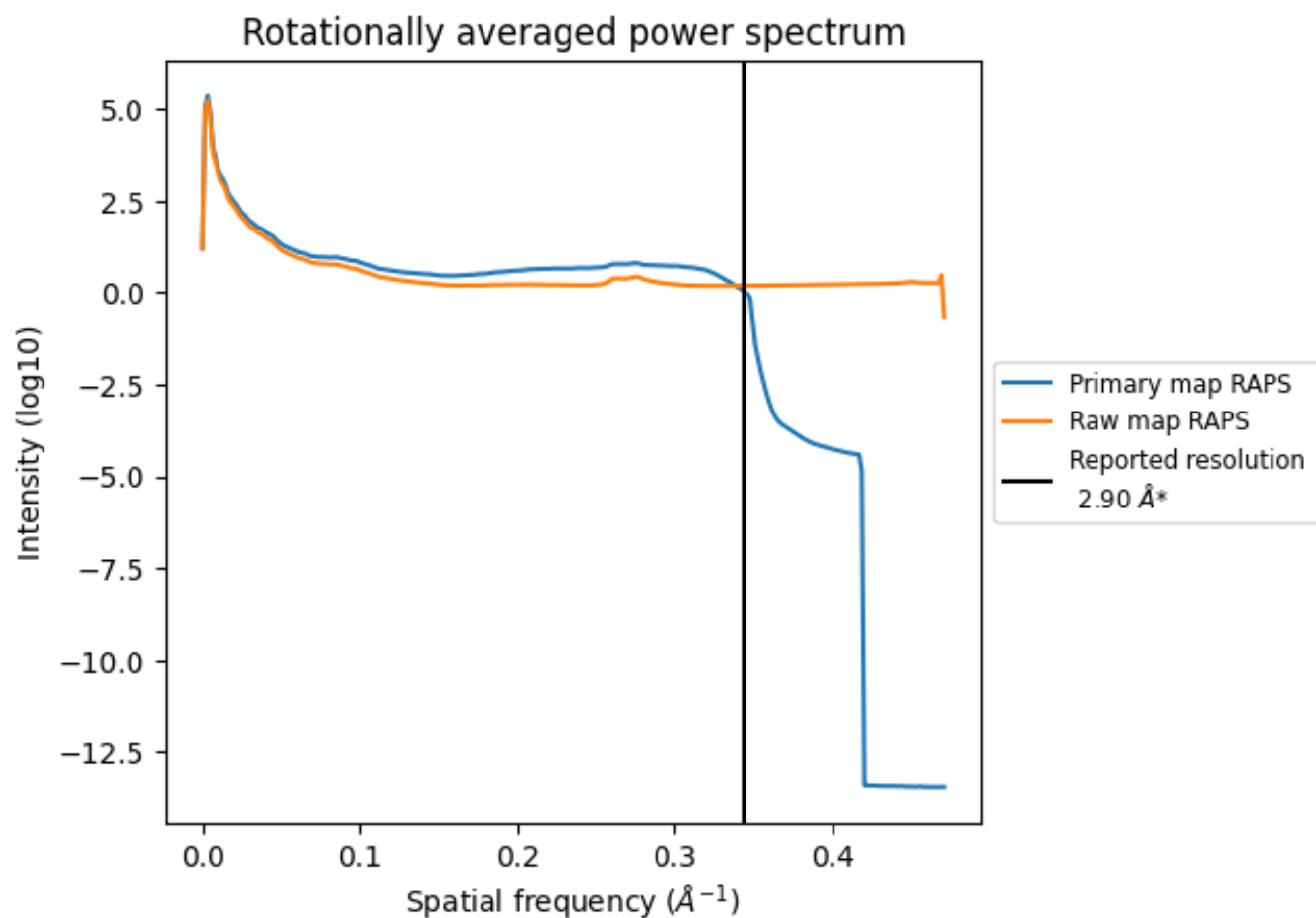
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 803  $\text{nm}^3$ ; this corresponds to an approximate mass of 726 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 ⓘ

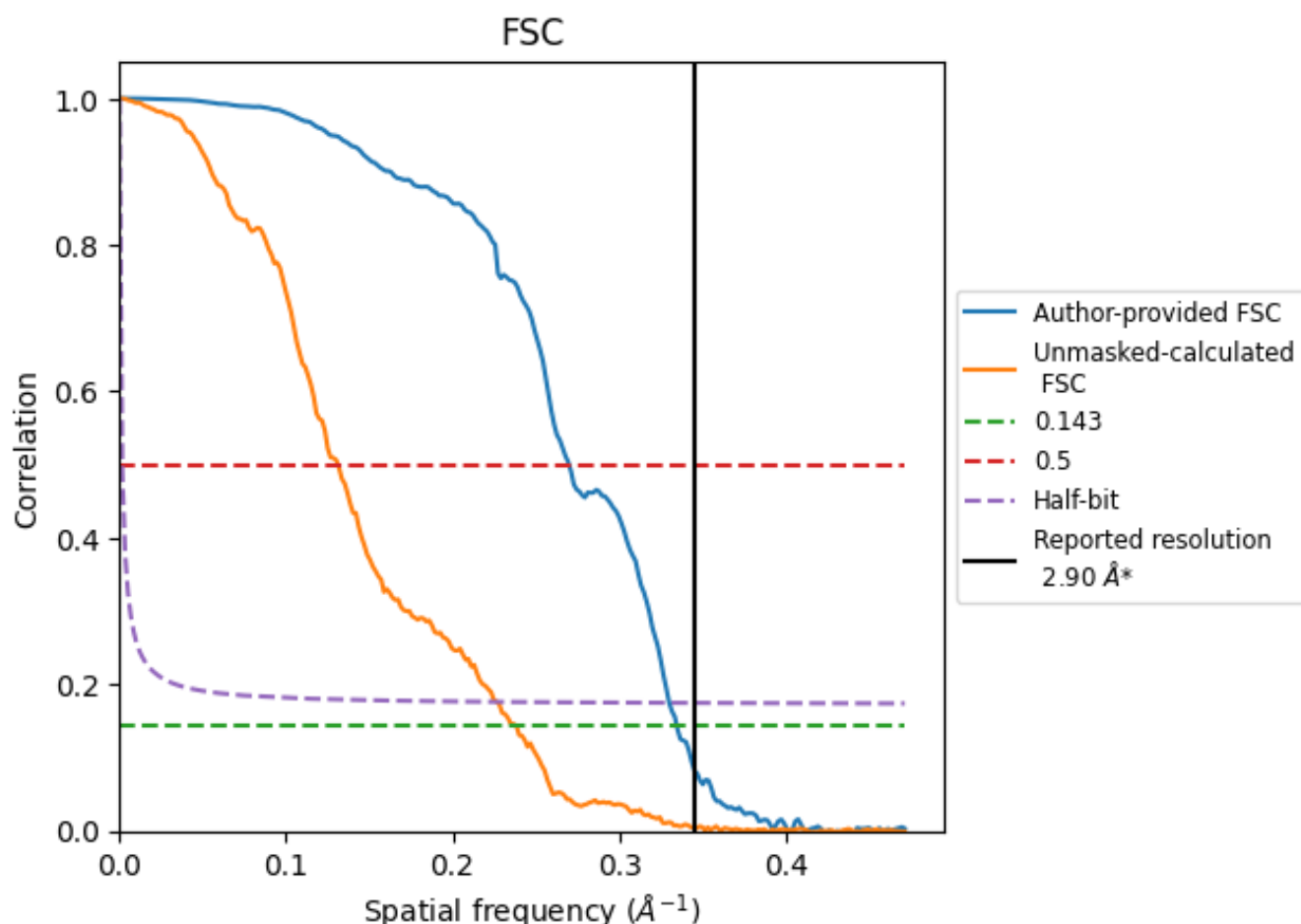


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 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 0.345 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.99	3.70	3.03
Unmasked-calculated*	4.19	7.63	4.41

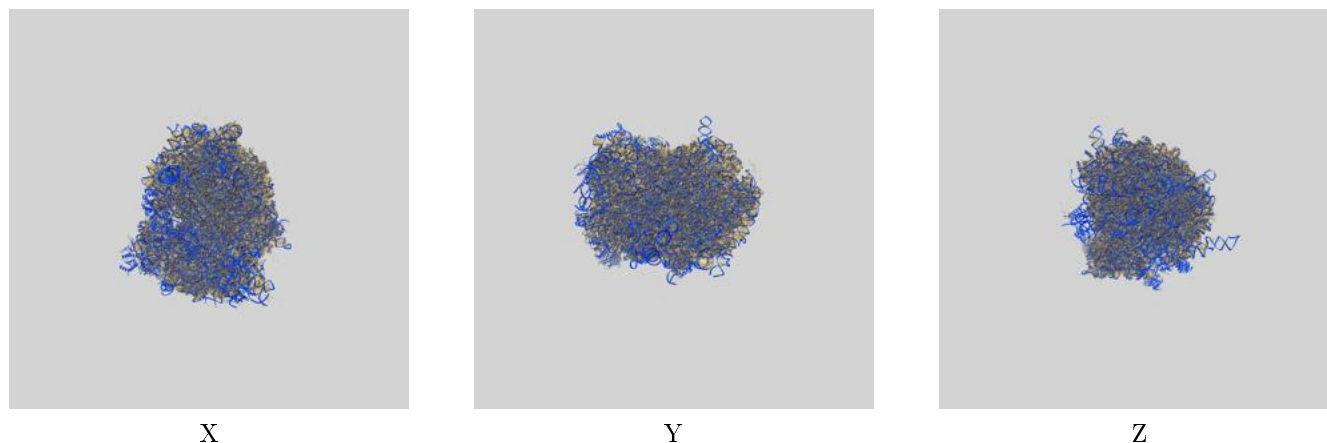
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.19 differs from the reported value 2.9 by more than 10 %



## 9 Map-model fit [i](#)

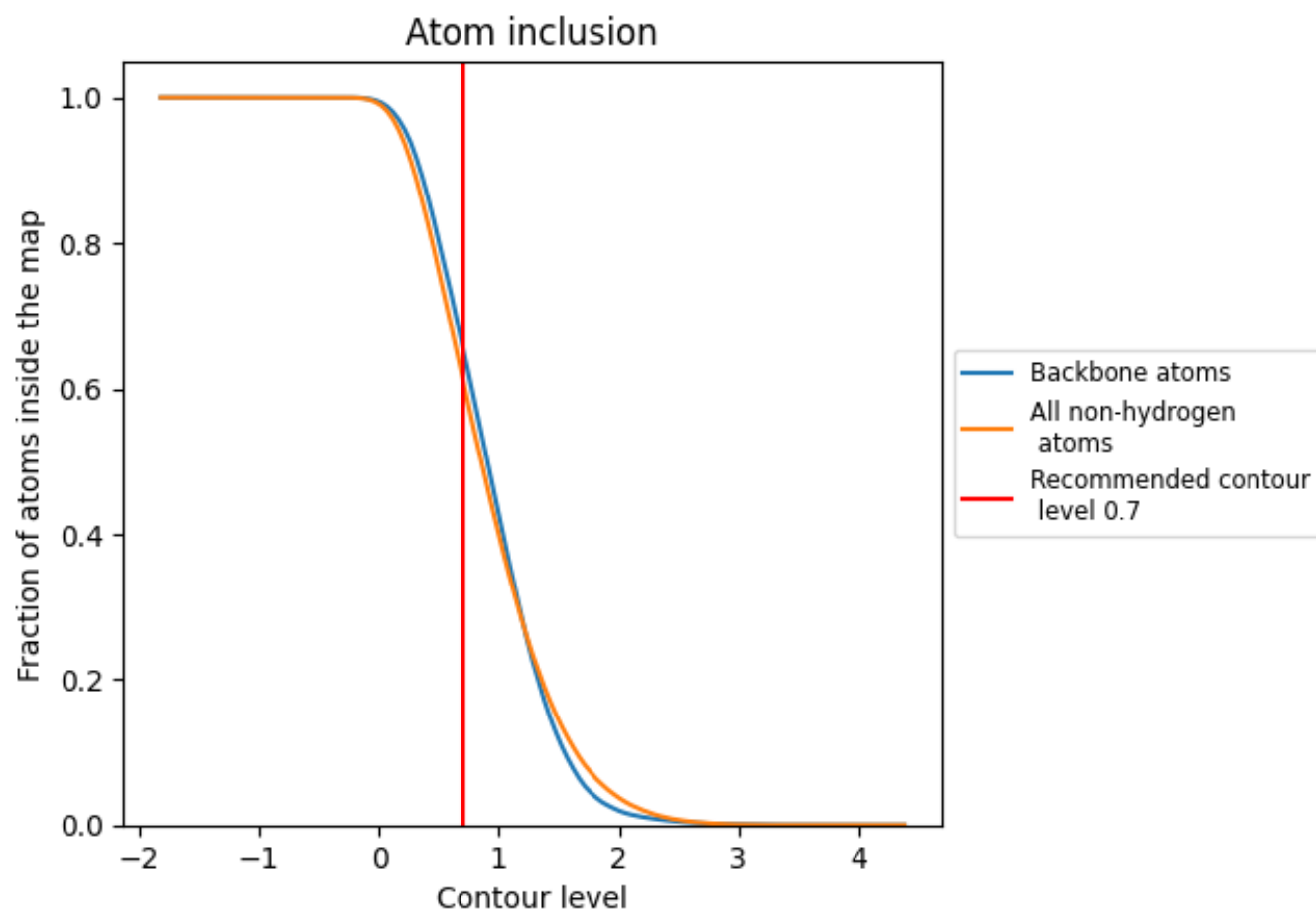
This section contains information regarding the fit between EMDB map EMD-12758 and PDB model 7O80. Per-residue inclusion information can be found in section [3](#) on page [27](#).

### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.7 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 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.