



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:01 PM UTC

PDB ID : 9S3D / pdb\_00009s3d  
EMDB ID : EMD-54530  
Title : NAC bound human RNC with 58 amino acid ARF1-linker  
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.  
Deposited on : 2025-07-24  
Resolution : 2.32 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.

The types of validation reports are described at

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

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

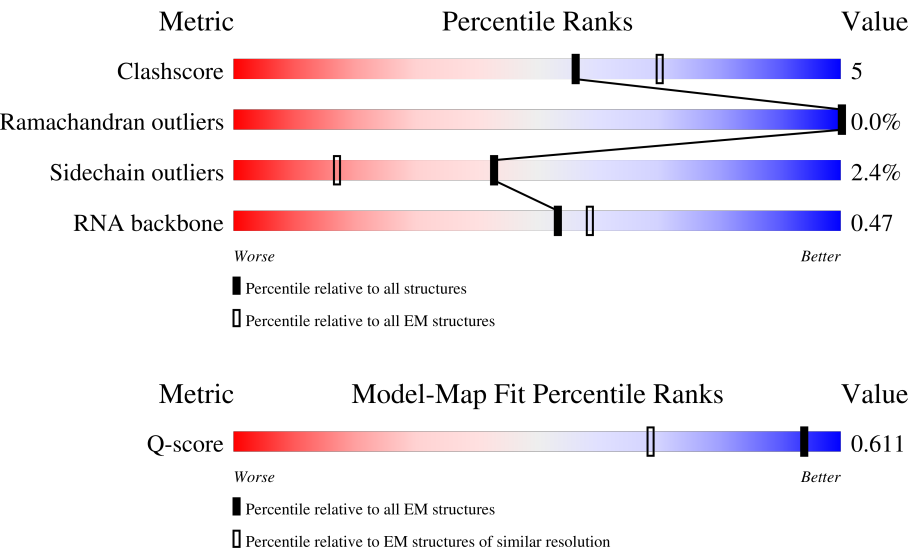
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.32 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4359 ( 1.82 - 2.82 )

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	NA	215	<div><div>18% 27% 69%</div></div>
2	NB	162	<div><div>32% 54% 11% 35%</div></div>
3	CM	586	<div><div>98%</div></div>











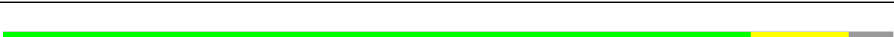


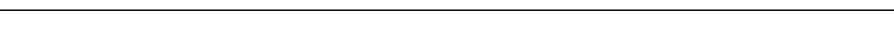
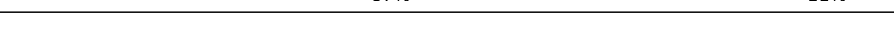
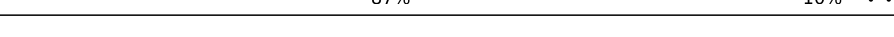



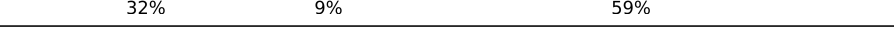





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Mol	Chain	Length	Quality of chain
4	CP	75	
5	CR	437	
6	CZ	95	
7	L5	5070	
8	L7	121	
9	L8	157	
10	LA	257	
11	LB	403	
12	LC	427	
13	LD	297	
14	LE	288	
15	LF	248	
16	LG	266	
17	LH	192	
18	LI	214	
19	LJ	178	
20	LL	211	
21	LM	215	
22	LN	204	
23	LO	203	
24	LP	184	
25	LQ	188	
26	LR	196	
27	LS	176	
28	LT	160	












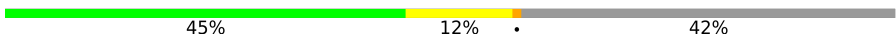













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Mol	Chain	Length	Quality of chain
29	LU	128	
30	LV	140	
31	LW	157	
32	LX	156	
33	LY	145	
34	LZ	136	
35	La	148	
36	Lb	159	
37	Lc	115	
38	Ld	125	
39	Le	135	
40	Lf	110	
41	Lg	117	
42	Lh	123	
43	Li	105	
44	Lj	97	
45	Lk	70	
46	Ll	51	
47	Lm	128	
48	Ln	25	
49	Lo	106	
50	Lp	92	
51	Lr	137	
52	Ls	317	
53	Lt	165	


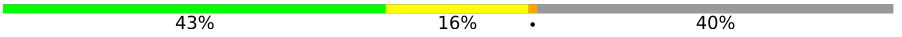






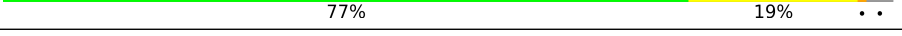
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Mol	Chain	Length	Quality of chain
54	S2	1869	
55	SA	295	
56	SB	264	
57	SC	293	
58	SD	243	
59	SE	263	
60	SF	204	
61	SG	249	
62	SH	194	
63	SI	208	
64	SJ	194	
65	SK	165	
66	SL	158	
67	SM	132	
68	SN	151	
69	SO	151	
70	SP	145	
71	SQ	146	
72	SR	135	
73	SS	152	
74	ST	145	
75	SU	119	
76	SV	83	
77	SW	130	
78	SX	143	

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Mol	Chain	Length	Quality of chain
79	SY	133	 67%26%8%
80	SZ	125	 43%16%40%
81	Sa	115	 73%13%14%
82	Sb	84	 83%13%..
83	Sc	69	 62%29%9%
84	Sd	56	 75%20%5%
85	Se	133	 35%6%59%
86	Sf	156	 29%11%60%
87	Sg	317	 77%19%..

## 2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 218816 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	NA	66	Total	C	N	O	S	0	0
			522	329	95	97	1		

- Molecule 2 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	NB	105	Total	C	N	O	S	0	0
			813	508	152	150	3		

- Molecule 3 is a RNA chain called 58 amino acid ARF1-linker - V5 peptide - hCMV staller mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CM	12	Total	C	N	O	P	0	0
			247	111	37	87	12		

- Molecule 4 is a RNA chain called prolyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CP	75	Total	C	N	O	P	0	0
			1602	713	284	530	75		

- Molecule 5 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CR	414	Total	C	N	O	S	0	0
			3269	2080	557	621	11		

- Molecule 6 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CZ	39	Total	C	N	O	S	0	0
			261	169	43	47	2		

- Molecule 7 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L5	3648	Total	C	N	O	P	0	0
			78199	34823	14307	25422	3647		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 9 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 11 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		

- Molecule 12 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		

- Molecule 13 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		

- Molecule 14 is a protein called Large ribosomal subunit protein eL6.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		

- Molecule 15 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		

- Molecule 17 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 18 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI	207	Total	C	N	O	S	0	0
			1666	1059	323	270	14		

- Molecule 19 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		

- Molecule 21 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		

- Molecule 22 is a protein called 60S ribosomal protein L15.

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

- Molecule 23 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		

- Molecule 24 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 25 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		

- Molecule 26 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		

- Molecule 27 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		

- Molecule 28 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

- Molecule 29 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	101	Total	C	N	O	S	0	0
			806	520	141	143	2		

- Molecule 30 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		

- Molecule 32 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		

- Molecule 33 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		

- Molecule 34 is a protein called 60S ribosomal protein L27.

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

- Molecule 35 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		

- Molecule 36 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		

- Molecule 38 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		

- Molecule 39 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		

- Molecule 40 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 41 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		

- Molecule 42 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 43 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		

- Molecule 44 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 45 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		

- Molecule 46 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 47 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		

- Molecule 48 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 49 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 50 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		

- Molecule 51 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ls	212	Total	C	N	O	S	0	0
			1640	1042	284	305	9		

- Molecule 53 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lt	160	Total	C	N	O	S	0	0
			1208	749	226	229	4		

- Molecule 54 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S2	1713	Total	C	N	O	P	0	0
			36562	16320	6564	11966	1712		

- Molecule 55 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 56 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 57 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 58 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SD	223	Total	C	N	O	S	0	0
			1594	1023	291	273	7		

- Molecule 59 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 60 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SF	181	Total	C	N	O	S	0	0
			1403	879	269	248	7		

- Molecule 61 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 62 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	SH	183	Total	C	N	O	0	0
			1274	819	242	213		

- Molecule 63 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 64 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 65 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 66 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 67 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SM	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 68 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 69 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 70 is a protein called 40S ribosomal protein S15.



Mol	Chain	Residues	Atoms					AltConf	Trace
70	SP	129	Total	C	N	O	S	0	0
			990	626	190	168	6		

- Molecule 71 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SQ	142	Total	C	N	O	S	0	0
			1075	689	204	179	3		

- Molecule 72 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 73 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SS	141	Total	C	N	O	S	0	0
			1130	712	232	185	1		

- Molecule 74 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 75 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 76 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- Molecule 77 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 78 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 79 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 80 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 81 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 82 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 83 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

- Molecule 84 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

- Molecule 85 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Se	55	Total	C	N	O	S	0	0
			416	254	93	68	1		

- Molecule 86 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Sf	63	Total	C	N	O	S	0	0
			515	324	98	86	7		

- Molecule 87 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Sg	308	Total	C	N	O	S	0	0
			2180	1393	381	395	11		

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	L5	127	Total	Mg	0
			127	127	
88	L7	3	Total	Mg	0
			3	3	
88	L8	3	Total	Mg	0
			3	3	
88	LA	1	Total	Mg	0
			1	1	
88	LC	1	Total	Mg	0
			1	1	
88	LN	1	Total	Mg	0
			1	1	
88	LP	1	Total	Mg	0
			1	1	
88	LV	1	Total	Mg	0
			1	1	
88	S2	53	Total	Mg	0
			53	53	

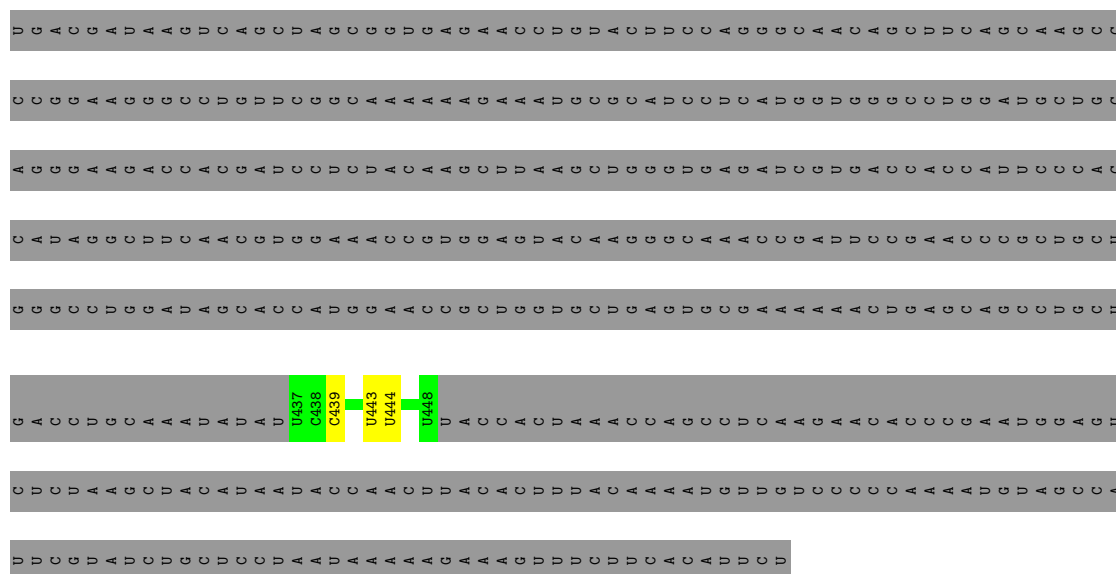
- Molecule 89 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
89	Lg	1	Total 1	Zn 1	0
89	Lj	1	Total 1	Zn 1	0
89	Lm	1	Total 1	Zn 1	0
89	Lo	1	Total 1	Zn 1	0
89	Lp	1	Total 1	Zn 1	0
89	Sa	1	Total 1	Zn 1	0
89	Sd	1	Total 1	Zn 1	0
89	Sf	1	Total 1	Zn 1	0

- Molecule 90 is water.

Mol	Chain	Residues	Atoms		AltConf
90	L5	4	Total 4	O 4	0
90	L7	1	Total 1	O 1	0
90	LI	1	Total 1	O 1	0
90	LN	1	Total 1	O 1	0
90	La	1	Total 1	O 1	0
90	S2	3	Total 3	O 3	0





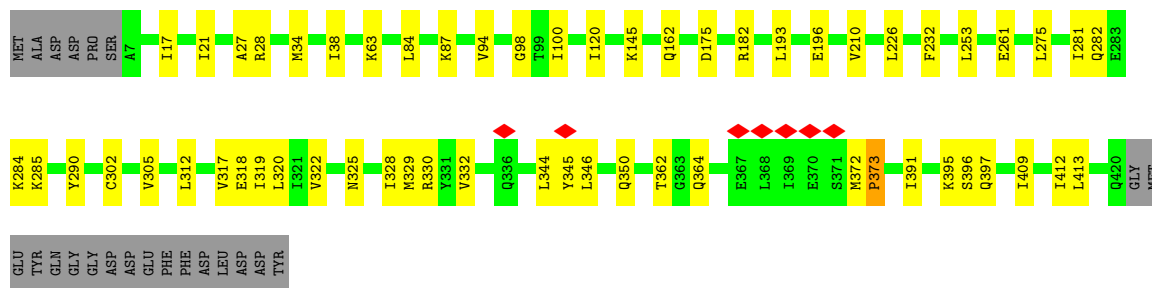
- Molecule 4: prolyl-tRNA

Chain CP: 60% 40%



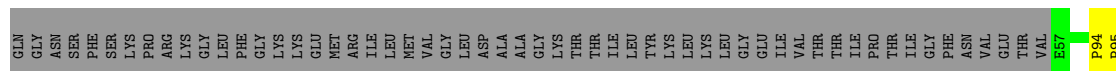
- Molecule 5: Eukaryotic peptide chain release factor subunit 1

Chain CR: 81% 13% 5%



- Molecule 6: nascent chain

Chain CZ: 39% 59%



- Molecule 7: 28S rRNA

Chain L5: 48% 22% 28%

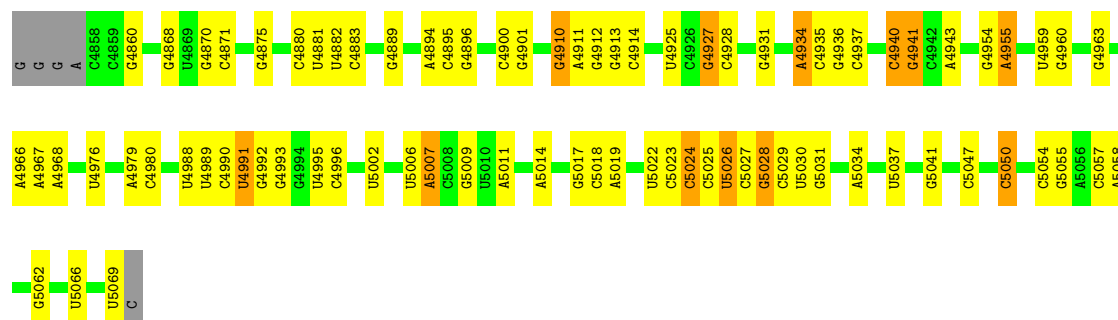






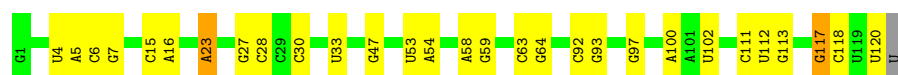






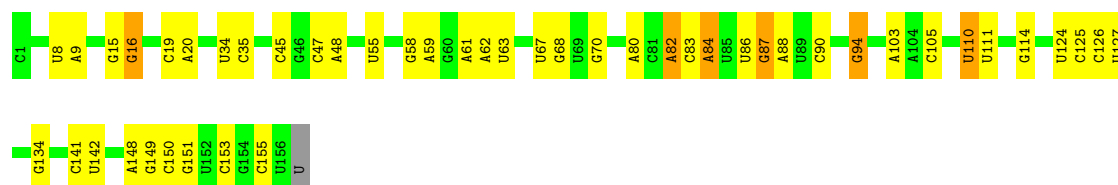
• Molecule 8: 5S rRNA

Chain L7: 75% 22% ..



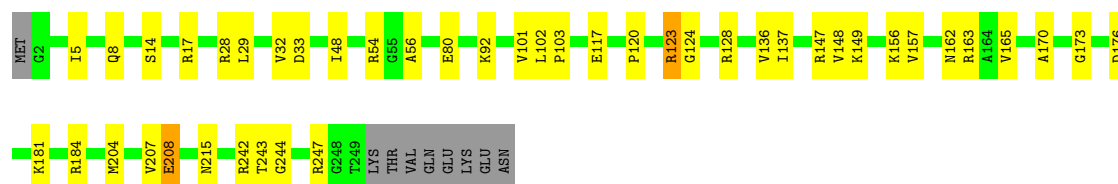
• Molecule 9: 5.8S rRNA

Chain L8: 69% 26% ..



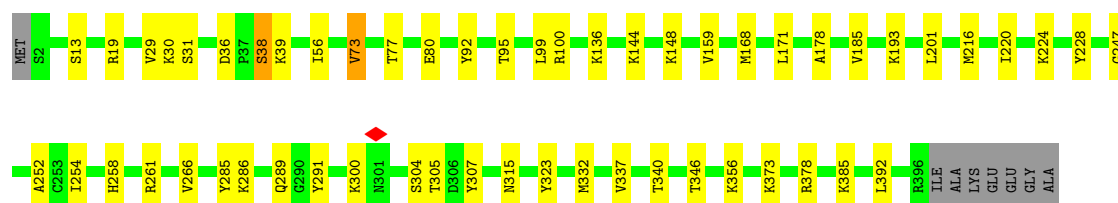
• Molecule 10: 60S ribosomal protein L8

Chain LA: 79% 16% ..




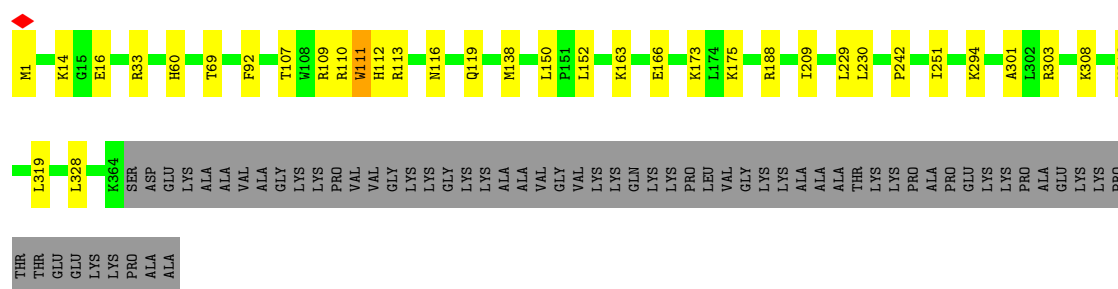
• Molecule 11: 60S ribosomal protein L3

Chain LB: 84% 13% .




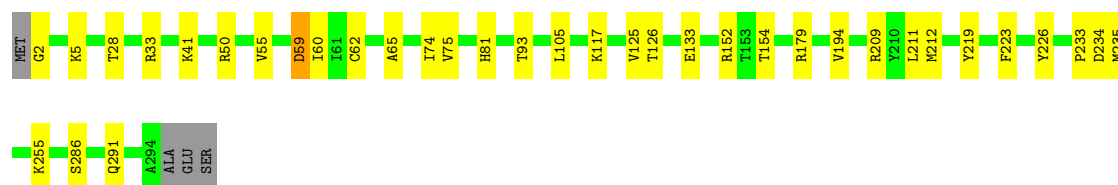
• Molecule 12: 60S ribosomal protein L4

Chain LC:  77% 8% 15%



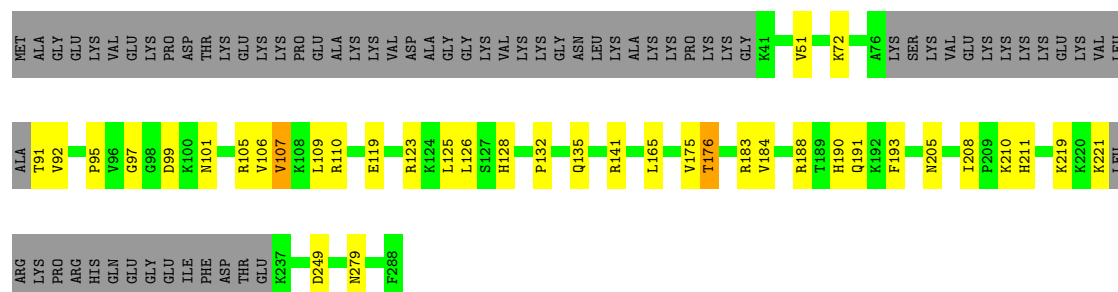
- Molecule 13: 60S ribosomal protein L5

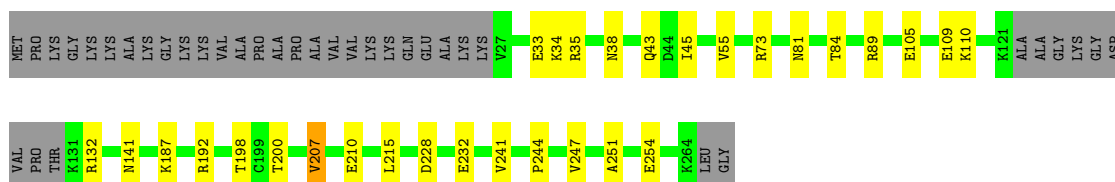
Chain LD:  87% 12%



- Molecule 14: Large ribosomal subunit protein eL6

Chain LE:  63% 12% 24%





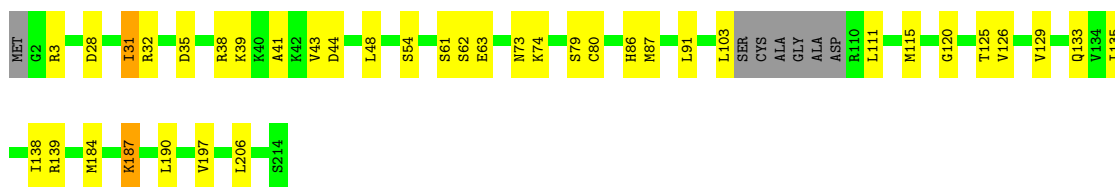
- Molecule 17: 60S ribosomal protein L9

Chain LH: 82% 17% ..



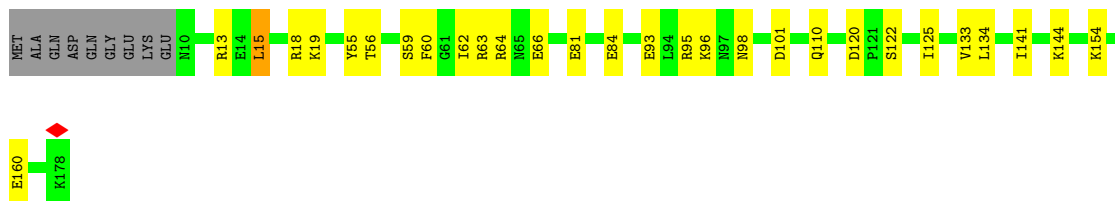
- Molecule 18: Ribosomal protein uL16-like

Chain LI: 79% 17% ..



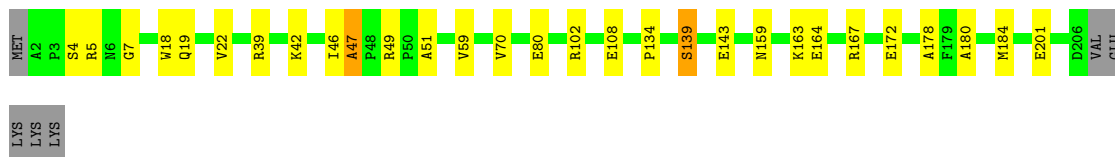
- Molecule 19: 60S ribosomal protein L11

Chain LJ: 79% 16% • 5%



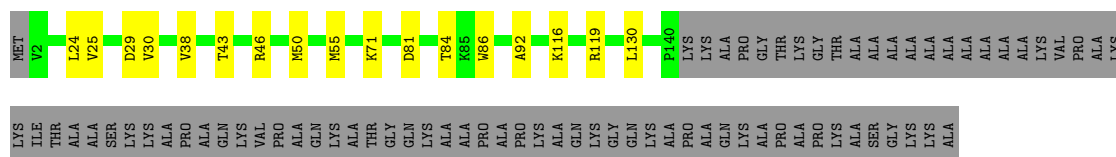
- Molecule 20: 60S ribosomal protein L13

Chain LL: 83% 13% ..



- Molecule 21: 60S ribosomal protein L14

Chain LM: 57% 8% 35%



- Molecule 22: 60S ribosomal protein L15

Chain LN: 88% 11%



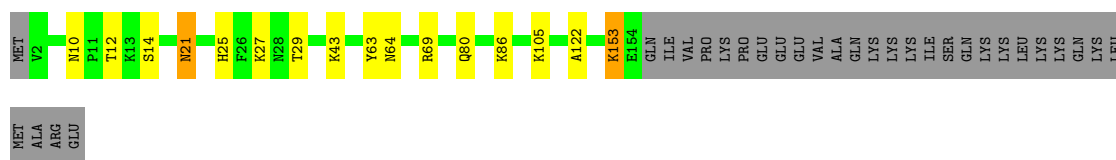
- Molecule 23: 60S ribosomal protein L13a

Chain LO: 85% 13%



- Molecule 24: 60S ribosomal protein L17

Chain LP: 74% 8% 17%



- Molecule 25: 60S ribosomal protein L18

Chain LQ: 87% 13%



- Molecule 26: 60S ribosomal protein L19

Chain LR: 80% 10% 10%




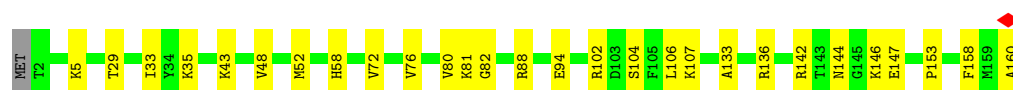
- Molecule 27: 60S ribosomal protein L18a

Chain LS: 83% 15%



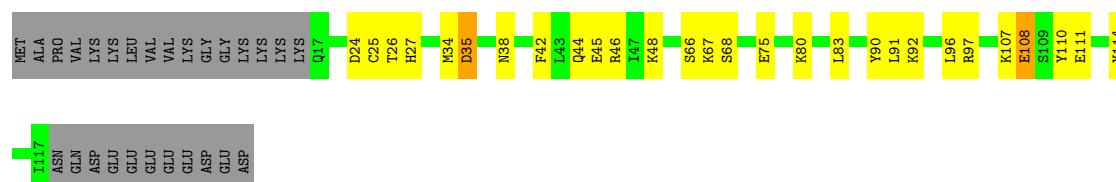
- Molecule 28: 60S ribosomal protein L21

Chain LT:  82% 18%




- Molecule 29: 60S ribosomal protein L22

Chain LU:  57% 20% 21%



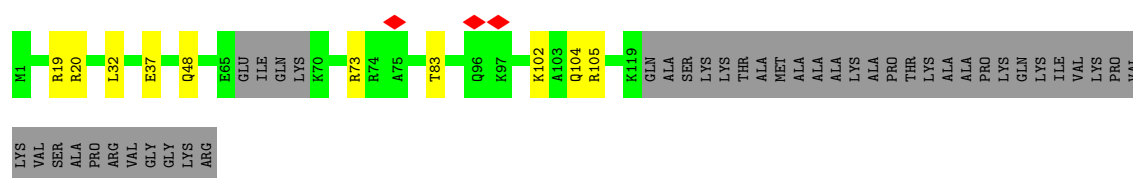
- Molecule 30: 60S ribosomal protein L23

Chain LV:  76% 17% 6%



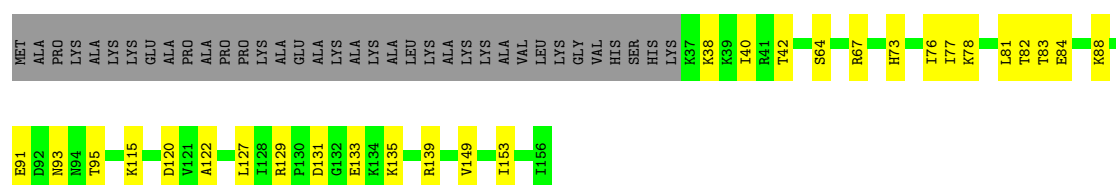
- Molecule 31: 60S ribosomal protein L24

Chain LW:  67% 6% 27%




- Molecule 32: 60S ribosomal protein L23a

Chain LX:  59% 18% 23%



- Molecule 33: 60S ribosomal protein L26

Chain LY:  77% 15% 8%





- Molecule 34: 60S ribosomal protein L27

Chain LZ: 87% 12% ..



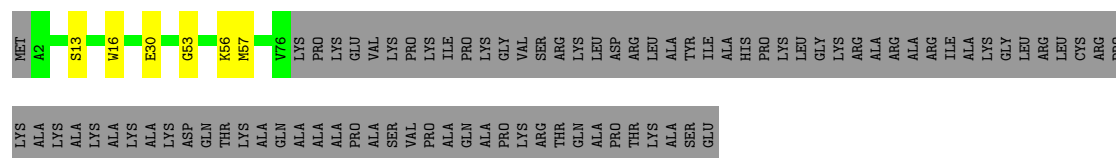
- Molecule 35: 60S ribosomal protein L27a

Chain La: 86% 13% .



- Molecule 36: 60S ribosomal protein L29

Chain Lb: 43% 53% .



- Molecule 37: 60S ribosomal protein L30

Chain Lc: 69% 16% 16%



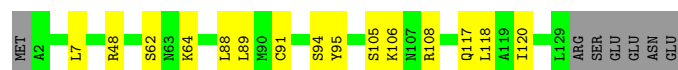
- Molecule 38: 60S ribosomal protein L31

Chain Ld: 74% 12% 14%




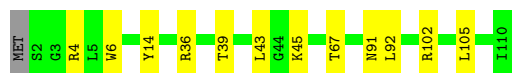
- Molecule 39: 60S ribosomal protein L32

Chain Le: 84% 11% 5%




- Molecule 40: 60S ribosomal protein L35a

Chain Lf:  88% 11%




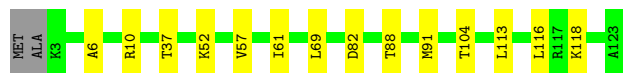
- Molecule 41: 60S ribosomal protein L34

Chain Lg:  86% 11%




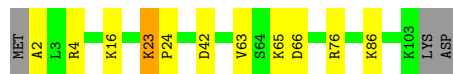
- Molecule 42: 60S ribosomal protein L35

Chain Lh:  87% 11%




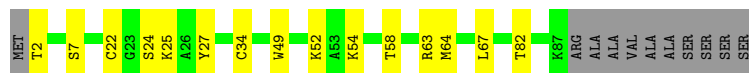
- Molecule 43: 60S ribosomal protein L36

Chain Li:  87% 10%




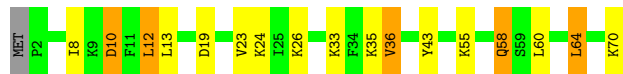
- Molecule 44: Large ribosomal subunit protein eL37

Chain Lj:  73% 15% 11%



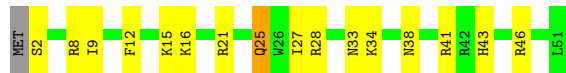
- Molecule 45: 60S ribosomal protein L38

Chain Lk:  74% 17% 7%



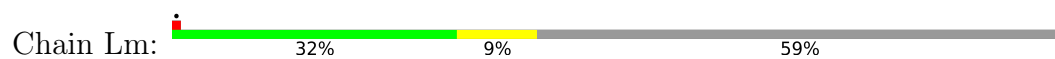
- Molecule 46: 60S ribosomal protein L39

Chain Ll:  67% 29%



- Molecule 47: Ubiquitin-60S ribosomal protein L40

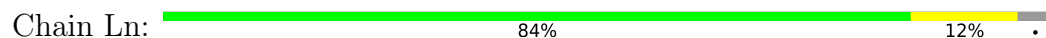




MET GLN ILE PHE VAL THR LEU THR GLY LYS THR ILE THR LEU GLU VAL PRO SER ASP THR ILE GLU ASN VAL LYS ALA LYS ILE LYS ASP LYS GLU ILE PRO PRO ASP GLN GLN ARG LEU PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP ASN

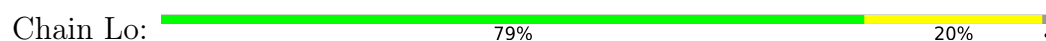
ILE GLN LYS SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY I77 P80 Q84 Y89 K38 C99 Y100 K113 T118 K124 V127 K128

- Molecule 48: 60S ribosomal protein L41



K1 M10 K14 S24 LYS

- Molecule 49: 60S ribosomal protein L36a



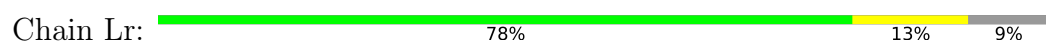
MET V2 N3 V4 F11 D31 S32 L33 Q36 G37 K38 T63 R69 L70 E71 C77 R78 S79 K80 R81 H90 E92 L93 R99 Q102 Q105 F106

- Molecule 50: 60S ribosomal protein L37a



MET A2 K3 R4 T5 G9 S21 T38 T45 K46 I54 S59 C60 T70 Y71 W72 Q82

- Molecule 51: 60S ribosomal protein L28



MET S2 Q6 K19 R20 N21 T44 V63 T64 K65 V78 R79 T80 N85 T89 S92 M96 I97 Y102 D105 L106 R107 V126 LYS ARG LYS ARG THR ARG PRO THR LYS SER

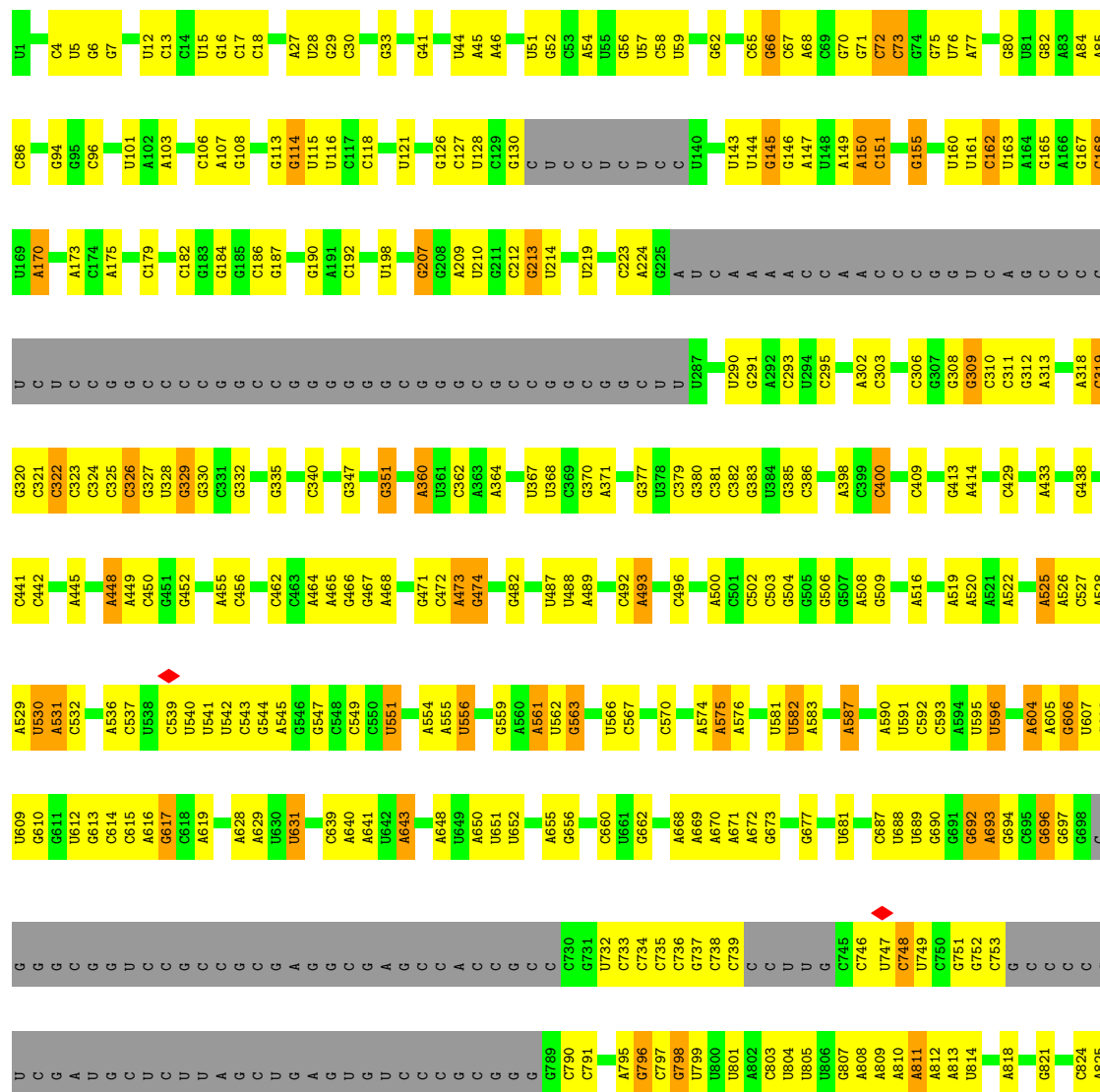
- Molecule 52: 60S acidic ribosomal protein P0



MET PRO ARG E4 Y13 I17 I18 Q19 Y24 VAL P25 K26 C27 F28 I29 V35 G36 K38 Q39 M40 Q41 Q42 M45 S46 L47 R48 G48 K50 A51 L54 M55 G56 K57 N58 T59 M60 M61 R62 H68 L69 E76 K77 L78 V89 F90 T91 K92 T96 R99

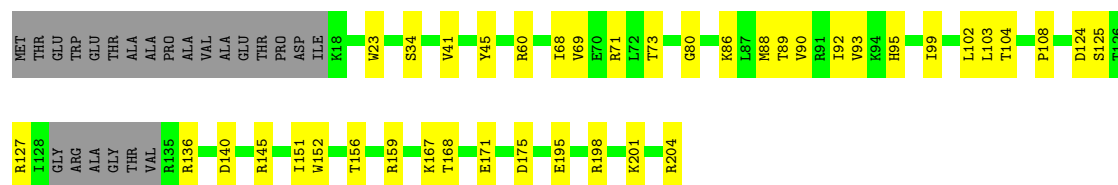
D100 M101 A104 V107 P108 A109 A113 G114 E120 A125 L130 S131 P132 E133 F138 I143 I154 K162 T163 G168 A169 S170 N176 S184 F185 L189 Q190 V191 V192 F193 D194 S197 I198 Y199 T207 F215 LEU GLY VAL ARG VAL

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



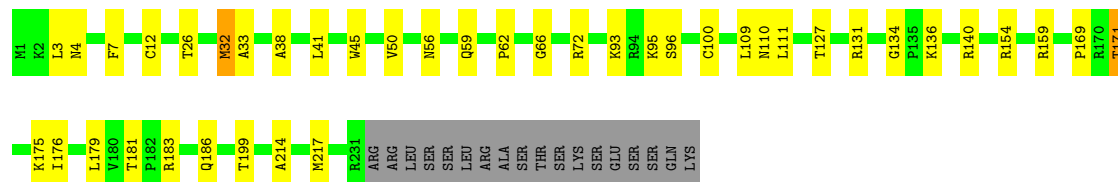


- Chain SF: 



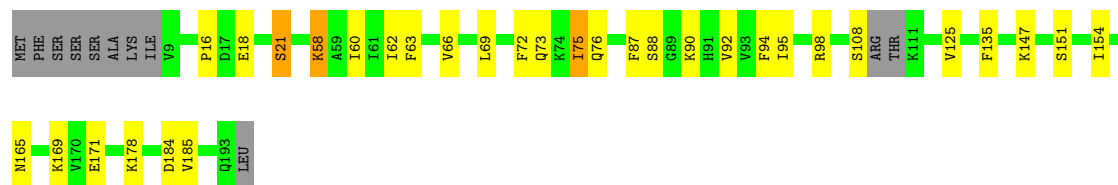
- Molecule 61: 40S ribosomal protein S6

Chain SG: 76% 16% • 7%



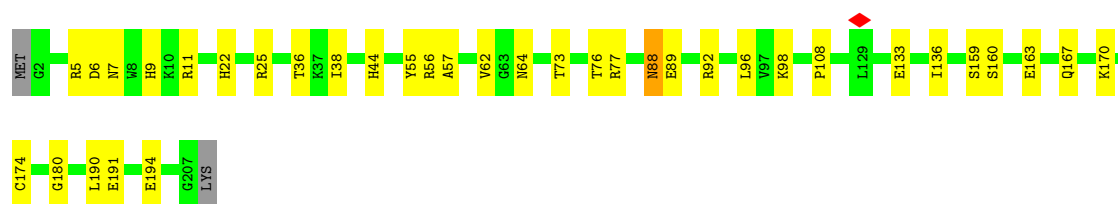
- Molecule 62: 40S ribosomal protein S7

Chain SH: 78% 15% • 6%



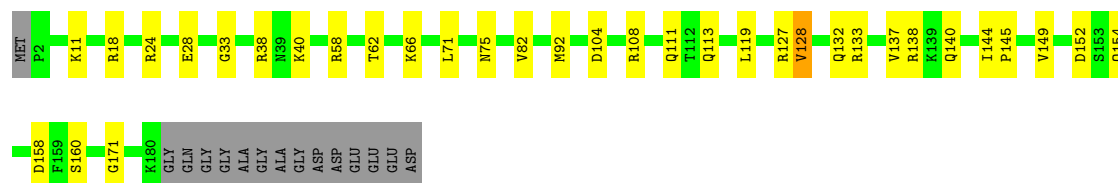
- Molecule 63: 40S ribosomal protein S8

Chain SI: 82% 17% •



- Molecule 64: 40S ribosomal protein S9


Chain SJ: 75% 17% • 8%



- Molecule 65: 40S ribosomal protein S10




- Molecule 71: 40S ribosomal protein S16

Chain SQ:  79% 18%



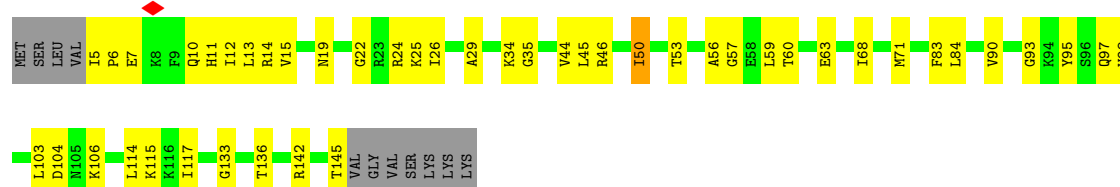
- Molecule 72: 40S ribosomal protein S17

Chain SR:  79% 19%




- Molecule 73: 40S ribosomal protein S18

Chain SS:  63% 30% 7%



- Molecule 74: 40S ribosomal protein S19

Chain ST:  76% 21%



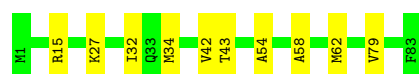
- Molecule 75: 40S ribosomal protein S20

Chain SU:  68% 16% 15%



- Molecule 76: 40S ribosomal protein S21

Chain SV:  88% 12%




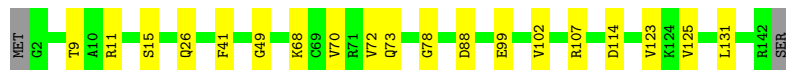
- Molecule 77: 40S ribosomal protein S15a

Chain SW:  87% 12% .



- Molecule 78: 40S ribosomal protein S23

Chain SX:  85% 13% .



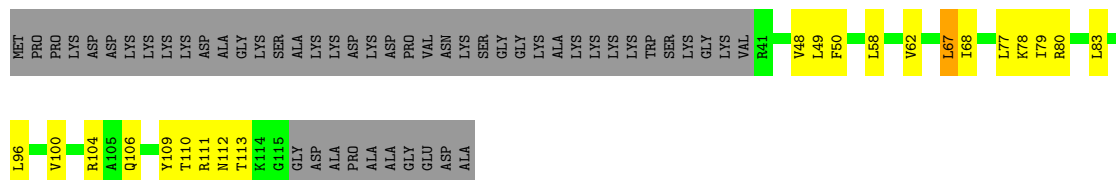
- Molecule 79: 40S ribosomal protein S24

Chain SY:  67% 26% 8%



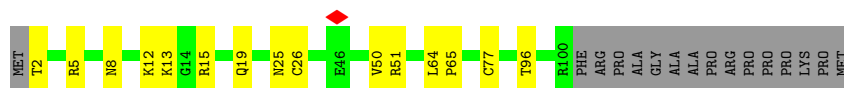
- Molecule 80: 40S ribosomal protein S25

Chain SZ:  43% 16% 40%




- Molecule 81: 40S ribosomal protein S26

Chain Sa:  73% 13% 14%



- Molecule 82: 40S ribosomal protein S27

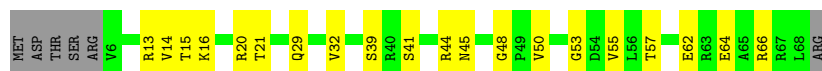
Chain Sb:  83% 13% ..




- Molecule 83: 40S ribosomal protein S28



Chain Sc:  62% 29% 9%




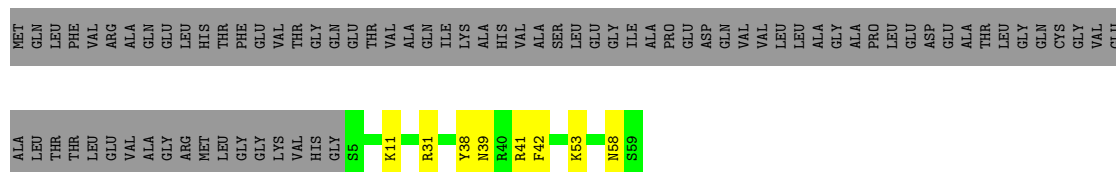
- Molecule 84: 40S ribosomal protein S29

Chain Sd:  75% 20% 5%



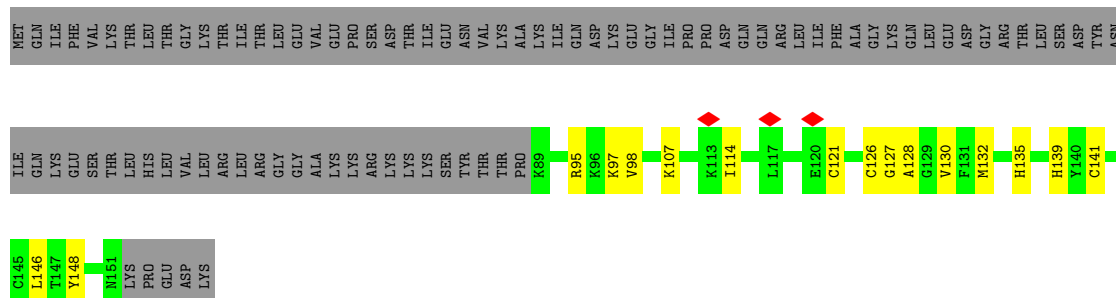
- Molecule 85: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

Chain Se:  35% 6% 59%




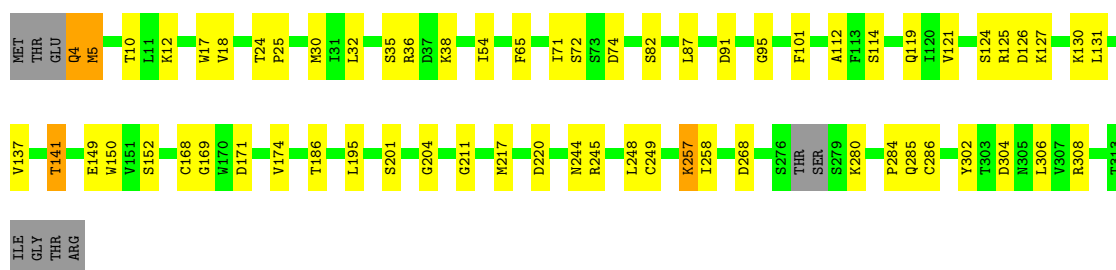
- Molecule 86: Ubiquitin

Chain Sf:  29% 11% 60%



- Molecule 87: Receptor of activated protein C kinase 1

Chain Sg:  77% 19% . .



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74754	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	6.553	Depositor
Minimum map value	-3.110	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.139	Depositor
Recommended contour level	0.0635	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	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, LYO, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	NA	0.11	0/527	0.32	0/704
2	NB	0.19	0/821	0.52	0/1101
3	CM	0.25	0/273	0.40	0/421
4	CP	0.25	0/1789	0.44	0/2788
5	CR	0.36	3/3311 (0.1%)	0.67	7/4452 (0.2%)
6	CZ	0.26	0/266	0.56	0/364
7	L5	0.28	0/87471	0.34	0/136443
8	L7	0.27	0/2858	0.31	0/4455
9	L8	0.28	0/3701	0.32	0/5766
10	LA	0.30	0/1936	0.55	0/2596
11	LB	0.28	0/3251	0.54	2/4352 (0.0%)
12	LC	0.26	0/2938	0.47	2/3947 (0.1%)
13	LD	0.24	0/2407	0.52	1/3227 (0.0%)
14	LE	0.27	0/1788	0.59	0/2399
15	LF	0.28	0/1905	0.52	0/2539
16	LG	0.27	0/1849	0.59	0/2496
17	LH	0.29	0/1529	0.61	0/2058
18	LI	0.28	0/1705	0.60	3/2277 (0.1%)
19	LJ	0.29	0/1352	0.69	0/1813
20	LL	0.30	0/1661	0.67	4/2229 (0.2%)
21	LM	0.26	0/1145	0.54	0/1536
22	LN	0.28	0/1746	0.48	1/2338 (0.0%)
23	LO	0.28	0/1665	0.55	1/2229 (0.0%)
24	LP	0.30	0/1260	0.56	1/1692 (0.1%)
25	LQ	0.27	0/1526	0.47	0/2038
26	LR	0.28	0/1468	0.59	0/1945
27	LS	0.27	0/1492	0.50	1/2003 (0.0%)
28	LT	0.28	0/1310	0.65	0/1752
29	LU	0.40	0/820	0.99	3/1102 (0.3%)
30	LV	0.28	0/985	0.54	0/1323
31	LW	0.30	0/820	0.72	1/1104 (0.1%)
32	LX	0.30	0/998	0.65	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	LY	0.32	0/1128	0.68	1/1500 (0.1%)
34	LZ	0.27	0/1130	0.57	0/1507
35	La	0.26	0/1183	0.43	0/1582
36	Lb	0.28	0/600	0.64	0/796
37	Lc	0.26	0/752	0.54	0/1011
38	Ld	0.26	0/889	0.47	0/1198
39	Le	0.28	0/1067	0.45	0/1425
40	Lf	0.29	0/891	0.55	0/1194
41	Lg	0.27	0/899	0.56	0/1200
42	Lh	0.26	0/1014	0.60	0/1340
43	Li	0.22	0/824	0.49	1/1093 (0.1%)
44	Lj	0.28	0/720	0.50	0/952
45	Lk	0.32	0/548	0.83	1/730 (0.1%)
46	Ll	0.32	0/454	0.62	0/599
47	Lm	0.24	0/431	0.49	0/570
48	Ln	0.25	0/231	0.43	0/294
49	Lo	0.31	0/876	0.66	0/1156
50	Lp	0.27	0/706	0.55	0/939
51	Lr	0.28	0/1012	0.50	0/1358
52	Ls	0.28	0/1666	0.73	2/2250 (0.1%)
53	Lt	0.33	0/1224	0.88	5/1651 (0.3%)
54	S2	0.27	0/40882	0.38	0/63715
55	SA	0.31	0/1708	0.69	0/2324
56	SB	0.25	0/1745	0.55	1/2337 (0.0%)
57	SC	0.29	0/1697	0.56	0/2301
58	SD	0.28	0/1620	0.65	2/2198 (0.1%)
59	SE	0.26	0/2014	0.53	0/2726
60	SF	0.29	0/1423	0.68	2/1913 (0.1%)
61	SG	0.24	0/1657	0.62	1/2247 (0.0%)
62	SH	0.26	0/1295	0.61	3/1763 (0.2%)
63	SI	0.26	0/1603	0.54	0/2161
64	SJ	0.28	0/1456	0.61	0/1957
65	SK	0.30	0/750	0.70	0/1026
66	SL	0.28	0/1163	0.48	0/1562
67	SM	0.27	0/960	0.84	1/1286 (0.1%)
68	SN	0.27	0/1206	0.51	0/1626
69	SO	0.28	0/982	0.65	0/1320
70	SP	0.28	0/1010	0.69	1/1362 (0.1%)
71	SQ	0.26	0/1093	0.60	0/1470
72	SR	0.30	0/955	0.79	2/1294 (0.2%)
73	SS	0.32	0/1148	0.77	0/1542
74	ST	0.27	0/1100	0.56	0/1479
75	SU	0.30	0/722	0.71	1/983 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	SV	0.30	0/625	0.60	0/837
77	SW	0.28	0/1043	0.51	0/1396
78	SX	0.29	0/1096	0.61	0/1467
79	SY	0.28	0/944	0.67	0/1271
80	SZ	0.32	0/565	0.74	0/764
81	Sa	0.29	0/794	0.58	0/1065
82	Sb	0.29	0/632	0.70	0/851
83	Sc	0.29	0/474	0.79	0/638
84	Sd	0.26	0/443	0.49	0/589
85	Se	0.28	0/420	0.64	1/554 (0.2%)
86	Sf	0.24	0/525	0.68	0/695
87	Sg	0.30	0/2235	0.74	3/3068 (0.1%)
All	All	0.28	3/234803 (0.0%)	0.47	55/344962 (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
2	NB	0	1
14	LE	0	1
20	LL	0	1
25	LQ	0	1
56	SB	0	1
61	SG	0	1
73	SS	0	1
82	Sb	0	1
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	CR	373	PRO	CG-CD	-10.21	1.16	1.50
5	CR	175	ASP	CA-CB	6.92	1.65	1.53
5	CR	373	PRO	N-CD	5.69	1.55	1.47

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CR	373	PRO	CA-N-CD	-12.64	94.30	112.00
5	CR	373	PRO	N-CD-CG	-10.84	86.94	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	Lt	7	PRO	CA-N-CD	-9.51	98.68	112.00
52	Ls	25	PRO	CA-N-CD	-8.12	100.63	112.00
29	LU	108	GLU	CA-CB-CG	7.92	129.94	114.10

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	LE	176	THR	Peptide
20	LL	47	ALA	Peptide
25	LQ	94	GLU	Peptide
2	NB	52	GLY	Peptide
56	SB	189	ILE	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	NA	522	0	560	6	0
2	NB	813	0	856	10	0
3	CM	247	0	128	1	0
4	CP	1602	0	809	5	0
5	CR	3269	0	3312	34	0
6	CZ	261	0	248	2	0
7	L5	78199	0	39523	455	0
8	L7	2558	0	1296	13	0
9	L8	3314	0	1683	19	0
10	LA	1898	0	1993	28	0
11	LB	3183	0	3316	36	0
12	LC	2884	0	3050	27	0
13	LD	2361	0	2378	22	0
14	LE	1754	0	1899	26	0
15	LF	1870	0	1996	26	0
16	LG	1818	0	1911	20	0
17	LH	1510	0	1579	20	0
18	LI	1666	0	1711	23	0
19	LJ	1329	0	1348	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	LL	1630	0	1715	18	0
21	LM	1122	0	1174	11	0
22	LN	1701	0	1749	16	0
23	LO	1633	0	1771	15	0
24	LP	1234	0	1254	10	0
25	LQ	1502	0	1616	16	0
26	LR	1452	0	1580	14	0
27	LS	1452	0	1490	20	0
28	LT	1282	0	1336	21	0
29	LU	806	0	826	17	0
30	LV	971	0	1024	16	0
31	LW	808	0	726	7	0
32	LX	981	0	1055	20	0
33	LY	1111	0	1194	17	0
34	LZ	1107	0	1182	12	0
35	La	1154	0	1198	12	0
36	Lb	590	0	613	6	0
37	Lc	742	0	774	9	0
38	Ld	874	0	918	8	0
39	Le	1049	0	1136	9	0
40	Lf	872	0	901	7	0
41	Lg	889	0	968	9	0
42	Lh	1006	0	1132	12	0
43	Li	813	0	887	7	0
44	Lj	705	0	737	11	0
45	Lk	542	0	590	13	0
46	Ll	444	0	483	13	0
47	Lm	425	0	462	7	0
48	Ln	230	0	276	3	0
49	Lo	862	0	929	13	0
50	Lp	696	0	744	8	0
51	Lr	997	0	1054	10	0
52	Ls	1640	0	1687	36	0
53	Lt	1208	0	1257	28	0
54	S2	36562	0	18472	281	0
55	SA	1671	0	1672	29	0
56	SB	1718	0	1786	32	0
57	SC	1661	0	1710	22	0
58	SD	1594	0	1568	22	0
59	SE	1972	0	2012	29	0
60	SF	1403	0	1421	30	0
61	SG	1634	0	1568	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	SH	1274	0	1196	20	0
63	SI	1574	0	1540	24	0
64	SJ	1431	0	1497	27	0
65	SK	726	0	674	16	0
66	SL	1143	0	1177	7	0
67	SM	950	0	987	23	0
68	SN	1182	0	1249	11	0
69	SO	969	0	982	14	0
70	SP	990	0	974	29	0
71	SQ	1075	0	1110	14	0
72	SR	942	0	913	16	0
73	SS	1130	0	1167	27	0
74	ST	1081	0	1093	20	0
75	SU	713	0	692	13	0
76	SV	618	0	617	7	0
77	SW	1026	0	1072	12	0
78	SX	1078	0	1130	11	0
79	SY	927	0	914	24	0
80	SZ	559	0	594	15	0
81	Sa	781	0	831	9	0
82	Sb	618	0	604	6	0
83	Sc	472	0	484	11	0
84	Sd	433	0	415	11	0
85	Se	416	0	439	6	0
86	Sf	515	0	521	12	0
87	Sg	2180	0	1968	38	0
88	L5	127	0	0	0	0
88	L7	3	0	0	0	0
88	L8	3	0	0	0	0
88	LA	1	0	0	0	0
88	LC	1	0	0	0	0
88	LN	1	0	0	0	0
88	LP	1	0	0	0	0
88	LV	1	0	0	0	0
88	S2	53	0	0	0	0
89	Lg	1	0	0	0	0
89	Lj	1	0	0	0	0
89	Lm	1	0	0	0	0
89	Lo	1	0	0	0	0
89	Lp	1	0	0	0	0
89	Sa	1	0	0	0	0
89	Sd	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	Sf	1	0	0	0	0
90	L5	4	0	0	0	0
90	L7	1	0	0	0	0
90	LI	1	0	0	0	0
90	LN	1	0	0	0	0
90	La	1	0	0	0	0
90	S2	3	0	0	0	0
All	All	218816	0	161083	1827	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1827 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:Sg:4:GLN:N	87:Sg:4:GLN:HE21	1.56	1.02
54:S2:1748:G:H1	54:S2:1786:U:H3	1.07	0.99
7:L5:1443:A:N6	7:L5:2104:G:C2	2.41	0.89
87:Sg:4:GLN:N	87:Sg:4:GLN:NE2	2.26	0.83
70:SP:93:MET:HE1	70:SP:106:GLU:HG2	1.61	0.82

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	NA	64/215 (30%)	62 (97%)	2 (3%)	0	100	100
2	NB	103/162 (64%)	95 (92%)	8 (8%)	0	100	100
5	CR	411/437 (94%)	402 (98%)	9 (2%)	0	100	100
6	CZ	37/95 (39%)	33 (89%)	4 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	LA	246/257 (96%)	229 (93%)	17 (7%)	0	100	100
11	LB	393/403 (98%)	370 (94%)	23 (6%)	0	100	100
12	LC	362/427 (85%)	342 (94%)	19 (5%)	1 (0%)	36	45
13	LD	291/297 (98%)	276 (95%)	14 (5%)	1 (0%)	36	45
14	LE	213/288 (74%)	193 (91%)	20 (9%)	0	100	100
15	LF	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
16	LG	225/266 (85%)	213 (95%)	12 (5%)	0	100	100
17	LH	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
18	LI	203/214 (95%)	190 (94%)	13 (6%)	0	100	100
19	LJ	167/178 (94%)	163 (98%)	4 (2%)	0	100	100
20	LL	203/211 (96%)	191 (94%)	12 (6%)	0	100	100
21	LM	137/215 (64%)	129 (94%)	8 (6%)	0	100	100
22	LN	201/204 (98%)	194 (96%)	7 (4%)	0	100	100
23	LO	198/203 (98%)	195 (98%)	3 (2%)	0	100	100
24	LP	151/184 (82%)	144 (95%)	7 (5%)	0	100	100
25	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
26	LR	174/196 (89%)	172 (99%)	2 (1%)	0	100	100
27	LS	173/176 (98%)	164 (95%)	9 (5%)	0	100	100
28	LT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100
29	LU	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
30	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
31	LW	111/157 (71%)	100 (90%)	11 (10%)	0	100	100
32	LX	118/156 (76%)	115 (98%)	3 (2%)	0	100	100
33	LY	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
34	LZ	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
35	La	145/148 (98%)	138 (95%)	7 (5%)	0	100	100
36	Lb	73/159 (46%)	68 (93%)	5 (7%)	0	100	100
37	Lc	95/115 (83%)	93 (98%)	2 (2%)	0	100	100
38	Ld	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
39	Le	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
40	Lf	107/110 (97%)	102 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	Lg	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
42	Lh	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
43	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
44	Lj	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
45	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
46	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
47	Lm	50/128 (39%)	50 (100%)	0	0	100	100
48	Ln	22/25 (88%)	22 (100%)	0	0	100	100
49	Lo	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
50	Lp	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
51	Lr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
52	Ls	210/317 (66%)	208 (99%)	2 (1%)	0	100	100
53	Lt	158/165 (96%)	157 (99%)	1 (1%)	0	100	100
55	SA	214/295 (72%)	203 (95%)	11 (5%)	0	100	100
56	SB	211/264 (80%)	206 (98%)	5 (2%)	0	100	100
57	SC	217/293 (74%)	207 (95%)	10 (5%)	0	100	100
58	SD	219/243 (90%)	209 (95%)	10 (5%)	0	100	100
59	SE	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
60	SF	177/204 (87%)	169 (96%)	7 (4%)	1 (1%)	21	25
61	SG	229/249 (92%)	215 (94%)	13 (6%)	1 (0%)	30	37
62	SH	179/194 (92%)	169 (94%)	10 (6%)	0	100	100
63	SI	204/208 (98%)	198 (97%)	6 (3%)	0	100	100
64	SJ	177/194 (91%)	172 (97%)	5 (3%)	0	100	100
65	SK	94/165 (57%)	88 (94%)	6 (6%)	0	100	100
66	SL	140/158 (89%)	131 (94%)	9 (6%)	0	100	100
67	SM	120/132 (91%)	111 (92%)	9 (8%)	0	100	100
68	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
69	SO	132/151 (87%)	120 (91%)	12 (9%)	0	100	100
70	SP	127/145 (88%)	121 (95%)	6 (5%)	0	100	100
71	SQ	140/146 (96%)	131 (94%)	9 (6%)	0	100	100
72	SR	129/135 (96%)	111 (86%)	18 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	SS	139/152 (91%)	120 (86%)	19 (14%)	0	100	100
74	ST	141/145 (97%)	135 (96%)	6 (4%)	0	100	100
75	SU	99/119 (83%)	91 (92%)	8 (8%)	0	100	100
76	SV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
77	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
78	SX	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
79	SY	121/133 (91%)	115 (95%)	6 (5%)	0	100	100
80	SZ	73/125 (58%)	66 (90%)	7 (10%)	0	100	100
81	Sa	97/115 (84%)	89 (92%)	8 (8%)	0	100	100
82	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
83	Sc	61/69 (88%)	54 (88%)	7 (12%)	0	100	100
84	Sd	51/56 (91%)	51 (100%)	0	0	100	100
85	Se	53/133 (40%)	51 (96%)	2 (4%)	0	100	100
86	Sf	61/156 (39%)	53 (87%)	7 (12%)	1 (2%)	7	7
87	Sg	304/317 (96%)	268 (88%)	36 (12%)	0	100	100
All	All	12108/14153 (86%)	11472 (95%)	631 (5%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
60	SF	80	GLY
12	LC	111	TRP
86	Sf	128	ALA
13	LD	59	ASP
61	SG	33	ALA

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	NA	59/183 (32%)	59 (100%)	0	100	100
2	NB	89/136 (65%)	86 (97%)	3 (3%)	32	47
5	CR	356/375 (95%)	351 (99%)	5 (1%)	59	75
6	CZ	25/83 (30%)	25 (100%)	0	100	100
10	LA	190/199 (96%)	184 (97%)	6 (3%)	34	50
11	LB	343/349 (98%)	338 (98%)	5 (2%)	57	73
12	LC	299/348 (86%)	296 (99%)	3 (1%)	68	81
13	LD	241/250 (96%)	238 (99%)	3 (1%)	63	78
14	LE	191/252 (76%)	184 (96%)	7 (4%)	30	44
15	LF	194/215 (90%)	193 (100%)	1 (0%)	81	89
16	LG	188/223 (84%)	185 (98%)	3 (2%)	55	72
17	LH	167/171 (98%)	161 (96%)	6 (4%)	31	45
18	LI	174/181 (96%)	171 (98%)	3 (2%)	53	70
19	LJ	136/149 (91%)	134 (98%)	2 (2%)	57	73
20	LL	164/177 (93%)	161 (98%)	3 (2%)	51	69
21	LM	114/161 (71%)	112 (98%)	2 (2%)	51	69
22	LN	171/172 (99%)	167 (98%)	4 (2%)	44	62
23	LO	170/174 (98%)	163 (96%)	7 (4%)	27	40
24	LP	132/163 (81%)	131 (99%)	1 (1%)	73	85
25	LQ	161/165 (98%)	160 (99%)	1 (1%)	78	88
26	LR	150/175 (86%)	149 (99%)	1 (1%)	76	86
27	LS	156/157 (99%)	155 (99%)	1 (1%)	78	88
28	LT	135/140 (96%)	131 (97%)	4 (3%)	36	52
29	LU	86/115 (75%)	81 (94%)	5 (6%)	18	25
30	LV	99/107 (92%)	95 (96%)	4 (4%)	28	41
31	LW	61/126 (48%)	59 (97%)	2 (3%)	33	48
32	LX	107/133 (80%)	106 (99%)	1 (1%)	70	83
33	LY	123/135 (91%)	123 (100%)	0	100	100
34	LZ	117/118 (99%)	112 (96%)	5 (4%)	26	38
35	La	118/121 (98%)	116 (98%)	2 (2%)	53	70
36	Lb	59/126 (47%)	59 (100%)	0	100	100
37	Lc	79/97 (81%)	76 (96%)	3 (4%)	29	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Ld	94/110 (86%)	92 (98%)	2 (2%)	47	65
39	Le	113/121 (93%)	111 (98%)	2 (2%)	51	69
40	Lf	87/89 (98%)	86 (99%)	1 (1%)	65	80
41	Lg	93/100 (93%)	91 (98%)	2 (2%)	45	63
42	Lh	108/110 (98%)	108 (100%)	0	100	100
43	Li	81/89 (91%)	79 (98%)	2 (2%)	42	59
44	Lj	73/80 (91%)	73 (100%)	0	100	100
45	Lk	57/65 (88%)	53 (93%)	4 (7%)	14	18
46	Ll	47/48 (98%)	46 (98%)	1 (2%)	47	65
47	Lm	47/116 (40%)	46 (98%)	1 (2%)	47	65
48	Ln	23/24 (96%)	23 (100%)	0	100	100
49	Lo	93/94 (99%)	91 (98%)	2 (2%)	45	63
50	Lp	71/75 (95%)	71 (100%)	0	100	100
51	Lr	107/121 (88%)	104 (97%)	3 (3%)	38	55
52	Ls	180/258 (70%)	174 (97%)	6 (3%)	33	48
53	Lt	132/137 (96%)	124 (94%)	8 (6%)	17	23
55	SA	170/243 (70%)	165 (97%)	5 (3%)	37	53
56	SB	191/231 (83%)	189 (99%)	2 (1%)	68	81
57	SC	175/225 (78%)	174 (99%)	1 (1%)	78	88
58	SD	148/202 (73%)	146 (99%)	2 (1%)	59	75
59	SE	196/225 (87%)	191 (97%)	5 (3%)	40	57
60	SF	142/170 (84%)	141 (99%)	1 (1%)	76	86
61	SG	138/218 (63%)	134 (97%)	4 (3%)	37	53
62	SH	109/174 (63%)	106 (97%)	3 (3%)	38	55
63	SI	149/180 (83%)	144 (97%)	5 (3%)	32	47
64	SJ	143/168 (85%)	141 (99%)	2 (1%)	59	75
65	SK	65/136 (48%)	60 (92%)	5 (8%)	12	15
66	SL	121/142 (85%)	118 (98%)	3 (2%)	42	59
67	SM	104/108 (96%)	99 (95%)	5 (5%)	23	33
68	SN	123/131 (94%)	120 (98%)	3 (2%)	43	60
69	SO	95/119 (80%)	92 (97%)	3 (3%)	34	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	SP	98/130 (75%)	92 (94%)	6 (6%)	17	23
71	SQ	103/121 (85%)	100 (97%)	3 (3%)	37	53
72	SR	84/122 (69%)	82 (98%)	2 (2%)	43	60
73	SS	112/132 (85%)	108 (96%)	4 (4%)	31	45
74	ST	105/115 (91%)	98 (93%)	7 (7%)	15	20
75	SU	68/107 (64%)	67 (98%)	1 (2%)	57	73
76	SV	62/67 (92%)	62 (100%)	0	100	100
77	SW	110/113 (97%)	108 (98%)	2 (2%)	51	69
78	SX	109/115 (95%)	105 (96%)	4 (4%)	30	44
79	SY	86/115 (75%)	82 (95%)	4 (5%)	23	34
80	SZ	56/103 (54%)	54 (96%)	2 (4%)	31	45
81	Sa	83/98 (85%)	80 (96%)	3 (4%)	31	45
82	Sb	65/76 (86%)	61 (94%)	4 (6%)	16	23
83	Sc	51/62 (82%)	46 (90%)	5 (10%)	7	9
84	Sd	44/49 (90%)	43 (98%)	1 (2%)	44	62
85	Se	39/104 (38%)	39 (100%)	0	100	100
86	Sf	56/140 (40%)	54 (96%)	2 (4%)	31	45
87	Sg	201/275 (73%)	192 (96%)	9 (4%)	24	36
All	All	9861/12029 (82%)	9626 (98%)	235 (2%)	43	60

5 of 235 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	Ls	69	LEU
83	Sc	50	VAL
61	SG	26	THR
83	Sc	21	THR
77	SW	43	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
44	Lj	13	ASN
60	SF	110	GLN
46	Ll	4	HIS

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Mol	Chain	Res	Type
52	Ls	159	GLN
63	SI	52	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	CM	11/586 (1%)	2 (18%)	0
4	CP	74/75 (98%)	23 (31%)	2 (2%)
54	S2	1704/1869 (91%)	465 (27%)	17 (0%)
7	L5	3633/5070 (71%)	737 (20%)	14 (0%)
8	L7	119/121 (98%)	12 (10%)	0
9	L8	155/157 (98%)	26 (16%)	1 (0%)
All	All	5696/7878 (72%)	1265 (22%)	34 (0%)

5 of 1265 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	CM	439	C
3	CM	444	U
4	CP	2	G
4	CP	4	U
4	CP	5	C

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	S2	1395	C
54	S2	1519	U
54	S2	1664	A
7	L5	3673	C
7	L5	3614	G

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z  > 2$
5	LYO	CR	63	5	7,9,10	0.81	0	7,10,12	1.10	1 (14%)

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
5	LYO	CR	63	5	-	3/8/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
5	CR	63	LYO	CE-CD-CG	-2.09	109.07	113.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CR	63	LYO	N-CA-CB-CG
5	CR	63	LYO	C-CA-CB-CG
5	CR	63	LYO	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 199 ligands modelled in this entry, 199 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

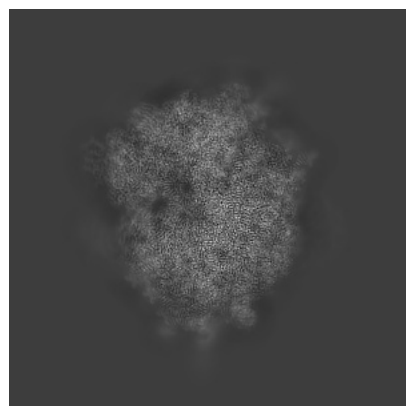
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54530. These allow visual inspection of the internal detail of the map and identification of artifacts.

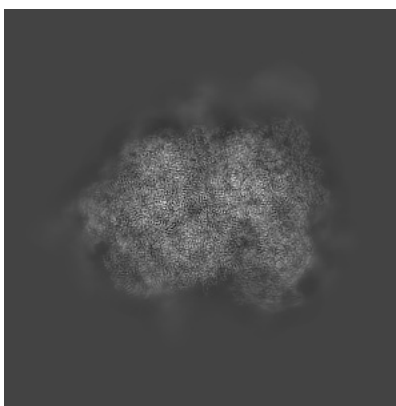
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

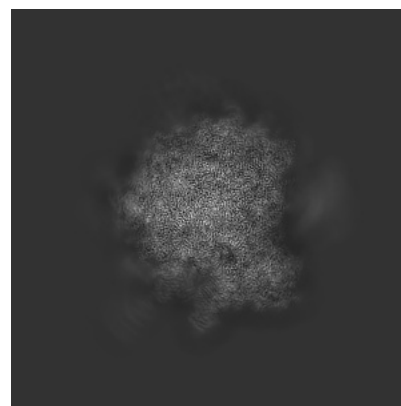
#### 6.1.1 Primary map



X

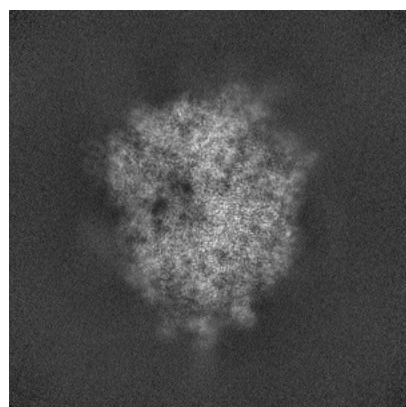


Y

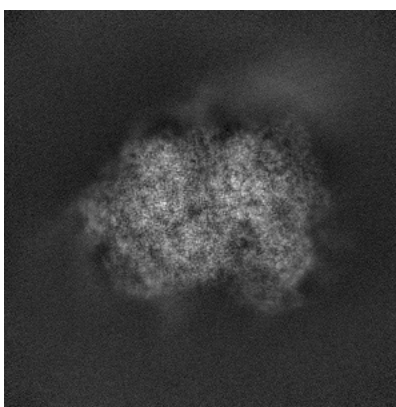


Z

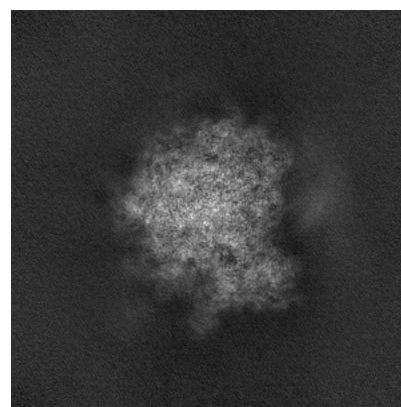
#### 6.1.2 Raw map



X



Y

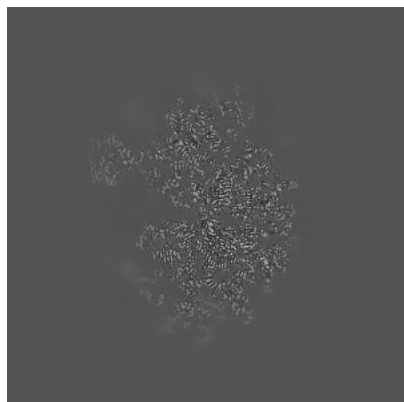


Z

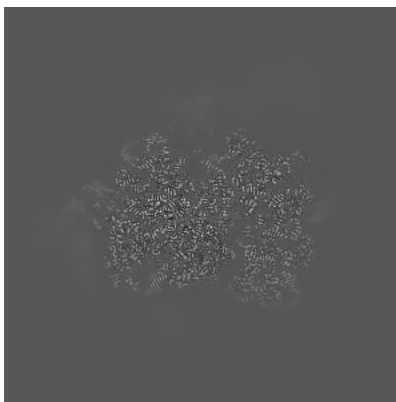
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

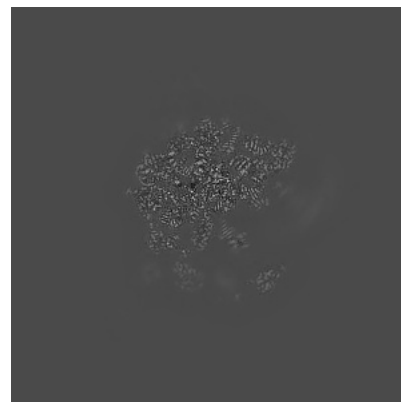
### 6.2.1 Primary map



X Index: 320

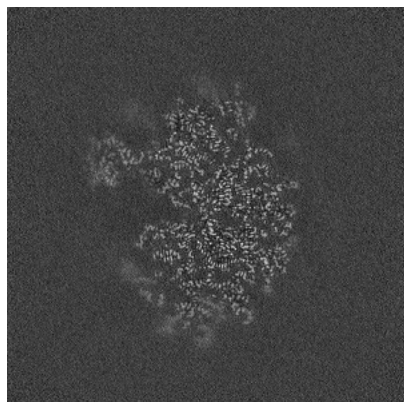


Y Index: 320

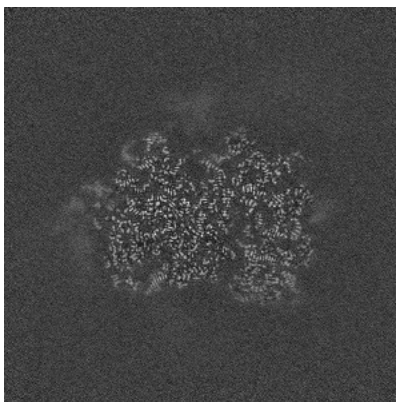


Z Index: 320

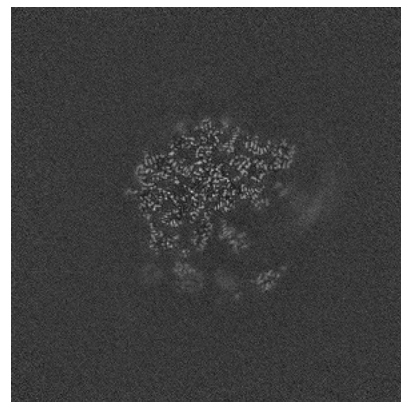
### 6.2.2 Raw map



X Index: 320



Y Index: 320

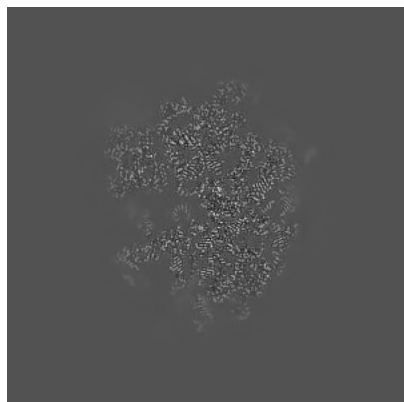


Z Index: 320

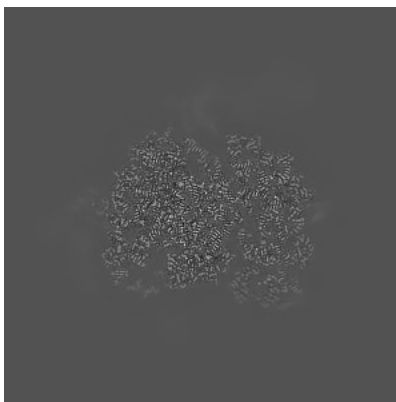
The images above show central slices of the map in three orthogonal directions.

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

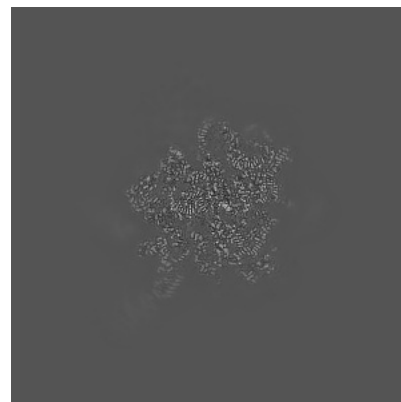
### 6.3.1 Primary map



X Index: 344

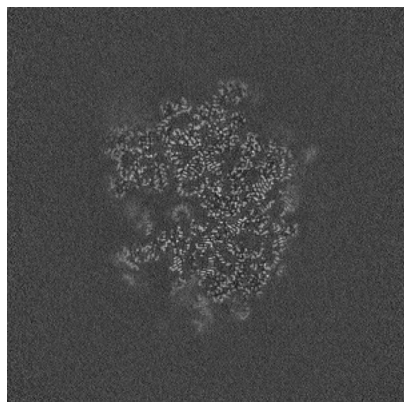


Y Index: 329

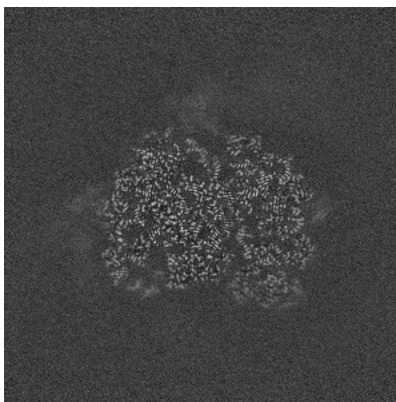


Z Index: 267

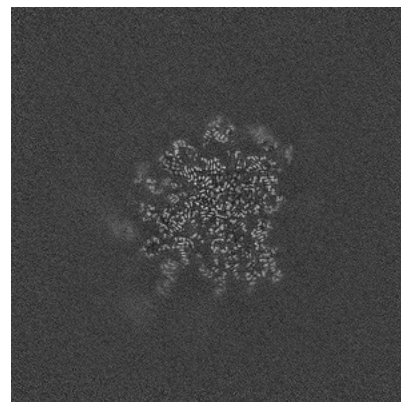
### 6.3.2 Raw map



X Index: 344



Y Index: 328



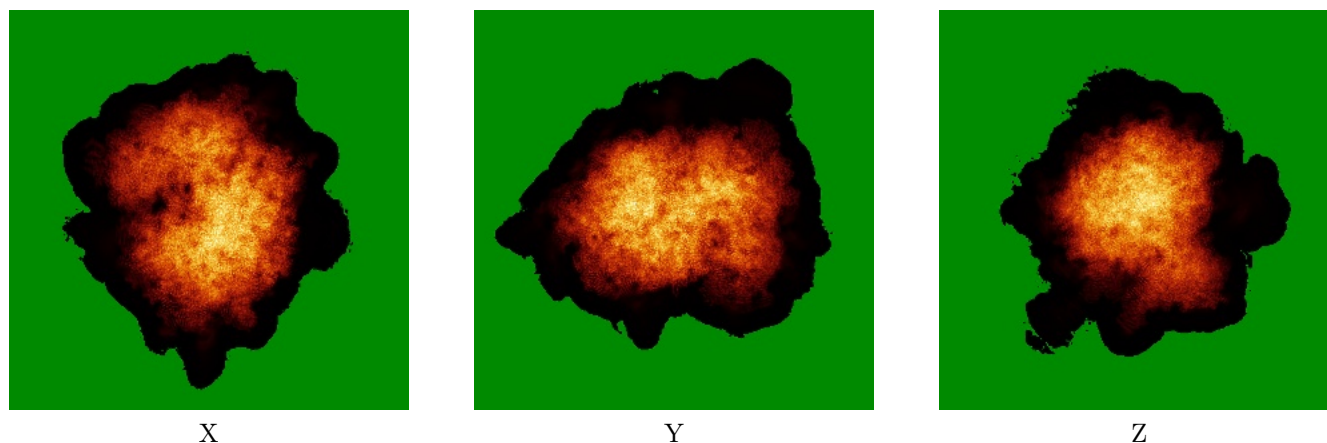
Z Index: 257

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

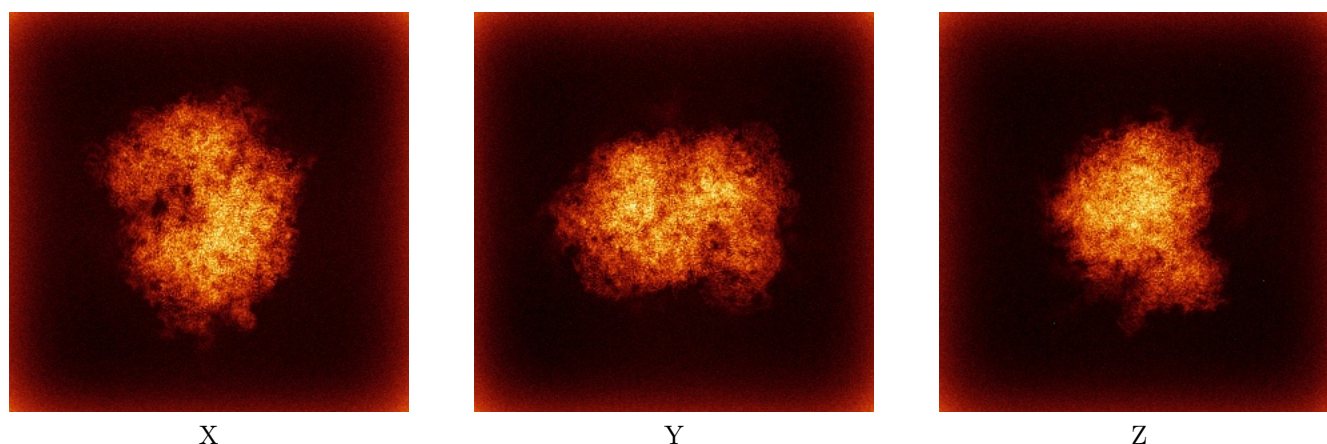


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

### 6.4.1 Primary map



### 6.4.2 Raw map



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

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

This section was not generated.

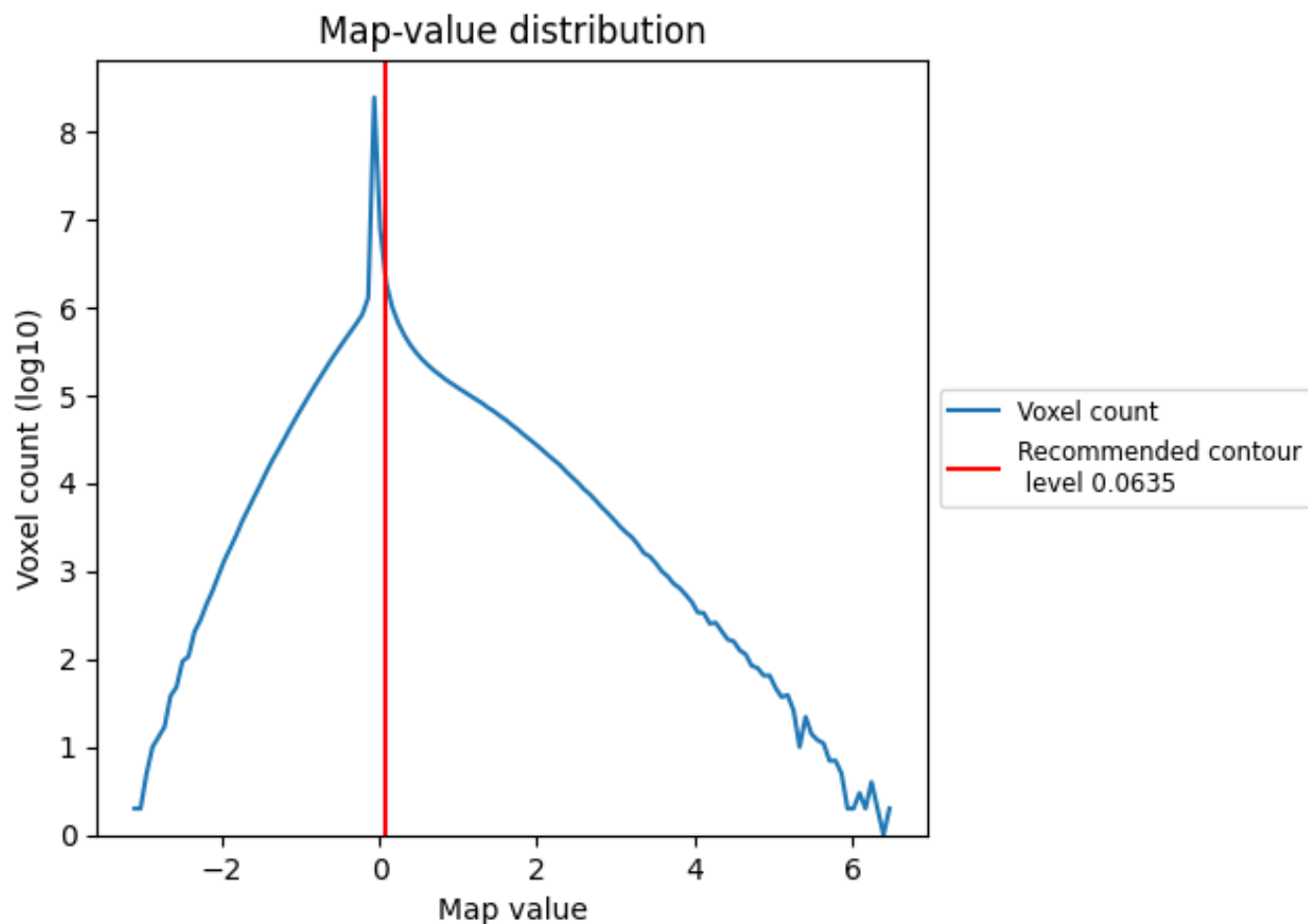
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

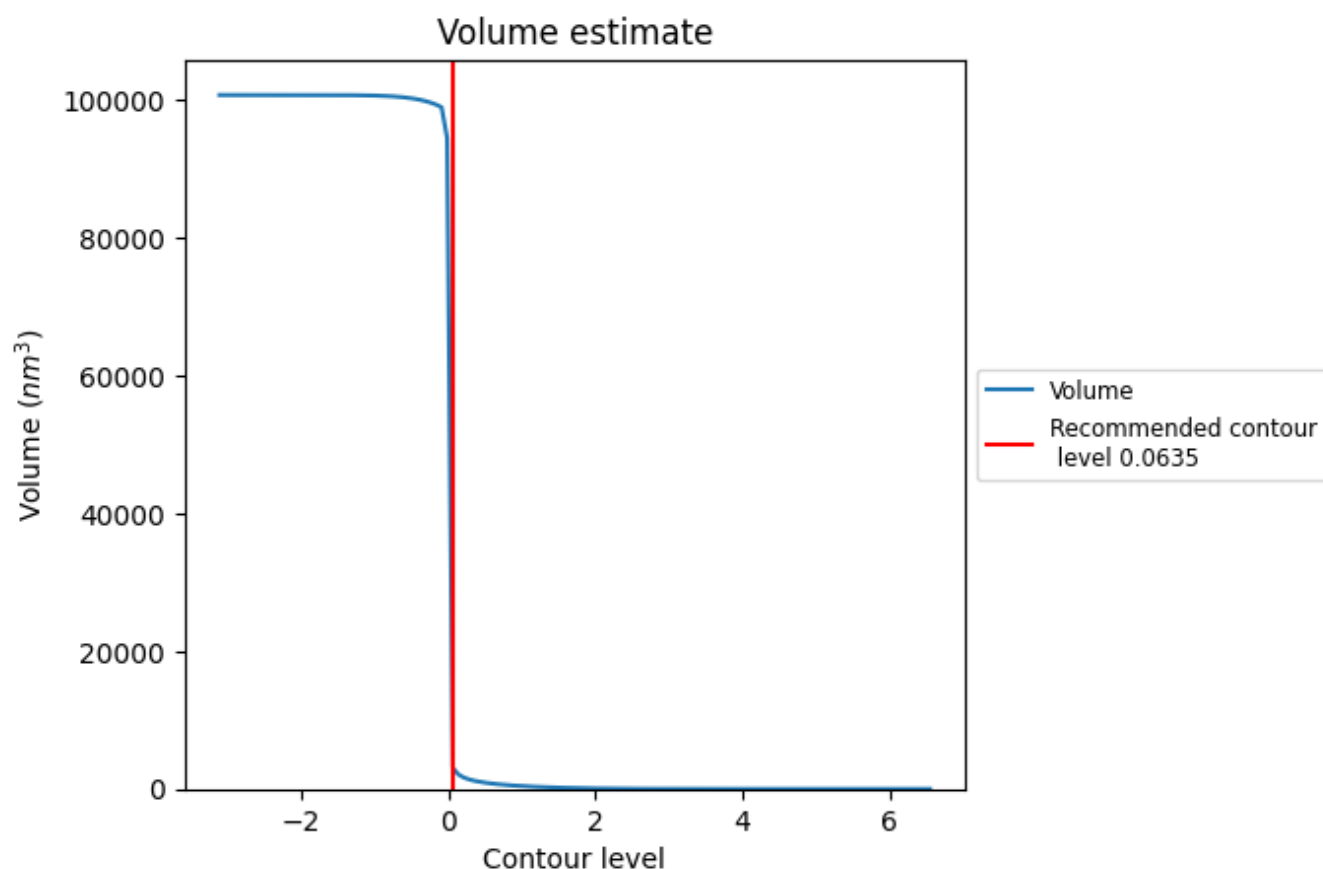
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

## 7.2 Volume estimate [i](#)

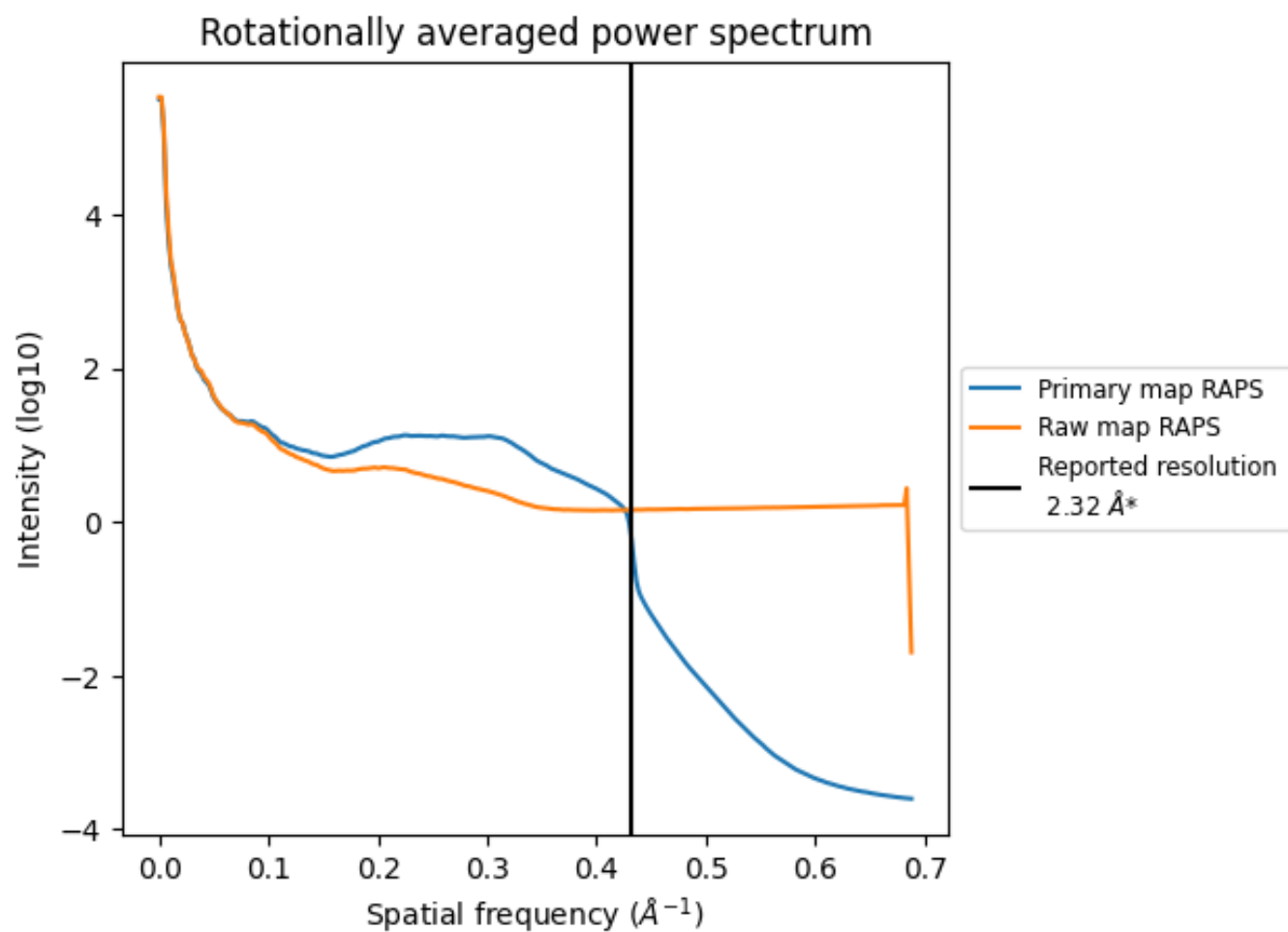


The volume at the recommended contour level is 3063  $\text{nm}^3$ ; this corresponds to an approximate mass of 2767 kDa.

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 ⓘ

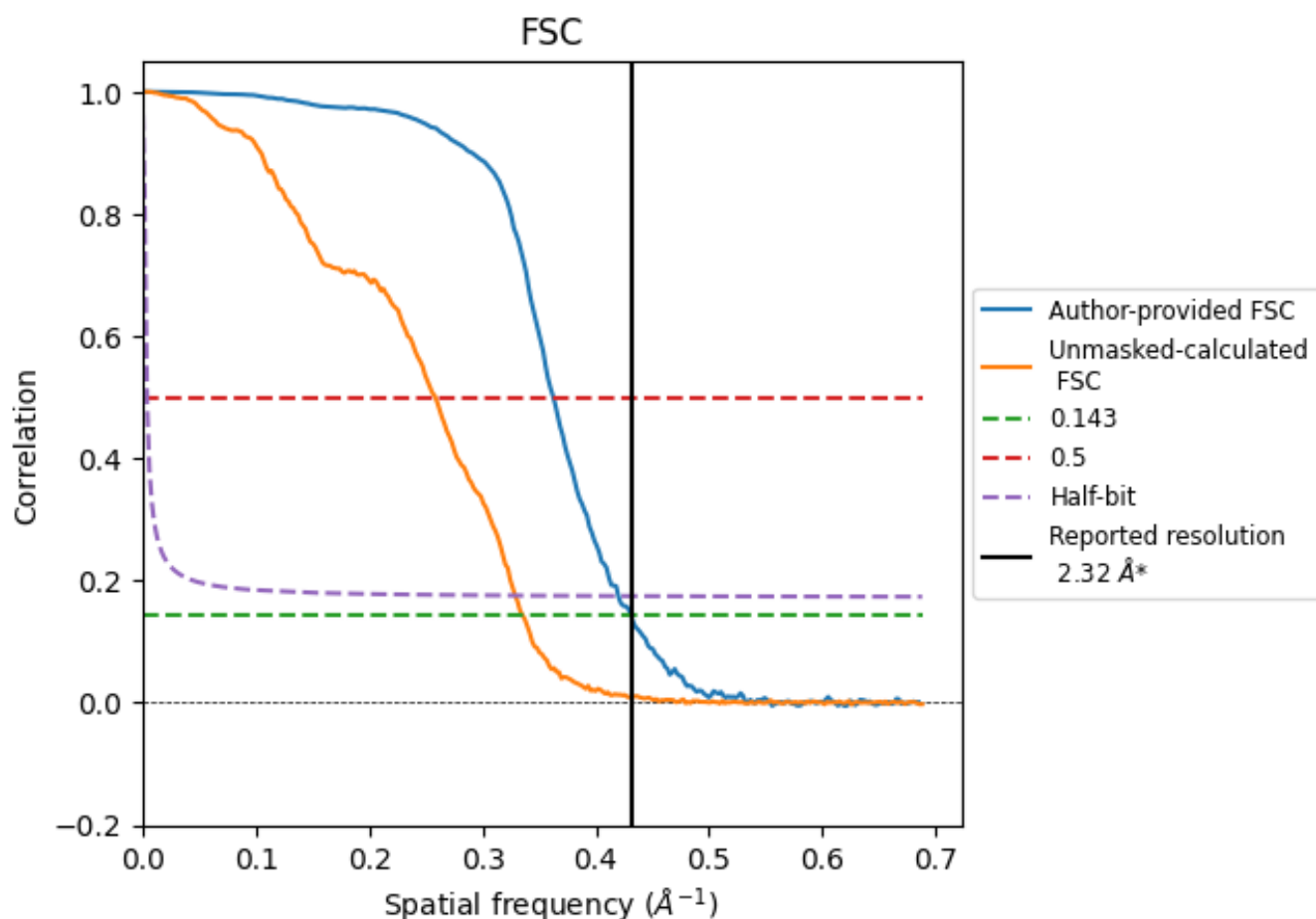


\*Reported resolution corresponds to spatial frequency of  $0.431 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.431  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

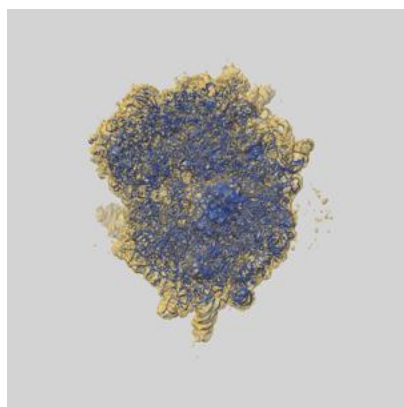
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.32	-	-
Author-provided FSC curve	2.32	2.76	2.38
Unmasked-calculated*	2.98	3.87	3.04

\*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 2.98 differs from the reported value 2.32 by more than 10 %

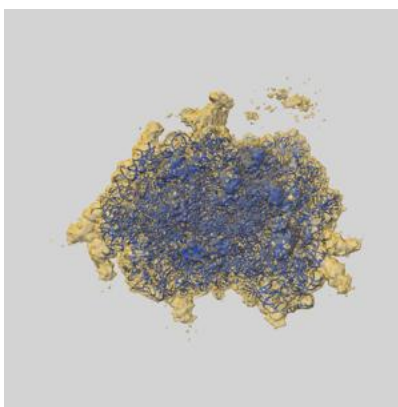
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54530 and PDB model 9S3D. Per-residue inclusion information can be found in section [3](#) on page [21](#).

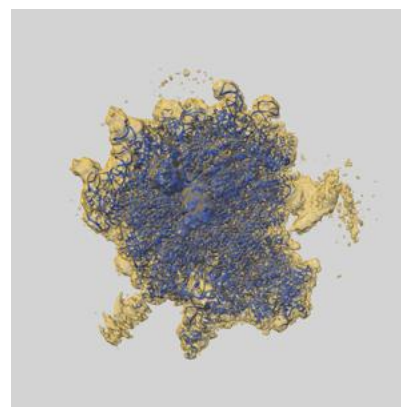
### 9.1 Map-model overlay [i](#)



X



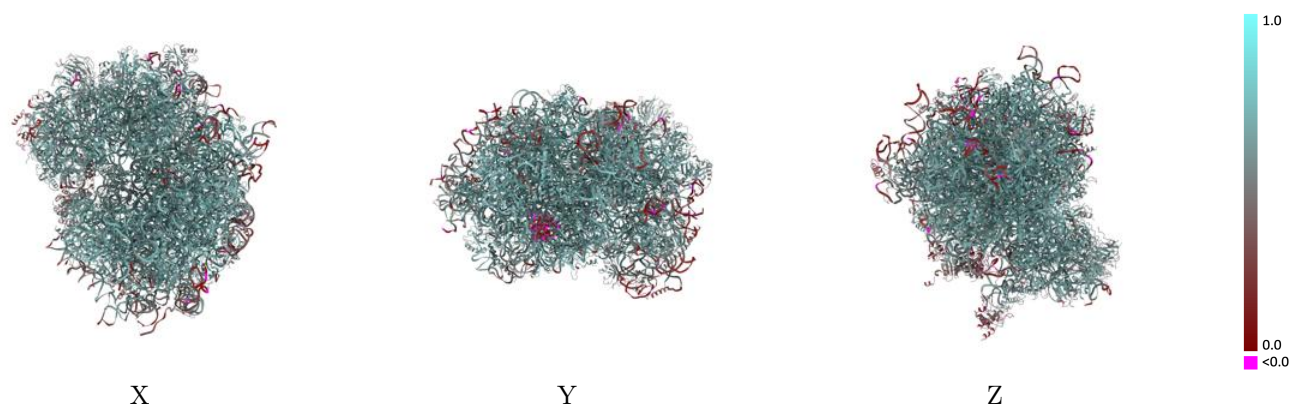
Y



Z

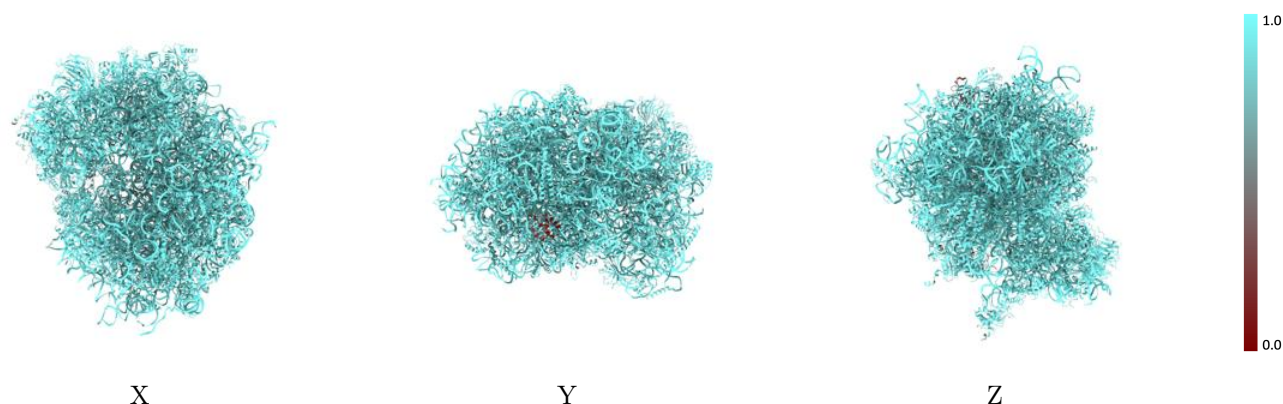
The images above show the 3D surface view of the map at the recommended contour level 0.0635 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



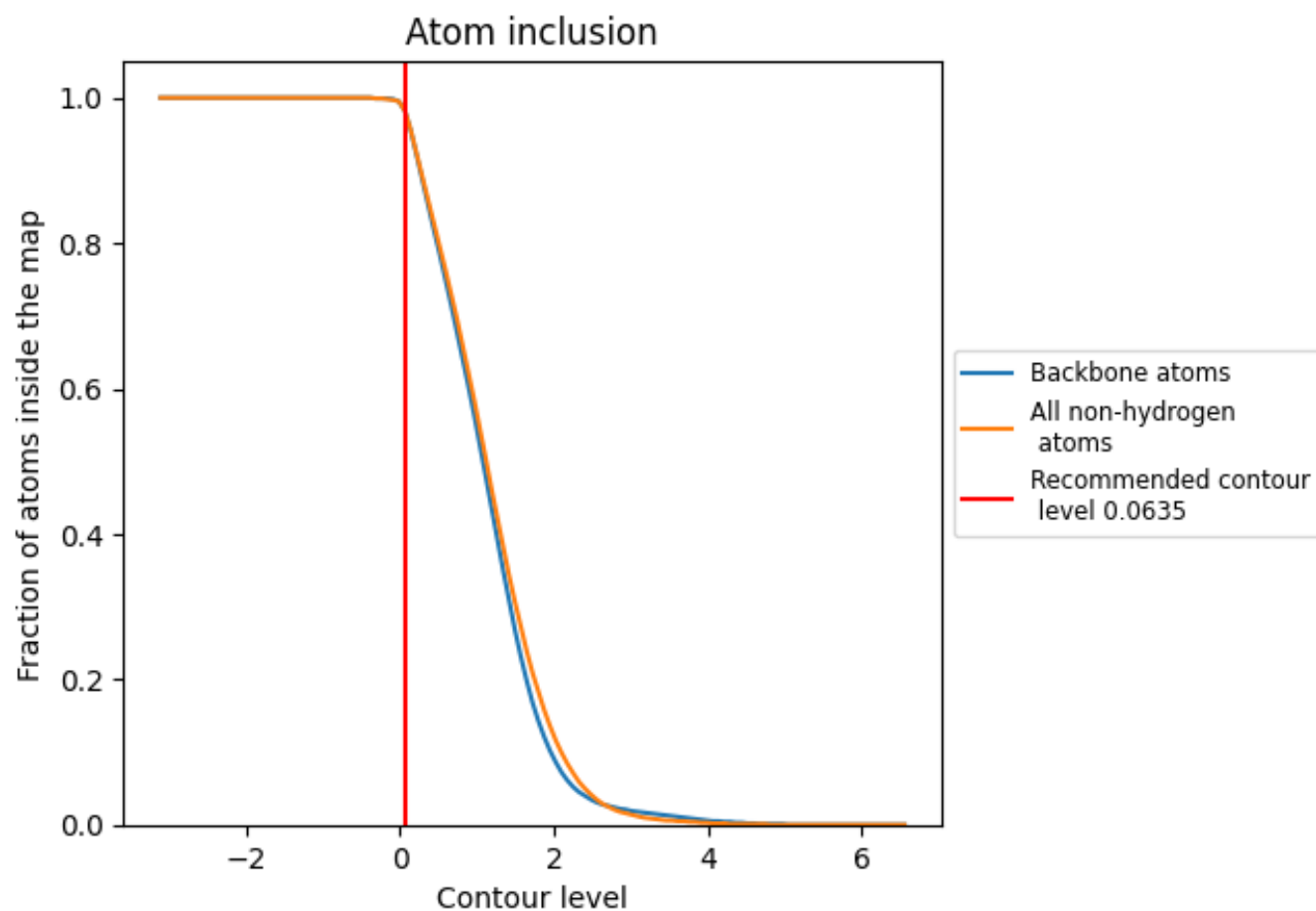
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0635).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.0635) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9820	 0.6110
CM	 0.9800	 0.5850
CP	 0.9880	 0.5880
CR	 0.9390	 0.5240
CZ	 0.9420	 0.5380
L5	 0.9910	 0.6190
L7	 0.9970	 0.6690
L8	 0.9910	 0.6340
LA	 0.9920	 0.6920
LB	 0.9870	 0.6750
LC	 0.9870	 0.6730
LD	 0.9830	 0.6210
LE	 0.9820	 0.6160
LF	 0.9860	 0.6720
LG	 0.9810	 0.6090
LH	 0.9850	 0.6340
LI	 0.9770	 0.6430
LJ	 0.9760	 0.5960
LL	 0.9780	 0.6340
LM	 0.9930	 0.6490
LN	 0.9960	 0.7020
LO	 0.9910	 0.6840
LP	 0.9910	 0.6830
LQ	 0.9940	 0.6890
LR	 0.9830	 0.6590
LS	 0.9890	 0.6770
LT	 0.9730	 0.6260
LU	 0.9750	 0.5400
LV	 0.9920	 0.6810
LW	 0.9620	 0.5230
LX	 0.9830	 0.6450
LY	 0.9890	 0.6410
LZ	 0.9890	 0.6470
La	 0.9900	 0.6810
Lb	 0.9670	 0.5860



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

















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Chain	Atom inclusion	Q-score
Lc	 0.9850	 0.6600
Ld	 0.9950	 0.6610
Le	 0.9940	 0.6900
Lf	 0.9860	 0.6840
Lg	 0.9850	 0.6570
Lh	 0.9810	 0.6420
Li	 0.9880	 0.6380
Lj	 0.9910	 0.6860
Lk	 0.9600	 0.5690
Ll	 0.9840	 0.6530
Lm	 0.9810	 0.6660
Ln	 0.9860	 0.6680
Lo	 0.9850	 0.6500
Lp	 0.9940	 0.6880
Lr	 0.9920	 0.6660
Ls	 0.9080	 0.2970
Lt	 0.9560	 0.3630
NA	 0.3410	 0.0840
NB	 0.4740	 0.1920
S2	 0.9870	 0.5960
SA	 0.9920	 0.6450
SB	 0.9830	 0.6260
SC	 0.9880	 0.6510
SD	 0.9860	 0.5940
SE	 0.9880	 0.6190
SF	 0.9680	 0.5930
SG	 0.9850	 0.5400
SH	 0.9850	 0.5670
SI	 0.9900	 0.6230
SJ	 0.9910	 0.6240
SK	 0.9830	 0.5790
SL	 0.9880	 0.6570
SM	 0.9040	 0.2960
SN	 0.9850	 0.6610
SO	 0.9890	 0.6460
SP	 0.9880	 0.5870
SQ	 0.9720	 0.6170
SR	 0.9550	 0.5520
SS	 0.9730	 0.5850
ST	 0.9790	 0.6070
SU	 0.9810	 0.5470
SV	 0.9870	 0.6390

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Chain	Atom inclusion	Q-score
SW	 0.9920	 0.6820
SX	 0.9850	 0.6390
SY	 0.9890	 0.5770
SZ	 0.9780	 0.5660
Sa	 0.9830	 0.6340
Sb	 0.9800	 0.5890
Sc	 0.9390	 0.5310
Sd	 0.9900	 0.6390
Se	 0.9800	 0.5820
Sf	 0.8750	 0.3110
Sg	 0.9770	 0.5390