



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 05:02 AM EDT

PDB ID : 9O3V / pdb_00009o3v
EMDB ID : EMD-70083
Title : Human 80S ribosome stalled on MYC nascent chain
Authors : Sauer, P.V.; Schuller, A.P.; Hamann, L.G.
Deposited on : 2025-04-07
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

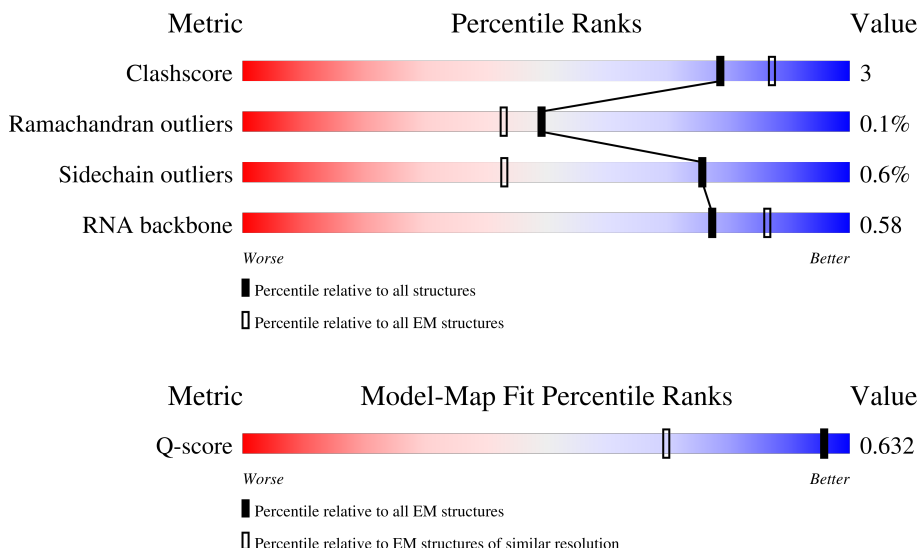
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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

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

The reported resolution of this entry is 2.20 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.



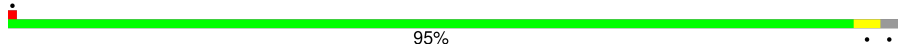
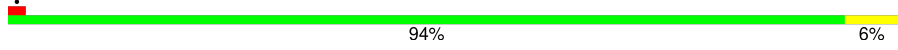
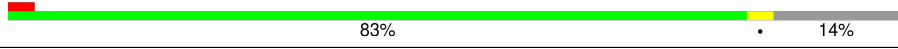
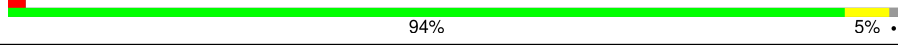
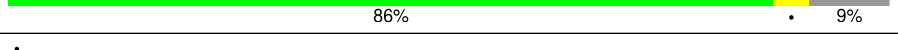
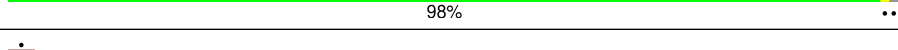
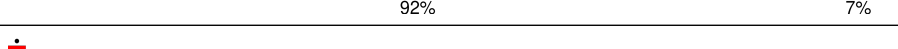
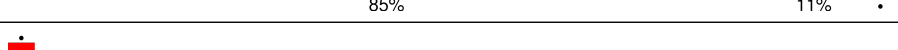
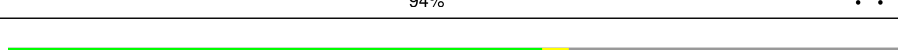
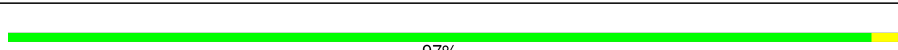
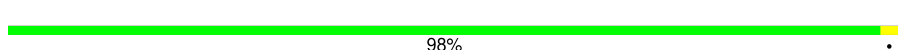
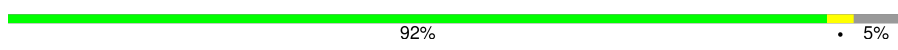
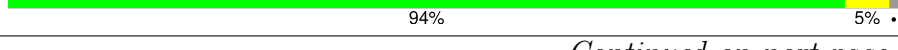
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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

Mol	Chain	Length	Quality of chain
1	L5	5069	
2	L7	120	
3	L8	156	

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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

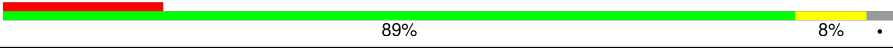
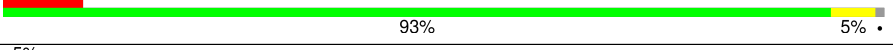
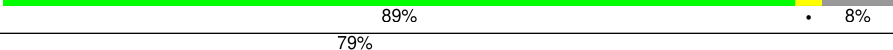
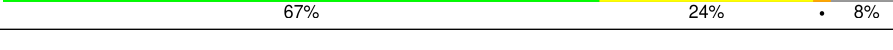
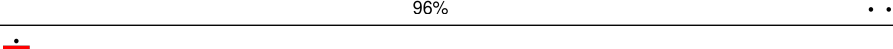
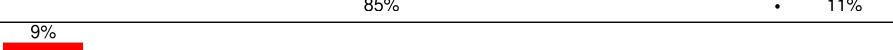
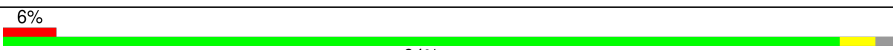
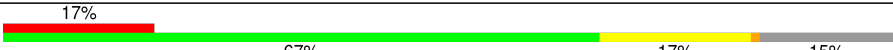
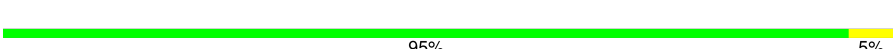
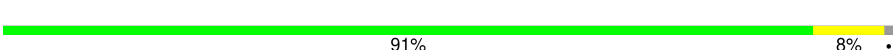
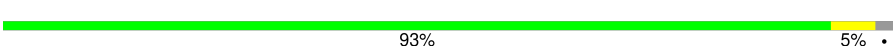
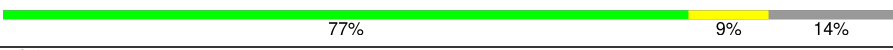
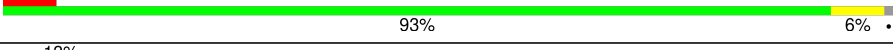
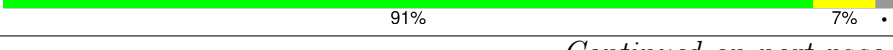
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	NC	19	
47	Pt	75	
48	S2	1869	
49	SA	295	
50	SB	264	
51	SC	293	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SG	249	
56	SH	194	
57	SI	208	
58	SJ	194	
59	SK	165	
60	SL	158	
61	SM	132	
62	SN	151	
63	SO	151	
64	SP	145	
65	SQ	146	
66	SR	135	
67	SS	152	
68	ST	145	
69	SU	119	
70	SV	84	
71	SW	130	
72	SX	143	
73	SY	133	
74	SZ	125	
75	Sa	115	
76	Sb	84	
77	Sc	69	
78	Sd	56	

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Mol	Chain	Length	Quality of chain
79	Se	133	35%62% .
80	Sf	156	30%31%10%60%
81	Sg	317	22%84%14% ..
82	mR	832	99% .

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 216990 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3546	Total	C	N	O	P	3	0
			76178	33963	13933	24733	3549		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3316	1482	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	251	Total	C	N	O	S	0	0
			1921	1204	393	318	6		

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	402	Total	C	N	O	S	0	0
			3240	2061	608	557	14		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	366	Total	C	N	O	S	0	0
			2914	1832	581	487	14		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	294	Total	C	N	O	S	0	0
			2391	1513	436	428	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	223	Total	C	N	O	S	0	0
			1787	1150	339	294	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1716	1086	331	285	14		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	206	Total	C	N	O	S	0	0
			1664	1041	345	274	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

- Molecule 16 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	202	Total	C	N	O	S	0	0
			1655	1066	322	262	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	133	Total	C	N	O	S	0	0
			989	623	186	175	5		

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	68	Total	C	N	O	S	0	0
			562	356	111	92	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	111	Total	C	N	O	S	0	0
			898	560	195	139	4		

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	99	Total	C	N	O	S	0	0
			770	488	136	140	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	110	Total	C	N	O	S	0	0
			884	560	175	145	4		

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

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

- Molecule 42 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			864	543	175	140	6		

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 45 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	126	Total	C	N	O	S	0	0
			1005	624	207	169	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lr	2	ACE	-	acetylation	UNP A0A2K6C1I7

- Molecule 46 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	NC	19	Total	C	N	O	0	0
			118	68	20	30		

- Molecule 47 is a RNA chain called P-site glutamyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Pt	75	Total	C	N	O	P	0	0
			1597	713	275	534	75		

- Molecule 48 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S2	1672	Total	C	N	O	P	0	0
			35736	15981	6403	11681	1671		

- Molecule 49 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	223	Total	C	N	O	S	0	0
			1750	1111	306	325	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SA	2	ACE	-	acetylation	UNP A0A2J8WY29

- Molecule 50 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	223	Total	C	N	O	S	0	0
			1806	1145	325	322	14		

- Molecule 51 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 52 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SD	226	Total	C	N	O	S	0	0
			1756	1119	315	314	8		

- Molecule 53 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 55 is a protein called Small ribosomal subunit protein eS6.

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

- Molecule 56 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SH	189	Total	C	N	O	S	0	0
			1517	966	279	271	1		

- Molecule 57 is a protein called Small ribosomal subunit protein eS8.

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

- Molecule 58 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS10.

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

- Molecule 60 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SL	146	Total	C	N	O	S	0	0
			1200	766	226	202	6		

- Molecule 61 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 62 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 63 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SO	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 64 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SP	131	Total	C	N	O	S	0	0
			1078	684	204	183	7		

- Molecule 65 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	134	Total	C	N	O	S	0	0
			1083	680	201	198	4		

- Molecule 67 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	148	Total	C	N	O	S	0	0
			1214	761	245	207	1		

- Molecule 68 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST	142	Total	C	N	O	S	0	0
			1103	691	212	197	3		

- Molecule 69 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 70 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV	84	Total	C	N	O	S	0	0
			640	395	117	123	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SV	0	ACE	-	acetylation	UNP P63220

- Molecule 71 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 72 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX	140	Total	C	N	O	S	0	0
			1088	687	215	183	3		

- Molecule 73 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 74 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sa	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 76 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sc	65	Total	C	N	O	S	0	0
			512	311	103	96	2		

- Molecule 78 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 79 is a protein called FAU ubiquitin-like and ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Se	50	Total	C	N	O	S	0	0
			395	241	88	65	1		

- Molecule 80 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

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

- Molecule 81 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 82 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	mR	6	Total	C	N	O	P	0	0
			133	59	27	41	6		

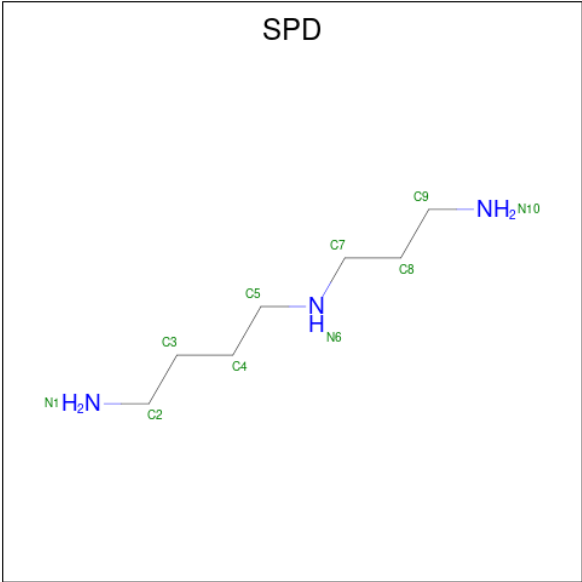
- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	L5	252	Total	Mg	0
			252	252	
83	L7	6	Total	Mg	0
			6	6	
83	L8	6	Total	Mg	0
			6	6	
83	LB	2	Total	Mg	0
			2	2	
83	LL	1	Total	Mg	0
			1	1	
83	LN	2	Total	Mg	0
			2	2	
83	LP	1	Total	Mg	0
			1	1	
83	LQ	1	Total	Mg	0
			1	1	
83	LV	1	Total	Mg	0
			1	1	
83	La	1	Total	Mg	0
			1	1	
83	Lo	1	Total	Mg	0
			1	1	
83	Pt	1	Total	Mg	0
			1	1	
83	S2	75	Total	Mg	0
			75	75	
83	ST	1	Total	Mg	0
			1	1	
83	Sd	1	Total	Mg	0
			1	1	

- Molecule 84 is POTASSIUM ION (CCD ID: K) (formula: K).

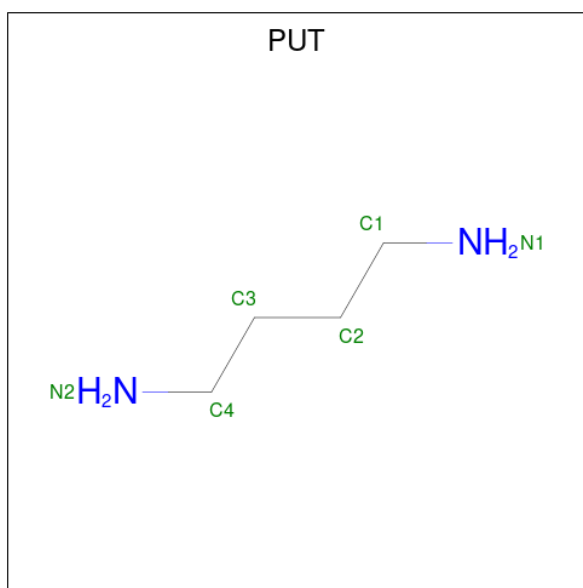
Mol	Chain	Residues	Atoms		AltConf
84	L5	115	Total 115	K 115	0
84	L7	3	Total 3	K 3	0
84	L8	2	Total 2	K 2	0
84	LA	3	Total 3	K 3	0
84	LH	1	Total 1	K 1	0
84	LI	1	Total 1	K 1	0
84	LL	1	Total 1	K 1	0
84	LN	1	Total 1	K 1	0
84	Lb	1	Total 1	K 1	0
84	Le	1	Total 1	K 1	0
84	Lf	1	Total 1	K 1	0
84	Lg	1	Total 1	K 1	0
84	Ll	1	Total 1	K 1	0
84	S2	31	Total 31	K 31	0
84	SL	1	Total 1	K 1	0
84	SO	1	Total 1	K 1	0

- Molecule 85 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



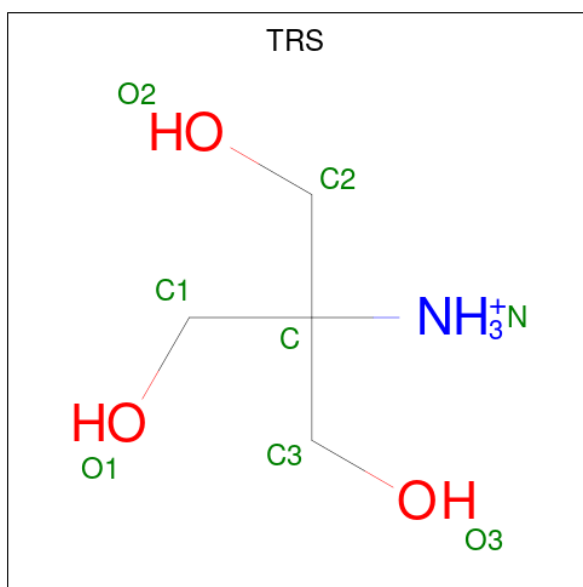
Mol	Chain	Residues	Atoms			AltConf
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	L5	1	Total	C	N	0
			10	7	3	
85	S2	1	Total	C	N	0
			10	7	3	
85	S2	1	Total	C	N	0
			10	7	3	

- Molecule 86 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms			AltConf
86	L5	1	Total	C	N	0
			6	4	2	
86	L5	1	Total	C	N	0
			6	4	2	
86	L5	1	Total	C	N	0
			6	4	2	
86	L5	1	Total	C	N	0
			6	4	2	
86	L5	1	Total	C	N	0
			6	4	2	
86	L5	1	Total	C	N	0
			6	4	2	

- Molecule 87 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				AltConf
87	L5	1	Total	C	N	O	0
			8	4	1	3	
87	L5	1	Total	C	N	O	0
			8	4	1	3	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 89 is water.

Mol	Chain	Residues	Atoms		AltConf
89	L5	3376	Total 3376	O 3376	0
89	L7	27	Total 27	O 27	0
89	L8	86	Total 86	O 86	0
89	LA	61	Total 61	O 61	0
89	LB	48	Total 48	O 48	0
89	LC	66	Total 66	O 66	0
89	LD	2	Total 2	O 2	0
89	LE	1	Total 1	O 1	0
89	LF	22	Total 22	O 22	0
89	LG	1	Total 1	O 1	0
89	LI	23	Total 23	O 23	0
89	LL	20	Total 20	O 20	0
89	LN	57	Total 57	O 57	0
89	LO	18	Total 18	O 18	0
89	LP	32	Total 32	O 32	0
89	LQ	28	Total 28	O 28	0
89	LR	13	Total 13	O 13	0
89	LS	5	Total 5	O 5	0
89	LT	19	Total 19	O 19	0
89	LV	21	Total 21	O 21	0
89	LW	3	Total 3	O 3	0
89	LX	5	Total 5	O 5	0

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Mol	Chain	Residues	Atoms		AltConf
89	LY	4	Total 4	O 4	0
89	La	34	Total 34	O 34	0
89	Lb	12	Total 12	O 12	0
89	Lc	1	Total 1	O 1	0
89	Ld	6	Total 6	O 6	0
89	Le	42	Total 42	O 42	0
89	Lf	15	Total 15	O 15	0
89	Lg	18	Total 18	O 18	0
89	Lh	3	Total 3	O 3	0
89	Li	3	Total 3	O 3	0
89	Lj	27	Total 27	O 27	0
89	Ll	12	Total 12	O 12	0
89	Lm	2	Total 2	O 2	0
89	Ln	3	Total 3	O 3	0
89	Lo	17	Total 17	O 17	0
89	Lp	13	Total 13	O 13	0
89	Lr	12	Total 12	O 12	0
89	NC	4	Total 4	O 4	0
89	Pt	6	Total 6	O 6	0
89	S2	506	Total 506	O 506	0
89	SA	1	Total 1	O 1	0

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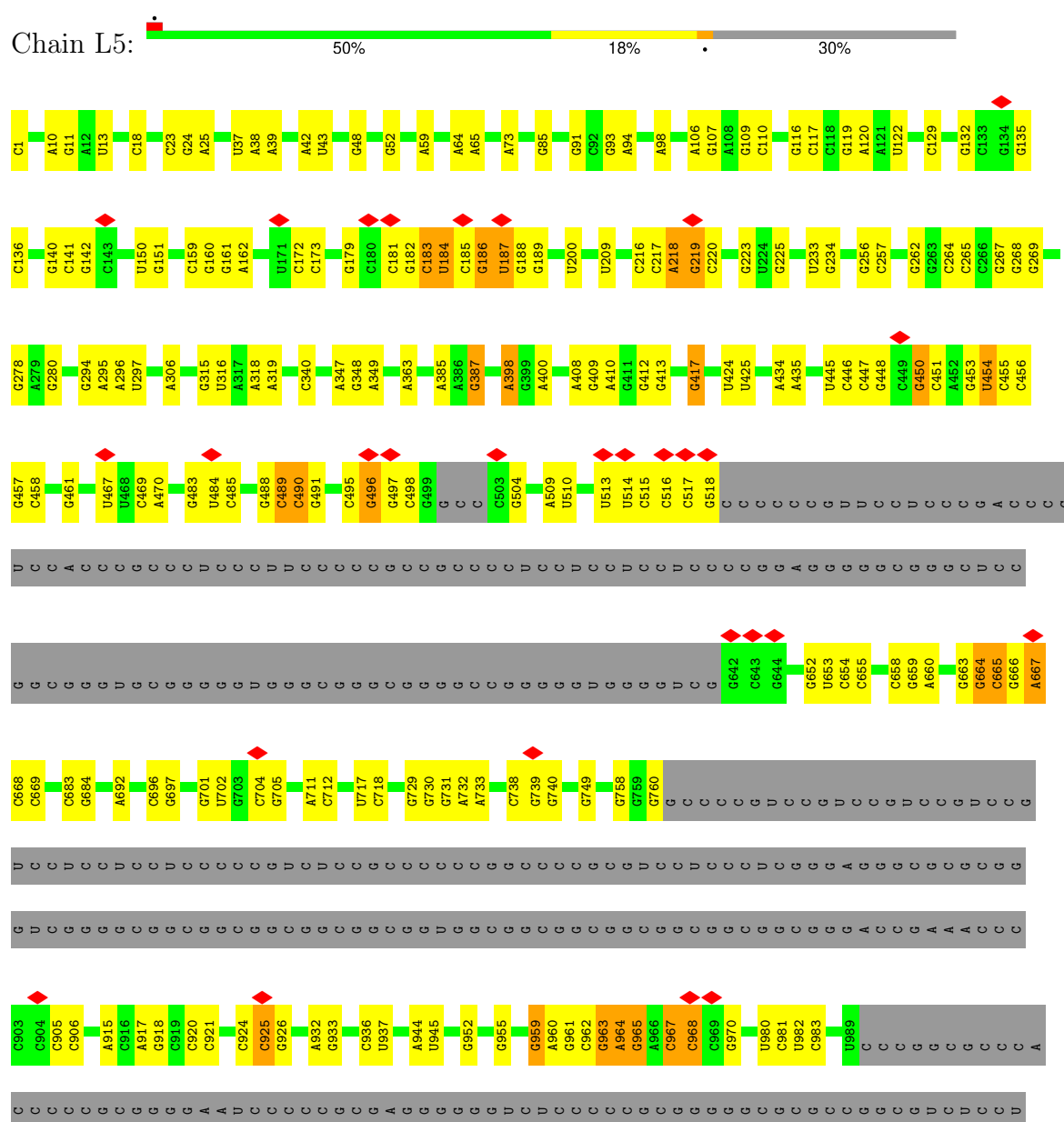
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Mol	Chain	Residues	Atoms		AltConf
89	SB	2	Total 2	O 2	0
89	SC	2	Total 2	O 2	0
89	SE	1	Total 1	O 1	0
89	SI	1	Total 1	O 1	0
89	SL	7	Total 7	O 7	0
89	SN	9	Total 9	O 9	0
89	SO	4	Total 4	O 4	0
89	SW	5	Total 5	O 5	0
89	SX	10	Total 10	O 10	0
89	Sa	11	Total 11	O 11	0
89	Sb	1	Total 1	O 1	0
89	Sc	1	Total 1	O 1	0
89	mR	1	Total 1	O 1	0

3 Residue-property plots

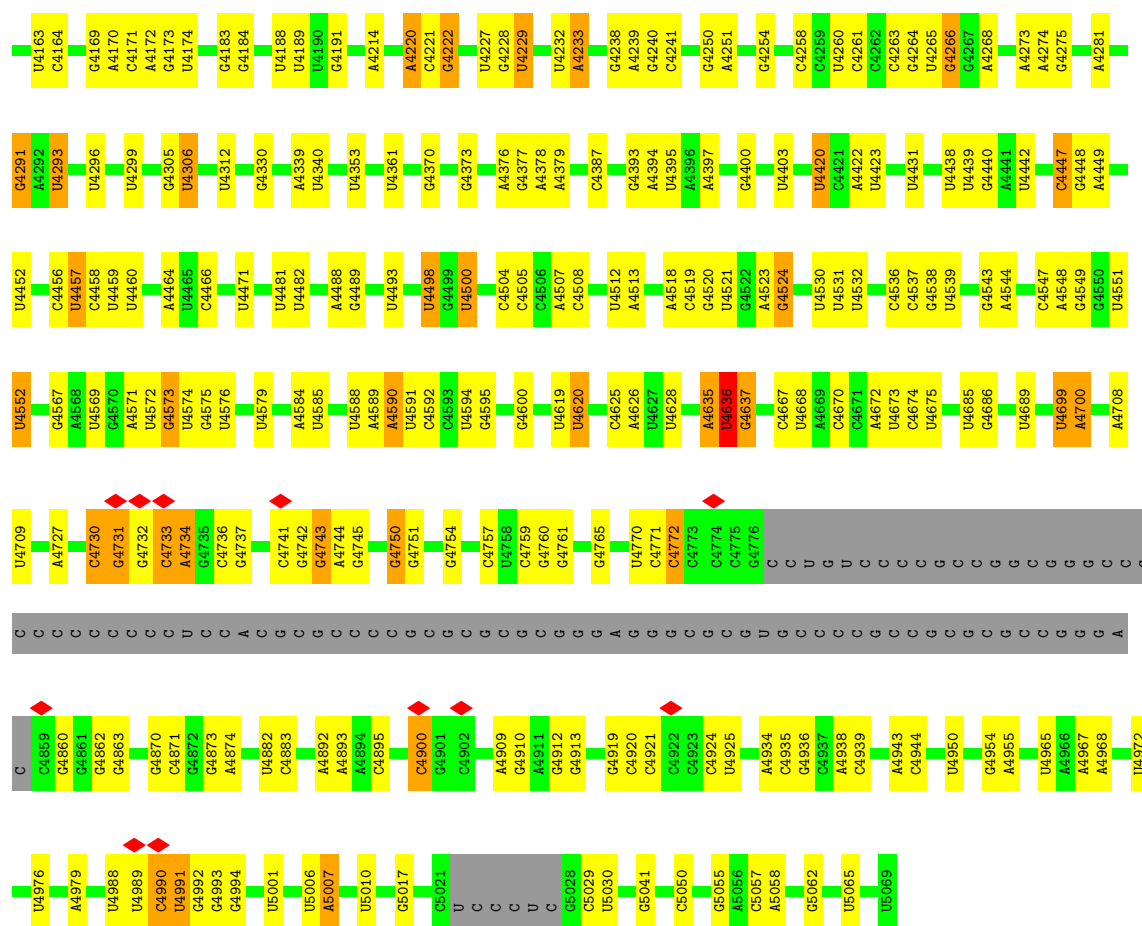
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S rRNA

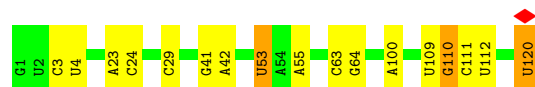
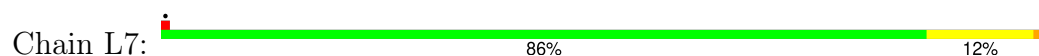




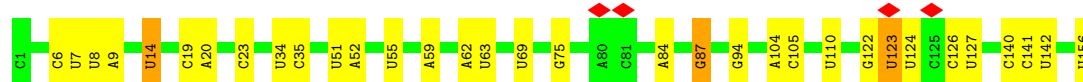
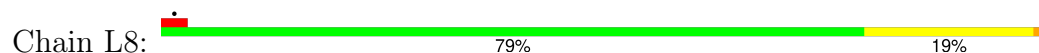
[illegible]



- Molecule 2: 5S rRNA



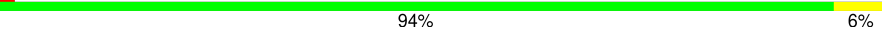
- Molecule 3: 5.8S rRNA

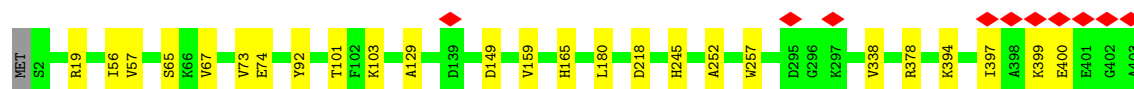


- Molecule 4: 60S ribosomal protein L8



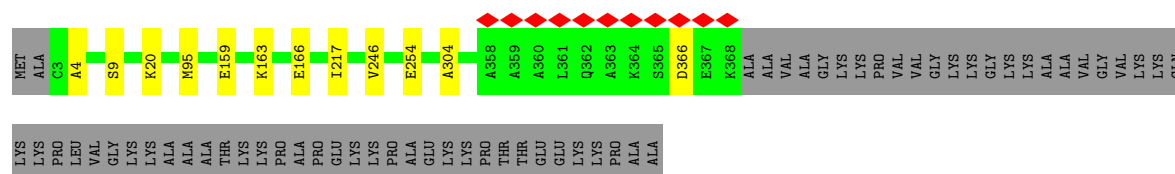
- Molecule 5: Large ribosomal subunit protein uL3

Chain LB:  94% 6%



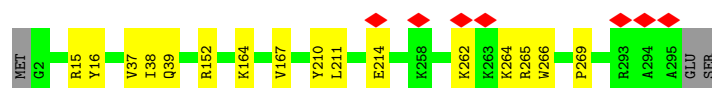
- Molecule 6: Large ribosomal subunit protein uL4

Chain LC:  83% 14%



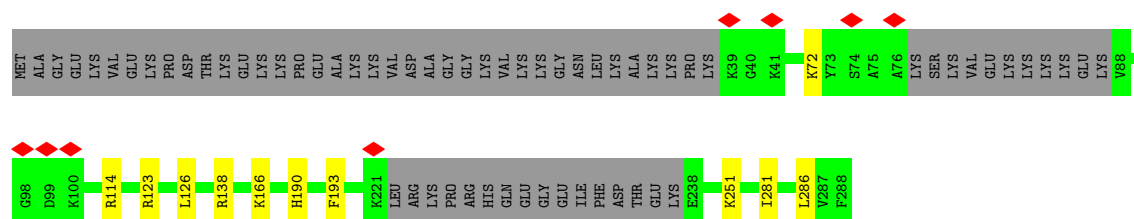
- Molecule 7: Large ribosomal subunit protein uL18

Chain LD:  94% 5%



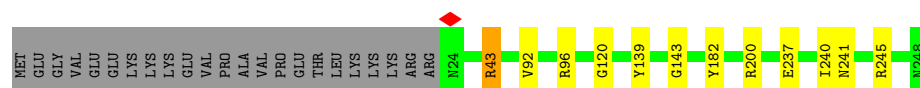
- Molecule 8: Large ribosomal subunit protein eL6

Chain LE:  74% 23%



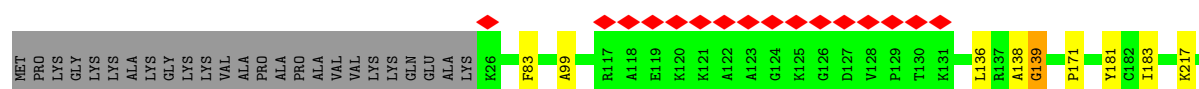
- Molecule 9: 60S ribosomal protein L7

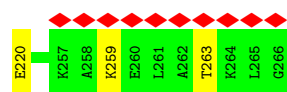
Chain LF:  86% 9%



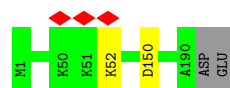
- Molecule 10: Large ribosomal subunit protein eL8

Chain LG:  10% 86% 9%

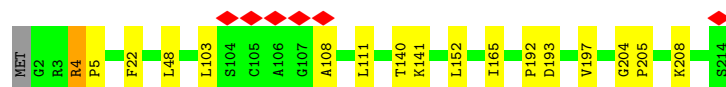




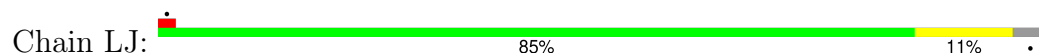
- Molecule 11: Large ribosomal subunit protein uL6



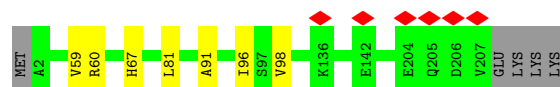
- Molecule 12: Large ribosomal subunit protein uL16



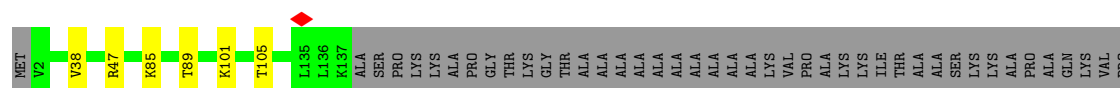
- Molecule 13: Large ribosomal subunit protein uL5



- Molecule 14: Large ribosomal subunit protein eL13



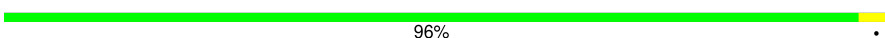
- Molecule 15: Large ribosomal subunit protein eL14



- Molecule 16: Large ribosomal subunit protein eL15



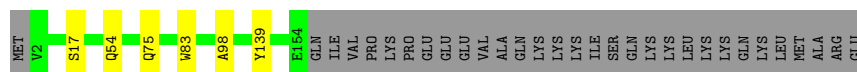
- Molecule 17: Large ribosomal subunit protein uL13

Chain LO:  96%

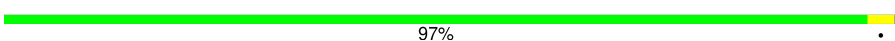


- Molecule 18: Large ribosomal subunit protein uL22

Chain LP:  80% 17%

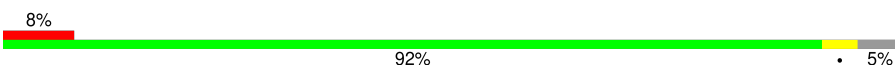


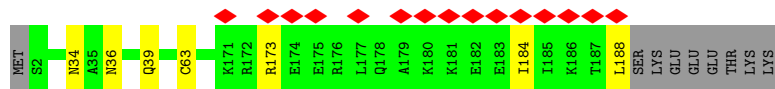
- Molecule 19: Large ribosomal subunit protein eL18

Chain LQ:  97%

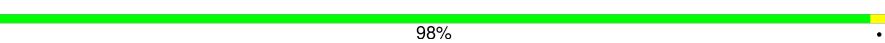


- Molecule 20: Large ribosomal subunit protein eL19

Chain LR:  8% 92% 5%

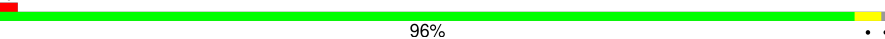


- Molecule 21: Large ribosomal subunit protein eL20

Chain LS:  98%



- Molecule 22: Large ribosomal subunit protein eL21

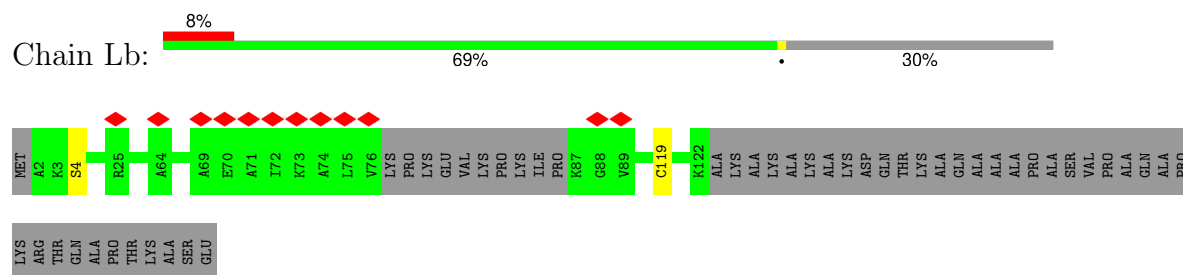
Chain LT:  96%



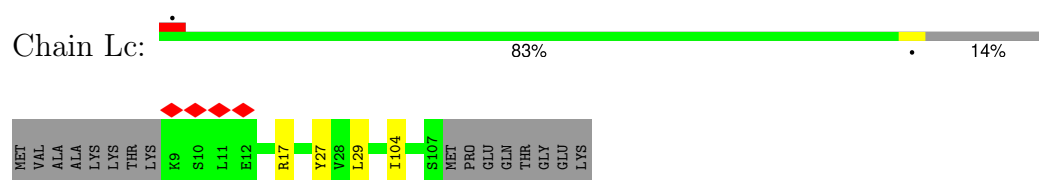
- Molecule 23: Large ribosomal subunit protein eL22

Chain LU:  68% 9% 23%

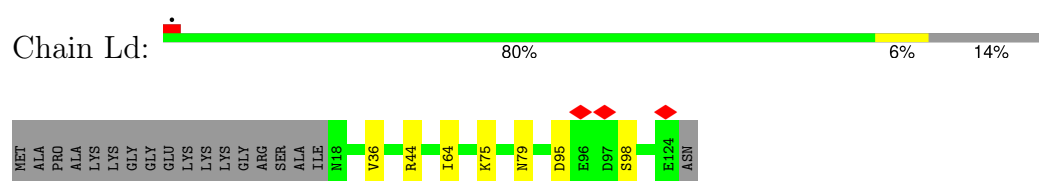
- Molecule 30: Large ribosomal subunit protein eL29



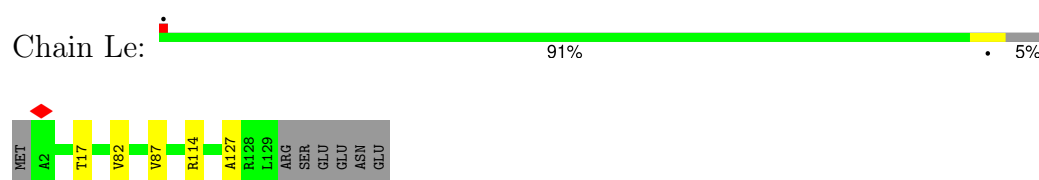
- Molecule 31: Large ribosomal subunit protein eL30



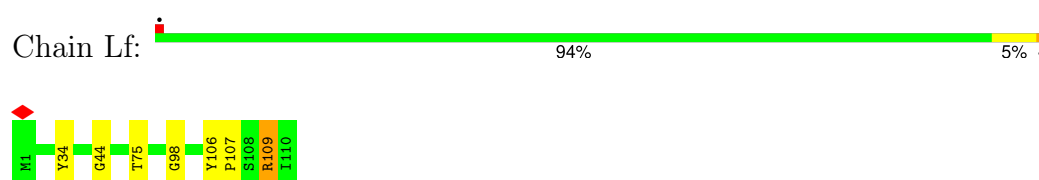
- Molecule 32: Large ribosomal subunit protein eL31



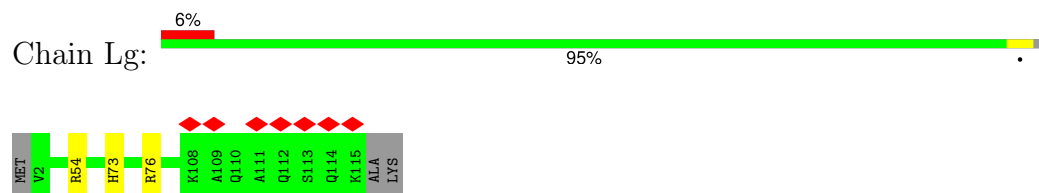
- Molecule 33: Large ribosomal subunit protein eL32



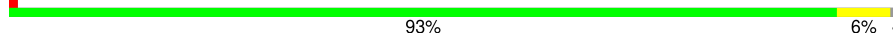
- Molecule 34: Large ribosomal subunit protein eL33



- Molecule 35: Large ribosomal subunit protein eL34

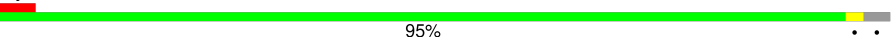


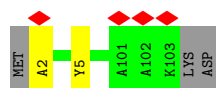
- Molecule 36: Large ribosomal subunit protein uL29

Chain Lh:  93% 6%



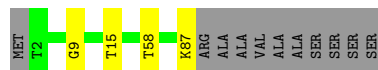
- Molecule 37: Large ribosomal subunit protein eL36

Chain Li:  95%

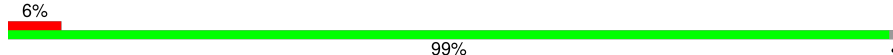


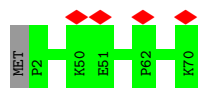
- Molecule 38: Large ribosomal subunit protein eL37

Chain Lj:  85% 11%



- Molecule 39: Large ribosomal subunit protein eL38

Chain Lk:  6% 99%



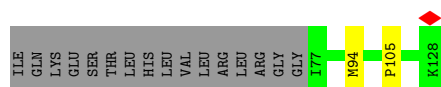
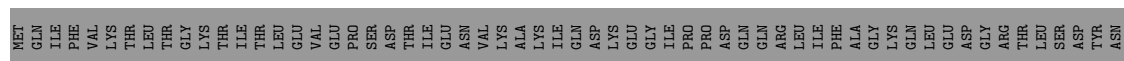
- Molecule 40: Large ribosomal subunit protein eL39

Chain Ll:  88% 10%



- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein

Chain Lm:  39% 59%

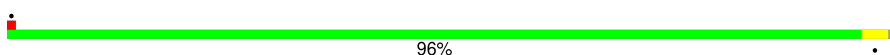


- Molecule 42: Small ribosomal subunit protein eS32

Chain Ln:  100%

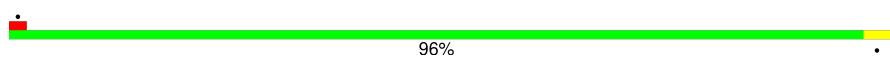
There are no outlier residues recorded for this chain.

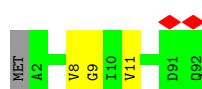
- Molecule 43: Large ribosomal subunit protein eL42

Chain Lo:  96%



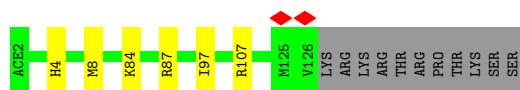
- Molecule 44: Large ribosomal subunit protein eL43

Chain Lp:  96%

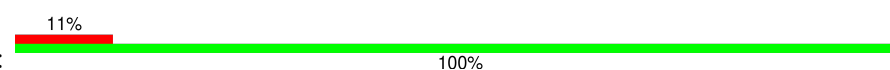


- Molecule 45: Large ribosomal subunit protein eL28

Chain Lr:  88%



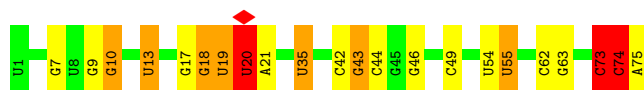
- Molecule 46: Nascent chain

Chain NC:  100%



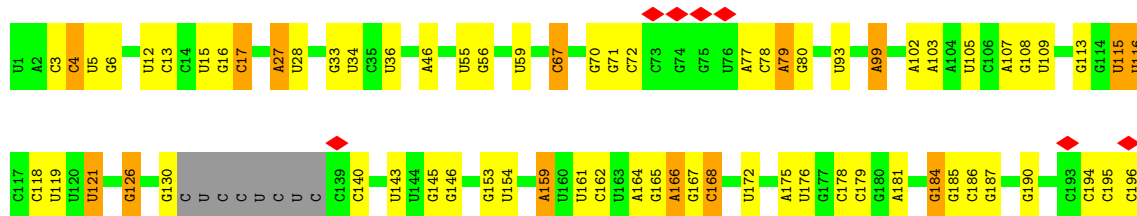
- Molecule 47: P-site glutamyl-tRNA

Chain Pt:  71%

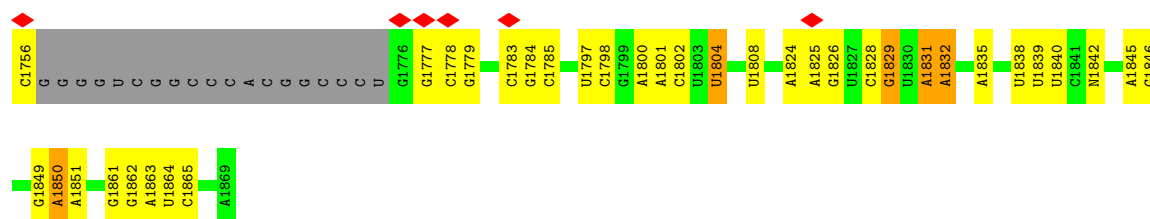


- Molecule 48: 18S rRNA

Chain S2:  60%

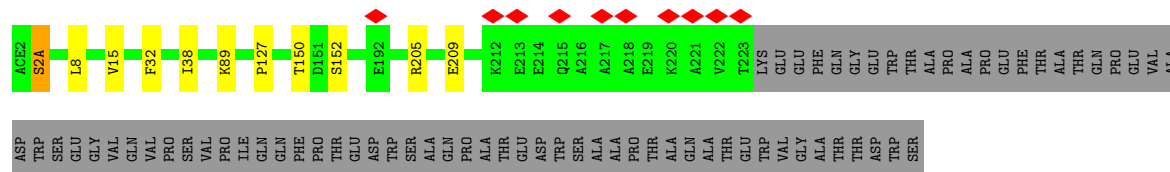






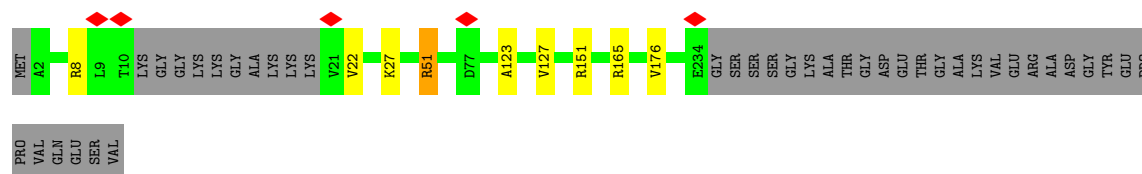
- Molecule 49: Small ribosomal subunit protein uS2

Chain SA: 72% 24%



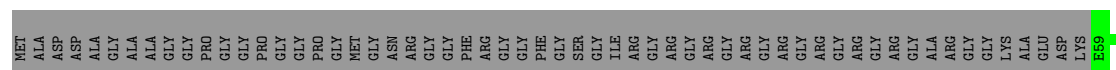
- Molecule 50: Small ribosomal subunit protein eS1

Chain SB: 81% 16%



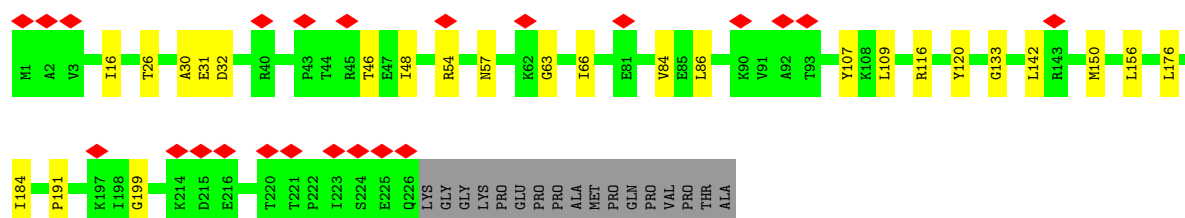
- Molecule 51: Small ribosomal subunit protein uS5

Chain SC: 70% 6% 24%



- Molecule 52: Small ribosomal subunit protein uS3

Chain SD: 9% 83% 10% 7%



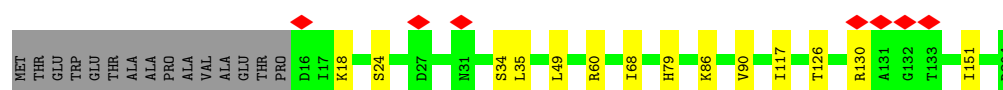
- Molecule 53: Small ribosomal subunit protein eS4, X isoform

Chain SE:  90% 9%



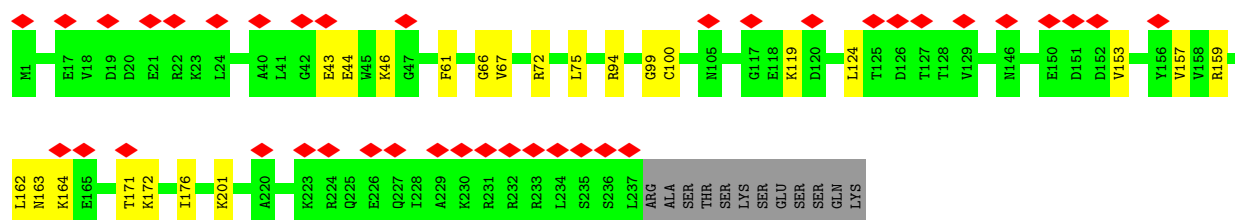
- Molecule 54: Small ribosomal subunit protein uS7

Chain SF:  86% 7% 7%



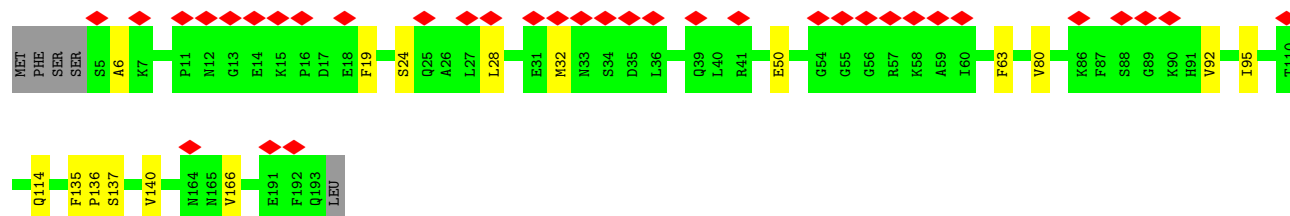
- Molecule 55: Small ribosomal subunit protein eS6

Chain SG:  16% 86% 9% 5%

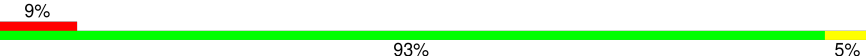


- Molecule 56: Small ribosomal subunit protein eS7

Chain SH:  18% 89% 8%



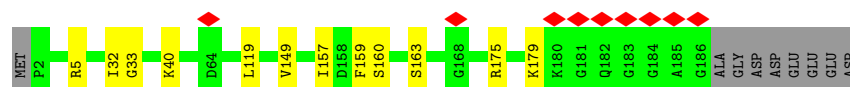
- Molecule 57: Small ribosomal subunit protein eS8

Chain SI:  9% 93% 5%

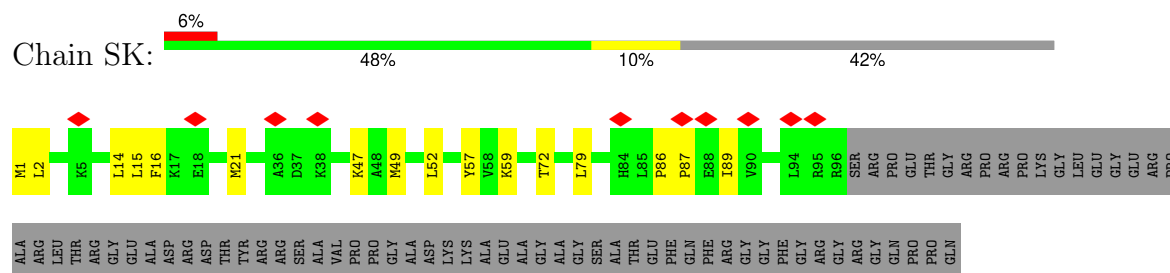


- Molecule 58: Small ribosomal subunit protein uS4

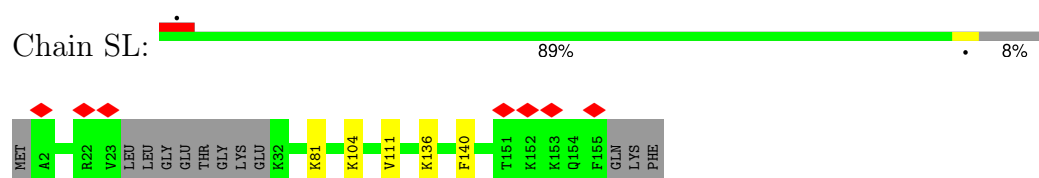
Chain SJ:  5% 89% 6% 5%



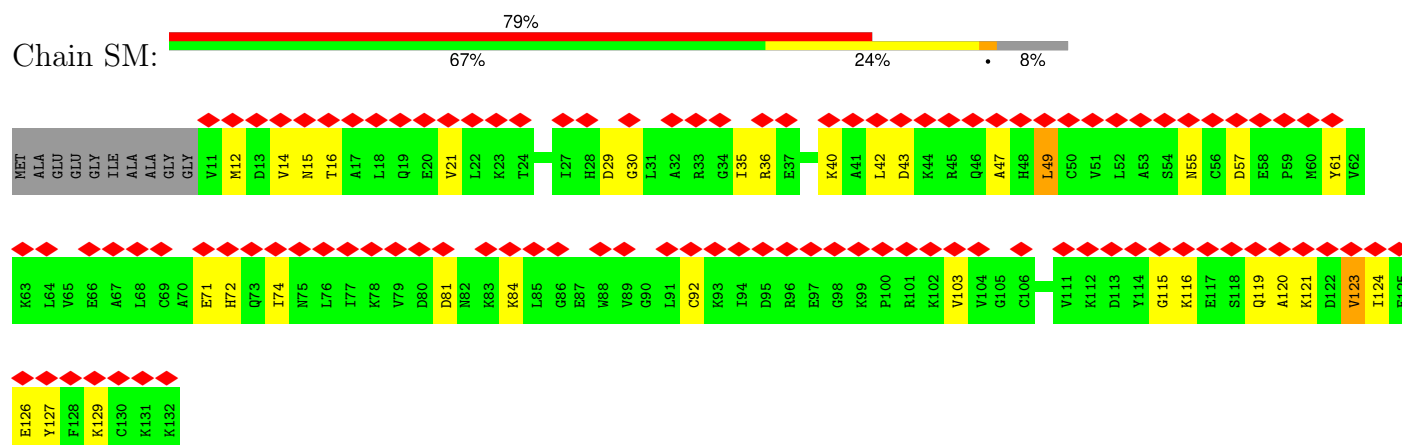
- Molecule 59: Small ribosomal subunit protein eS10



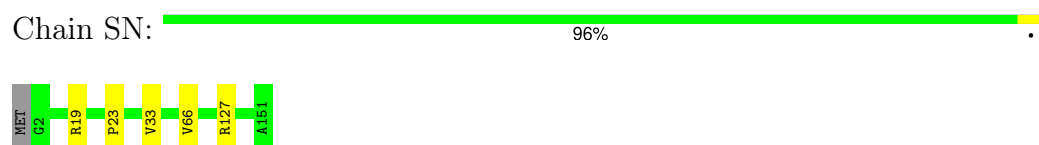
- Molecule 60: Small ribosomal subunit protein uS17



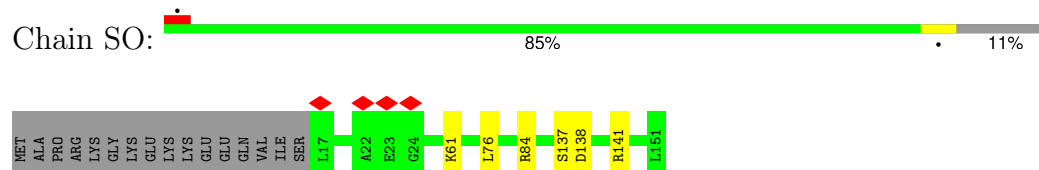
- Molecule 61: Small ribosomal subunit protein eS12



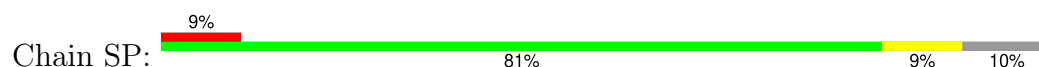
- Molecule 62: Small ribosomal subunit protein uS15

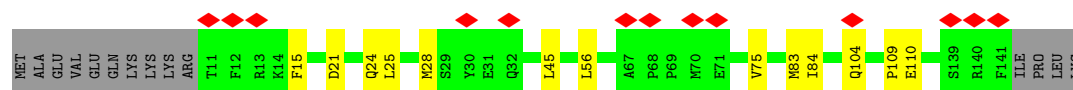


- Molecule 63: Small ribosomal subunit protein uS11

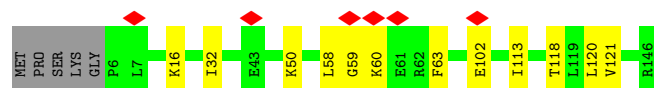
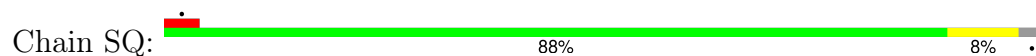


- Molecule 64: Small ribosomal subunit protein uS19

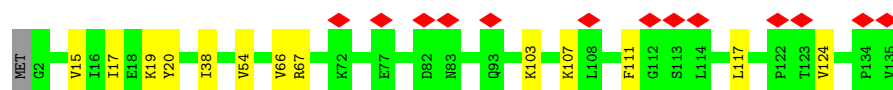
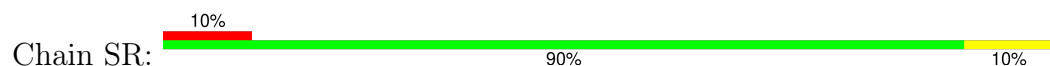




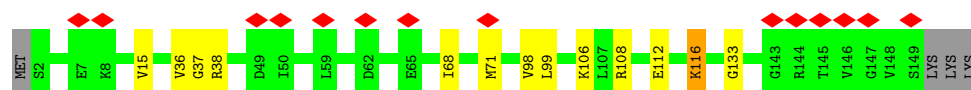
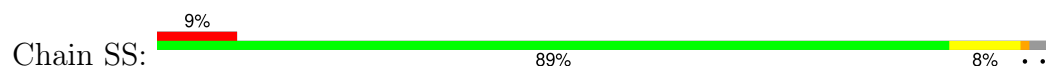
- Molecule 65: Small ribosomal subunit protein uS9



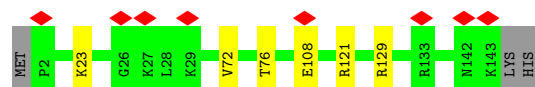
- Molecule 66: Small ribosomal subunit protein eS17



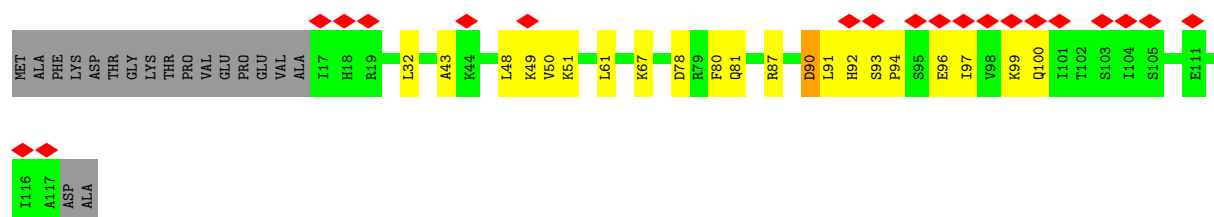
- Molecule 67: Small ribosomal subunit protein uS13



- Molecule 68: Small ribosomal subunit protein eS19



- Molecule 69: Small ribosomal subunit protein uS10



- Molecule 70: 40S ribosomal protein S21





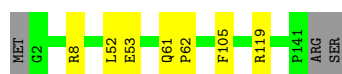
- Molecule 71: Small ribosomal subunit protein uS8

Chain SW: 91% 8%



- Molecule 72: Small ribosomal subunit protein uS12

Chain SX: 93% 5%



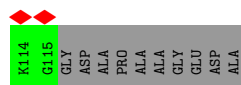
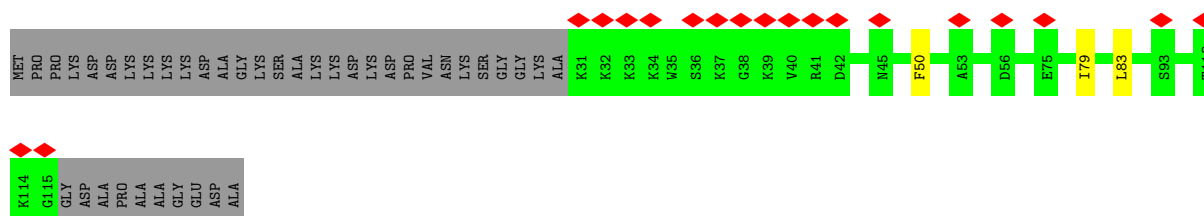
- Molecule 73: 40S ribosomal protein S24

Chain SY: 9% 83% 16%



- Molecule 74: Small ribosomal subunit protein eS25

Chain SZ: 15% 66% 32%



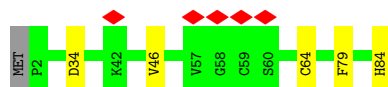
- Molecule 75: Small ribosomal subunit protein eS26

Chain Sa: 77% 9% 14%



- Molecule 76: Small ribosomal subunit protein eS27

Chain Sb: 6% 93% 6%



- | |
|------|
| Q143 | D144 | C153 | V154 | R155 | N159 | S160 | S161 | N162 | P163 | I164 | I165 | K172 | L173 | V174 | W177 | M178 | L179 | A180 | N181 | C182 | K183 | T186 | N187 | H188 | H191 | T192 | G193 | Y194 | L195 | V198 | T199 | V200 | G204 | S209 | G210 | G214 | D220 | L221 | N222 | E223 | G224 | K225 | H226 | L227 | Y228 | D231 |
|------|



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	171177	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.263	Depositor
Minimum map value	-0.503	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	427.008, 427.008, 427.008	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.834, 0.834, 0.834	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, G7M, 5MC, 1MA, M3L, 4AC, K, PSU, HY3, HIC, MLZ, OMU, 6MZ, H2U, TRS, B8N, SPD, OMG, MG, OMC, 2MU, ACE, UY1, UR3, ZN, 2MG, A2M, PUT

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	L5	0.48	0/82149	0.58	7/128155 (0.0%)
2	L7	0.41	0/2858	0.56	1/4455 (0.0%)
3	L8	0.46	0/3609	0.56	0/5623
4	LA	0.37	0/1959	0.58	0/2627
5	LB	0.32	0/3295	0.54	0/4406
6	LC	0.34	0/2968	0.53	0/3985
7	LD	0.27	0/2437	0.49	0/3263
8	LE	0.27	0/1821	0.48	0/2442
9	LF	0.33	0/1905	0.51	0/2539
10	LG	0.29	0/1960	0.60	1/2637 (0.0%)
11	LH	0.30	0/1537	0.49	0/2066
12	LI	0.30	0/1755	0.48	0/2344
13	LJ	0.26	0/1385	0.54	0/1852
14	LL	0.29	0/1695	0.50	0/2270
15	LM	0.29	0/1142	0.49	0/1527
16	LN	0.37	0/1746	0.57	0/2338
17	LO	0.34	0/1687	0.53	0/2257
18	LP	0.35	0/1268	0.51	0/1701
19	LQ	0.34	0/1537	0.57	0/2052
20	LR	0.29	0/1582	0.47	0/2091
21	LS	0.31	0/1501	0.46	0/2013
22	LT	0.32	0/1326	0.51	0/1770
23	LU	0.26	0/822	0.53	0/1103
24	LV	0.33	0/1003	0.55	0/1345
25	LW	0.31	0/574	0.48	0/763
26	LX	0.30	0/984	0.50	0/1323
27	LY	0.30	0/1132	0.50	0/1504
28	LZ	0.30	0/1130	0.55	0/1507
29	La	0.37	0/1191	0.56	0/1591
30	Lb	0.29	0/900	0.53	0/1187
31	Lc	0.32	0/780	0.53	0/1046

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Ld	0.32	0/903	0.49	0/1216
33	Le	0.37	0/1071	0.57	0/1429
34	Lf	0.35	0/903	0.56	0/1208
35	Lg	0.31	0/916	0.49	0/1220
36	Lh	0.29	0/1023	0.48	0/1351
37	Li	0.27	0/843	0.47	0/1115
38	Lj	0.38	0/720	0.61	0/952
39	Lk	0.28	0/575	0.49	0/761
40	Ll	0.36	0/454	0.54	0/599
41	Lm	0.32	0/426	0.51	0/564
42	Ln	0.37	0/241	0.58	0/305
43	Lo	0.33	0/867	0.53	0/1141
44	Lp	0.36	0/718	0.59	0/953
45	Lr	0.33	0/1018	0.49	0/1366
46	NC	0.38	0/52	0.71	0/68
47	Pt	0.38	0/1640	0.85	6/2555 (0.2%)
48	S2	0.41	1/37935 (0.0%)	0.54	1/59125 (0.0%)
49	SA	0.27	0/1785	0.47	0/2426
50	SB	0.27	0/1832	0.47	0/2449
51	SC	0.31	0/1762	0.50	0/2381
52	SD	0.24	0/1784	0.46	0/2403
53	SE	0.28	0/2118	0.51	0/2849
54	SF	0.25	0/1516	0.51	0/2037
55	SG	0.24	0/1946	0.51	0/2590
56	SH	0.26	0/1540	0.48	0/2064
57	SI	0.29	0/1715	0.52	0/2287
58	SJ	0.27	0/1550	0.50	0/2069
59	SK	0.22	0/834	0.49	0/1125
60	SL	0.30	0/1221	0.46	0/1632
61	SM	0.19	0/960	0.50	0/1286
62	SN	0.29	0/1232	0.45	0/1656
63	SO	0.30	0/1023	0.57	0/1372
64	SP	0.23	0/1100	0.53	0/1470
65	SQ	0.27	0/1142	0.51	1/1528 (0.1%)
66	SR	0.24	0/1098	0.47	0/1474
67	SS	0.23	0/1232	0.49	0/1651
68	ST	0.24	0/1122	0.46	0/1504
69	SU	0.25	0/813	0.51	0/1092
70	SV	0.37	1/645 (0.2%)	0.50	0/862
71	SW	0.31	0/1051	0.49	0/1406
72	SX	0.29	0/1096	0.51	0/1461
73	SY	0.25	0/1083	0.51	0/1438
74	SZ	0.22	0/691	0.53	0/922

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sa	0.32	0/805	0.52	0/1079
76	Sb	0.26	0/665	0.47	0/891
77	Sc	0.26	0/514	0.56	0/688
78	Sd	0.25	0/470	0.50	0/623
79	Se	0.23	0/397	0.48	0/519
80	Sf	0.21	0/525	0.53	0/695
81	Sg	0.22	0/2493	0.54	0/3394
82	mR	0.34	0/149	1.07	0/231
All	All	0.40	2/221852 (0.0%)	0.55	17/325264 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	LB	0	1
7	LD	0	2
8	LE	0	1
9	LF	0	1
10	LG	0	2
12	LI	0	1
16	LN	0	1
34	Lf	0	2
35	Lg	0	1
36	Lh	0	1
50	SB	0	1
51	SC	0	1
58	SJ	0	1
62	SN	0	1
63	SO	0	2
65	SQ	0	1
67	SS	0	2
72	SX	0	1
75	Sa	0	1
All	All	0	24

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	SV	0	ACE	C-N	5.97	1.45	1.33
48	S2	1383	A2M	O3'-P	5.06	1.61	1.56

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	Pt	73	C	OP2-P-O3'	-23.41	37.76	108.00
10	LG	139	GLY	N-CA-C	8.52	133.37	113.18
47	Pt	74	C	P-O5'-C5'	7.54	132.22	120.90
47	Pt	74	C	C3'-C2'-C1'	6.53	107.83	101.30
1	L5	2304	U	C2'-C3'-O3'	-6.30	100.06	109.50

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	LB	378	ARG	Sidechain
7	LD	152	ARG	Sidechain
7	LD	37	VAL	Peptide
8	LE	138	ARG	Sidechain
9	LF	43	ARG	Sidechain

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	L5	76178	0	38554	414	0
2	L7	2558	0	1295	9	0
3	L8	3316	0	1686	13	0
4	LA	1921	0	2022	5	0
5	LB	3240	0	3377	14	0
6	LC	2914	0	3087	6	0
7	LD	2391	0	2426	10	0
8	LE	1787	0	1945	9	0
9	LF	1870	0	1996	6	0
10	LG	1927	0	2074	5	0
11	LH	1518	0	1601	1	0
12	LI	1716	0	1765	9	0
13	LJ	1362	0	1399	11	0
14	LL	1664	0	1773	3	0
15	LM	1120	0	1187	3	0
16	LN	1701	0	1749	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	LO	1655	0	1799	3	0
18	LP	1242	0	1269	5	0
19	LQ	1513	0	1628	3	0
20	LR	1566	0	1729	4	0
21	LS	1461	0	1502	3	0
22	LT	1298	0	1366	3	0
23	LU	808	0	831	7	0
24	LV	989	0	1047	2	0
25	LW	562	0	569	1	0
26	LX	967	0	1040	6	0
27	LY	1115	0	1205	1	0
28	LZ	1107	0	1182	3	0
29	La	1162	0	1213	5	0
30	Lb	898	0	983	2	0
31	Lc	770	0	809	3	0
32	Ld	888	0	930	4	0
33	Le	1053	0	1147	3	0
34	Lf	884	0	923	4	0
35	Lg	906	0	998	0	0
36	Lh	1015	0	1148	4	0
37	Li	832	0	917	1	0
38	Lj	705	0	737	3	0
39	Lk	569	0	637	0	0
40	Ll	444	0	482	3	0
41	Lm	432	0	471	1	0
42	Ln	240	0	289	0	0
43	Lo	864	0	929	2	0
44	Lp	708	0	756	2	0
45	Lr	1005	0	1072	5	0
46	NC	118	0	52	0	0
47	Pt	1597	0	817	13	0
48	S2	35736	0	18082	253	0
49	SA	1750	0	1755	7	0
50	SB	1806	0	1888	6	0
51	SC	1725	0	1813	8	0
52	SD	1756	0	1852	14	0
53	SE	2076	0	2177	15	0
54	SF	1495	0	1549	9	0
55	SG	1923	0	2089	12	0
56	SH	1517	0	1605	9	0
57	SI	1686	0	1772	6	0
58	SJ	1525	0	1640	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	SK	810	0	836	10	0
60	SL	1200	0	1271	5	0
61	SM	950	0	987	21	0
62	SN	1208	0	1293	3	0
63	SO	1010	0	1034	5	0
64	SP	1078	0	1121	7	0
65	SQ	1124	0	1193	7	0
66	SR	1083	0	1137	6	0
67	SS	1214	0	1275	7	0
68	ST	1103	0	1133	4	0
69	SU	803	0	873	17	0
70	SV	640	0	638	2	0
71	SW	1034	0	1080	6	0
72	SX	1088	0	1149	3	0
73	SY	1065	0	1142	11	0
74	SZ	683	0	761	1	0
75	Sa	792	0	841	5	0
76	Sb	651	0	672	3	0
77	Sc	512	0	541	3	0
78	Sd	459	0	448	4	0
79	Se	395	0	434	3	0
80	Sf	515	0	521	14	0
81	Sg	2436	0	2393	25	0
82	mR	133	0	66	0	0
83	L5	252	0	0	0	0
83	L7	6	0	0	0	0
83	L8	6	0	0	0	0
83	LB	2	0	0	0	0
83	LL	1	0	0	0	0
83	LN	2	0	0	0	0
83	LP	1	0	0	0	0
83	LQ	1	0	0	0	0
83	LV	1	0	0	0	0
83	La	1	0	0	0	0
83	Lo	1	0	0	0	0
83	Pt	1	0	0	0	0
83	S2	75	0	0	0	0
83	ST	1	0	0	0	0
83	Sd	1	0	0	0	0
84	L5	115	0	0	0	0
84	L7	3	0	0	0	0
84	L8	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	LA	3	0	0	0	0
84	LH	1	0	0	0	0
84	LI	1	0	0	0	0
84	LL	1	0	0	0	0
84	LN	1	0	0	0	0
84	Lb	1	0	0	0	0
84	Le	1	0	0	0	0
84	Lf	1	0	0	0	0
84	Lg	1	0	0	0	0
84	Ll	1	0	0	0	0
84	S2	31	0	0	0	0
84	SL	1	0	0	0	0
84	SO	1	0	0	0	0
85	L5	120	0	228	1	0
85	S2	20	0	38	0	0
86	L5	42	0	84	3	0
87	L5	16	0	24	1	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
89	L5	3376	0	0	1	0
89	L7	27	0	0	0	0
89	L8	86	0	0	1	0
89	LA	61	0	0	0	0
89	LB	48	0	0	0	0
89	LC	66	0	0	0	0
89	LD	2	0	0	0	0
89	LE	1	0	0	0	0
89	LF	22	0	0	0	0
89	LG	1	0	0	0	0
89	LI	23	0	0	0	0
89	LL	20	0	0	0	0
89	LN	57	0	0	0	0
89	LO	18	0	0	0	0
89	LP	32	0	0	0	0
89	LQ	28	0	0	0	0
89	LR	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	LS	5	0	0	0	0
89	LT	19	0	0	0	0
89	LV	21	0	0	0	0
89	LW	3	0	0	0	0
89	LX	5	0	0	0	0
89	LY	4	0	0	0	0
89	La	34	0	0	0	0
89	Lb	12	0	0	0	0
89	Lc	1	0	0	0	0
89	Ld	6	0	0	0	0
89	Le	42	0	0	0	0
89	Lf	15	0	0	0	0
89	Lg	18	0	0	0	0
89	Lh	3	0	0	0	0
89	Li	3	0	0	0	0
89	Lj	27	0	0	0	0
89	Ll	12	0	0	0	0
89	Lm	2	0	0	0	0
89	Ln	3	0	0	0	0
89	Lo	17	0	0	0	0
89	Lp	13	0	0	0	0
89	Lr	12	0	0	0	0
89	NC	4	0	0	0	0
89	Pt	6	0	0	0	0
89	S2	506	0	0	0	0
89	SA	1	0	0	0	0
89	SB	2	0	0	0	0
89	SC	2	0	0	0	0
89	SE	1	0	0	0	0
89	SI	1	0	0	0	0
89	SL	7	0	0	0	0
89	SN	9	0	0	0	0
89	SO	4	0	0	0	0
89	SW	5	0	0	0	0
89	SX	10	0	0	0	0
89	Sa	11	0	0	0	0
89	Sb	1	0	0	0	0
89	Sc	1	0	0	0	0
89	mR	1	0	0	0	0
All	All	216990	0	157848	1027	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 3.

The worst 5 of 1027 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)
1:L5:664:G:N2	1:L5:667:A:H61	1.60	0.98
1:L5:664:G:H21	1:L5:667:A:H61	1.16	0.92
1:L5:664:G:H21	1:L5:667:A:N6	1.71	0.89
50:SB:22:VAL:HG11	63:SO:84:ARG:HH22	1.37	0.89
1:L5:4108:G:H2'	1:L5:4109:G:C8	2.17	0.80

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	
4	LA	249/257 (97%)	246 (99%)	3 (1%)	0	100	100
5	LB	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
6	LC	364/427 (85%)	356 (98%)	8 (2%)	0	100	100
7	LD	292/297 (98%)	283 (97%)	8 (3%)	1 (0%)	36	42
8	LE	217/288 (75%)	206 (95%)	10 (5%)	1 (0%)	24	27
9	LF	223/248 (90%)	217 (97%)	5 (2%)	1 (0%)	30	34
10	LG	239/266 (90%)	230 (96%)	9 (4%)	0	100	100
11	LH	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
12	LI	211/214 (99%)	207 (98%)	4 (2%)	0	100	100
13	LJ	168/178 (94%)	163 (97%)	4 (2%)	1 (1%)	21	23
14	LL	204/211 (97%)	201 (98%)	3 (2%)	0	100	100
15	LM	134/215 (62%)	132 (98%)	2 (2%)	0	100	100
16	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	LO	200/203 (98%)	197 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LP	151/184 (82%)	148 (98%)	3 (2%)	0	100	100
19	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
20	LR	185/196 (94%)	185 (100%)	0	0	100	100
21	LS	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
22	LT	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
23	LU	97/128 (76%)	95 (98%)	2 (2%)	0	100	100
24	LV	131/140 (94%)	130 (99%)	1 (1%)	0	100	100
25	LW	64/157 (41%)	64 (100%)	0	0	100	100
26	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
27	LY	132/145 (91%)	128 (97%)	4 (3%)	0	100	100
28	LZ	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
29	La	145/148 (98%)	139 (96%)	4 (3%)	2 (1%)	9	7
30	Lb	106/159 (67%)	102 (96%)	4 (4%)	0	100	100
31	Lc	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
32	Ld	105/125 (84%)	105 (100%)	0	0	100	100
33	Le	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
34	Lf	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
38	Lj	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
39	Lk	67/70 (96%)	67 (100%)	0	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	49/128 (38%)	49 (100%)	0	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	124/137 (90%)	122 (98%)	2 (2%)	0	100	100
46	NC	4/19 (21%)	3 (75%)	1 (25%)	0	100	100
49	SA	221/295 (75%)	218 (99%)	3 (1%)	0	100	100
50	SB	219/264 (83%)	218 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	SC	220/293 (75%)	215 (98%)	5 (2%)	0	100	100
52	SD	224/243 (92%)	221 (99%)	3 (1%)	0	100	100
53	SE	260/263 (99%)	252 (97%)	7 (3%)	1 (0%)	30	34
54	SF	187/204 (92%)	175 (94%)	11 (6%)	1 (0%)	24	27
55	SG	235/249 (94%)	231 (98%)	4 (2%)	0	100	100
56	SH	187/194 (96%)	182 (97%)	5 (3%)	0	100	100
57	SI	204/208 (98%)	196 (96%)	7 (3%)	1 (0%)	24	27
58	SJ	183/194 (94%)	178 (97%)	5 (3%)	0	100	100
59	SK	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
60	SL	142/158 (90%)	139 (98%)	3 (2%)	0	100	100
61	SM	120/132 (91%)	114 (95%)	6 (5%)	0	100	100
62	SN	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
63	SO	133/151 (88%)	129 (97%)	4 (3%)	0	100	100
64	SP	129/145 (89%)	125 (97%)	4 (3%)	0	100	100
65	SQ	139/146 (95%)	131 (94%)	8 (6%)	0	100	100
66	SR	132/135 (98%)	125 (95%)	7 (5%)	0	100	100
67	SS	146/152 (96%)	143 (98%)	3 (2%)	0	100	100
68	ST	140/145 (97%)	139 (99%)	1 (1%)	0	100	100
69	SU	99/119 (83%)	97 (98%)	2 (2%)	0	100	100
70	SV	82/84 (98%)	81 (99%)	1 (1%)	0	100	100
71	SW	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
72	SX	137/143 (96%)	133 (97%)	4 (3%)	0	100	100
73	SY	129/133 (97%)	126 (98%)	3 (2%)	0	100	100
74	SZ	83/125 (66%)	80 (96%)	3 (4%)	0	100	100
75	Sa	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
76	Sb	81/84 (96%)	80 (99%)	1 (1%)	0	100	100
77	Sc	63/69 (91%)	61 (97%)	2 (3%)	0	100	100
78	Sd	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
79	Se	46/133 (35%)	45 (98%)	1 (2%)	0	100	100
80	Sf	61/156 (39%)	57 (93%)	4 (7%)	0	100	100
81	Sg	311/317 (98%)	294 (94%)	15 (5%)	2 (1%)	21	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11255/12782 (88%)	10982 (98%)	262 (2%)	11 (0%)	49	57

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	SI	131	PRO
8	LE	166	LYS
81	Sg	134	THR
7	LD	39	GLN
9	LF	237	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	193/199 (97%)	191 (99%)	2 (1%)	68	81
5	LB	347/348 (100%)	343 (99%)	4 (1%)	63	78
6	LC	305/348 (88%)	302 (99%)	3 (1%)	68	81
7	LD	247/250 (99%)	247 (100%)	0	100	100
8	LE	196/252 (78%)	196 (100%)	0	100	100
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	168 (99%)	1 (1%)	78	89
12	LI	180/181 (99%)	178 (99%)	2 (1%)	65	79
13	LJ	143/149 (96%)	142 (99%)	1 (1%)	76	87
14	LL	172/177 (97%)	171 (99%)	1 (1%)	78	89
15	LM	116/161 (72%)	115 (99%)	1 (1%)	70	84
16	LN	171/172 (99%)	170 (99%)	1 (1%)	78	89
17	LO	173/174 (99%)	171 (99%)	2 (1%)	63	78
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	LR	166/175 (95%)	164 (99%)	2 (1%)	63	78
21	LS	157/157 (100%)	157 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	89/115 (77%)	89 (100%)	0	100	100
24	LV	102/107 (95%)	102 (100%)	0	100	100
25	LW	58/126 (46%)	57 (98%)	1 (2%)	53	69
26	LX	106/133 (80%)	106 (100%)	0	100	100
27	LY	124/135 (92%)	123 (99%)	1 (1%)	73	85
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	84
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	90/125 (72%)	90 (100%)	0	100	100
31	Lc	84/97 (87%)	84 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	113 (99%)	1 (1%)	70	84
34	Lf	89/89 (100%)	88 (99%)	1 (1%)	65	79
35	Lg	98/100 (98%)	96 (98%)	2 (2%)	48	64
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	71 (97%)	2 (3%)	39	53
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	47/115 (41%)	47 (100%)	0	100	100
42	Ln	24/24 (100%)	24 (100%)	0	100	100
43	Lo	92/93 (99%)	92 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/120 (91%)	109 (100%)	0	100	100
46	NC	6/6 (100%)	6 (100%)	0	100	100
49	SA	184/242 (76%)	183 (100%)	1 (0%)	81	90
50	SB	202/231 (87%)	201 (100%)	1 (0%)	81	90
51	SC	188/225 (84%)	185 (98%)	3 (2%)	55	71
52	SD	189/202 (94%)	189 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	SE	224/225 (100%)	222 (99%)	2 (1%)	70	84
54	SF	159/170 (94%)	159 (100%)	0	100	100
55	SG	207/218 (95%)	205 (99%)	2 (1%)	68	81
56	SH	168/174 (97%)	168 (100%)	0	100	100
57	SI	178/180 (99%)	175 (98%)	3 (2%)	53	69
58	SJ	161/168 (96%)	161 (100%)	0	100	100
59	SK	87/136 (64%)	87 (100%)	0	100	100
60	SL	132/142 (93%)	132 (100%)	0	100	100
61	SM	104/108 (96%)	99 (95%)	5 (5%)	23	30
62	SN	130/131 (99%)	130 (100%)	0	100	100
63	SO	105/119 (88%)	105 (100%)	0	100	100
64	SP	117/130 (90%)	116 (99%)	1 (1%)	70	84
65	SQ	117/121 (97%)	116 (99%)	1 (1%)	70	84
66	SR	121/122 (99%)	119 (98%)	2 (2%)	53	69
67	SS	128/132 (97%)	127 (99%)	1 (1%)	73	85
68	ST	112/115 (97%)	112 (100%)	0	100	100
69	SU	93/107 (87%)	92 (99%)	1 (1%)	65	79
70	SV	67/67 (100%)	67 (100%)	0	100	100
71	SW	112/113 (99%)	112 (100%)	0	100	100
72	SX	111/114 (97%)	111 (100%)	0	100	100
73	SY	113/115 (98%)	113 (100%)	0	100	100
74	SZ	75/103 (73%)	74 (99%)	1 (1%)	61	76
75	Sa	86/98 (88%)	84 (98%)	2 (2%)	44	59
76	Sb	75/76 (99%)	75 (100%)	0	100	100
77	Sc	58/62 (94%)	58 (100%)	0	100	100
78	Sd	48/49 (98%)	48 (100%)	0	100	100
79	Se	40/104 (38%)	40 (100%)	0	100	100
80	Sf	56/140 (40%)	55 (98%)	1 (2%)	51	68
81	Sg	272/275 (99%)	269 (99%)	3 (1%)	65	79
All	All	9808/10856 (90%)	9748 (99%)	60 (1%)	76	89

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Lj	58	THR
75	Sa	82	LYS
53	SE	69	PHE
75	Sa	51	ARG
81	Sg	177	TRP

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

Mol	Chain	Res	Type
54	SF	179	ASN
67	SS	135	HIS
56	SH	168	HIS
61	SM	46	GLN
72	SX	92	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3528/5069 (69%)	447 (12%)	68 (1%)
2	L7	119/120 (99%)	7 (5%)	1 (0%)
3	L8	155/156 (99%)	18 (11%)	2 (1%)
47	Pt	74/75 (98%)	13 (17%)	0
48	S2	1667/1869 (89%)	205 (12%)	32 (1%)
82	mR	5/832 (0%)	0	0
All	All	5548/8121 (68%)	690 (12%)	103 (1%)

5 of 690 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	13	U
1	L5	25	A
1	L5	39	A
1	L5	42	A
1	L5	43	U

5 of 103 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4266	G
48	S2	55	U
48	S2	1556	A

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Mol	Chain	Res	Type
1	L5	4626	A
1	L5	4965	U

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

229 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	$\# Z > 2$
48	A2M	S2	576	48	22,25,26	1.32	2 (9%)	30,36,39	1.46	6 (20%)
48	PSU	S2	573	48	18,21,22	1.01	2 (11%)	21,30,33	1.52	4 (19%)
1	OMC	L5	2351	83,1	19,22,23	0.86	1 (5%)	25,31,34	0.76	0
1	PSU	L5	1781	1	18,21,22	1.02	1 (5%)	21,30,33	1.58	4 (19%)
1	PSU	L5	3884	1	18,21,22	1.10	1 (5%)	21,30,33	1.40	4 (19%)
48	A2M	S2	484	48	22,25,26	1.08	1 (4%)	30,36,39	1.25	3 (10%)
1	PSU	L5	4293	1	18,21,22	0.83	0	21,30,33	1.44	3 (14%)
1	A2M	L5	3830	1	22,25,26	1.20	2 (9%)	30,36,39	1.28	5 (16%)
47	H2U	Pt	20	47	18,21,22	0.53	0	19,30,33	1.09	1 (5%)
48	OMG	S2	644	48	23,26,27	0.62	0	32,38,41	0.67	0
1	PSU	L5	1792	84,1	18,21,22	0.92	1 (5%)	21,30,33	1.46	4 (19%)
1	OMG	L5	4637	84,1	23,26,27	0.70	0	32,38,41	0.58	0
1	OMG	L5	4499	1	23,26,27	0.64	0	32,38,41	0.61	0
48	A2M	S2	468	48	22,25,26	1.28	2 (9%)	30,36,39	1.47	6 (20%)
48	PSU	S2	1445	48	18,21,22	1.01	1 (5%)	21,30,33	1.54	4 (19%)
1	PSU	L5	2843	1	18,21,22	1.45	2 (11%)	21,30,33	1.74	5 (23%)
1	OMG	L5	4196	47,1	23,26,27	0.77	0	32,38,41	0.54	0
1	OMG	L5	1522	1	23,26,27	0.69	0	32,38,41	0.71	1 (3%)
1	OMC	L5	4536	1	19,22,23	0.84	1 (5%)	25,31,34	0.61	0
1	PSU	L5	1744	84,1	18,21,22	0.76	0	21,30,33	1.63	4 (19%)
48	OMU	S2	121	48	19,22,23	0.60	0	25,31,34	1.28	5 (20%)
1	PSU	L5	4521	84,83,1	18,21,22	1.19	2 (11%)	21,30,33	1.53	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L5	3770	1	18,21,22	0.89	1 (5%)	21,30,33	1.46	4 (19%)
1	PSU	L5	1582	1	18,21,22	1.12	1 (5%)	21,30,33	1.48	4 (19%)
48	A2M	S2	166	48	22,25,26	1.20	1 (4%)	30,36,39	1.53	9 (30%)
1	OMG	L5	4618	84,1	23,26,27	0.62	0	32,38,41	0.62	0
1	A2M	L5	3867	1	22,25,26	1.38	3 (13%)	30,36,39	1.36	4 (13%)
1	A2M	L5	2401	1	22,25,26	1.26	2 (9%)	30,36,39	1.31	3 (10%)
1	A2M	L5	3760	48,1	22,25,26	1.37	3 (13%)	30,36,39	1.69	10 (33%)
1	OMG	L5	3944	1	23,26,27	0.53	0	32,38,41	0.43	0
1	OMG	L5	3899	83,1	23,26,27	0.82	0	32,38,41	0.77	0
48	UY1	S2	1326	83,48	19,22,23	4.14	7 (36%)	21,31,34	2.41	6 (28%)
47	PSU	Pt	55	47	18,21,22	1.18	3 (16%)	21,30,33	1.46	4 (19%)
48	OMC	S2	174	83,48	19,22,23	0.62	0	25,31,34	0.59	0
1	PSU	L5	1782	1	18,21,22	0.90	0	21,30,33	1.58	4 (19%)
1	OMU	L5	4227	1	19,22,23	0.59	0	25,31,34	1.43	6 (24%)
48	PSU	S2	1177	48	18,21,22	1.05	1 (5%)	21,30,33	1.59	4 (19%)
48	PSU	S2	105	48	18,21,22	1.00	1 (5%)	21,30,33	1.58	4 (19%)
1	UY1	L5	3818	84,1	19,22,23	3.93	8 (42%)	21,31,34	2.10	5 (23%)
1	PSU	L5	2839	1	18,21,22	1.14	3 (16%)	21,30,33	1.68	4 (19%)
1	PSU	L5	3758	1	18,21,22	1.06	2 (11%)	21,30,33	1.54	4 (19%)
48	PSU	S2	1238	48	18,21,22	0.96	1 (5%)	21,30,33	1.53	4 (19%)
48	PSU	S2	918	48	18,21,22	1.00	2 (11%)	21,30,33	1.72	5 (23%)
1	PSU	L5	4579	1	18,21,22	1.06	2 (11%)	21,30,33	1.42	4 (19%)
3	OMU	L8	14	3,1,84	19,22,23	0.54	0	25,31,34	1.28	5 (20%)
1	PSU	L5	3768	1	18,21,22	0.84	1 (5%)	21,30,33	1.53	4 (19%)
1	OMG	L5	4370	1	23,26,27	0.74	0	32,38,41	0.59	1 (3%)
48	MA6	S2	1850	48	23,26,27	1.42	4 (17%)	33,38,41	2.83	12 (36%)
1	OMC	L5	3841	1	19,22,23	0.83	1 (5%)	25,31,34	0.65	0
48	PSU	S2	814	48	18,21,22	0.96	1 (5%)	21,30,33	1.59	4 (19%)
1	A2M	L5	3724	1	22,25,26	1.35	3 (13%)	30,36,39	1.45	6 (20%)
1	PSU	L5	1779	1	18,21,22	0.98	1 (5%)	21,30,33	1.61	4 (19%)
1	PSU	L5	4471	1	18,21,22	1.11	3 (16%)	21,30,33	1.64	4 (19%)
48	MA6	S2	1851	48	23,26,27	1.41	4 (17%)	33,38,41	2.93	13 (39%)
72	HY3	SX	62	72	7,8,9	6.63	5 (71%)	7,10,12	1.35	1 (14%)
1	PSU	L5	4500	1	18,21,22	0.97	1 (5%)	21,30,33	1.63	4 (19%)
1	PSU	L5	3844	1	18,21,22	1.08	2 (11%)	21,30,33	1.54	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	L5	4296	1	18,21,22	0.98	1 (5%)	21,30,33	1.56	4 (19%)
1	OMU	L5	4498	84,83,1	19,22,23	0.67	0	25,31,34	1.30	3 (12%)
48	OMU	S2	428	48	19,22,23	0.77	1 (5%)	25,31,34	1.26	4 (16%)
1	OMG	L5	4392	1	23,26,27	0.79	0	32,38,41	0.48	0
1	OMC	L5	3701	84,1	19,22,23	0.84	1 (5%)	25,31,34	0.70	0
48	PSU	S2	218	48	18,21,22	0.92	1 (5%)	21,30,33	1.48	4 (19%)
48	PSU	S2	1004	48	18,21,22	0.93	1 (5%)	21,30,33	1.57	4 (19%)
1	PSU	L5	3764	1	18,21,22	1.36	2 (11%)	21,30,33	1.52	4 (19%)
48	A2M	S2	159	48	22,25,26	1.28	2 (9%)	30,36,39	1.57	6 (20%)
48	PSU	S2	649	48	18,21,22	1.00	1 (5%)	21,30,33	1.49	4 (19%)
48	PSU	S2	34	48	18,21,22	1.01	1 (5%)	21,30,33	1.55	4 (19%)
1	A2M	L5	2815	83,1	22,25,26	1.19	2 (9%)	30,36,39	1.37	4 (13%)
48	PSU	S2	609	48	18,21,22	0.93	1 (5%)	21,30,33	1.57	4 (19%)
1	OMU	L5	2415	1	19,22,23	0.55	0	25,31,34	1.27	4 (16%)
47	PSU	Pt	13	47	18,21,22	1.11	1 (5%)	21,30,33	1.61	4 (19%)
1	A2M	L5	1524	1	22,25,26	1.30	1 (4%)	30,36,39	1.38	6 (20%)
48	PSU	S2	1643	83,48	18,21,22	0.97	2 (11%)	21,30,33	1.56	4 (19%)
48	A2M	S2	1031	48	22,25,26	1.24	2 (9%)	30,36,39	1.25	5 (16%)
1	PSU	L5	3851	1	18,21,22	0.93	1 (5%)	21,30,33	1.66	4 (19%)
1	PSU	L5	3734	1	18,21,22	1.07	2 (11%)	21,30,33	1.68	5 (23%)
1	PSU	L5	4531	1	18,21,22	0.80	1 (5%)	21,30,33	1.64	4 (19%)
1	PSU	L5	3639	1	18,21,22	1.37	3 (16%)	21,30,33	1.58	4 (19%)
48	PSU	S2	1174	84,48	18,21,22	0.93	2 (11%)	21,30,33	1.68	4 (19%)
43	MLZ	Lo	53	43	8,9,10	0.64	0	4,9,11	0.73	0
1	PSU	L5	4361	1	18,21,22	0.94	1 (5%)	21,30,33	1.66	4 (19%)
48	PSU	S2	1056	48	18,21,22	0.97	1 (5%)	21,30,33	1.54	4 (19%)
1	6MZ	L5	4220	1	22,25,26	3.86	12 (54%)	29,36,39	2.55	11 (37%)
48	PSU	S2	93	48	18,21,22	0.89	1 (5%)	21,30,33	1.51	4 (19%)
48	PSU	S2	681	48	18,21,22	1.19	2 (11%)	21,30,33	1.60	4 (19%)
30	MLZ	Lb	5	84,30	8,9,10	0.80	0	4,9,11	0.78	0
1	PSU	L5	2632	1	18,21,22	0.90	0	21,30,33	1.46	4 (19%)
1	A2M	L5	1871	83,1	22,25,26	1.31	3 (13%)	30,36,39	1.41	6 (20%)
1	OMG	L5	1625	84,1	23,26,27	0.73	0	32,38,41	0.70	0
1	A2M	L5	398	1	22,25,26	1.19	2 (9%)	30,36,39	1.40	6 (20%)
48	PSU	S2	1136	48	18,21,22	1.05	1 (5%)	21,30,33	1.66	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
48	PSU	S2	1244	48	18,21,22	1.02	1 (5%)	21,30,33	1.63	4 (19%)
48	B8N	S2	1248	48	25,29,30	0.67	0	28,42,45	1.11	3 (10%)
48	PSU	S2	296	48	18,21,22	0.84	0	21,30,33	1.55	4 (19%)
1	PSU	L5	4673	83,1	18,21,22	0.93	2 (11%)	21,30,33	1.56	4 (19%)
1	OMG	L5	3627	1	23,26,27	0.81	0	32,38,41	0.74	1 (3%)
1	PSU	L5	5001	1	18,21,22	0.98	1 (5%)	21,30,33	1.63	4 (19%)
48	PSU	S2	866	48	18,21,22	0.97	1 (5%)	21,30,33	1.56	4 (19%)
1	OMG	L5	3744	1	23,26,27	0.66	0	32,38,41	0.55	0
1	PSU	L5	1862	1	18,21,22	0.92	1 (5%)	21,30,33	1.79	4 (19%)
1	OMG	L5	3792	1	23,26,27	0.71	0	32,38,41	0.50	0
1	A2M	L5	1534	83,1	22,25,26	1.54	3 (13%)	30,36,39	1.51	5 (16%)
48	PSU	S2	119	48	18,21,22	1.07	1 (5%)	21,30,33	1.39	4 (19%)
48	PSU	S2	651	48	18,21,22	0.92	1 (5%)	21,30,33	1.65	4 (19%)
1	PSU	L5	1536	1	18,21,22	1.33	1 (5%)	21,30,33	1.67	4 (19%)
1	PSU	L5	4457	1	18,21,22	1.06	2 (11%)	21,30,33	1.61	4 (19%)
1	A2M	L5	3718	1	22,25,26	1.19	2 (9%)	30,36,39	1.35	4 (13%)
48	A2M	S2	1383	48	22,25,26	1.12	1 (4%)	30,36,39	1.40	6 (20%)
1	PSU	L5	4493	84,1	18,21,22	1.02	2 (11%)	21,30,33	1.69	4 (19%)
48	OMU	S2	627	48	19,22,23	0.60	0	25,31,34	1.30	3 (12%)
48	PSU	S2	109	48	18,21,22	0.92	0	21,30,33	1.53	4 (19%)
48	PSU	S2	822	48	18,21,22	1.02	1 (5%)	21,30,33	1.60	5 (23%)
1	OMC	L5	2365	1	19,22,23	0.80	1 (5%)	25,31,34	0.63	0
1	OMG	L5	4228	1	23,26,27	0.68	0	32,38,41	0.56	0
48	PSU	S2	572	48	18,21,22	1.01	1 (5%)	21,30,33	1.47	4 (19%)
1	PSU	L5	2508	1	18,21,22	1.04	2 (11%)	21,30,33	1.64	5 (23%)
1	PSU	L5	4423	1	18,21,22	0.94	1 (5%)	21,30,33	1.66	4 (19%)
48	A2M	S2	512	48	22,25,26	1.20	3 (13%)	30,36,39	1.40	4 (13%)
1	A2M	L5	1326	1	22,25,26	1.31	2 (9%)	30,36,39	1.34	6 (20%)
1	A2M	L5	3785	1	22,25,26	1.46	2 (9%)	30,36,39	1.49	7 (23%)
48	PSU	S2	406	48	18,21,22	0.90	1 (5%)	21,30,33	1.53	4 (19%)
48	OMC	S2	517	48	19,22,23	0.66	0	25,31,34	0.64	0
1	PSU	L5	1677	1	18,21,22	1.35	3 (16%)	21,30,33	1.69	5 (23%)
48	PSU	S2	1243	48	18,21,22	1.07	1 (5%)	21,30,33	1.58	4 (19%)
47	5MC	Pt	49	47	19,22,23	3.76	8 (42%)	26,32,35	1.07	2 (7%)
48	A2M	S2	27	83,48	22,25,26	1.25	2 (9%)	30,36,39	1.35	8 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	L5	4523	83,1	22,25,26	1.35	3 (13%)	30,36,39	1.39	5 (16%)
48	OMU	S2	116	48	19,22,23	0.55	0	25,31,34	1.13	1 (4%)
1	OMU	L5	3925	1	19,22,23	0.68	0	25,31,34	1.39	4 (16%)
48	PSU	S2	686	48	18,21,22	0.94	1 (5%)	21,30,33	1.50	4 (19%)
47	2MU	Pt	54	47	20,23,24	1.15	2 (10%)	27,33,36	1.94	7 (25%)
1	PSU	L5	4299	1	18,21,22	0.92	0	21,30,33	1.60	4 (19%)
1	5MC	L5	4447	84,1	19,22,23	3.50	8 (42%)	26,32,35	1.48	4 (15%)
1	PSU	L5	4636	1	18,21,22	0.92	1 (5%)	21,30,33	1.56	5 (23%)
48	OMU	S2	1804	48	19,22,23	0.72	0	25,31,34	1.34	4 (16%)
48	A2M	S2	668	83,48	22,25,26	1.52	2 (9%)	30,36,39	1.36	5 (16%)
48	PSU	S2	966	48	18,21,22	0.93	1 (5%)	21,30,33	1.51	4 (19%)
1	PSU	L5	4431	1	18,21,22	1.03	1 (5%)	21,30,33	1.65	4 (19%)
48	OMG	S2	601	48	23,26,27	0.64	0	32,38,41	0.47	0
1	OMG	L5	2424	1	23,26,27	0.62	0	32,38,41	0.45	0
1	PSU	L5	4972	84,1	18,21,22	1.08	2 (11%)	21,30,33	1.51	4 (19%)
1	A2M	L5	4590	1	22,25,26	1.10	2 (9%)	30,36,39	1.42	5 (16%)
1	PSU	L5	3695	84,1	18,21,22	1.00	2 (11%)	21,30,33	1.62	4 (19%)
1	PSU	L5	4312	1	18,21,22	0.85	0	21,30,33	1.54	4 (19%)
1	OMG	L5	4623	1	23,26,27	0.65	0	32,38,41	0.64	0
48	PSU	S2	815	48	18,21,22	0.84	1 (5%)	21,30,33	1.57	4 (19%)
48	PSU	S2	1692	48	18,21,22	1.06	1 (5%)	21,30,33	1.43	4 (19%)
48	4AC	S2	1842	48	21,24,25	3.09	11 (52%)	28,34,37	1.23	4 (14%)
1	PSU	L5	4403	1	18,21,22	1.01	1 (5%)	21,30,33	1.68	4 (19%)
1	PSU	L5	3637	84,1	18,21,22	1.12	1 (5%)	21,30,33	1.72	4 (19%)
1	PSU	L5	1860	1	18,21,22	0.77	0	21,30,33	1.64	4 (19%)
48	6MZ	S2	1832	84,83,48	22,25,26	3.75	10 (45%)	29,36,39	2.69	12 (41%)
3	PSU	L8	69	3	18,21,22	0.98	1 (5%)	21,30,33	1.60	4 (19%)
48	OMU	S2	354	48	19,22,23	0.57	0	25,31,34	1.42	6 (24%)
1	OMG	L5	2876	1	23,26,27	0.72	0	32,38,41	0.77	0
1	OMG	L5	2364	1	23,26,27	0.77	0	32,38,41	0.60	0
48	PSU	S2	1367	48	18,21,22	0.92	1 (5%)	21,30,33	1.53	4 (19%)
1	OMC	L5	4456	1	19,22,23	0.86	1 (5%)	25,31,34	0.55	0
48	OMU	S2	1288	48	19,22,23	0.85	2 (10%)	25,31,34	1.28	4 (16%)
1	PSU	L5	3853	84,83,1	18,21,22	1.04	1 (5%)	21,30,33	1.45	5 (23%)
47	2MG	Pt	10	47	23,26,27	1.30	2 (8%)	33,38,41	1.39	4 (12%)
1	PSU	L5	4689	1	18,21,22	0.88	1 (5%)	21,30,33	1.55	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
48	OMG	S2	683	48	23,26,27	0.60	0	32,38,41	0.66	0
1	A2M	L5	3723	1	22,25,26	1.19	1 (4%)	30,36,39	1.43	8 (26%)
1	OMC	L5	1881	83,1	19,22,23	0.78	1 (5%)	25,31,34	0.72	0
48	PSU	S2	1625	48	18,21,22	1.04	1 (5%)	21,30,33	1.56	4 (19%)
3	OMG	L8	75	3	23,26,27	0.60	0	32,38,41	0.60	0
48	4AC	S2	1337	48	21,24,25	3.23	11 (52%)	28,34,37	0.98	1 (3%)
1	OMC	L5	2824	1	19,22,23	0.72	0	25,31,34	0.80	1 (4%)
48	OMG	S2	1447	48	23,26,27	0.49	0	32,38,41	0.55	0
1	OMC	L5	2804	1	19,22,23	0.76	1 (5%)	25,31,34	0.66	0
1	A2M	L5	3825	1	22,25,26	1.26	2 (9%)	30,36,39	1.33	6 (20%)
48	OMG	S2	1490	83,48	23,26,27	0.67	0	32,38,41	0.48	0
48	OMG	S2	1328	48	23,26,27	0.60	0	32,38,41	0.45	0
1	OMC	L5	3808	1	19,22,23	0.75	0	25,31,34	0.49	0
1	PSU	L5	4576	1	18,21,22	0.89	0	21,30,33	1.64	4 (19%)
48	G7M	S2	1639	48,47	23,26,27	2.59	7 (30%)	34,39,42	2.44	9 (26%)
48	A2M	S2	590	48	22,25,26	1.29	2 (9%)	30,36,39	1.44	6 (20%)
1	PSU	L5	4532	1	18,21,22	1.35	2 (11%)	21,30,33	1.48	4 (19%)
1	PSU	L5	1683	84,1	18,21,22	1.12	2 (11%)	21,30,33	1.64	4 (19%)
1	OMU	L5	2837	1	19,22,23	0.62	0	25,31,34	1.48	5 (20%)
1	PSU	L5	3920	83,1	18,21,22	1.14	1 (5%)	21,30,33	1.66	4 (19%)
1	PSU	L5	4353	1	18,21,22	0.91	1 (5%)	21,30,33	1.59	4 (19%)
48	A2M	S2	1678	48	22,25,26	1.28	3 (13%)	30,36,39	1.53	7 (23%)
48	OMU	S2	172	48	19,22,23	0.61	0	25,31,34	1.38	5 (20%)
1	PSU	L5	4552	1	18,21,22	1.24	2 (11%)	21,30,33	1.61	4 (19%)
1	PSU	L5	3715	1	18,21,22	1.01	1 (5%)	21,30,33	1.60	4 (19%)
1	OMC	L5	3887	1	19,22,23	0.76	0	25,31,34	0.63	1 (4%)
48	PSU	S2	1239	48	18,21,22	1.09	1 (5%)	21,30,33	1.52	4 (19%)
1	OMC	L5	2422	83,1	19,22,23	0.73	0	25,31,34	0.60	0
48	OMU	S2	1442	48	19,22,23	0.58	0	25,31,34	1.30	5 (20%)
48	OMC	S2	1703	84,48	19,22,23	0.72	0	25,31,34	0.50	0
1	UR3	L5	4530	1	19,22,23	2.68	6 (31%)	26,32,35	1.62	4 (15%)
3	PSU	L8	55	3	18,21,22	0.99	2 (11%)	21,30,33	1.54	4 (19%)
1	PSU	L5	4569	1	18,21,22	1.21	2 (11%)	21,30,33	1.43	4 (19%)
48	OMG	S2	509	48	23,26,27	0.57	0	32,38,41	0.57	0
48	PSU	S2	1081	48	18,21,22	1.12	3 (16%)	21,30,33	1.65	5 (23%)
48	OMG	S2	867	48	23,26,27	0.54	0	32,38,41	0.44	0
48	PSU	S2	36	48	18,21,22	0.88	1 (5%)	21,30,33	1.64	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	L5	2363	83,1	22,25,26	1.20	2 (9%)	30,36,39	1.28	5 (16%)
5	HIC	LB	245	5	10,11,12	0.68	0	9,14,16	0.50	0
48	PSU	S2	863	48	18,21,22	0.98	1 (5%)	21,30,33	1.59	4 (19%)
1	1MA	L5	1322	83,1	21,25,26	0.84	1 (4%)	30,37,40	0.84	1 (3%)
1	PSU	L5	4442	1	18,21,22	0.99	1 (5%)	21,30,33	1.56	4 (19%)
48	PSU	S2	1232	48	18,21,22	0.99	1 (5%)	21,30,33	1.67	4 (19%)
1	OMC	L5	1340	1	19,22,23	0.80	1 (5%)	25,31,34	0.78	0
48	OMC	S2	1391	48	19,22,23	0.65	0	25,31,34	0.50	0
1	OMC	L5	2861	1	19,22,23	0.64	0	25,31,34	0.62	0
48	A2M	S2	99	83,48	22,25,26	1.19	2 (9%)	30,36,39	1.33	5 (16%)
1	PSU	L5	5010	1	18,21,22	0.86	1 (5%)	21,30,33	1.52	4 (19%)
1	A2M	L5	4571	1	22,25,26	1.44	3 (13%)	30,36,39	1.52	5 (16%)
48	OMC	S2	462	48	19,22,23	0.61	0	25,31,34	0.58	0
48	OMG	S2	436	48	23,26,27	0.66	0	32,38,41	0.61	0
1	A2M	L5	400	1	22,25,26	1.39	3 (13%)	30,36,39	1.37	6 (20%)
1	A2M	L5	2787	1	22,25,26	1.25	1 (4%)	30,36,39	1.35	2 (6%)
1	PSU	L5	3762	1	18,21,22	1.07	1 (5%)	21,30,33	1.36	4 (19%)
1	PSU	L5	4628	1	18,21,22	1.07	1 (5%)	21,30,33	1.58	4 (19%)
1	OMU	L5	4306	1	19,22,23	0.60	0	25,31,34	1.37	5 (20%)
1	OMC	L5	3869	1	19,22,23	0.75	1 (5%)	25,31,34	0.56	0
1	PSU	L5	4420	1	18,21,22	1.08	3 (16%)	21,30,33	1.40	4 (19%)
1	OMU	L5	4620	1	19,22,23	0.55	0	25,31,34	1.31	5 (20%)
1	5MC	L5	3782	83,1	19,22,23	3.61	8 (42%)	26,32,35	1.26	3 (11%)
48	PSU	S2	801	48	18,21,22	1.00	1 (5%)	21,30,33	1.60	4 (19%)
41	M3L	Lm	98	41	10,11,12	0.53	0	9,14,16	0.52	0
1	PSU	L5	3729	1	18,21,22	1.04	1 (5%)	21,30,33	1.56	4 (19%)
1	OMG	L5	1316	1	23,26,27	0.82	0	32,38,41	0.73	1 (3%)
1	OMG	L5	4494	1	23,26,27	0.66	0	32,38,41	0.61	0
48	PSU	S2	1347	48	18,21,22	0.93	1 (5%)	21,30,33	1.69	4 (19%)

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
48	A2M	S2	576	48	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	PSU	S2	573	48	-	1/7/25/26	0/2/2/2
1	OMC	L5	2351	83,1	-	2/9/27/28	0/2/2/2
1	PSU	L5	1781	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3884	1	-	0/7/25/26	0/2/2/2
48	A2M	S2	484	48	-	0/9/27/28	0/3/3/3
1	PSU	L5	4293	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	3830	1	-	0/9/27/28	0/3/3/3
47	H2U	Pt	20	47	-	3/7/38/39	0/2/2/2
48	OMG	S2	644	48	-	3/9/27/28	0/3/3/3
1	PSU	L5	1792	84,1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4637	84,1	-	1/9/27/28	0/3/3/3
1	OMG	L5	4499	1	-	0/9/27/28	0/3/3/3
48	A2M	S2	468	48	-	0/9/27/28	0/3/3/3
48	PSU	S2	1445	48	-	1/7/25/26	0/2/2/2
1	PSU	L5	2843	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4196	47,1	-	1/9/27/28	0/3/3/3
1	OMG	L5	1522	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	4536	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1744	84,1	-	0/7/25/26	0/2/2/2
48	OMU	S2	121	48	-	0/9/27/28	0/2/2/2
1	PSU	L5	4521	84,83,1	-	2/7/25/26	0/2/2/2
1	PSU	L5	3770	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1582	1	-	0/7/25/26	0/2/2/2
48	A2M	S2	166	48	-	0/9/27/28	0/3/3/3
1	OMG	L5	4618	84,1	-	0/9/27/28	0/3/3/3
1	A2M	L5	3867	1	-	1/9/27/28	0/3/3/3
1	A2M	L5	2401	1	-	0/9/27/28	0/3/3/3
1	A2M	L5	3760	48,1	-	4/9/27/28	0/3/3/3
1	OMG	L5	3944	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	3899	83,1	-	0/9/27/28	0/3/3/3
48	UY1	S2	1326	83,48	-	1/9/27/28	0/2/2/2
47	PSU	Pt	55	47	-	0/7/25/26	0/2/2/2
48	OMC	S2	174	83,48	-	0/9/27/28	0/2/2/2
1	PSU	L5	1782	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	4227	1	-	0/9/27/28	0/2/2/2
48	PSU	S2	1177	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	105	48	-	0/7/25/26	0/2/2/2
1	UY1	L5	3818	84,1	-	2/9/27/28	0/2/2/2
1	PSU	L5	2839	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3758	1	-	0/7/25/26	0/2/2/2
48	PSU	S2	1238	48	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	PSU	S2	918	48	-	0/7/25/26	0/2/2/2
1	PSU	L5	4579	1	-	0/7/25/26	0/2/2/2
3	OMU	L8	14	3,1,84	-	1/9/27/28	0/2/2/2
1	PSU	L5	3768	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4370	1	-	0/9/27/28	0/3/3/3
48	MA6	S2	1850	48	-	0/11/29/30	0/3/3/3
1	OMC	L5	3841	1	-	0/9/27/28	0/2/2/2
48	PSU	S2	814	48	-	0/7/25/26	0/2/2/2
1	A2M	L5	3724	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1779	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4471	1	-	0/7/25/26	0/2/2/2
48	MA6	S2	1851	48	-	3/11/29/30	0/3/3/3
72	HY3	SX	62	72	-	1/1/12/14	0/1/1/1
1	PSU	L5	4500	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	3844	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	4296	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	4498	84,83,1	-	0/9/27/28	0/2/2/2
48	OMU	S2	428	48	-	2/9/27/28	0/2/2/2
1	OMG	L5	4392	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	3701	84,1	-	4/9/27/28	0/2/2/2
48	PSU	S2	218	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	1004	48	-	0/7/25/26	0/2/2/2
1	PSU	L5	3764	1	-	3/7/25/26	0/2/2/2
48	A2M	S2	159	48	-	1/9/27/28	0/3/3/3
48	PSU	S2	649	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	34	48	-	0/7/25/26	0/2/2/2
1	A2M	L5	2815	83,1	-	3/9/27/28	0/3/3/3
48	PSU	S2	609	48	-	0/7/25/26	0/2/2/2
1	OMU	L5	2415	1	-	0/9/27/28	0/2/2/2
47	PSU	Pt	13	47	-	0/7/25/26	0/2/2/2
1	A2M	L5	1524	1	-	0/9/27/28	0/3/3/3
48	PSU	S2	1643	83,48	-	0/7/25/26	0/2/2/2
48	A2M	S2	1031	48	-	0/9/27/28	0/3/3/3
1	PSU	L5	3851	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	3734	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4531	1	-	1/7/25/26	0/2/2/2
1	PSU	L5	3639	1	-	0/7/25/26	0/2/2/2
48	PSU	S2	1174	84,48	-	0/7/25/26	0/2/2/2
43	MLZ	Lo	53	43	-	0/7/8/10	-
1	PSU	L5	4361	1	-	0/7/25/26	0/2/2/2
48	PSU	S2	1056	48	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	6MZ	L5	4220	1	-	0/9/27/28	0/3/3/3
48	PSU	S2	93	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	681	48	-	0/7/25/26	0/2/2/2
30	MLZ	Lb	5	84,30	-	1/7/8/10	-
1	PSU	L5	2632	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	1871	83,1	-	0/9/27/28	0/3/3/3
1	OMG	L5	1625	84,1	-	2/9/27/28	0/3/3/3
1	A2M	L5	398	1	-	1/9/27/28	0/3/3/3
48	PSU	S2	1136	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	1244	48	-	0/7/25/26	0/2/2/2
48	B8N	S2	1248	48	-	5/16/34/35	0/2/2/2
48	PSU	S2	296	48	-	0/7/25/26	0/2/2/2
1	PSU	L5	4673	83,1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3627	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	5001	1	-	0/7/25/26	0/2/2/2
48	PSU	S2	866	48	-	0/7/25/26	0/2/2/2
1	OMG	L5	3744	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1862	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3792	1	-	0/9/27/28	0/3/3/3
1	A2M	L5	1534	83,1	-	1/9/27/28	0/3/3/3
48	PSU	S2	119	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	651	48	-	0/7/25/26	0/2/2/2
1	PSU	L5	1536	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4457	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	3718	1	-	0/9/27/28	0/3/3/3
48	A2M	S2	1383	48	-	0/9/27/28	0/3/3/3
1	PSU	L5	4493	84,1	-	0/7/25/26	0/2/2/2
48	OMU	S2	627	48	-	0/9/27/28	0/2/2/2
48	PSU	S2	109	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	822	48	-	0/7/25/26	0/2/2/2
1	OMC	L5	2365	1	-	1/9/27/28	0/2/2/2
1	OMG	L5	4228	1	-	1/9/27/28	0/3/3/3
48	PSU	S2	572	48	-	0/7/25/26	0/2/2/2
1	PSU	L5	2508	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4423	1	-	0/7/25/26	0/2/2/2
48	A2M	S2	512	48	-	1/9/27/28	0/3/3/3
1	A2M	L5	1326	1	-	1/9/27/28	0/3/3/3
1	A2M	L5	3785	1	-	1/9/27/28	0/3/3/3
48	PSU	S2	406	48	-	0/7/25/26	0/2/2/2
48	OMC	S2	517	48	-	0/9/27/28	0/2/2/2
1	PSU	L5	1677	1	-	4/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	PSU	S2	1243	48	-	3/7/25/26	0/2/2/2
47	5MC	Pt	49	47	-	0/7/25/26	0/2/2/2
48	A2M	S2	27	83,48	-	0/9/27/28	0/3/3/3
1	A2M	L5	4523	83,1	-	0/9/27/28	0/3/3/3
48	OMU	S2	116	48	-	0/9/27/28	0/2/2/2
1	OMU	L5	3925	1	-	0/9/27/28	0/2/2/2
48	PSU	S2	686	48	-	0/7/25/26	0/2/2/2
47	2MU	Pt	54	47	-	1/9/27/28	0/2/2/2
1	PSU	L5	4299	1	-	0/7/25/26	0/2/2/2
1	5MC	L5	4447	84,1	-	4/7/25/26	0/2/2/2
1	PSU	L5	4636	1	-	3/7/25/26	0/2/2/2
48	OMU	S2	1804	48	-	0/9/27/28	0/2/2/2
48	A2M	S2	668	83,48	-	2/9/27/28	0/3/3/3
48	PSU	S2	966	48	-	0/7/25/26	0/2/2/2
1	PSU	L5	4431	1	-	0/7/25/26	0/2/2/2
48	OMG	S2	601	48	-	1/9/27/28	0/3/3/3
1	OMG	L5	2424	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	4972	84,1	-	0/7/25/26	0/2/2/2
1	A2M	L5	4590	1	-	1/9/27/28	0/3/3/3
1	PSU	L5	3695	84,1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4312	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4623	1	-	0/9/27/28	0/3/3/3
48	PSU	S2	815	48	-	0/7/25/26	0/2/2/2
48	PSU	S2	1692	48	-	0/7/25/26	0/2/2/2
48	4AC	S2	1842	48	-	0/11/29/30	0/2/2/2
1	PSU	L5	4403	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3637	84,1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1860	1	-	0/7/25/26	0/2/2/2
48	6MZ	S2	1832	84,83,48	-	0/9/27/28	0/3/3/3
3	PSU	L8	69	3	-	0/7/25/26	0/2/2/2
48	OMU	S2	354	48	-	0/9/27/28	0/2/2/2
1	OMG	L5	2876	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	2364	1	-	1/9/27/28	0/3/3/3
48	PSU	S2	1367	48	-	0/7/25/26	0/2/2/2
1	OMC	L5	4456	1	-	0/9/27/28	0/2/2/2
48	OMU	S2	1288	48	-	0/9/27/28	0/2/2/2
1	PSU	L5	3853	84,83,1	-	0/7/25/26	0/2/2/2
47	2MG	Pt	10	47	-	0/9/27/28	0/3/3/3
1	PSU	L5	4689	1	-	0/7/25/26	0/2/2/2
48	OMG	S2	683	48	-	1/9/27/28	0/3/3/3
1	A2M	L5	3723	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	L5	1881	83,1	-	0/9/27/28	0/2/2/2
48	PSU	S2	1625	48	-	0/7/25/26	0/2/2/2
3	OMG	L8	75	3	-	1/9/27/28	0/3/3/3
48	4AC	S2	1337	48	-	0/11/29/30	0/2/2/2
1	OMC	L5	2824	1	-	0/9/27/28	0/2/2/2
48	OMG	S2	1447	48	-	1/9/27/28	0/3/3/3
1	OMC	L5	2804	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3825	1	-	0/9/27/28	0/3/3/3
48	OMG	S2	1490	83,48	-	3/9/27/28	0/3/3/3
48	OMG	S2	1328	48	-	0/9/27/28	0/3/3/3
1	OMC	L5	3808	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4576	1	-	0/7/25/26	0/2/2/2
48	G7M	S2	1639	48,47	-	0/7/25/26	0/3/3/3
48	A2M	S2	590	48	-	3/9/27/28	0/3/3/3
1	PSU	L5	4532	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	1683	84,1	-	0/7/25/26	0/2/2/2
1	OMU	L5	2837	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3920	83,1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4353	1	-	0/7/25/26	0/2/2/2
48	A2M	S2	1678	48	-	1/9/27/28	0/3/3/3
48	OMU	S2	172	48	-	0/9/27/28	0/2/2/2
1	PSU	L5	4552	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	3715	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	3887	1	-	0/9/27/28	0/2/2/2
48	PSU	S2	1239	48	-	0/7/25/26	0/2/2/2
1	OMC	L5	2422	83,1	-	0/9/27/28	0/2/2/2
48	OMU	S2	1442	48	-	0/9/27/28	0/2/2/2
48	OMC	S2	1703	84,48	-	0/9/27/28	0/2/2/2
1	UR3	L5	4530	1	-	0/7/25/26	0/2/2/2
3	PSU	L8	55	3	-	0/7/25/26	0/2/2/2
1	PSU	L5	4569	1	-	0/7/25/26	0/2/2/2
48	OMG	S2	509	48	-	0/9/27/28	0/3/3/3
48	PSU	S2	1081	48	-	1/7/25/26	0/2/2/2
48	OMG	S2	867	48	-	1/9/27/28	0/3/3/3
48	PSU	S2	36	48	-	0/7/25/26	0/2/2/2
1	A2M	L5	2363	83,1	-	0/9/27/28	0/3/3/3
5	HIC	LB	245	5	-	1/5/6/8	0/1/1/1
48	PSU	S2	863	48	-	0/7/25/26	0/2/2/2
1	1MA	L5	1322	83,1	-	0/7/25/26	0/3/3/3
1	PSU	L5	4442	1	-	0/7/25/26	0/2/2/2
48	PSU	S2	1232	48	-	0/7/25/26	0/2/2/2
1	OMC	L5	1340	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	OMC	S2	1391	48	-	0/9/27/28	0/2/2/2
1	OMC	L5	2861	1	-	0/9/27/28	0/2/2/2
48	A2M	S2	99	83,48	-	2/9/27/28	0/3/3/3
1	PSU	L5	5010	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	4571	1	-	0/9/27/28	0/3/3/3
48	OMC	S2	462	48	-	0/9/27/28	0/2/2/2
48	OMG	S2	436	48	-	0/9/27/28	0/3/3/3
1	A2M	L5	400	1	-	0/9/27/28	0/3/3/3
1	A2M	L5	2787	1	-	3/9/27/28	0/3/3/3
1	PSU	L5	3762	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4628	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	4306	1	-	1/9/27/28	0/2/2/2
1	OMC	L5	3869	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4420	1	-	3/7/25/26	0/2/2/2
1	OMU	L5	4620	1	-	0/9/27/28	0/2/2/2
1	5MC	L5	3782	83,1	-	0/7/25/26	0/2/2/2
48	PSU	S2	801	48	-	0/7/25/26	0/2/2/2
41	M3L	Lm	98	41	-	0/9/10/12	-
1	PSU	L5	3729	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	1316	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	4494	1	-	0/9/27/28	0/3/3/3
48	PSU	S2	1347	48	-	0/7/25/26	0/2/2/2

The worst 5 of 331 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
72	SX	62	HY3	C4-C3	-11.14	1.32	1.52
48	S2	1326	UY1	C6-C5	10.91	1.47	1.35
1	L5	3818	UY1	C6-C5	10.59	1.47	1.35
1	L5	4220	6MZ	C6-N6	9.97	1.45	1.34
48	S2	1326	UY1	C2-N1	9.69	1.49	1.36

The worst 5 of 801 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	S2	1851	MA6	N1-C6-N6	-8.84	106.09	116.86
48	S2	1850	MA6	N1-C6-N6	-7.98	107.14	116.86
48	S2	1639	G7M	C1'-N9-C4	-6.77	106.48	126.49
48	S2	1832	6MZ	C9-N6-C6	-6.42	116.89	122.85
48	S2	1851	MA6	N1-C2-N3	-5.94	119.59	128.58

There are no chirality outliers.

5 of 103 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L8	14	OMU	C1'-C2'-O2'-CM2
3	L8	75	OMG	C1'-C2'-O2'-CM2
5	LB	245	HIC	O-C-CA-CB
72	SX	62	HY3	O-C-CA-C3
1	L5	398	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

57 monomers are involved in 73 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	S2	576	A2M	2	0
48	S2	573	PSU	1	0
1	L5	2351	OMC	2	0
1	L5	1781	PSU	1	0
48	S2	484	A2M	1	0
1	L5	4293	PSU	1	0
47	Pt	20	H2U	1	0
1	L5	4637	OMG	1	0
48	S2	468	A2M	1	0
48	S2	121	OMU	1	0
48	S2	166	A2M	1	0
1	L5	3867	A2M	2	0
1	L5	3760	A2M	1	0
1	L5	3899	OMG	1	0
47	Pt	55	PSU	1	0
3	L8	14	OMU	1	0
1	L5	3768	PSU	2	0
48	S2	1850	MA6	1	0
1	L5	4498	OMU	1	0
1	L5	3701	OMC	1	0
48	S2	159	A2M	1	0
1	L5	2415	OMU	1	0
47	Pt	13	PSU	1	0
1	L5	3734	PSU	1	0
1	L5	4220	6MZ	2	0
1	L5	398	A2M	1	0
1	L5	3744	OMG	1	0
1	L5	3792	OMG	1	0
1	L5	1534	A2M	1	0
1	L5	4457	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	3718	A2M	4	0
1	L5	4228	OMG	2	0
48	S2	512	A2M	1	0
48	S2	27	A2M	1	0
48	S2	116	OMU	3	0
1	L5	4447	5MC	1	0
1	L5	4636	PSU	1	0
48	S2	1804	OMU	1	0
1	L5	2424	OMG	1	0
48	S2	1832	6MZ	1	0
1	L5	2876	OMG	1	0
1	L5	3723	A2M	2	0
3	L8	75	OMG	1	0
48	S2	1490	OMG	1	0
48	S2	1639	G7M	1	0
1	L5	4552	PSU	1	0
48	S2	509	OMG	2	0
48	S2	867	OMG	1	0
1	L5	2363	A2M	1	0
5	LB	245	HIC	1	0
1	L5	1340	OMC	1	0
48	S2	1391	OMC	2	0
48	S2	462	OMC	2	0
1	L5	3762	PSU	2	0
1	L5	4620	OMU	1	0
48	S2	801	PSU	2	0
48	S2	1347	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 548 ligands modelled in this entry, 525 are monoatomic - leaving 23 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	$\# Z > 2$
85	SPD	L5	5447	-	9,9,9	0.27	0	8,8,8	0.51	0
85	SPD	L5	5370	83	9,9,9	0.28	0	8,8,8	0.46	0
85	SPD	L5	5449	-	9,9,9	0.31	0	8,8,8	0.29	0
85	SPD	L5	5454	-	9,9,9	0.36	0	8,8,8	0.74	0
86	PUT	L5	5455	-	5,5,5	0.09	0	4,4,4	0.42	0
86	PUT	L5	5432	-	5,5,5	0.13	0	4,4,4	0.17	0
85	SPD	L5	5422	-	9,9,9	0.26	0	8,8,8	0.19	0
85	SPD	L5	5430	-	9,9,9	0.26	0	8,8,8	0.90	0
86	PUT	L5	5408	-	5,5,5	0.10	0	4,4,4	0.25	0
85	SPD	L5	5438	-	9,9,9	0.26	0	8,8,8	0.44	0
87	TRS	L5	5440	-	7,7,7	0.44	0	9,9,9	0.59	0
86	PUT	L5	5429	-	5,5,5	0.15	0	4,4,4	0.25	0
85	SPD	S2	1940	-	9,9,9	0.26	0	8,8,8	0.79	0
85	SPD	L5	5437	-	9,9,9	0.33	0	8,8,8	0.47	0
85	SPD	L5	5436	-	9,9,9	0.25	0	8,8,8	0.58	0
86	PUT	L5	5458	-	5,5,5	0.12	0	4,4,4	0.21	0
85	SPD	L5	5423	-	9,9,9	0.26	0	8,8,8	0.47	0
85	SPD	L5	5427	-	9,9,9	0.28	0	8,8,8	0.53	0
85	SPD	S2	1941	-	9,9,9	0.24	0	8,8,8	0.39	0
86	PUT	L5	5371	-	5,5,5	0.13	0	4,4,4	0.33	0
86	PUT	L5	5441	-	5,5,5	0.14	0	4,4,4	0.20	0
87	TRS	L5	5457	-	7,7,7	0.54	0	9,9,9	0.71	0
85	SPD	L5	5442	-	9,9,9	0.29	0	8,8,8	0.13	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
85	SPD	L5	5447	-	-	1/7/7/7	-
85	SPD	L5	5370	83	-	4/7/7/7	-
85	SPD	L5	5449	-	-	0/7/7/7	-
85	SPD	L5	5454	-	-	1/7/7/7	-
86	PUT	L5	5455	-	-	0/3/3/3	-
86	PUT	L5	5432	-	-	2/3/3/3	-
85	SPD	L5	5422	-	-	0/7/7/7	-
85	SPD	L5	5430	-	-	2/7/7/7	-
86	PUT	L5	5408	-	-	1/3/3/3	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	SPD	L5	5438	-	-	1/7/7/7	-
87	TRS	L5	5440	-	-	3/9/9/9	-
86	PUT	L5	5429	-	-	0/3/3/3	-
85	SPD	S2	1940	-	-	2/7/7/7	-
85	SPD	L5	5437	-	-	1/7/7/7	-
85	SPD	L5	5436	-	-	1/7/7/7	-
86	PUT	L5	5458	-	-	1/3/3/3	-
85	SPD	L5	5423	-	-	0/7/7/7	-
85	SPD	L5	5427	-	-	3/7/7/7	-
85	SPD	S2	1941	-	-	1/7/7/7	-
86	PUT	L5	5371	-	-	1/3/3/3	-
86	PUT	L5	5441	-	-	0/3/3/3	-
87	TRS	L5	5457	-	-	1/9/9/9	-
85	SPD	L5	5442	-	-	0/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	S2	1940	SPD	C4-C5-N6-C7
85	L5	5370	SPD	C3-C4-C5-N6
85	L5	5436	SPD	C3-C4-C5-N6
85	L5	5430	SPD	N6-C7-C8-C9
86	L5	5371	PUT	C1-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	L5	5370	SPD	1	0
86	L5	5432	PUT	1	0
86	L5	5441	PUT	2	0
87	L5	5457	TRS	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	NC	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	NC	20:UNK	C	26:GLU	N	15.93

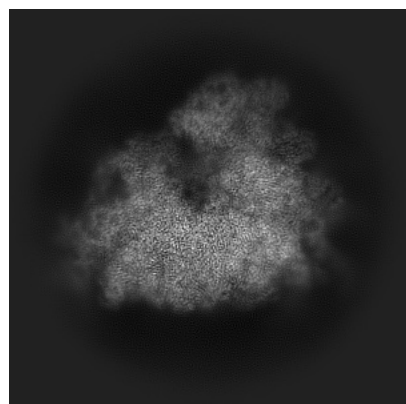
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70083. These allow visual inspection of the internal detail of the map and identification of artifacts.

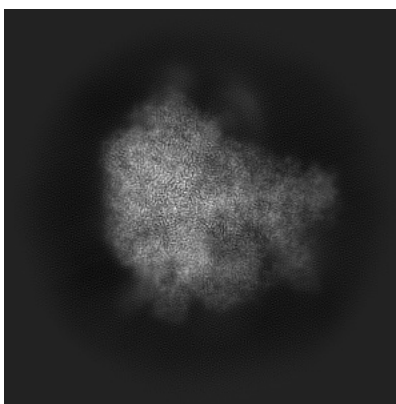
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

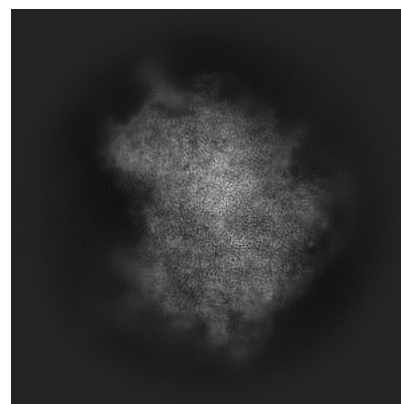
6.1.1 Primary map



X

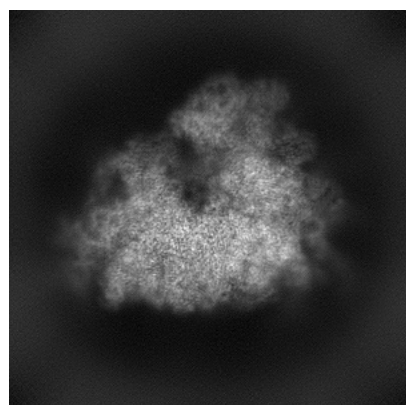


Y

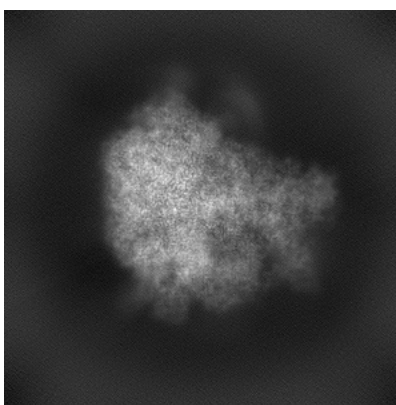


Z

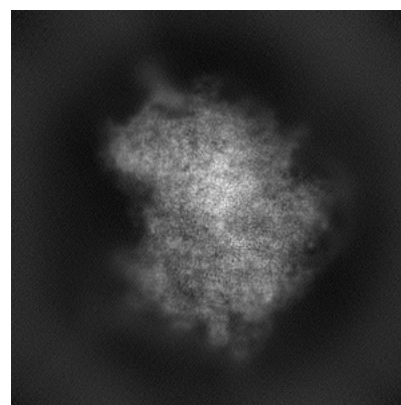
6.1.2 Raw map



X



Y

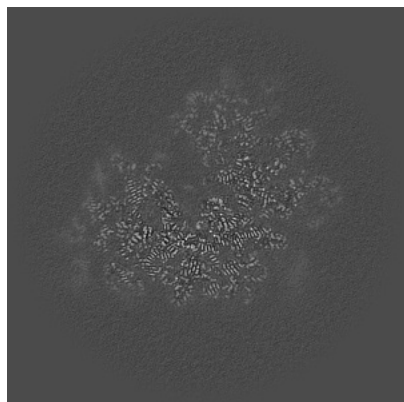


Z

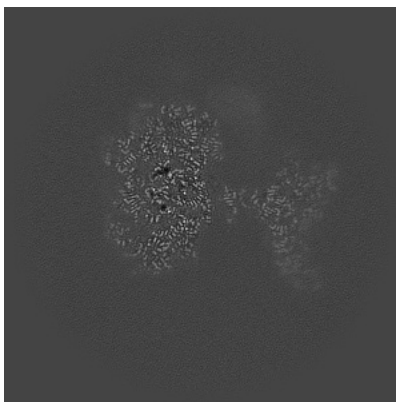
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

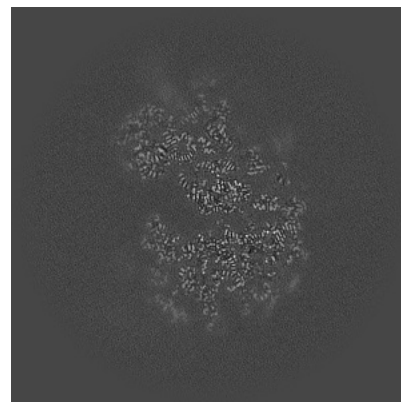
6.2.1 Primary map



X Index: 256

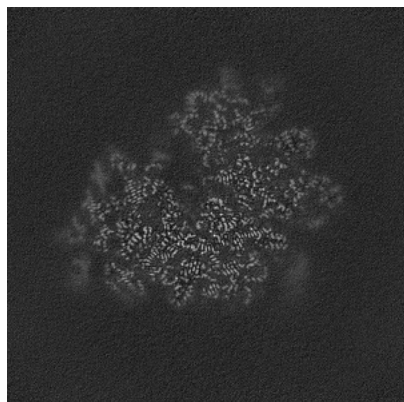


Y Index: 256

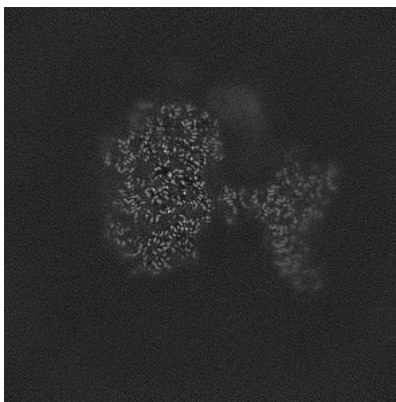


Z Index: 256

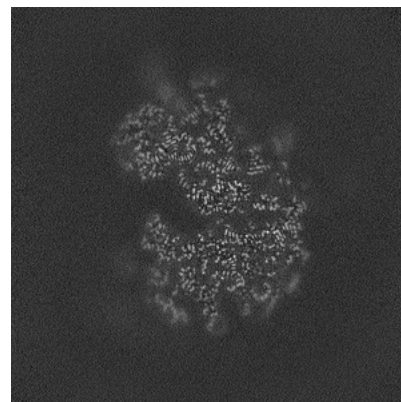
6.2.2 Raw map



X Index: 256



Y Index: 256

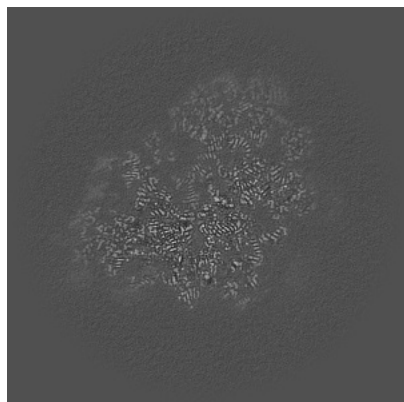


Z Index: 256

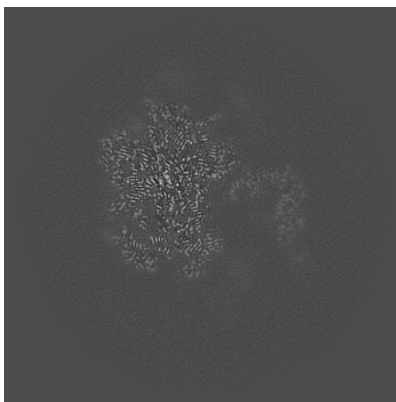
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

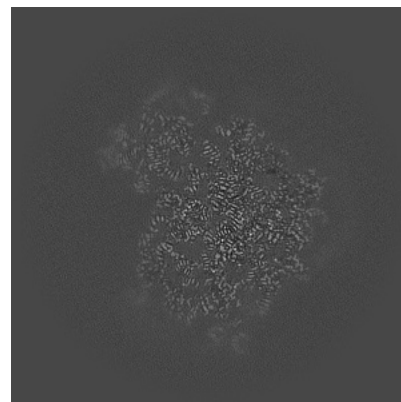
6.3.1 Primary map



X Index: 269

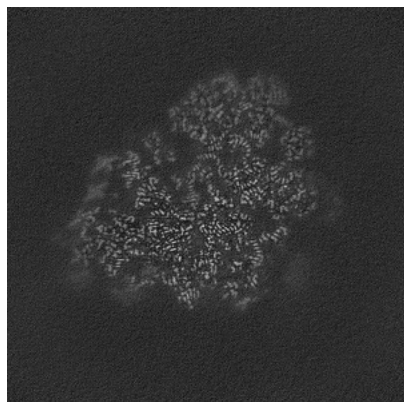


Y Index: 215

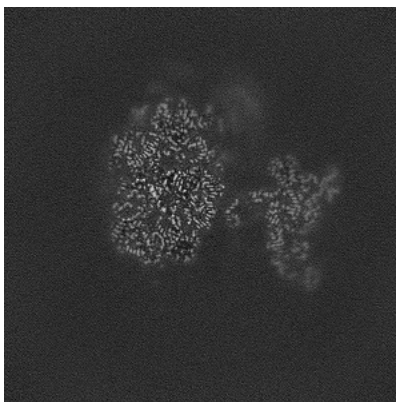


Z Index: 228

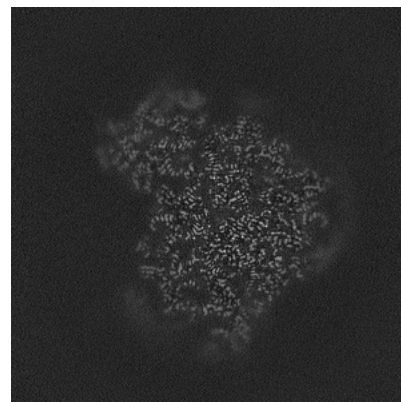
6.3.2 Raw map



X Index: 269



Y Index: 266

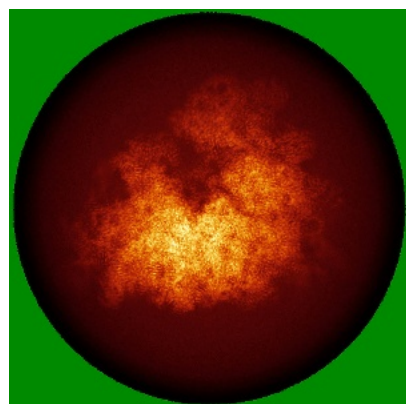


Z Index: 222

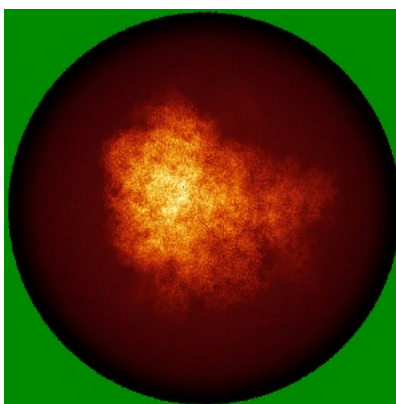
The images above show the largest variance slices of the map in three orthogonal directions.

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

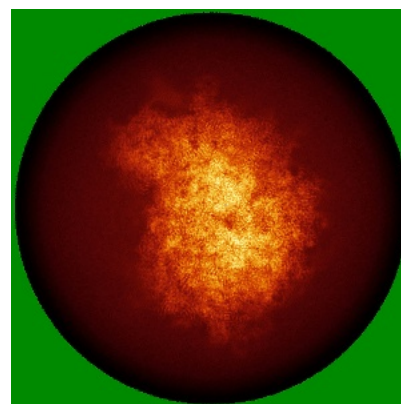
6.4.1 Primary map



X

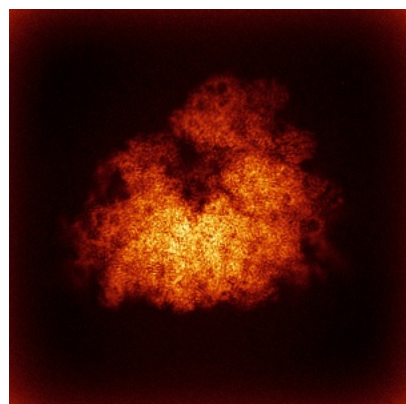


Y

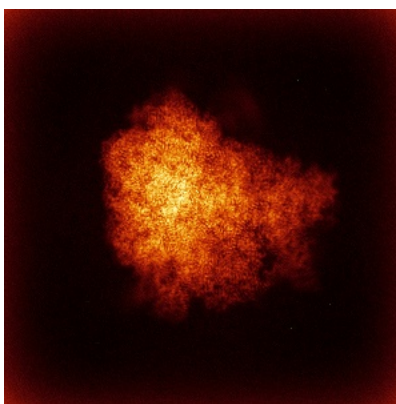


Z

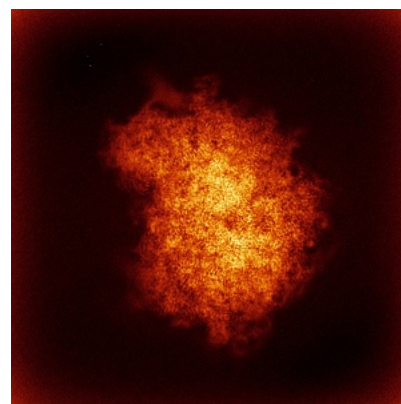
6.4.2 Raw map



X



Y

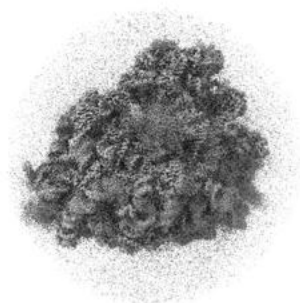


Z

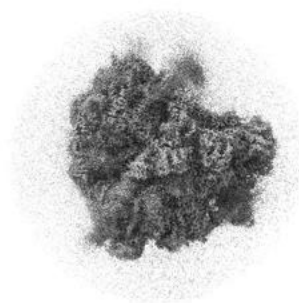
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

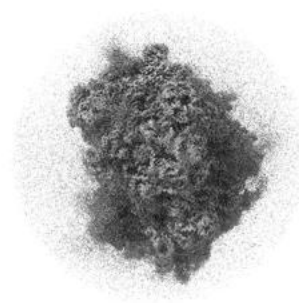
6.5.1 Primary map



X



Y



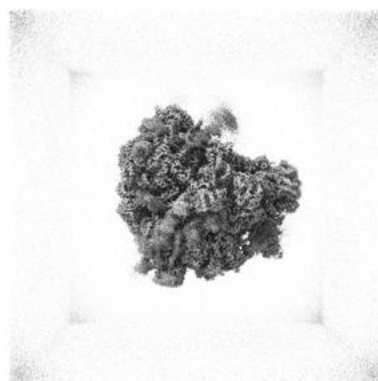
Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

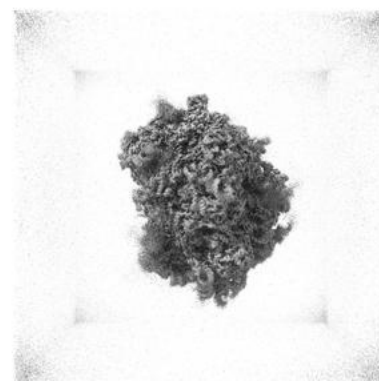
6.5.2 Raw map



X



Y



Z

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

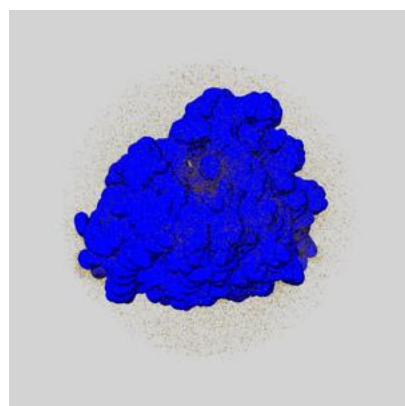
6.6 Mask visualisation [i](#)

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

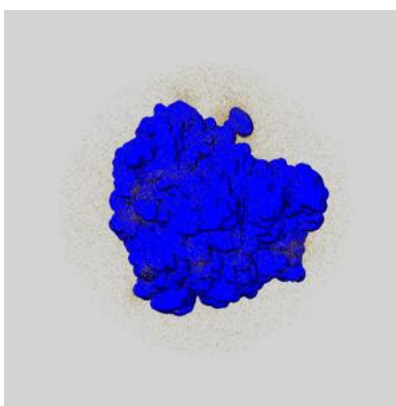
A mask typically either:

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

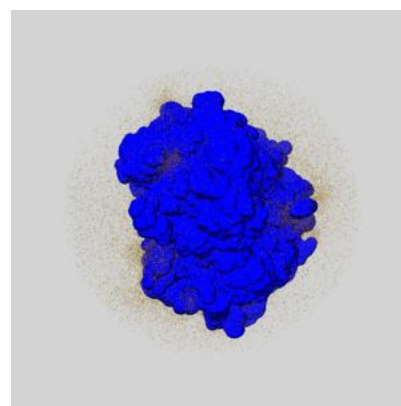
6.6.1 emd_70083_msk_1.map [i](#)



X



Y

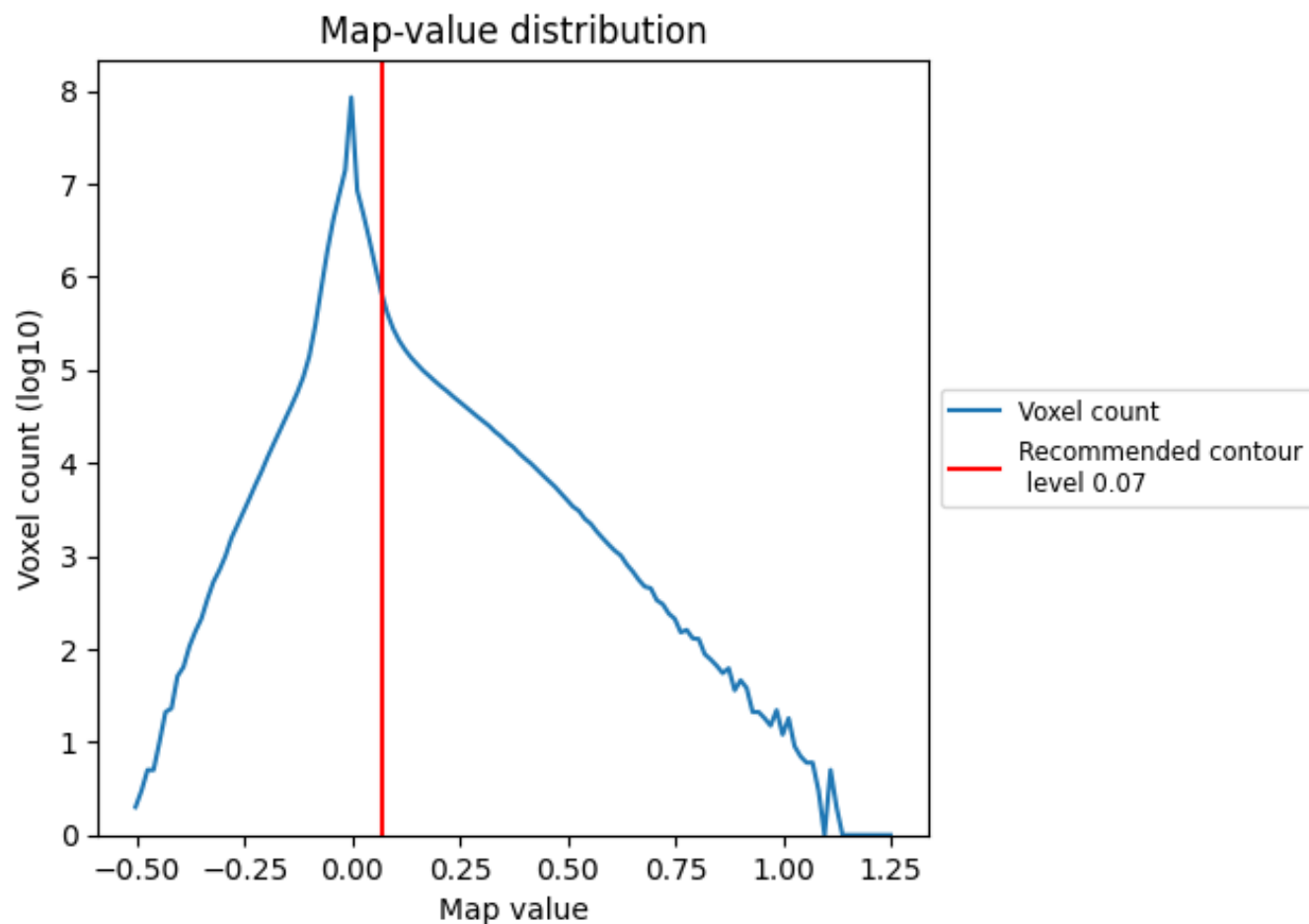


Z

7 Map analysis [i](#)

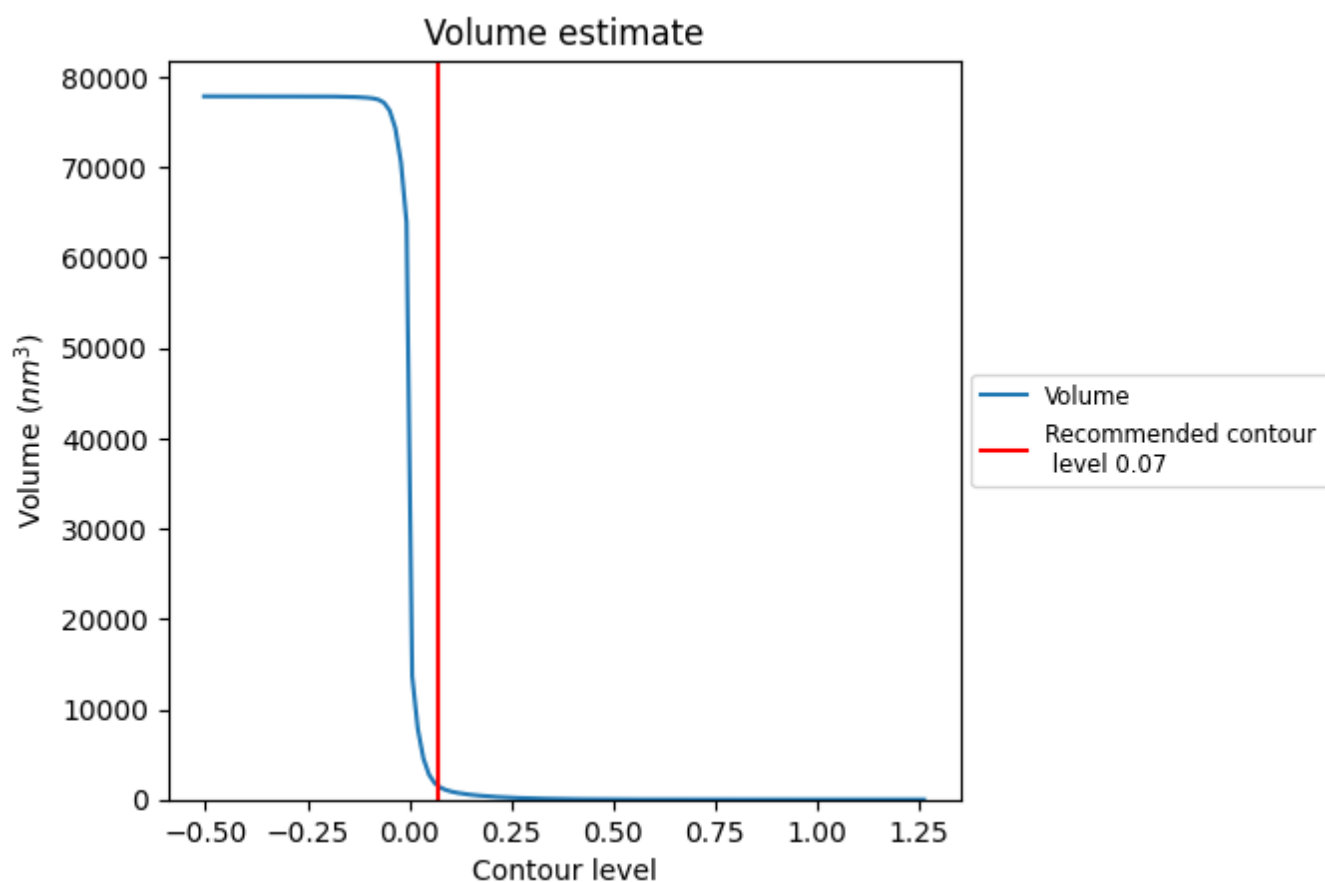
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

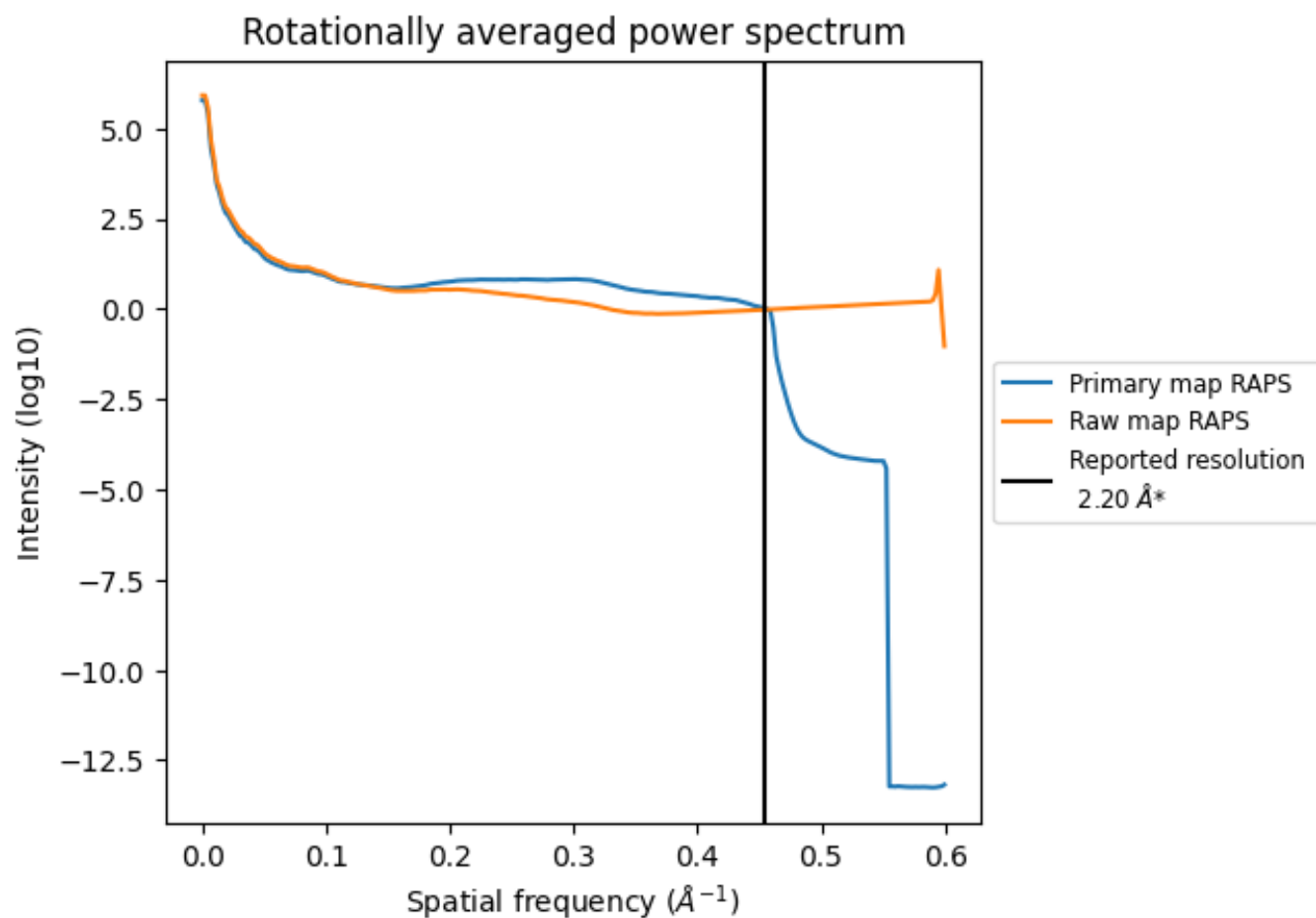
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1557 nm³; this corresponds to an approximate mass of 1407 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 ⓘ

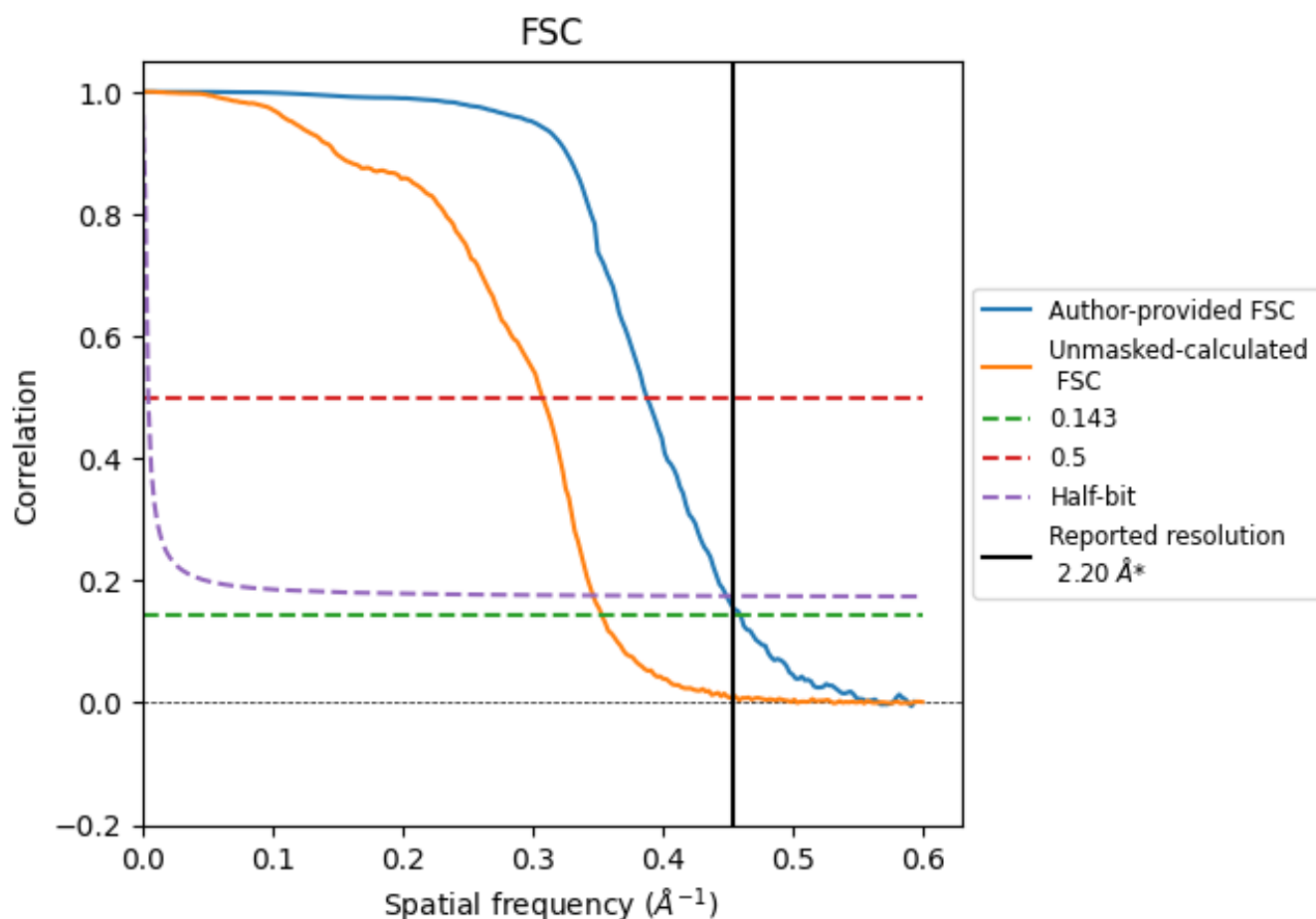


*Reported resolution corresponds to spatial frequency of 0.455 $\text{\AA}^{-1}$

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 $0.455 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

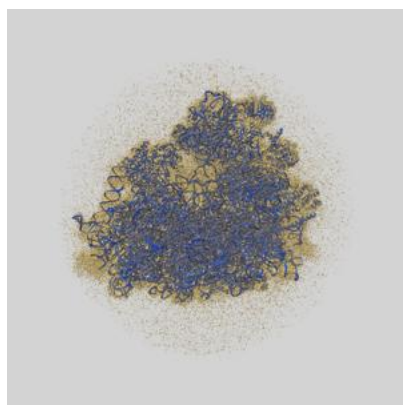
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	2.17	2.58	2.23
Unmasked-calculated*	2.83	3.25	2.89

*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 2.83 differs from the reported value 2.2 by more than 10 %

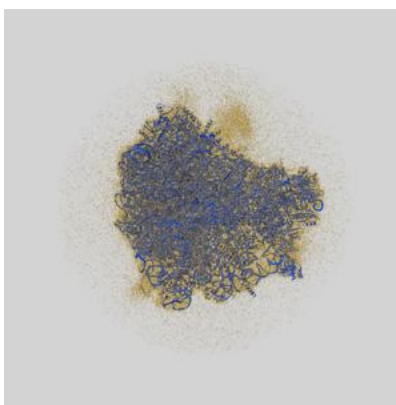
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70083 and PDB model 9O3V. Per-residue inclusion information can be found in [section 3](#) on [page 27](#).

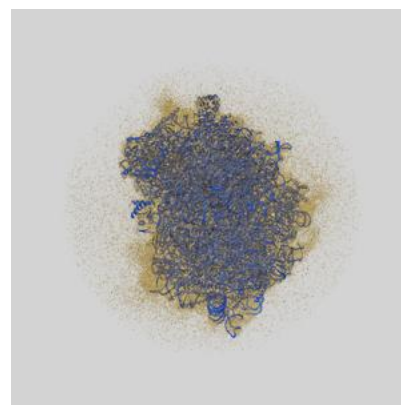
9.1 Map-model overlay [i](#)



X



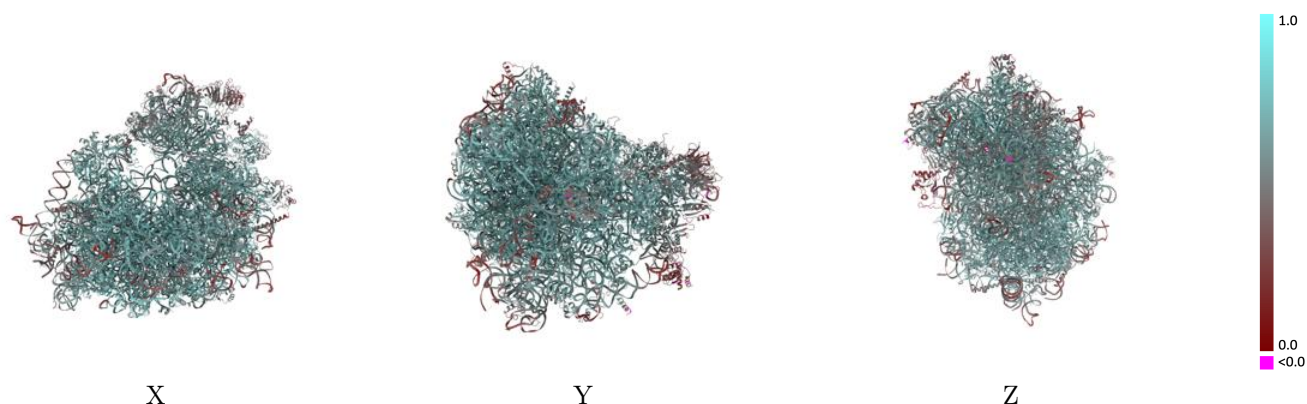
Y



Z

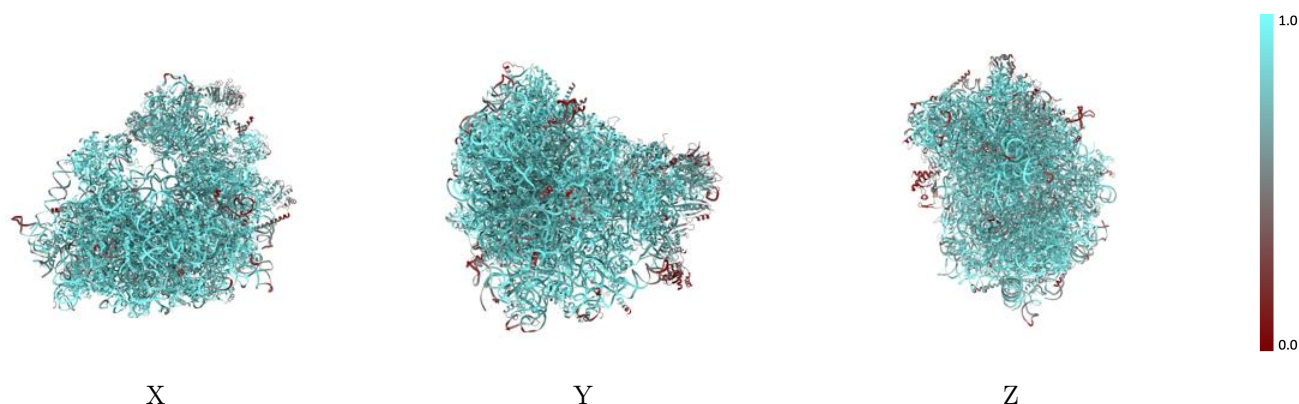
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



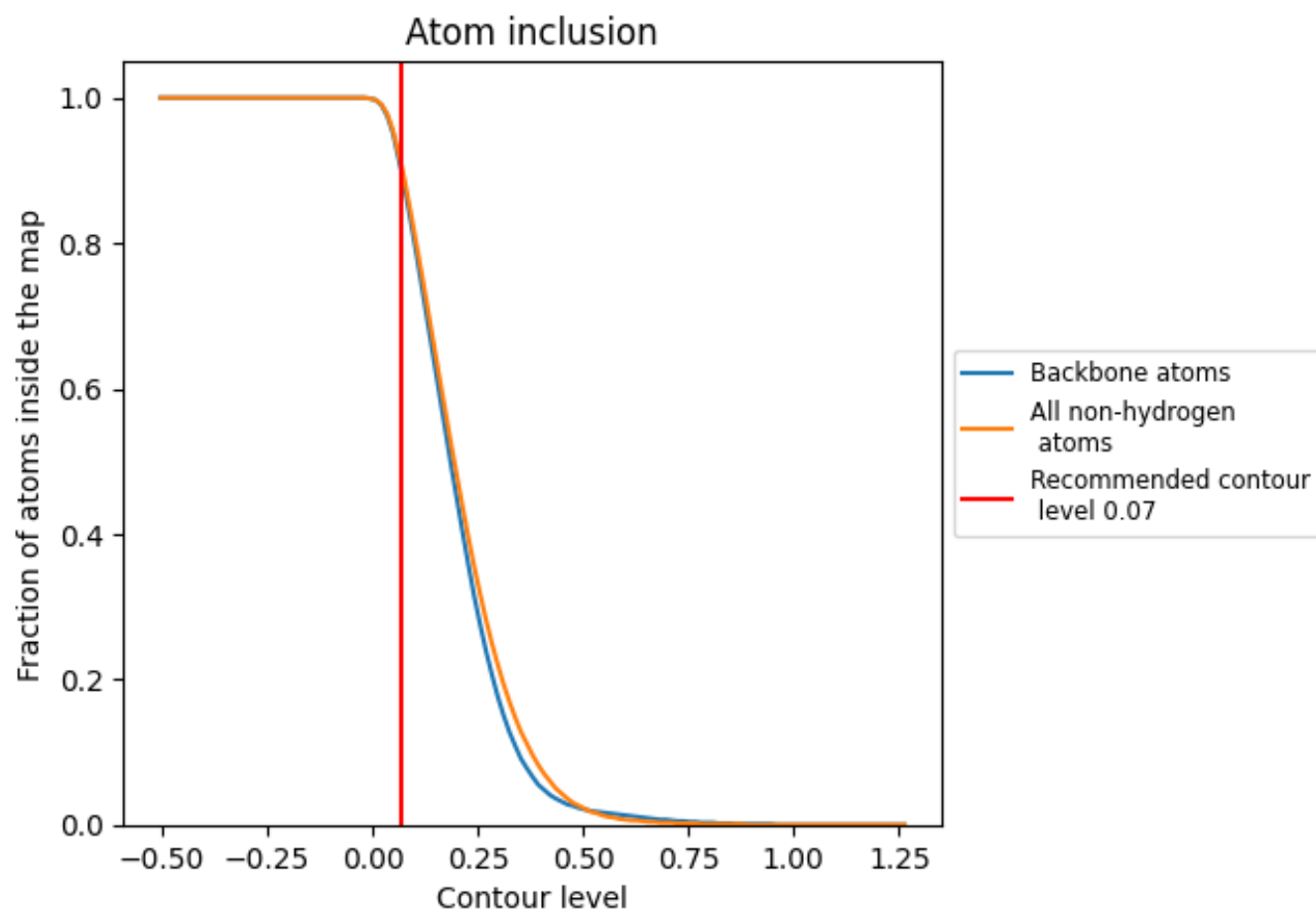
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9040	 0.6320
L5	 0.9310	 0.6440
L7	 0.9880	 0.6720
L8	 0.9620	 0.6700
LA	 0.9780	 0.7280
LB	 0.9430	 0.6880
LC	 0.9500	 0.6930
LD	 0.8920	 0.6170
LE	 0.8960	 0.6190
LF	 0.9550	 0.6940
LG	 0.8260	 0.5910
LH	 0.9230	 0.6540
LI	 0.9290	 0.6720
LJ	 0.8560	 0.6010
LL	 0.9160	 0.6610
LM	 0.9310	 0.6450
LN	 0.9940	 0.7260
LO	 0.9490	 0.6960
LP	 0.9590	 0.7090
LQ	 0.9720	 0.7120
LR	 0.8650	 0.6430
LS	 0.9710	 0.6960
LT	 0.9190	 0.6660
LU	 0.8000	 0.5670
LV	 0.9670	 0.7110
LW	 0.9000	 0.6730
LX	 0.9280	 0.6660
LY	 0.9290	 0.6670
LZ	 0.9190	 0.6360
La	 0.9670	 0.7050
Lb	 0.8110	 0.5980
Lc	 0.9280	 0.6620
Ld	 0.9250	 0.6710
Le	 0.9750	 0.7180
Lf	 0.9720	 0.7100



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Chain	Atom inclusion	Q-score
Lg	 0.9200	 0.6760
Lh	 0.9150	 0.6520
Li	 0.8860	 0.6410
Lj	 0.9900	 0.7300
Lk	 0.7920	 0.5720
Ll	 0.9720	 0.7030
Lm	 0.9330	 0.6700
Ln	 0.9730	 0.7110
Lo	 0.9360	 0.6870
Lp	 0.9460	 0.7090
Lr	 0.9670	 0.6910
NC	 0.7460	 0.5070
Pt	 0.9360	 0.6280
S2	 0.9300	 0.6200
SA	 0.8890	 0.6180
SB	 0.8930	 0.6340
SC	 0.9290	 0.6600
SD	 0.7620	 0.5340
SE	 0.8850	 0.5960
SF	 0.8380	 0.5870
SG	 0.6900	 0.4750
SH	 0.6780	 0.5020
SI	 0.8600	 0.6150
SJ	 0.8700	 0.5980
SK	 0.7220	 0.4640
SL	 0.9130	 0.6670
SM	 0.2110	 0.2440
SN	 0.9470	 0.6810
SO	 0.9430	 0.6740
SP	 0.7230	 0.5040
SQ	 0.8200	 0.5590
SR	 0.7500	 0.5320
SS	 0.7660	 0.5460
ST	 0.7620	 0.5240
SU	 0.6740	 0.4880
SV	 0.9090	 0.6370
SW	 0.9650	 0.6830
SX	 0.9580	 0.6840
SY	 0.7490	 0.5150
SZ	 0.6340	 0.4870
Sa	 0.9420	 0.6840
Sb	 0.8440	 0.5970

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Chain	Atom inclusion	Q-score
Sc	 0.7760	 0.5770
Sd	 0.9050	 0.6250
Se	 0.8340	 0.5950
Sf	 0.2910	 0.2800
Sg	 0.5760	 0.4120
mR	 0.7370	 0.6240