



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:20 AM UTC

PDB ID : 8PV6 / pdb_00008pv6
EMDB ID : EMD-17955
Title : Chaetomium thermophilum pre-60S State 3 - post-5S rotation with Rix1 complex with Foot - composite structure
Authors : Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2023-07-17
Resolution : 2.94 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:

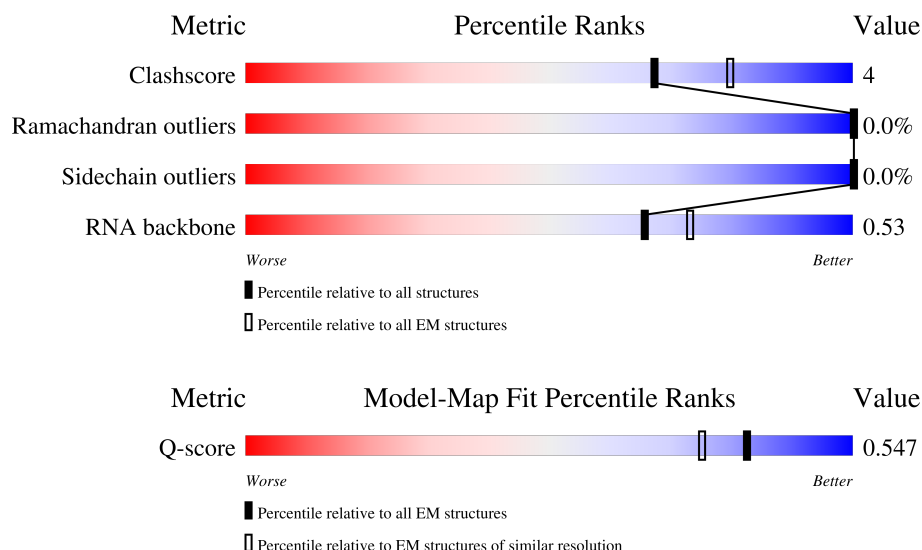
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.94 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.



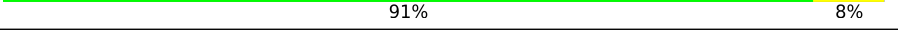
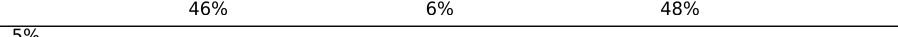
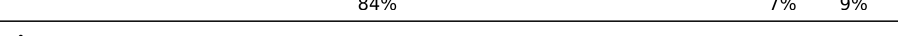
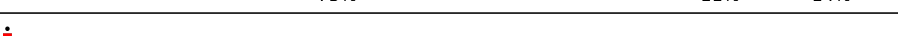
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13068 (2.44 - 3.44)

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	C1	3342	
2	C2	156	
3	C3	162	

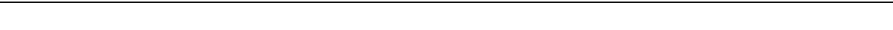
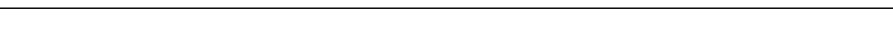
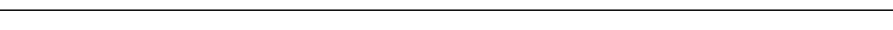
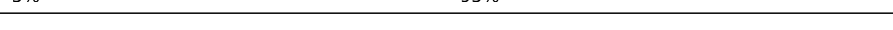
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Mol	Chain	Length	Quality of chain
4	C4	119	
5	CF	270	
6	CH	661	
7	CI	414	
8	CJ	679	
9	CK	261	
10	CL	558	
11	CM	249	
11	LF	249	
12	CN	246	
13	CO	120	
14	CQ	225	
15	CR	767	
16	CS	338	
17	CT	437	
17	CU	437	
18	CV	781	
18	CW	781	
19	Cb	117	
20	Cd	627	
21	Ce	443	
22	Ch	517	
23	Cz	123	
24	LA	254	
25	LB	392	

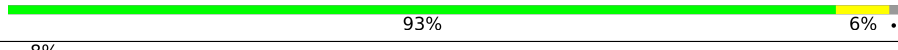
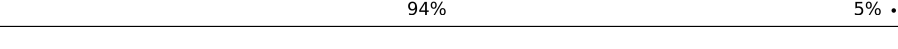
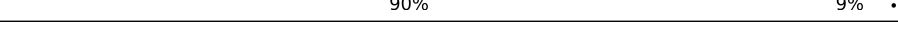
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Mol	Chain	Length	Quality of chain
26	LC	365	
27	LD	304	
28	LE	200	
29	LG	262	
30	LH	229	
31	LJ	173	
32	LK	165	
33	LL	213	
34	LM	142	
35	LN	203	
36	LO	204	
37	LP	187	
38	LQ	213	
39	LR	2898	
40	LS	174	
41	LT	160	
42	LU	127	
43	LV	139	
44	LX	156	
45	LY	138	
46	LZ	135	
47	La	149	
48	Lb	65	
49	Lc	108	
50	Ld	120	

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Mol	Chain	Length	Quality of chain
51	Le	131	
52	Lf	109	
53	Lg	119	
54	Lh	935	
55	Li	110	
56	Lj	95	
57	Lk	94	
58	Ll	51	
59	Lp	92	
60	Lq	147	
61	Lr	217	

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 172014 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 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	3100	Total	C	N	O	P	0	0
			66359	29636	12012	21611	3100		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	156	Total	C	N	O	P	0	0
			3319	1484	589	1090	156		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	3	Total	C	N	O	P	0	0
			60	27	7	23	3		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C4	115	Total	C	N	O	P	0	0
			2451	1093	438	805	115		

- Molecule 5 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CF	245	Total	C	N	O	S	0	0
			1934	1215	350	360	9		

- Molecule 6 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CH	627	Total	C	N	O	S	0	0
			5061	3180	924	938	19		

- Molecule 7 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CI	93	Total	C	N	O	S	0	0
			729	472	132	122	3		

- Molecule 8 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CJ	382	Total	C	N	O	S	0	0
			3116	2008	548	550	10		

- Molecule 9 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CK	233	Total	C	N	O	S	0	0
			1878	1183	363	328	4		

- Molecule 10 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	CL	79	Total	C	N	O	0	0
			618	386	124	108		

- Molecule 11 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CM	217	Total	C	N	O	S	0	0
			1773	1144	329	297	3		
11	LF	248	Total	C	N	O	S	0	0
			2023	1297	377	346	3		

- Molecule 12 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CN	246	Total	C	N	O	S	0	0
			1850	1154	322	368	6		

- Molecule 13 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 14 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CQ	183	Total	C	N	O	S	0	0
			1476	923	304	239	10		

- Molecule 15 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CR	516	Total	C	N	O	S	0	0
			3844	2445	683	703	13		

- Molecule 16 is a protein called Pre-rRNA-processing protein IPI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CS	307	Total	C	N	O	S	0	0
			2391	1520	418	446	7		

- Molecule 17 is a protein called Pre-rRNA-processing protein IPI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CT	393	Total	C	N	O	S	0	0
			2941	1865	492	566	18		
17	CU	393	Total	C	N	O	S	0	0
			2953	1873	494	568	18		

- Molecule 18 is a protein called Pre-rRNA-processing protein RIX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CV	550	Total	C	N	O	S	0	0
			4217	2691	735	777	14		
18	CW	550	Total	C	N	O	S	0	0
			4204	2685	729	776	14		

- Molecule 19 is a protein called Zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Cb	101	Total	C	N	O	S	0	0
			830	517	161	148	4		

- Molecule 20 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cd	451	Total	C	N	O	S	0	0
			3614	2301	660	642	11		

- Molecule 21 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ce	302	Total	C	N	O	S	0	0
			2476	1541	471	460	4		

- Molecule 22 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ch	389	Total	C	N	O	S	1	0
			3050	1916	568	557	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ch	117	ASP	GLU	engineered mutation	UNP G0SC29

- Molecule 23 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Cz	103	Total	C	N	O	S	0	0
			884	548	183	149	4		

- Molecule 24 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LA	247	Total	C	N	O	S	0	0
			1878	1175	374	326	3		

- Molecule 25 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LB	388	Total	C	N	O	S	0	0
			3097	1969	578	537	13		

- Molecule 26 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LC	363	Total	C	N	O	S	0	0
			2745	1734	524	478	9		

- Molecule 27 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LD	298	Total	C	N	O	S	0	0
			2366	1496	424	443	3		

- Molecule 28 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LE	191	Total	C	N	O	S	0	0
			1470	941	267	259	3		

- Molecule 29 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LG	235	Total	C	N	O	S	0	0
			1880	1204	348	323	5		

- Molecule 30 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LH	190	Total	C	N	O	S	0	0
			1495	949	268	272	6		

- Molecule 31 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LJ	168	Total	C	N	O	S	0	0
			1367	854	266	241	6		

- Molecule 32 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LK	158	Total	C	N	O	S	0	0
			1184	743	215	224	2		

- Molecule 33 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LL	203	Total	C	N	O	S	0	0
			1587	989	325	271	2		

- Molecule 34 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LM	141	Total	C	N	O	S	0	0
			1126	714	216	195	1		

- Molecule 35 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LN	202	Total	C	N	O	S	0	0
			1704	1062	360	278	4		

- Molecule 36 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LO	203	Total	C	N	O	S	0	0
			1611	1034	305	267	5		

- Molecule 37 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LP	171	Total	C	N	O	S	0	0
			1343	834	274	232	3		

- Molecule 38 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LQ	146	Total	C	N	O	S	0	0
			1156	730	228	196	2		

- Molecule 39 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LR	155	Total	C	N	O	S	0	0
			1241	772	262	203	4		

- Molecule 40 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LS	174	Total	C	N	O	S	0	0
			1430	920	267	238	5		

- Molecule 41 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LT	141	Total	C	N	O	S	0	0
			1124	712	215	195	2		

- Molecule 42 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LU	105	Total	C	N	O	S	0	0
			838	542	144	151	1		

- Molecule 43 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LV	135	Total	C	N	O	S	0	0
			991	630	184	170	7		

- Molecule 44 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LX	145	Total	C	N	O	S	0	0
			1113	709	206	198			

- Molecule 45 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LY	133	Total	C	N	O	S	0	0
			1056	658	213	183	2		

- Molecule 46 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LZ	135	Total	C	N	O	S	0	0
			1102	707	203	188	4		

- Molecule 47 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	La	108	Total	C	N	O	S	0	0
			872	556	168	147	1		

- Molecule 48 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lb	36	Total	C	N	O		0	0
			286	178	61	47			

- Molecule 49 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lc	95	Total	C	N	O	S	0	0
			705	449	122	129	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ld	110	Total	C	N	O	S	0	0
			875	555	171	148	1		

- Molecule 51 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Le	126	Total	C	N	O	S	0	0
			1017	640	208	163	6		

- Molecule 52 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 53 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lg	118	Total	C	N	O	S	0	0
			901	561	184	152	4		

- Molecule 54 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	Lh	122	Total	C	N	O	0	0
			1003	637	198	168		

- Molecule 55 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Li	101	Total	C	N	O	S	0	0
			821	506	178	136	1		

- Molecule 56 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lj	88	Total	C	N	O	S	0	0
			698	427	154	112	5		

- Molecule 57 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Lk	76	Total	C	N	O	S	0	0
			624	394	119	109	2		

- Molecule 58 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	Ll	50	Total	C	N	O	0	0
			436	275	97	64		

- Molecule 59 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Lp	91	Total	C	N	O	S	0	0
			694	428	138	122	6		

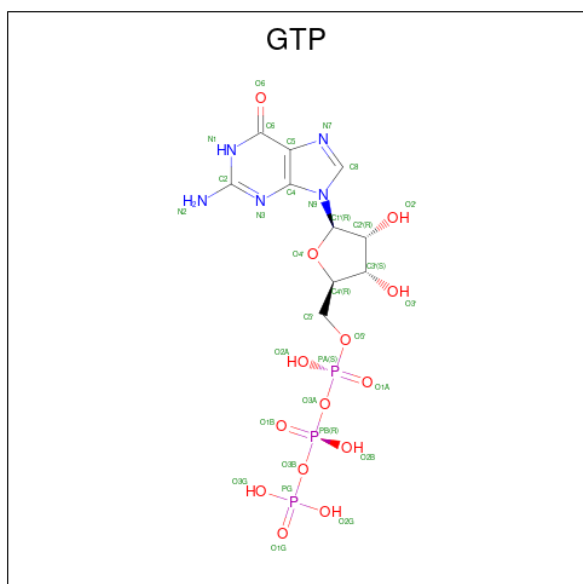
- Molecule 60 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	Lq	139	Total	C	N	O	0	0
			1061	666	207	188		

- Molecule 61 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lr	214	Total	C	N	O	S	0	0
			1660	1056	296	300	8		

- Molecule 62 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
62	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	
62	Cd	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
63	CH	1	Total	Mg	0
			1	1	
63	Cd	2	Total	Mg	0
			2	2	

- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
64	CQ	1	Total	Zn	0
			1	1	
64	Cb	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
64	Lg	1	Total 1	Zn 1	0
64	Lj	1	Total 1	Zn 1	0
64	Lp	1	Total 1	Zn 1	0

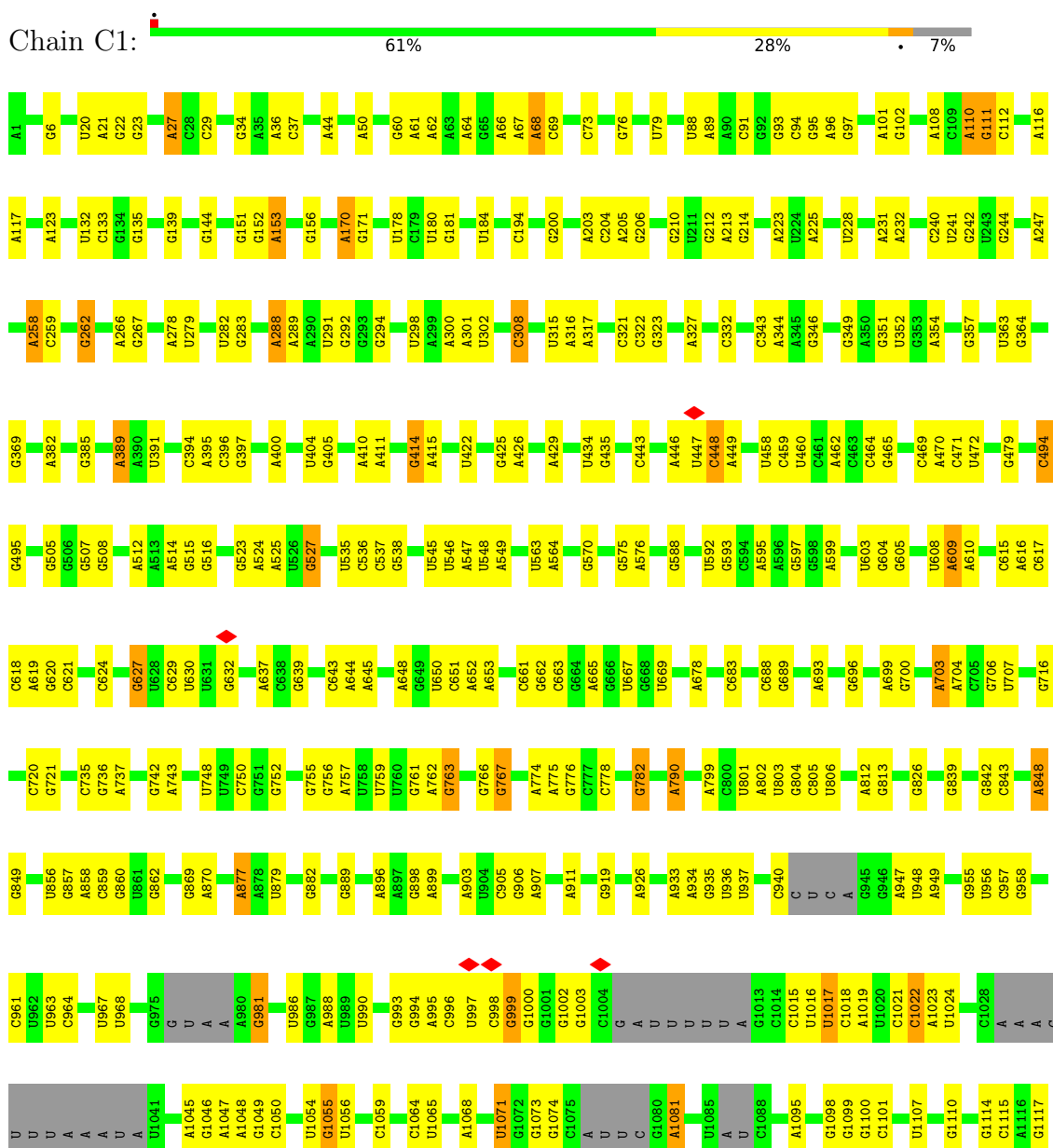
- Molecule 65 is water.

Mol	Chain	Residues	Atoms		AltConf
65	C1	1	Total 1	O 1	0
65	CH	1	Total 1	O 1	0
65	Cd	2	Total 2	O 2	0

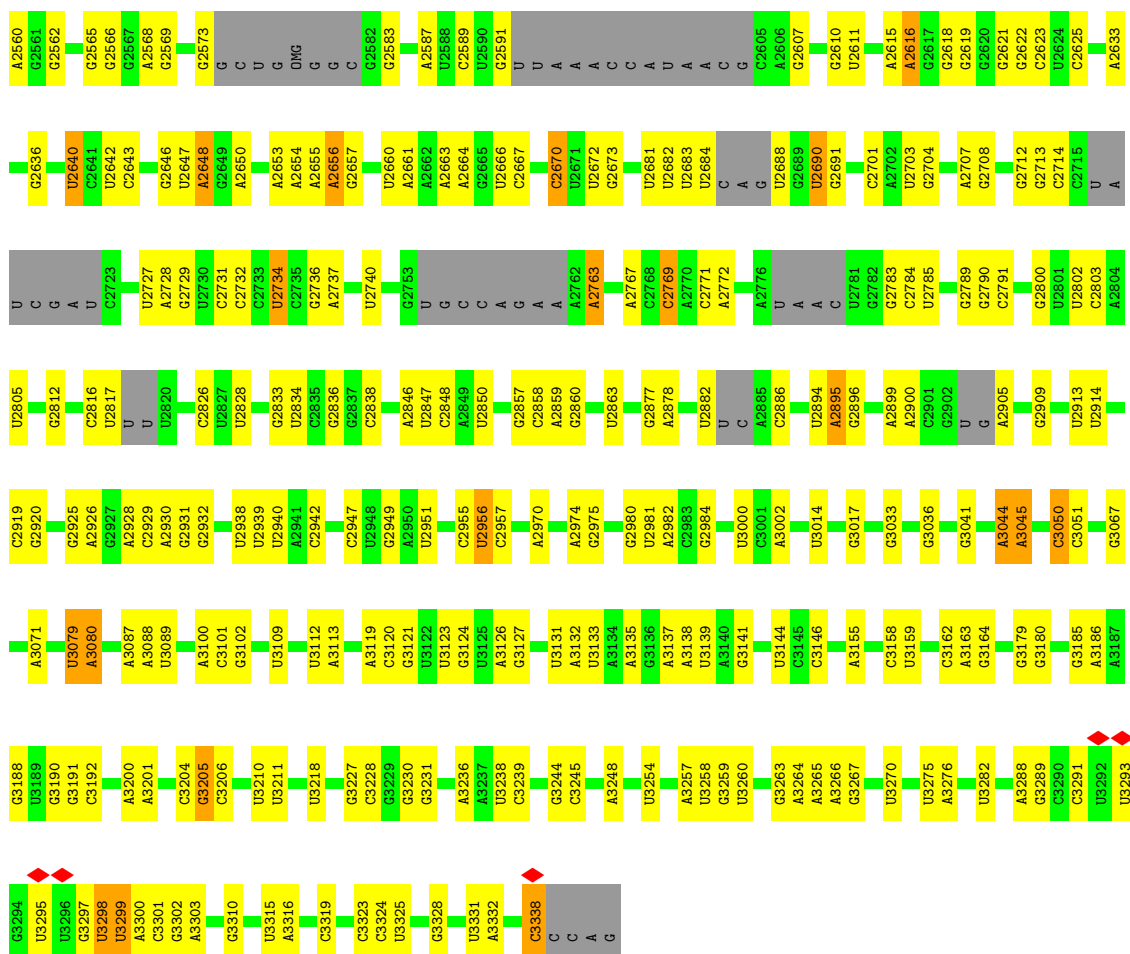
3 Residue-property plots

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

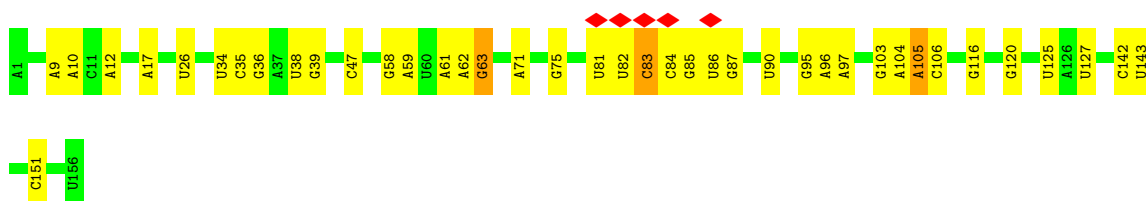
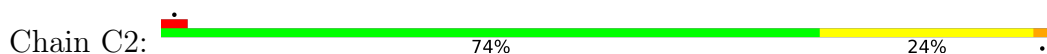
• Molecule 1: 26S rRNA



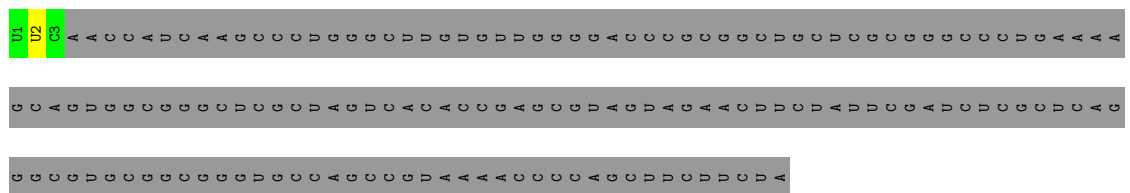
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A2382	C2383	U2384	U2389	U2390	U2392	U2393	U2394	U2396	U2397	U2398	U2399	U2403	U2404	U2405	U2406	U2409	U2410	U2411	U2412	U2413	U2414	U2415	U2420	U2423	U2424	U2425	U2426	U2427	U2428	U2431	U2432	U2435	U2436	U2437	U2440	U2441	U2444	U2445	U2446	U2447	U2448	U2449	U2450	U2454	U2455	U2456	U2457	
G	A	A	ONU	G	A	U2281	U2282	U2283	U2289	U2297	U2298	U2299	U2307	U2308	U2309	U2314	U2315	U2320	U2321	U2329	U2330	U2331	U2334	U2335	U2336	U2337	U2338	U2339	U2340	U2346	U2351	U2356	U2357	U2362	U2365	U2366	U2367	U2368	U2374	U2375	U2376	U2377	U2380	U2381				
A2207	C2208	G2209	G2212	G2213	G2214	A2219	C2220	U2221	U2222	U2223	G2224	U2227	U2231	U2232	A2233	A2234	G2235	G2236	U	G	C	C	A	A	U	G	C	C	A	A	U	A	U	A	U	U	A	U	U	G	A	A	U					
G2084	G2085	A2089	U2092	G2093	A2094	U2100	A2101	U2102	U2103	U2104	A2105	A2112	A2115	A2121	U2122	U2123	G2124	G2132	U2139	G2150	A2151	C2155	U	G2157	A2161	C2167	U2168	G2047	U2048	G2049	C2050	G2051	U2052	U2053	U2054	A2055	A2069	A2070	G2073	G2074	A2185	A2186	U2188	A2192	A2205	A2206		
C	C	C	G	G	G	U	U	U	U	U	U	U	U	A	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C			
G1837	A1838	A1839	G1840	A1844	A1845	C1846	A1847	U1851	U1856	U1857	G1858	A1859	U1860	A1866	A1867	U1868	A1873	U1874	A1875	A1876	G1877	G1878	G1879	G1886	C1887	U1892	A1893	G1894	U1917	G1920	C1923	G1929	G1933	G1934	C1935	C1937	U1939	U	G	G	G	G	G	U	U			
G1737	A1738	C1741	U1742	U1743	C1744	U1745	U1746	C1747	U1748	G1758	C1759	G1760	G1766	A1767	G1776	A1777	A1778	A1779	A1780	C1783	G1784	G1785	G1786	G1787	G1788	A1789	G1790	G1791	G1792	A1793	A1794	U1795	U1796	C1800	U1801	G1809	U1814	A1815	C1816	A1821	A1822	C1823	U1824	G1825	C1826	C1829	A1830	C1836
U1609	G1610	C1611	G1612	C1613	G1614	G1615	A1618	C1619	A1622	A1623	C1624	U1625	G1626	G1638	A1639	C1640	G1641	C1642	C1643	G1644	G1645	G1646	G1647	C1650	G1658	U1661	U1662	A1676	A1677	U1683	A1684	U1685	C1697	A1698	G1699	U1700	U1701	U1704	A1709	U1722	C1726	A1730	G1731					
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C1238	G1239	U1240	U1241	A1242	A1246	C1247	U1248	U1252	C1255	C1260	A1261	C1262	C1263	U1264	C1265	C1267	C1268	A1269	A1270	G1278	G1283	A1287	U1288	G1289	C1290	A1291	U1292	C1296	A1301	C1306	A1313	C1319	G1320	A1331	G1332	A1333	A1334	A1335	G1337	U1339	G1345	A1346						
U1361	G1362	G1363	G1366	A1369	G1370	A1373	C1380	U1381	G1382	G1383	G1387	A1390	G1400	A1401	G1404	G1405	C1409	G1414	G1417	A1418	U1419	U1421	A1429	G1430	U1431	A1432	G1433	C1434	A1435	U1438	G1447	A1448	G1449	A1450	U1454	G1455	U1458	U1463	A1464	A1465	G1466							
A1118	U1127	G1132	G1135	A1136	G1140	A1141	A1142	C1143	U1151	A1152	G1157	C1158	C1159	G1163	U1164	G1165	G1169	C1175	A1176	G1177	A1178	C1181	C1182	A1185	A1186	A1187	G1192	U1193	U1197	A1198	C1199	G1205	A1206	G1209	C1210	A1211	G1216	A1223	A1228	G1229								



- Molecule 2: 5.8S rRNA



- Molecule 3: ITS2



- Molecule 4: 5S rRNA

- Chain CF:

- Chain CH:
-
- 88% 7% 5%
- THR
ALA
ASP
PRO
ASP
ALA
MET
ASP
ILE
ASP
ASP
GLY
ALA
SER
SF682
E585
R586
L587
A588
R589
R593
A616
E635
K646
S650
R661
- R342
H352
S353
N354
G355
N356
I357
V364
D375
D397
R405
E408
R422
D435
E476
D477
ASP
ASP
LEU
PRO
D482
R509
K513
L534
D540
L546
R549
T552
ALA
GLN
SER
SER
ARG
GLY
ARG
SER
LEU
VAL
ARG
SER
ARG
GLY
THR

- [illegible]

[illegible]

- Molecule 8: Pescadillo homolog

Chain CJ:

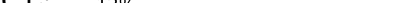
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ARG	ASP	ASP	Y450	ALA	ALA
ARG	PRO	GLU	R453	ILE	K25
ARG	LYS	GLN		ASP	GLN
ILE	VAL	GLU		LYS	ASN
GLU	LYS	ASP		PHE	L36
GLU	ALA	ASP	K491	GLU	L42
MET	LEU	PHE		PRO	GLN
ALA	GLU	GLY	THR	VAL	E46
ALA	ALA	PHE	GLN	ALA	
LYS	LYS	SER	GLY	PRO	A59
LYS	LYS	ASP	GLN	GLY	THR
ALA	ALA	ASP	TYR	GLY	ASN
	ALA	GLU	ASP	ASP	T66
	LEU	ASP	PRO	VAL	GLY
	GLU	GLU	THR	LEU	GLU
ARG	ARG	GLU	LYS	LEU	Q70
LYS	LYS	GLN	PRO	PRO	Y71
LYS	LYS	GLN	PRO	GLN	L72
LYS	LYS	SER	LEU	PRO	L73
ILE	GLN	ASP	GLU	SER	H74
GLU	GLN	GLU	GLU	TYR	ASP
ALA	GLY	GLY	GLN	TYR	E75
	SER	GLN	GLN	SER	
	GLU	SER	THR	SER	Q84
	GLU	GLU	GLU	GLN	R120
LEU	GLY	ASP	ALA	ALA	
GLU	GLU	GLU	D362	GLU	R128
ARG	GLU	ASP	W397	VAL	
ALA	ALA	GLU	ALA	ASP	L141
LYS	LYS	GLU	LEU	LYS	
GLY	GLY	GLU	L401	LEU	
MET	ASP	ASP	E410	VAL	S156
LEU	ASP	GLU	ALA	ALA	
SER	SER	GLU	Q418	LYS	A162
	GLU	ASP		LEU	F189
LYS	LYS	GLU	P423	ARG	
LYS	LYS	GLU	ALA	GLU	Y196
ARG	ARG	GLU	ILE	GLU	
LYS	LYS	ALA	ARG	GLU	
LEU	LYS	THR	GLN	GLN	N200
PHE	PHE	LEU	GLN	ALA	
GLU	GLU	ARG	GLU	VAL	D205
MET	MET	GLN	GLY	SER	
GLN	GLN	ARG	SER	ASN	D223
TYR	TYR	LEU	ASP	GLY	
		LEU	GLU	ASP	I226
		GLU	GLY	LYS	
SER	SER	LEU	GLY	THR	V231
ASN	ASN	ALA	GLY	ASP	
ALA	ALA	GLU	GLU	GLU	M235
LYS	LYS	LEU	SER	LYS	
ASN	ASN	GLY	ASN	GLY	V241
ALA	ALA	GLY	GLN	GLU	
GLU	GLU	LYS	THR	GLU	P254
ASP	ASP	VAL	SER	ASN	P255
ALA	ALA	SER	MET	GLU	
LYS	LYS	SER	LYS	GLY	A266
LEU	LEU	GLY	ALA	ASP	
		TYR	VAL	ASP	V270

- Molecule 9: Ribosome biogenesis protein NSA2 homolog

Chain CK:  79% 11% 11%

K140	R141	T142	R149	P154	R163	R164	P165	V166	E169	P174	L177	L198	E222	S234	R241	P249	V261	MET	P2	R11	R16	R43	Q53	Q57	R62	R66	V73	LYS	GLY	ARG	PRO	ALA	GLU	LYS	E81	D84	P87	L90	A94	ASN	PRO	THR	THR	ALA	LYS	ALA	LEU	SER	SER	GLN	ILE	LYS	LYS	ASN	LYS	ARG	ALA	GLU	LYS	ALA	A115	E129	F133
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------

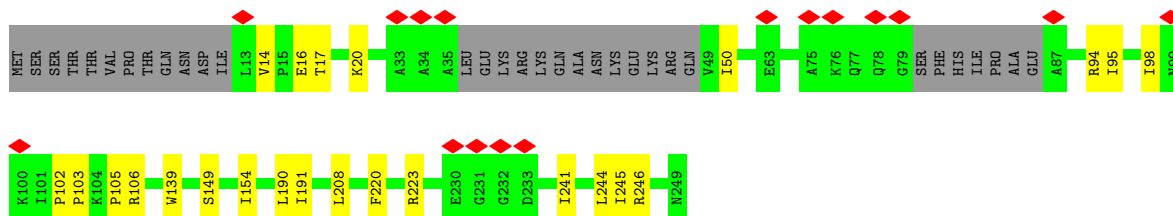
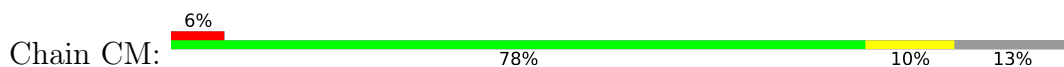
- Molecule 10: Putative GTP binding protein

Chain CL:  12% : 86%

ASU	LYS	ASP	GLU	GLN	MET	GLM	GLU	ASP	ASP	ASP	GLU	GLU	GLU	LEU	LEU	LEU	ASP	ASP	ALA	MET	ASP	GLU	GLY	GLY	VAL	ASP	ASP	GLU	SER	SER	ASN	PRO	LEU	ALA	ALA	ALA	LEU	VAL	ARG	SER	ALA	ARG	LYS	LYS	ALA	LEU	ARG	LYS	LYS	LYS	GLU	GLU	LEU	ALA	LYS	LYS	ALA	GLN	SER	GLY
MET	A2	I5	R27	E30	K31	L38	A39	R40	K41	H42	P43	E44	K50	K51	D52	N57	Y61	R64	L65	L66	Q67	Q68	I69	Y70	E71	E72	R73	I74	R75	R76	K77	R78	E79	L80	LEU	ARG	LYS	LYS	GLU	GLU	LEU	ALA	LYS	LYS	ALA	GLN <td>SER<td>GLY<td>ASP<td>GLY</td> </td></td></td>	SER <td>GLY<td>ASP<td>GLY</td> </td></td>	GLY <td>ASP<td>GLY</td> </td>	ASP <td>GLY</td>	GLY										

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

- Molecule 11: 60S ribosomal protein 17-like protein



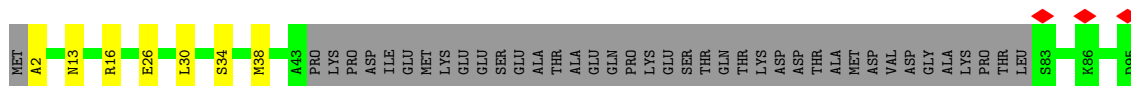
- Molecule 11: 60S ribosomal protein l7-like protein



- Molecule 12: Eukaryotic translation initiation factor 6

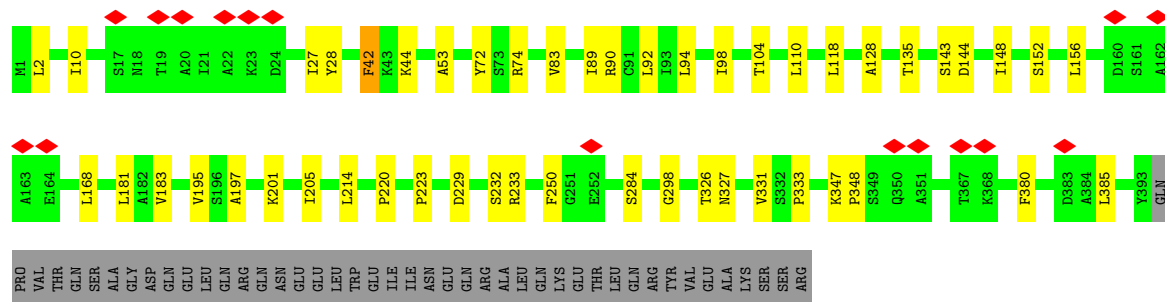
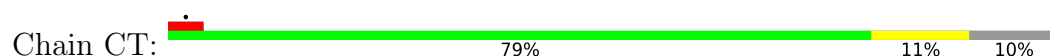


- Molecule 13: DUF2423 domain-containing protein

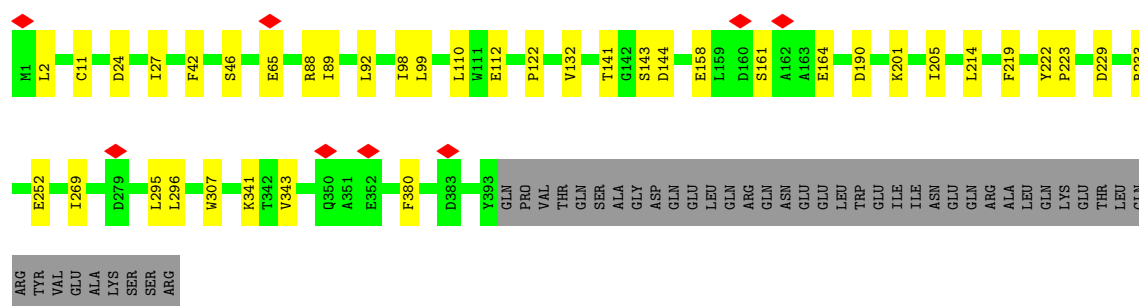
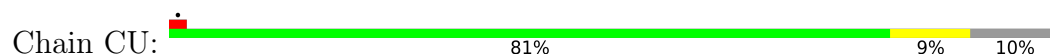




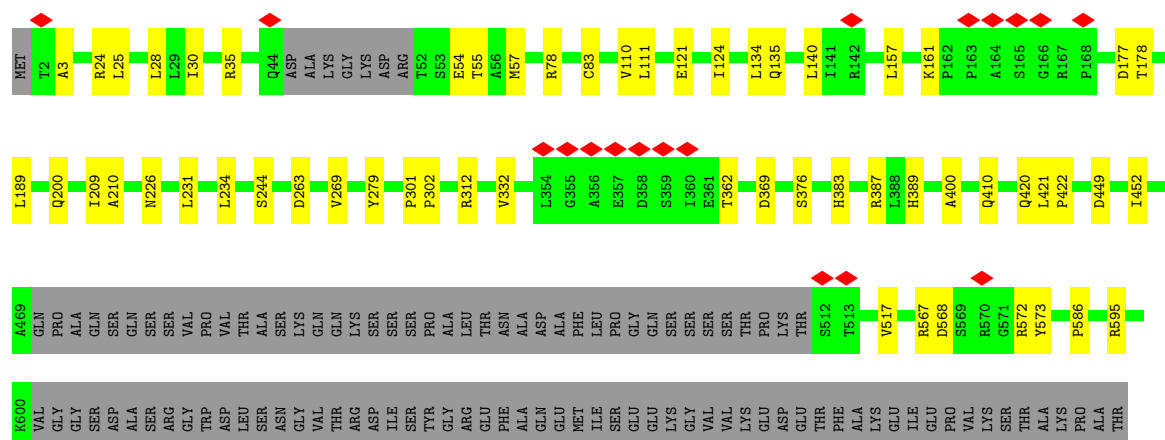
- Molecule 17: Pre-rRNA-processing protein IPI3

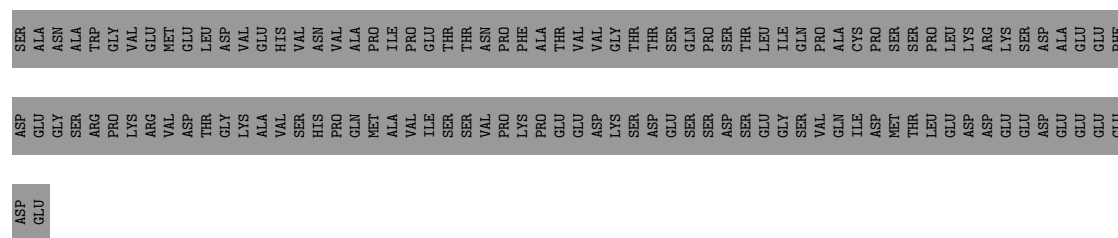


- Molecule 17: Pre-rRNA-processing protein IPI3



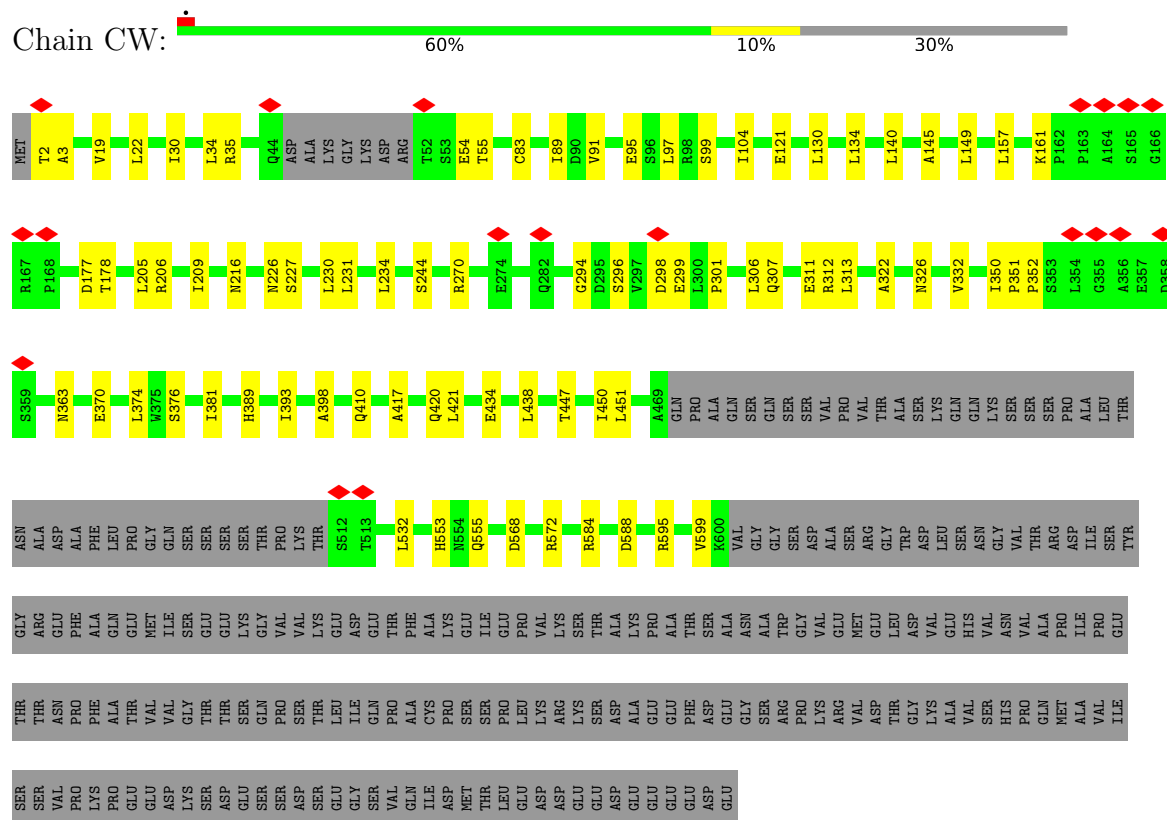
- Molecule 18: Pre-rRNA-processing protein RIX1





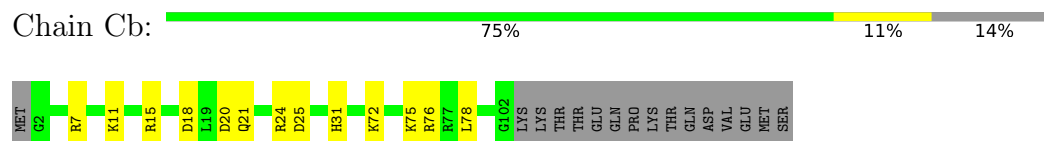
• Molecule 18: Pre-rRNA-processing protein RIX1

Chain CW:



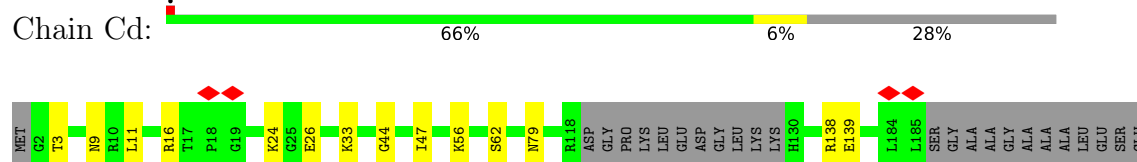
• Molecule 19: Zinc finger domain-containing protein

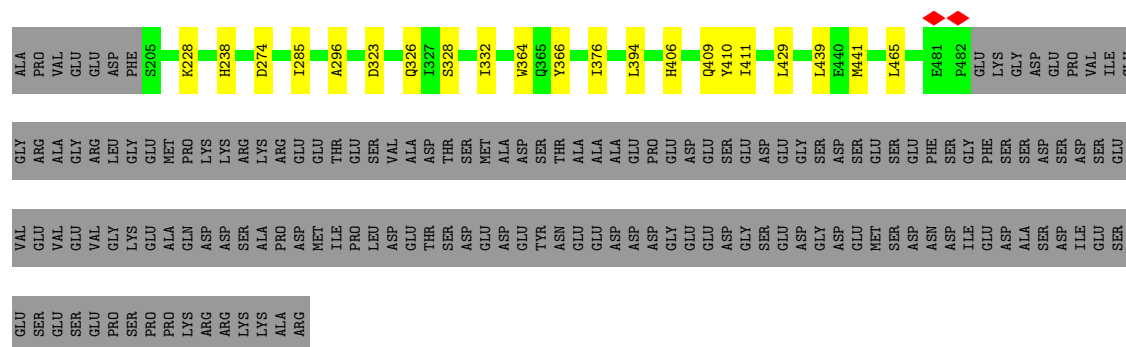
Chain Cb:



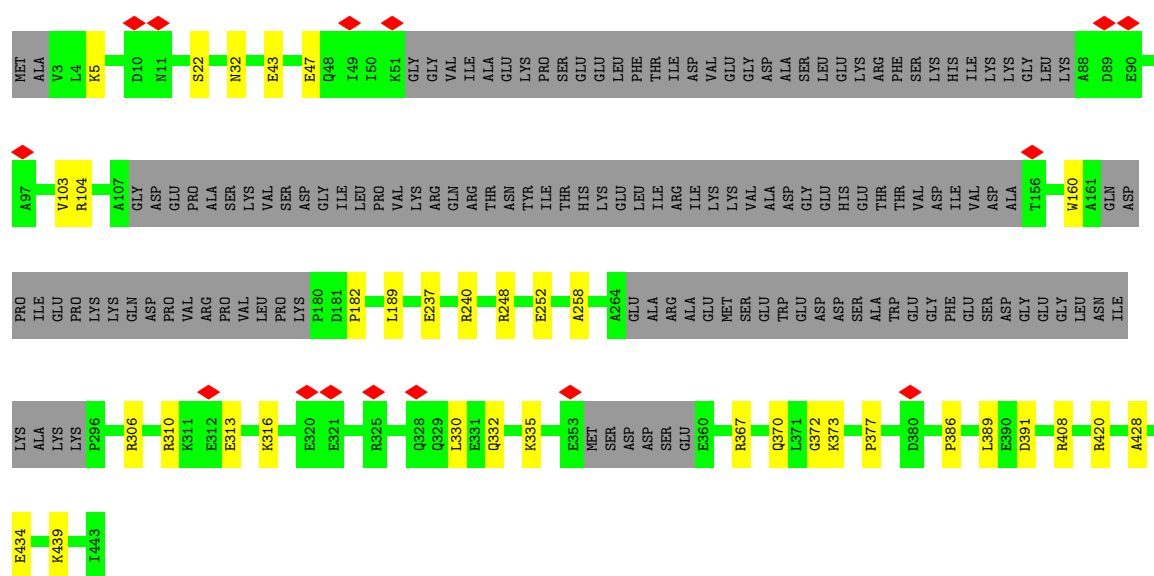
• Molecule 20: Nucleolar GTP-binding protein 2

Chain Cd:

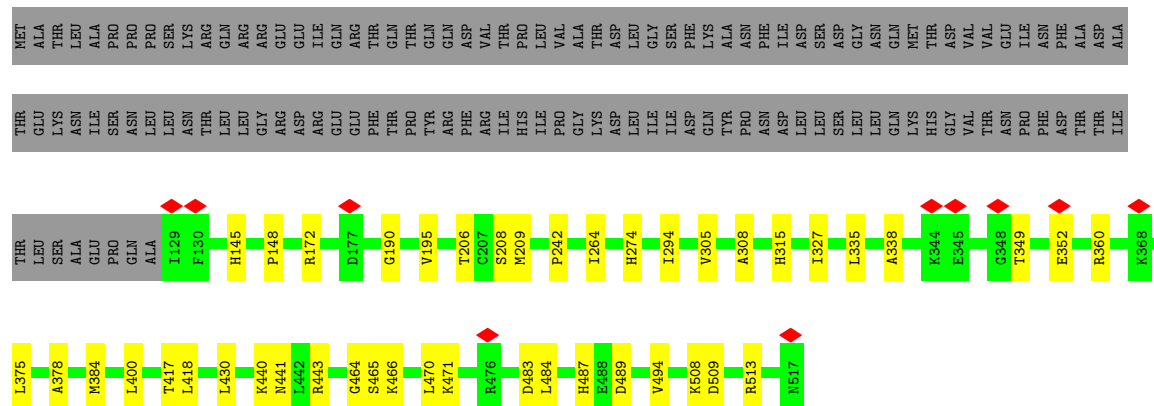




• Molecule 21: Ribosome biogenesis protein NOP53



• Molecule 22: Ribosome assembly protein 4



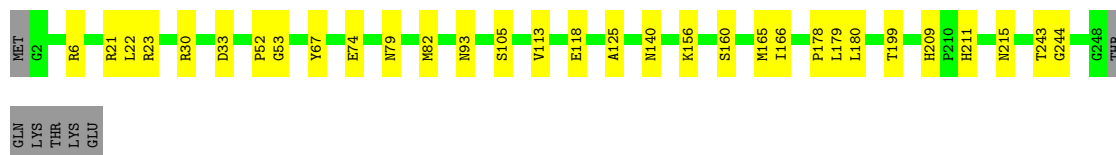
• Molecule 23: rRNA-processing protein

Chain Cz:  75% 9% 16%



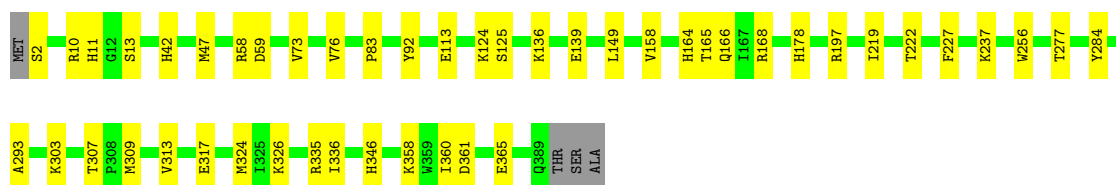
- Molecule 24: 60S ribosomal protein L2-like protein

Chain LA:  85% 12%

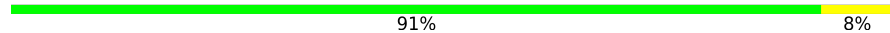


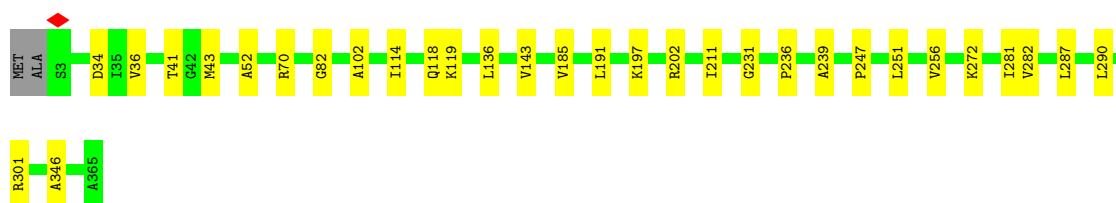
- Molecule 25: 60S ribosomal protein L3-like protein

Chain LB:  87% 12%



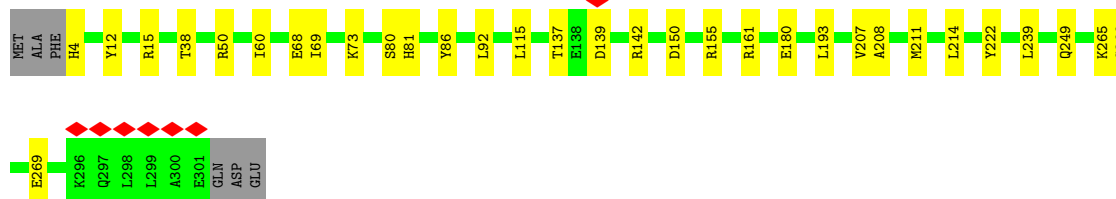
- Molecule 26: 60S ribosomal protein L4-like protein

Chain LC:  91% 8%



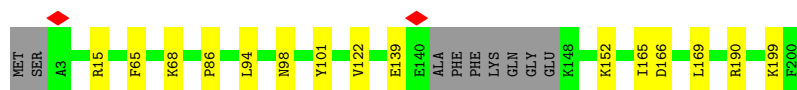
- Molecule 27: 60S ribosomal protein L5-like protein

Chain LD:  88% 11%

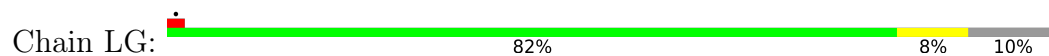


- Molecule 28: 60S ribosomal protein L6

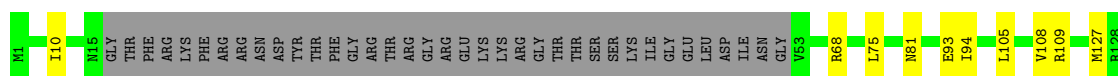
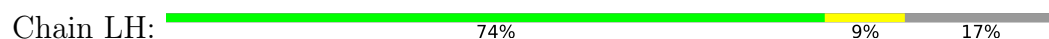
Chain LE:  88% 8%



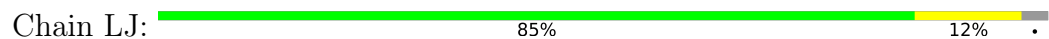
- Molecule 29: 60S ribosomal protein L8



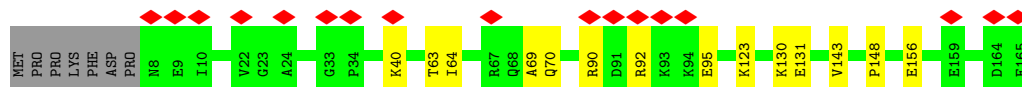
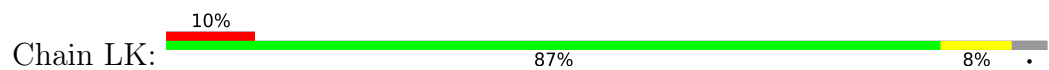
- Molecule 30: 60S ribosomal protein l9-like protein



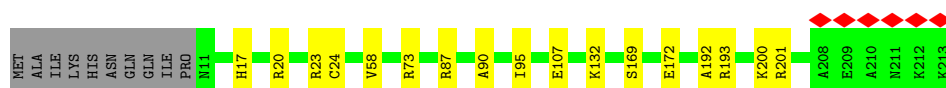
- Molecule 31: Putative ribosomal protein



- Molecule 32: 60S ribosomal protein L12-like protein



- Molecule 33: 60S ribosomal protein L13



- Molecule 34: 60S ribosomal protein L14-like protein

MET	A2	R13	V19	R18	G25	I30	V31	E32	R54	L59	L72	P73	A76	K93	T97	L112	D116	R117	V120	M121	K124	A142
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- Chain LN: 89% 11%

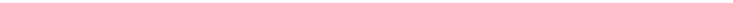
MET	G2	L7	E8	K14	I36	R44	R50	K56	Y62	R63	V64	R68	R73	P84	Q87	R96	E104	R108	D124	S125	L134	D145	L174	R179	E213
-----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------

- Chain LO: 92% 8%

MET	S2	K13	L28	F49	R64	Y65	N66	R87	G88	M89	I90	P91	R103	R127	V128	L129	R130	L131	E159	R162	Y170	K174	Y204
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- Chain LP: 86% 6% 9%

ME1	V2	R3	T7	R16	R62	K115	H116	A122	Q125	S141	P142	T149	L150	T151	E154	GLU	THR	VAL	GLN	LYS	SER	GLU	ALA	VAL	VAL	ARG	ASP	VAL	E168	T185	ALA	ALA
-----	----	----	----	-----	-----	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----

- Chain LQ:  60% 8% 31%

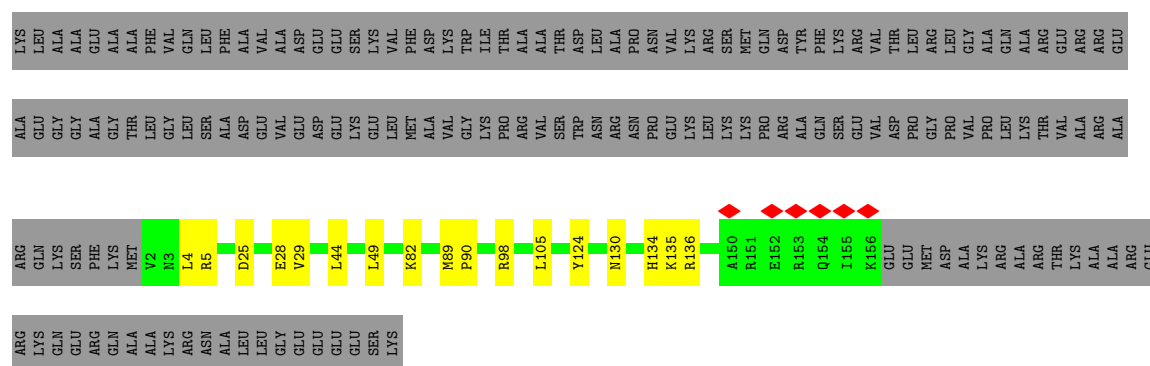
T150	T151	D152	L167	R168	R174	V177	F180	GLY	PHE	GLY	GLY	PRO	PRO	HIS	LYS	HIS	LYS	LYS	LYS	GLU	GLU	TYR	VAL	ARG	VAL	SER	LYS	GLY	GLY	ARG	LYS	PHE	GLU	ARG	ALA	ALA	ARG	TRP	ARG	L34	G31	SER	SER	SER	GLU	LEU	ASN	ARG	ALA	ALA	PHE	ILE	GLY	LEU	CYS	VAL	ASP	LEU	ASP	MET
------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain LR: 5% . 95%

[illegible]







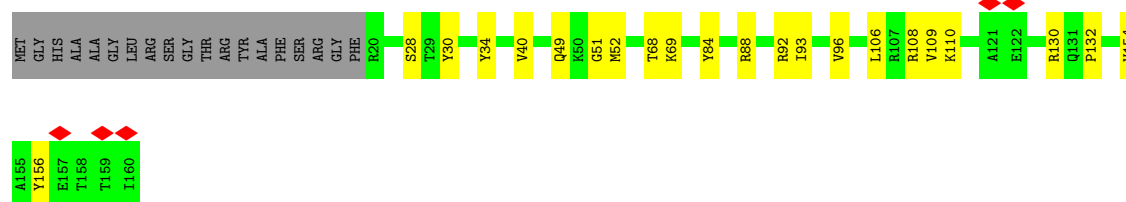
- Molecule 40: 60S ribosomal protein L20

Chain LS: 83% 17% .



- Molecule 41: 60S ribosomal protein l21-like protein

Chain LT: 74% 14% 12%



- Molecule 42: 60S ribosomal protein L22-like protein

Chain LU: 69% 13% 17%



- Molecule 43: 60S ribosomal protein l23-like protein

Chain LV: 88% 9% .

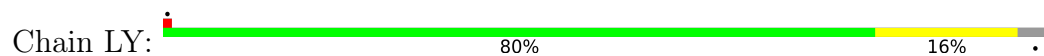


- Molecule 44: 60S ribosomal protein L25-like protein

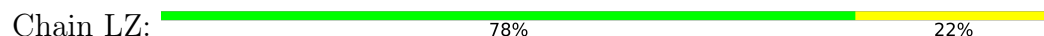
Chain LX: 85% 8% 7%



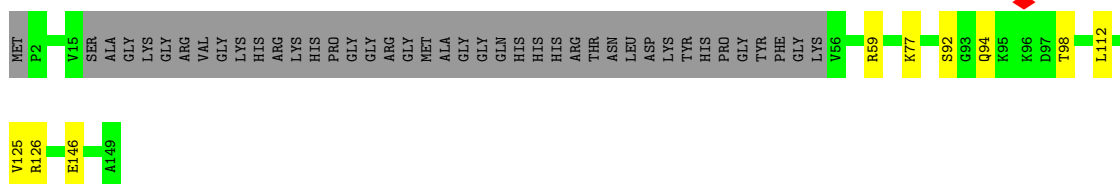
- Molecule 45: 60S ribosomal protein L26-like protein



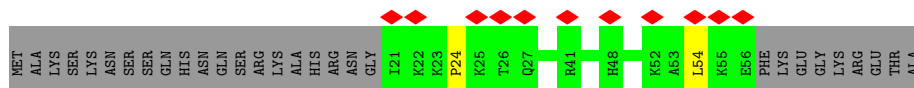
- Molecule 46: 60S ribosomal protein L27



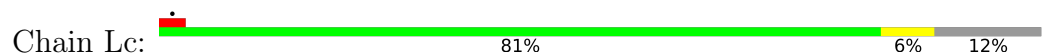
- Molecule 47: 60S ribosomal protein L28-like protein



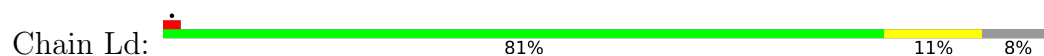
- Molecule 48: 60S ribosomal protein L29

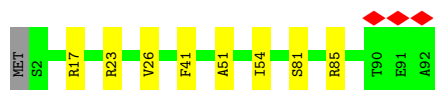


- Molecule 49: 60S ribosomal protein l30-like protein



- Molecule 50: Putative 60S ribosomal protein





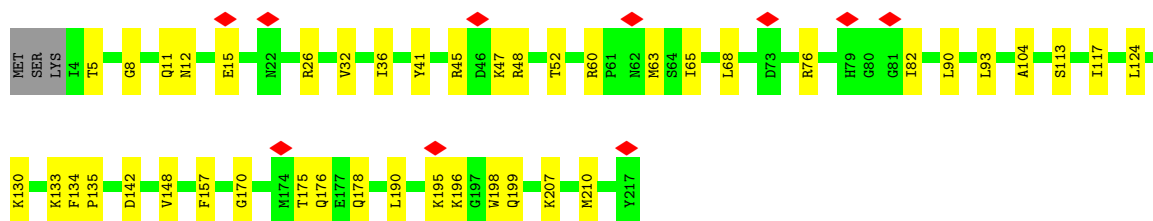
- Molecule 60: Putative 60S ribosomal protein

Chain Lq: 84% 10% 5%



- Molecule 61: Ribosomal protein

Chain Lr: 5% 79% 20%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25753	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.708	Depositor
Minimum map value	0.000	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ZN, OMG, OMC, MG, A2M, OMU

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	C1	0.17	2/73447 (0.0%)	0.31	0/114487
2	C2	0.15	0/3710	0.29	0/5778
3	C3	0.09	0/65	0.21	0/98
4	C4	0.16	0/2737	0.33	0/4262
5	CF	0.15	0/1972	0.39	0/2660
6	CH	0.17	0/5145	0.39	0/6923
7	CI	0.19	0/749	0.58	0/1013
8	CJ	0.16	0/3196	0.36	0/4319
9	CK	0.17	0/1913	0.40	0/2571
10	CL	0.23	0/627	0.61	1/839 (0.1%)
11	CM	0.17	0/1805	0.42	0/2417
11	LF	0.18	0/2061	0.43	0/2765
12	CN	0.18	0/1875	0.46	0/2552
13	CO	0.21	0/470	0.51	0/619
14	CQ	0.20	0/1500	0.46	0/1995
15	CR	0.18	0/3912	0.43	0/5320
16	CS	0.20	0/2442	0.41	0/3315
17	CT	0.19	0/3009	0.49	0/4113
17	CU	0.18	0/3021	0.47	0/4128
18	CV	0.20	0/4312	0.48	2/5897 (0.0%)
18	CW	0.21	0/4299	0.48	2/5882 (0.0%)
19	Cb	0.19	0/845	0.47	0/1128
20	Cd	0.16	0/3691	0.39	2/4975 (0.0%)
21	Ce	0.16	0/2506	0.40	0/3338
22	Ch	0.17	0/3137	0.47	0/4262
23	Cz	0.19	0/892	0.45	0/1167
24	LA	0.19	0/1917	0.42	0/2580
25	LB	0.17	0/3165	0.39	0/4250
26	LC	0.17	0/2802	0.36	0/3778
27	LD	0.16	0/2412	0.43	0/3247
28	LE	0.18	0/1497	0.41	0/2018
29	LG	0.18	0/1909	0.41	0/2556

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	LH	0.16	0/1515	0.41	0/2037
31	LJ	0.19	0/1389	0.49	0/1856
32	LK	0.18	0/1198	0.46	0/1611
33	LL	0.17	0/1614	0.38	0/2168
34	LM	0.16	0/1145	0.37	0/1539
35	LN	0.19	0/1741	0.41	0/2332
36	LO	0.16	0/1645	0.37	0/2205
37	LP	0.16	0/1364	0.40	0/1835
38	LQ	0.16	0/1170	0.37	0/1573
39	LR	0.16	0/1260	0.33	0/1683
40	LS	0.17	0/1465	0.42	1/1970 (0.1%)
41	LT	0.18	0/1146	0.45	0/1546
42	LU	0.18	0/851	0.45	0/1143
43	LV	0.17	0/1009	0.38	0/1357
44	LX	0.19	0/1131	0.45	0/1526
45	LY	0.20	0/1070	0.50	0/1432
46	LZ	0.20	0/1125	0.49	0/1508
47	La	0.16	0/892	0.37	0/1200
48	Lb	0.15	0/293	0.38	0/392
49	Lc	0.17	0/714	0.43	0/960
50	Ld	0.19	0/889	0.43	1/1192 (0.1%)
51	Le	0.21	0/1035	0.50	0/1379
52	Lf	0.18	0/883	0.39	0/1187
53	Lg	0.20	0/914	0.47	0/1228
54	Lh	0.18	0/1014	0.40	0/1349
55	Li	0.16	0/828	0.40	0/1092
56	Lj	0.17	0/712	0.43	0/944
57	Lk	0.21	0/632	0.48	1/842 (0.1%)
58	Ll	0.17	0/446	0.34	0/593
59	Lp	0.20	0/702	0.45	0/935
60	Lq	0.17	0/1079	0.40	0/1454
61	Lr	0.21	0/1684	0.53	1/2266 (0.0%)
All	All	0.17	2/181595 (0.0%)	0.38	11/261586 (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
17	CT	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	1847	A2M	O3'-P	5.04	1.61	1.56
1	C1	848	A2M	O3'-P	5.03	1.61	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	CV	400	ALA	CA-C-N	6.47	124.32	120.24
18	CV	400	ALA	C-N-CA	6.47	124.32	120.24
20	Cd	410	TYR	CA-C-N	5.52	123.72	120.24
20	Cd	410	TYR	C-N-CA	5.52	123.72	120.24
18	CW	451	LEU	CA-C-N	5.47	123.68	120.24

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	CT	42	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	66359	0	33489	431	0
2	C2	3319	0	1678	17	0
3	C3	60	0	32	0	0
4	C4	2451	0	1244	11	0
5	CF	1934	0	1945	19	0
6	CH	5061	0	5152	30	0
7	CI	729	0	707	9	0
8	CJ	3116	0	3122	25	0
9	CK	1878	0	1963	23	0
10	CL	618	0	630	9	0
11	CM	1773	0	1879	14	0
11	LF	2023	0	2132	12	0
12	CN	1850	0	1845	19	0
13	CO	468	0	503	5	0
14	CQ	1476	0	1519	13	0
15	CR	3844	0	3684	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	CS	2391	0	2411	18	0
17	CT	2941	0	2877	28	0
17	CU	2953	0	2906	25	0
18	CV	4217	0	4334	35	0
18	CW	4204	0	4309	48	0
19	Cb	830	0	838	10	0
20	Cd	3614	0	3741	24	0
21	Ce	2476	0	2584	28	0
22	Ch	3050	0	2974	25	0
23	Cz	884	0	967	10	0
24	LA	1878	0	1940	21	0
25	LB	3097	0	3214	30	0
26	LC	2745	0	2864	23	0
27	LD	2366	0	2315	22	0
28	LE	1470	0	1561	10	0
29	LG	1880	0	2018	15	0
30	LH	1495	0	1573	10	0
31	LJ	1367	0	1399	13	0
32	LK	1184	0	1249	11	0
33	LL	1587	0	1655	15	0
34	LM	1126	0	1198	16	0
35	LN	1704	0	1767	16	0
36	LO	1611	0	1702	13	0
37	LP	1343	0	1369	7	0
38	LQ	1156	0	1252	12	0
39	LR	1241	0	1298	12	0
40	LS	1430	0	1492	24	0
41	LT	1124	0	1170	16	0
42	LU	838	0	861	11	0
43	LV	991	0	1044	7	0
44	LX	1113	0	1184	9	0
45	LY	1056	0	1143	14	0
46	LZ	1102	0	1159	22	0
47	La	872	0	903	6	0
48	Lb	286	0	286	2	0
49	Lc	705	0	751	4	0
50	Ld	875	0	918	9	0
51	Le	1017	0	1092	9	0
52	Lf	862	0	891	5	0
53	Lg	901	0	941	5	0
54	Lh	1003	0	1116	7	0
55	Li	821	0	895	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	Lj	698	0	726	12	0
57	Lk	624	0	671	10	0
58	Ll	436	0	473	7	0
59	Lp	694	0	733	8	0
60	Lq	1061	0	1108	12	0
61	Lr	1660	0	1768	30	0
62	CH	32	0	12	1	0
62	Cd	32	0	12	0	0
63	CH	1	0	0	0	0
63	Cd	2	0	0	0	0
64	CQ	1	0	0	0	0
64	Cb	1	0	0	0	0
64	Lg	1	0	0	0	0
64	Lj	1	0	0	0	0
64	Lp	1	0	0	0	0
65	C1	1	0	0	0	0
65	CH	1	0	0	0	0
65	Cd	2	0	0	0	0
All	All	172014	0	139188	1144	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 4.

The worst 5 of 1144 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:C1:1107:U:H3	1:C1:1117:G:H1	1.19	0.86
8:CJ:128:ARG:HH12	21:Ce:160:TRP:H	1.23	0.83
1:C1:1809:G:HO2'	8:CJ:2:GLY:N	1.79	0.81
1:C1:3289:G:H1	1:C1:3298:U:H3	1.27	0.81
40:LS:93:GLU:HG3	40:LS:140:ILE:HD12	1.66	0.75

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
5	CF	243/270 (90%)	241 (99%)	2 (1%)	0	100	100
6	CH	621/661 (94%)	616 (99%)	5 (1%)	0	100	100
7	CI	91/414 (22%)	90 (99%)	1 (1%)	0	100	100
8	CJ	376/679 (55%)	374 (100%)	2 (0%)	0	100	100
9	CK	227/261 (87%)	223 (98%)	4 (2%)	0	100	100
10	CL	77/558 (14%)	76 (99%)	1 (1%)	0	100	100
11	CM	211/249 (85%)	206 (98%)	5 (2%)	0	100	100
11	LF	246/249 (99%)	241 (98%)	4 (2%)	1 (0%)	30	54
12	CN	244/246 (99%)	237 (97%)	7 (3%)	0	100	100
13	CO	56/120 (47%)	54 (96%)	2 (4%)	0	100	100
14	CQ	181/225 (80%)	178 (98%)	3 (2%)	0	100	100
15	CR	510/767 (66%)	504 (99%)	6 (1%)	0	100	100
16	CS	301/338 (89%)	298 (99%)	3 (1%)	0	100	100
17	CT	391/437 (90%)	384 (98%)	7 (2%)	0	100	100
17	CU	391/437 (90%)	380 (97%)	11 (3%)	0	100	100
18	CV	544/781 (70%)	535 (98%)	9 (2%)	0	100	100
18	CW	544/781 (70%)	536 (98%)	8 (2%)	0	100	100
19	Cb	99/117 (85%)	98 (99%)	1 (1%)	0	100	100
20	Cd	445/627 (71%)	437 (98%)	8 (2%)	0	100	100
21	Ce	290/443 (66%)	285 (98%)	5 (2%)	0	100	100
22	Ch	388/517 (75%)	375 (97%)	13 (3%)	0	100	100
23	Cz	101/123 (82%)	100 (99%)	1 (1%)	0	100	100
24	LA	245/254 (96%)	238 (97%)	7 (3%)	0	100	100
25	LB	386/392 (98%)	380 (98%)	6 (2%)	0	100	100
26	LC	361/365 (99%)	356 (99%)	5 (1%)	0	100	100
27	LD	296/304 (97%)	289 (98%)	7 (2%)	0	100	100
28	LE	187/200 (94%)	182 (97%)	5 (3%)	0	100	100
29	LG	233/262 (89%)	230 (99%)	3 (1%)	0	100	100
30	LH	188/229 (82%)	184 (98%)	4 (2%)	0	100	100
31	LJ	166/173 (96%)	163 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	LK	156/165 (94%)	156 (100%)	0	0	100	100
33	LL	201/213 (94%)	199 (99%)	2 (1%)	0	100	100
34	LM	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
35	LN	200/203 (98%)	196 (98%)	4 (2%)	0	100	100
36	LO	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
37	LP	167/187 (89%)	164 (98%)	3 (2%)	0	100	100
38	LQ	142/213 (67%)	140 (99%)	2 (1%)	0	100	100
39	LR	153/2898 (5%)	152 (99%)	1 (1%)	0	100	100
40	LS	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
41	LT	139/160 (87%)	136 (98%)	3 (2%)	0	100	100
42	LU	103/127 (81%)	100 (97%)	3 (3%)	0	100	100
43	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
44	LX	143/156 (92%)	139 (97%)	4 (3%)	0	100	100
45	LY	131/138 (95%)	126 (96%)	5 (4%)	0	100	100
46	LZ	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
47	La	104/149 (70%)	101 (97%)	3 (3%)	0	100	100
48	Lb	34/65 (52%)	34 (100%)	0	0	100	100
49	Lc	93/108 (86%)	92 (99%)	1 (1%)	0	100	100
50	Ld	108/120 (90%)	108 (100%)	0	0	100	100
51	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
52	Lf	106/109 (97%)	103 (97%)	3 (3%)	0	100	100
53	Lg	116/119 (98%)	114 (98%)	2 (2%)	0	100	100
54	Lh	120/935 (13%)	116 (97%)	4 (3%)	0	100	100
55	Li	99/110 (90%)	99 (100%)	0	0	100	100
56	Lj	86/95 (90%)	86 (100%)	0	0	100	100
57	Lk	74/94 (79%)	74 (100%)	0	0	100	100
58	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
59	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
60	Lq	137/147 (93%)	134 (98%)	3 (2%)	0	100	100
61	Lr	212/217 (98%)	209 (99%)	3 (1%)	0	100	100
All	All	12502/19275 (65%)	12289 (98%)	212 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	LF	197	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CF	212/236 (90%)	212 (100%)	0	100	100
6	CH	548/575 (95%)	548 (100%)	0	100	100
7	CI	70/336 (21%)	70 (100%)	0	100	100
8	CJ	331/579 (57%)	331 (100%)	0	100	100
9	CK	203/225 (90%)	203 (100%)	0	100	100
10	CL	60/458 (13%)	60 (100%)	0	100	100
11	CM	185/215 (86%)	185 (100%)	0	100	100
11	LF	213/215 (99%)	213 (100%)	0	100	100
12	CN	204/206 (99%)	204 (100%)	0	100	100
13	CO	48/99 (48%)	48 (100%)	0	100	100
14	CQ	143/192 (74%)	143 (100%)	0	100	100
15	CR	374/663 (56%)	374 (100%)	0	100	100
16	CS	260/291 (89%)	260 (100%)	0	100	100
17	CT	323/376 (86%)	323 (100%)	0	100	100
17	CU	327/376 (87%)	327 (100%)	0	100	100
18	CV	472/675 (70%)	472 (100%)	0	100	100
18	CW	469/675 (70%)	469 (100%)	0	100	100
19	Cb	85/101 (84%)	85 (100%)	0	100	100
20	Cd	395/541 (73%)	395 (100%)	0	100	100
21	Ce	262/383 (68%)	262 (100%)	0	100	100
22	Ch	322/436 (74%)	322 (100%)	0	100	100
23	Cz	91/107 (85%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	LA	190/198 (96%)	190 (100%)	0	100	100
25	LB	328/331 (99%)	328 (100%)	0	100	100
26	LC	281/285 (99%)	281 (100%)	0	100	100
27	LD	233/253 (92%)	233 (100%)	0	100	100
28	LE	155/166 (93%)	155 (100%)	0	100	100
29	LG	197/222 (89%)	197 (100%)	0	100	100
30	LH	167/200 (84%)	167 (100%)	0	100	100
31	LJ	144/150 (96%)	143 (99%)	1 (1%)	76	86
32	LK	127/136 (93%)	127 (100%)	0	100	100
33	LL	158/176 (90%)	158 (100%)	0	100	100
34	LM	116/117 (99%)	116 (100%)	0	100	100
35	LN	179/180 (99%)	179 (100%)	0	100	100
36	LO	162/163 (99%)	162 (100%)	0	100	100
37	LP	133/152 (88%)	133 (100%)	0	100	100
38	LQ	124/178 (70%)	124 (100%)	0	100	100
39	LR	125/2396 (5%)	125 (100%)	0	100	100
40	LS	153/154 (99%)	153 (100%)	0	100	100
41	LT	120/135 (89%)	120 (100%)	0	100	100
42	LU	90/108 (83%)	90 (100%)	0	100	100
43	LV	98/102 (96%)	98 (100%)	0	100	100
44	LX	117/129 (91%)	117 (100%)	0	100	100
45	LY	116/119 (98%)	116 (100%)	0	100	100
46	LZ	119/121 (98%)	119 (100%)	0	100	100
47	La	93/122 (76%)	93 (100%)	0	100	100
48	Lb	28/55 (51%)	28 (100%)	0	100	100
49	Lc	76/88 (86%)	76 (100%)	0	100	100
50	Ld	90/105 (86%)	90 (100%)	0	100	100
51	Le	109/114 (96%)	109 (100%)	0	100	100
52	Lf	89/90 (99%)	89 (100%)	0	100	100
53	Lg	91/102 (89%)	91 (100%)	0	100	100
54	Lh	109/781 (14%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	Li	84/93 (90%)	84 (100%)	0	100	100
56	Lj	72/78 (92%)	72 (100%)	0	100	100
57	Lk	71/88 (81%)	71 (100%)	0	100	100
58	Ll	45/46 (98%)	45 (100%)	0	100	100
59	Lp	72/74 (97%)	72 (100%)	0	100	100
60	Lq	107/112 (96%)	107 (100%)	0	100	100
61	Lr	186/189 (98%)	186 (100%)	0	100	100
All	All	10551/16268 (65%)	10550 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	LJ	40	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
47	La	11	HIS
47	La	94	GLN
56	Lj	13	ASN
18	CV	553	HIS
18	CV	383	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3079/3342 (92%)	557 (18%)	17 (0%)
2	C2	155/156 (99%)	21 (13%)	0
3	C3	2/162 (1%)	1 (50%)	0
4	C4	113/119 (94%)	21 (18%)	0
All	All	3349/3779 (88%)	600 (17%)	17 (0%)

5 of 600 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	G
1	C1	23	G

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Mol	Chain	Res	Type
1	C1	27	A
1	C1	50	A
1	C1	60	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3258	U
1	C1	3301	C
1	C1	2409	U
1	C1	2712	G
1	C1	3079	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMC	C1	778	1	19,22,23	0.56	0	25,31,34	0.90	1 (4%)
1	A2M	C1	848	1	22,25,26	4.01	12 (54%)	30,36,39	3.44	15 (50%)
1	A2M	C1	2289	1	22,25,26	4.01	12 (54%)	30,36,39	3.32	14 (46%)
1	OMG	C1	646	1	23,26,27	0.48	0	32,38,41	0.49	0
1	OMC	C1	1812	1	19,22,23	0.55	0	25,31,34	0.76	0
1	OMC	C1	1836	1	19,22,23	0.59	0	25,31,34	0.97	1 (4%)
1	OMG	C1	2358	1	23,26,27	0.48	0	32,38,41	0.53	0
1	A2M	C1	389	1	22,25,26	3.98	11 (50%)	30,36,39	3.40	13 (43%)
1	A2M	C1	1223	1	22,25,26	3.98	11 (50%)	30,36,39	3.32	12 (40%)
1	OMG	C1	2881	1	23,26,27	0.47	0	32,38,41	0.45	0
1	OMG	C1	2876	1	23,26,27	0.48	0	32,38,41	0.48	0
1	A2M	C1	1847	1	22,25,26	3.98	12 (54%)	30,36,39	3.51	14 (46%)
1	OMU	C1	2683	1	19,22,23	3.11	6 (31%)	25,31,34	1.85	5 (20%)
1	A2M	C1	637	1	22,25,26	3.99	11 (50%)	30,36,39	3.38	13 (43%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	C1	1420	1	19,22,23	0.56	0	25,31,34	1.04	1 (4%)
1	OMG	C1	627	1	23,26,27	0.53	0	32,38,41	0.48	0
1	OMU	C1	2688	1	19,22,23	3.17	6 (31%)	25,31,34	1.77	4 (16%)
1	OMG	C1	1433	1	23,26,27	0.48	0	32,38,41	0.50	0
1	OMU	C1	1917	1	19,22,23	3.14	6 (31%)	25,31,34	1.90	5 (20%)
1	A2M	C1	858	1	22,25,26	4.00	11 (50%)	30,36,39	3.43	13 (43%)
1	OMC	C1	2300	1	19,22,23	0.51	0	25,31,34	0.71	0
1	OMG	C1	385	1	23,26,27	0.47	0	32,38,41	0.58	0
1	OMC	C1	2918	1	19,22,23	0.55	0	25,31,34	0.78	0
1	OMU	C1	2380	1	19,22,23	3.05	6 (31%)	25,31,34	1.81	5 (20%)
1	OMC	C1	1491	1	19,22,23	0.54	0	25,31,34	0.76	0
1	A2M	C1	1432	1	22,25,26	3.99	12 (54%)	30,36,39	3.39	13 (43%)
1	OMU	C1	2384	1	19,22,23	3.09	6 (31%)	25,31,34	1.77	4 (16%)
1	OMG	C1	2774	1	23,26,27	0.47	0	32,38,41	0.46	0
1	OMG	C1	787	1	23,26,27	0.49	0	32,38,41	0.59	0
1	OMC	C1	2838	1	19,22,23	0.59	0	25,31,34	0.97	2 (8%)
1	OMU	C1	1868	1	19,22,23	3.09	6 (31%)	25,31,34	1.87	5 (20%)
1	OMU	C1	2690	1	19,22,23	3.24	6 (31%)	25,31,34	1.87	7 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	C1	778	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	848	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	2289	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	646	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	1812	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1836	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2358	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	389	1	-	2/9/27/28	0/3/3/3
1	A2M	C1	1223	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	2881	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	2876	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	1847	1	-	3/9/27/28	0/3/3/3
1	OMU	C1	2683	1	-	2/9/27/28	0/2/2/2
1	A2M	C1	637	1	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	C1	1420	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	627	1	-	2/9/27/28	0/3/3/3
1	OMU	C1	2688	1	-	2/9/27/28	0/2/2/2
1	OMG	C1	1433	1	-	2/9/27/28	0/3/3/3
1	OMU	C1	1917	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	858	1	-	1/9/27/28	0/3/3/3
1	OMC	C1	2300	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	385	1	-	2/9/27/28	0/3/3/3
1	OMC	C1	2918	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2380	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1491	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	1432	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2384	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	2774	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	787	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	2838	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2690	1	-	3/9/27/28	0/2/2/2

The worst 5 of 134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2289	A2M	C3'-C2'	-13.09	1.24	1.53
1	C1	848	A2M	C3'-C2'	-13.04	1.24	1.53
1	C1	858	A2M	C3'-C2'	-13.03	1.24	1.53
1	C1	1223	A2M	C3'-C2'	-12.98	1.24	1.53
1	C1	637	A2M	C3'-C2'	-12.97	1.24	1.53

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1847	A2M	C1'-N9-C8	-9.66	105.66	127.09
1	C1	858	A2M	C1'-N9-C8	-9.38	106.28	127.09
1	C1	1432	A2M	C1'-N9-C8	-9.28	106.49	127.09
1	C1	389	A2M	C1'-N9-C8	-9.22	106.63	127.09
1	C1	637	A2M	C1'-N9-C8	-9.18	106.72	127.09

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	389	A2M	C1'-C2'-O2'-CM'
1	C1	637	A2M	C1'-C2'-O2'-CM'
1	C1	1223	A2M	C1'-C2'-O2'-CM'
1	C1	1433	OMG	O4'-C4'-C5'-O5'
1	C1	2384	OMU	C1'-C2'-O2'-CM2

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	848	A2M	1	0
1	C1	389	A2M	1	0
1	C1	1223	A2M	1	0
1	C1	1420	OMC	1	0
1	C1	627	OMG	1	0
1	C1	1432	A2M	1	0
1	C1	2384	OMU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	$\# Z > 2$
62	GTP	Cd	1000	63	33,34,34	0.96	1 (3%)	50,54,54	1.61	9 (18%)
62	GTP	CH	701	63	33,34,34	0.89	1 (3%)	50,54,54	1.57	9 (18%)

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
62	GTP	Cd	1000	63	-	3/22/38/38	0/3/3/3
62	GTP	CH	701	63	-	4/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	Cd	1000	GTP	C2-N3	2.19	1.38	1.33
62	CH	701	GTP	C2-N3	2.07	1.38	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	Cd	1000	GTP	C5-C4-N3	-5.09	120.29	128.39
62	CH	701	GTP	C5-C4-N3	-4.78	120.78	128.39
62	Cd	1000	GTP	C2-N3-C4	4.64	120.29	112.30
62	CH	701	GTP	C2-N3-C4	4.55	120.13	112.30
62	Cd	1000	GTP	N9-C4-N3	3.31	132.56	125.95

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	CH	701	GTP	C5'-O5'-PA-O1A
62	CH	701	GTP	O4'-C4'-C5'-O5'
62	Cd	1000	GTP	C3'-C4'-C5'-O5'
62	Cd	1000	GTP	O4'-C4'-C5'-O5'
62	CH	701	GTP	PB-O3A-PA-O1A

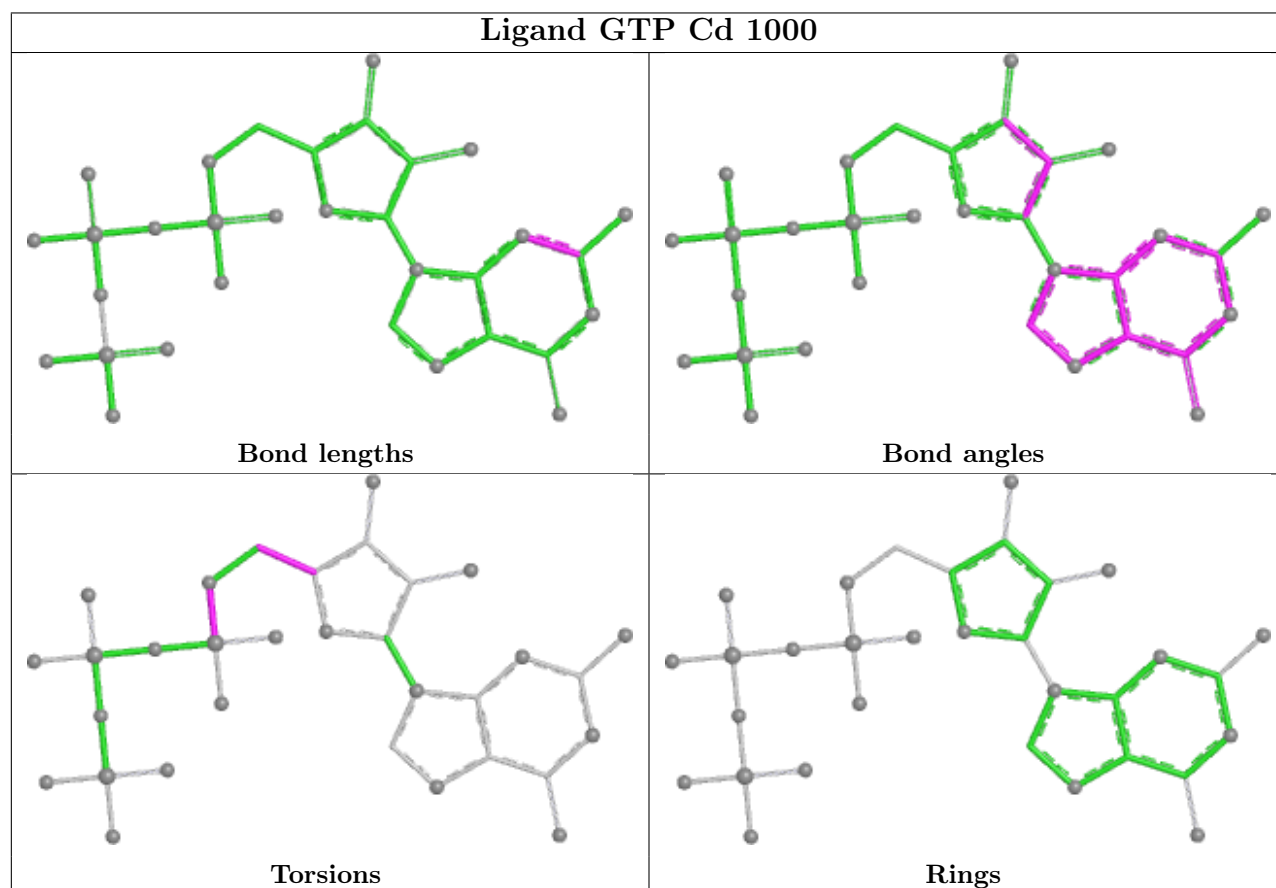
There are no ring outliers.

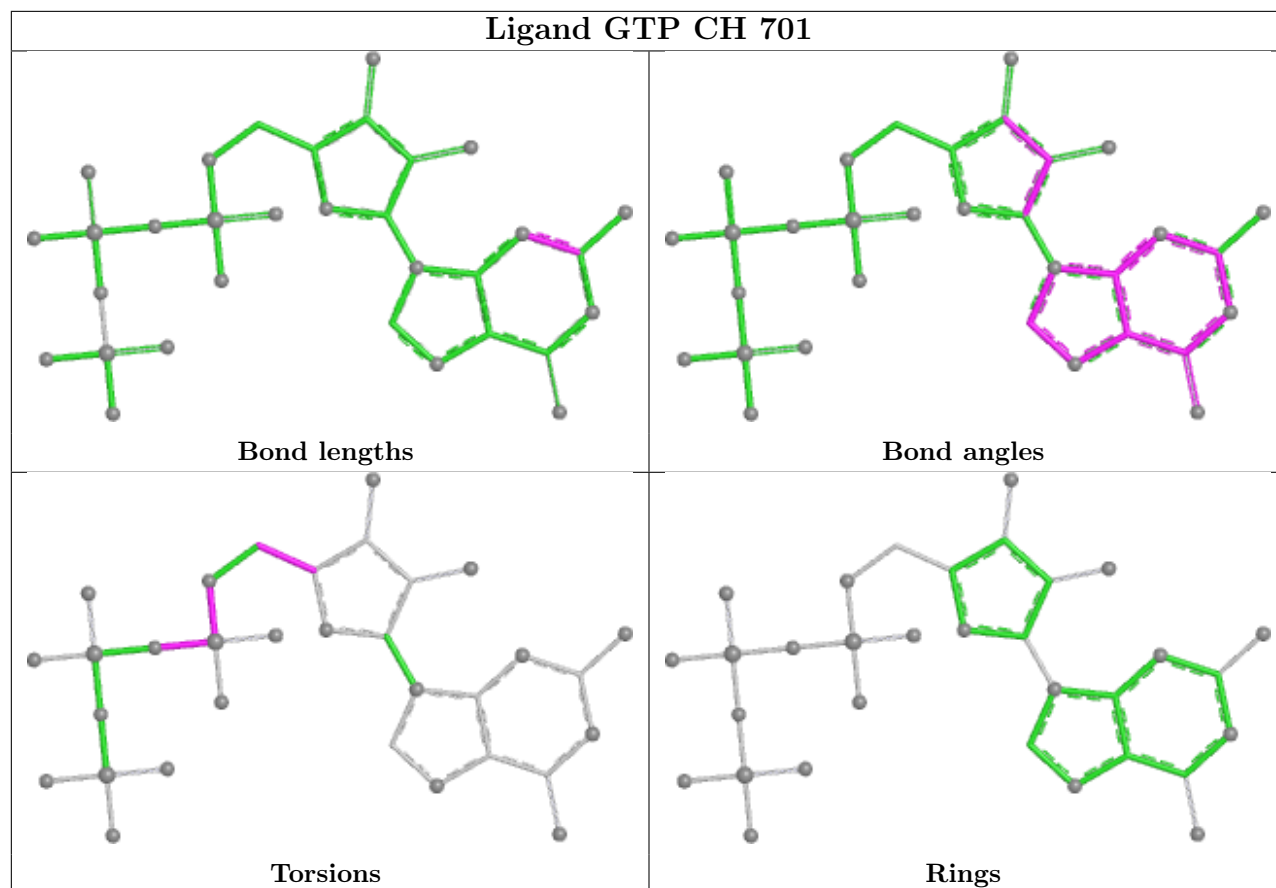
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	CH	701	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

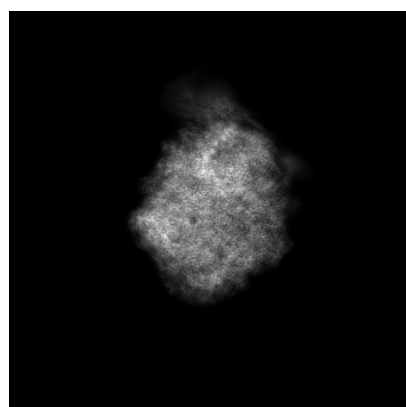
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17955. These allow visual inspection of the internal detail of the map and identification of artifacts.

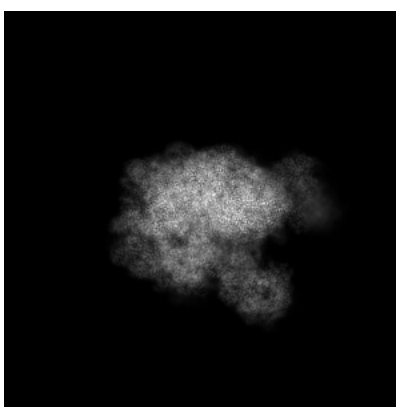
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

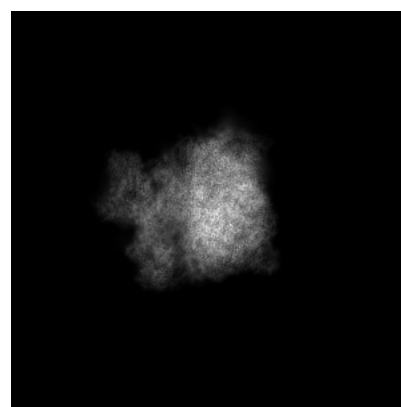
6.1.1 Primary map



X



Y

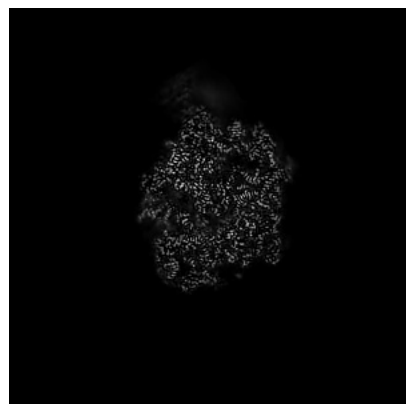


Z

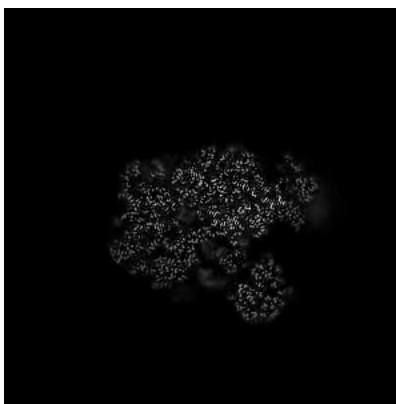
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

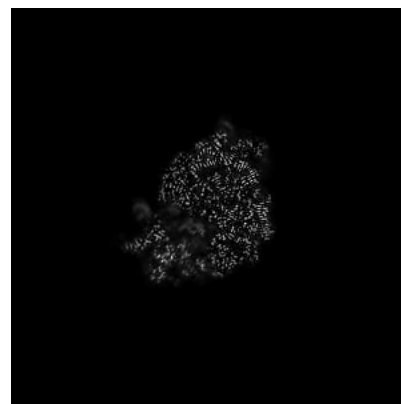
6.2.1 Primary map



X Index: 250



Y Index: 250

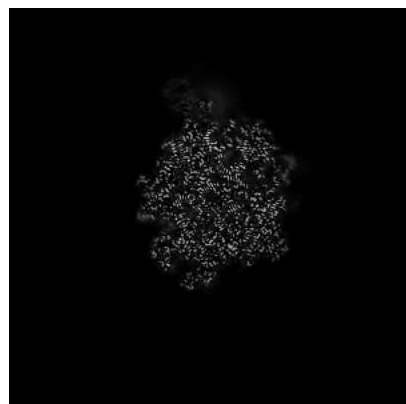


Z Index: 250

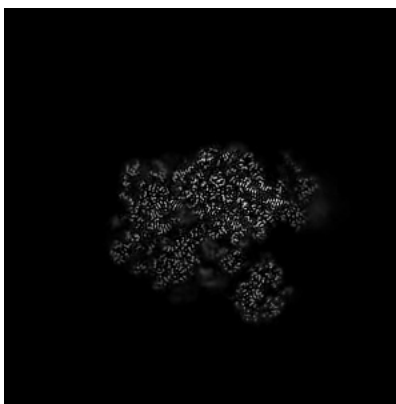
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

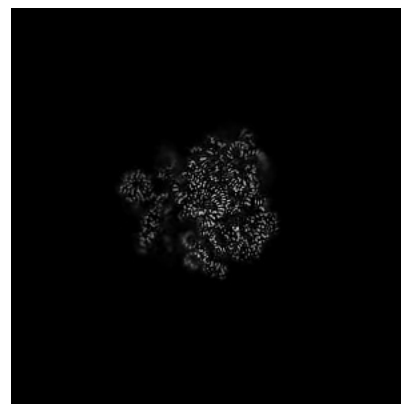
6.3.1 Primary map



X Index: 259



Y Index: 248

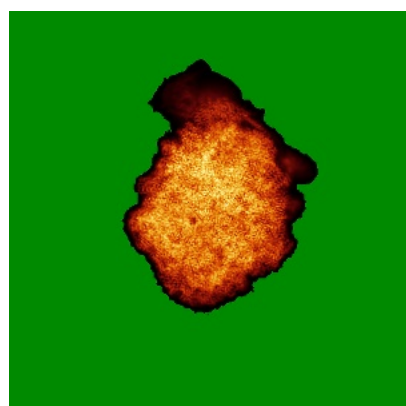


Z Index: 274

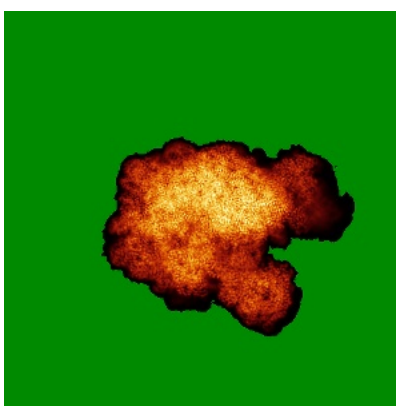
The images above show the largest variance slices of the map in three orthogonal directions.

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

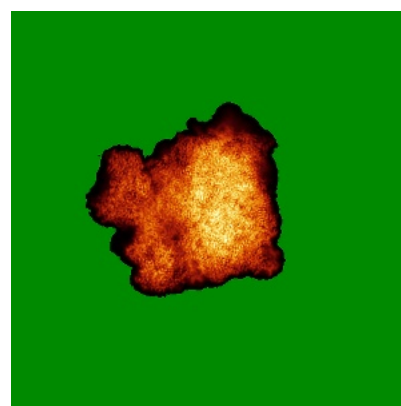
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

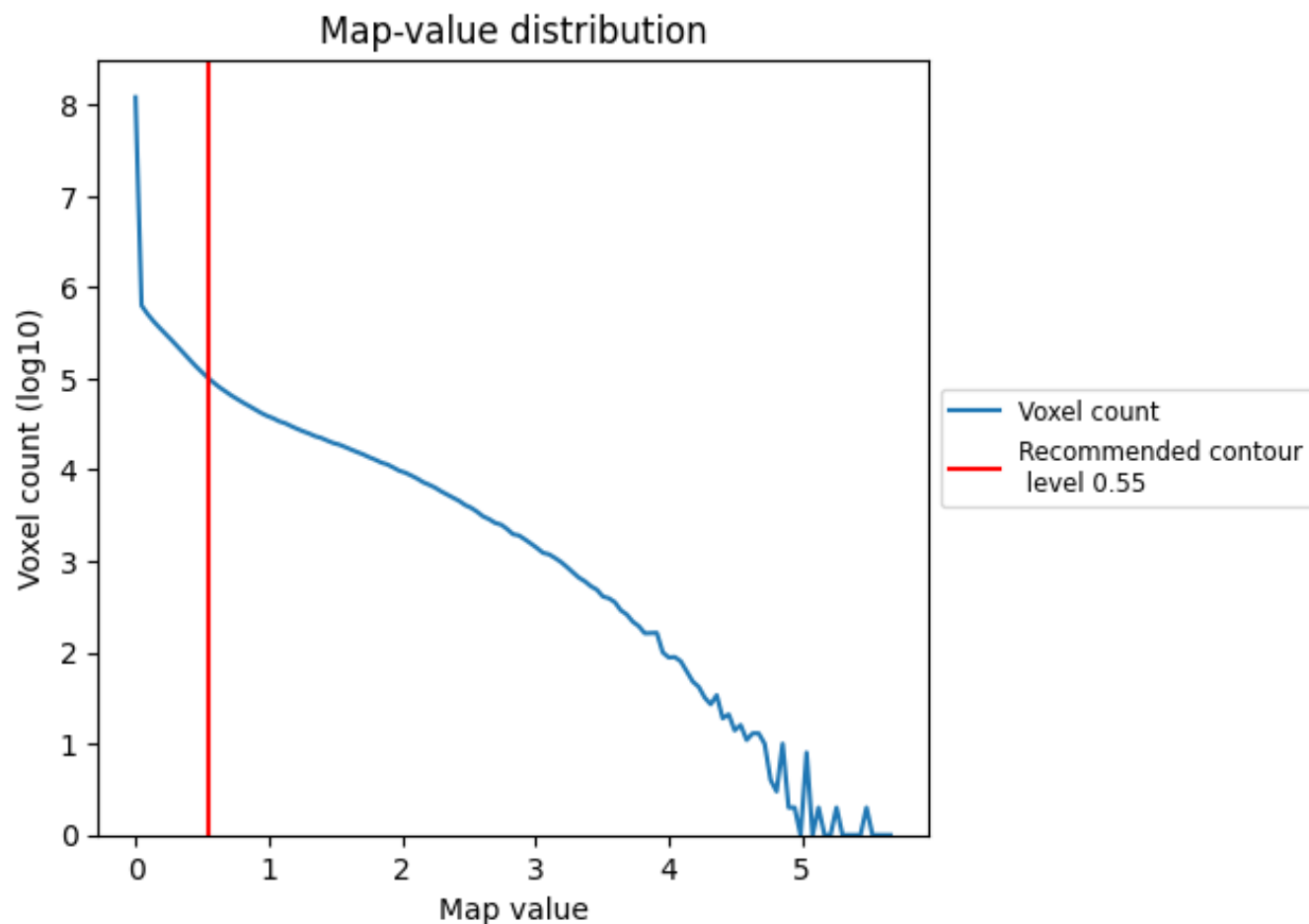
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

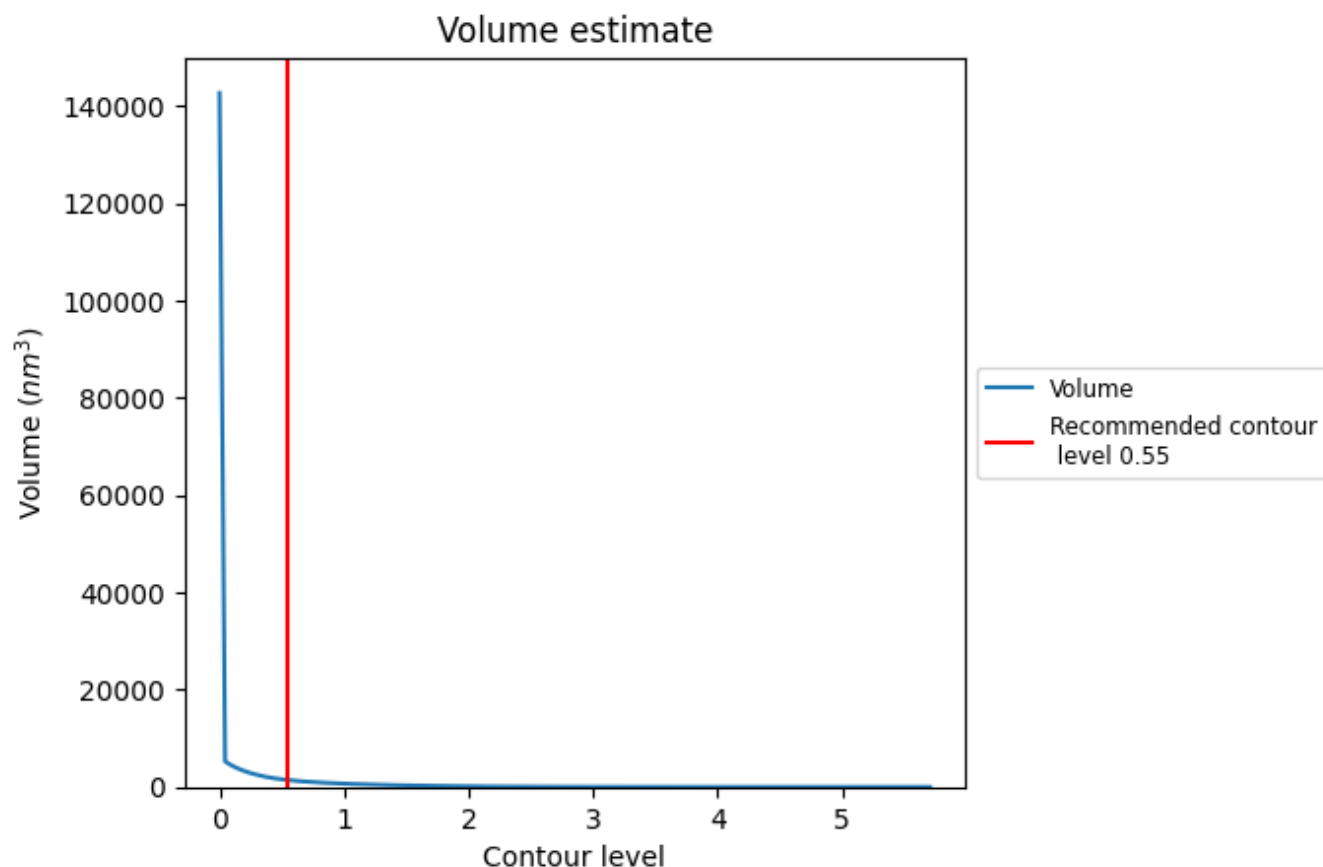
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

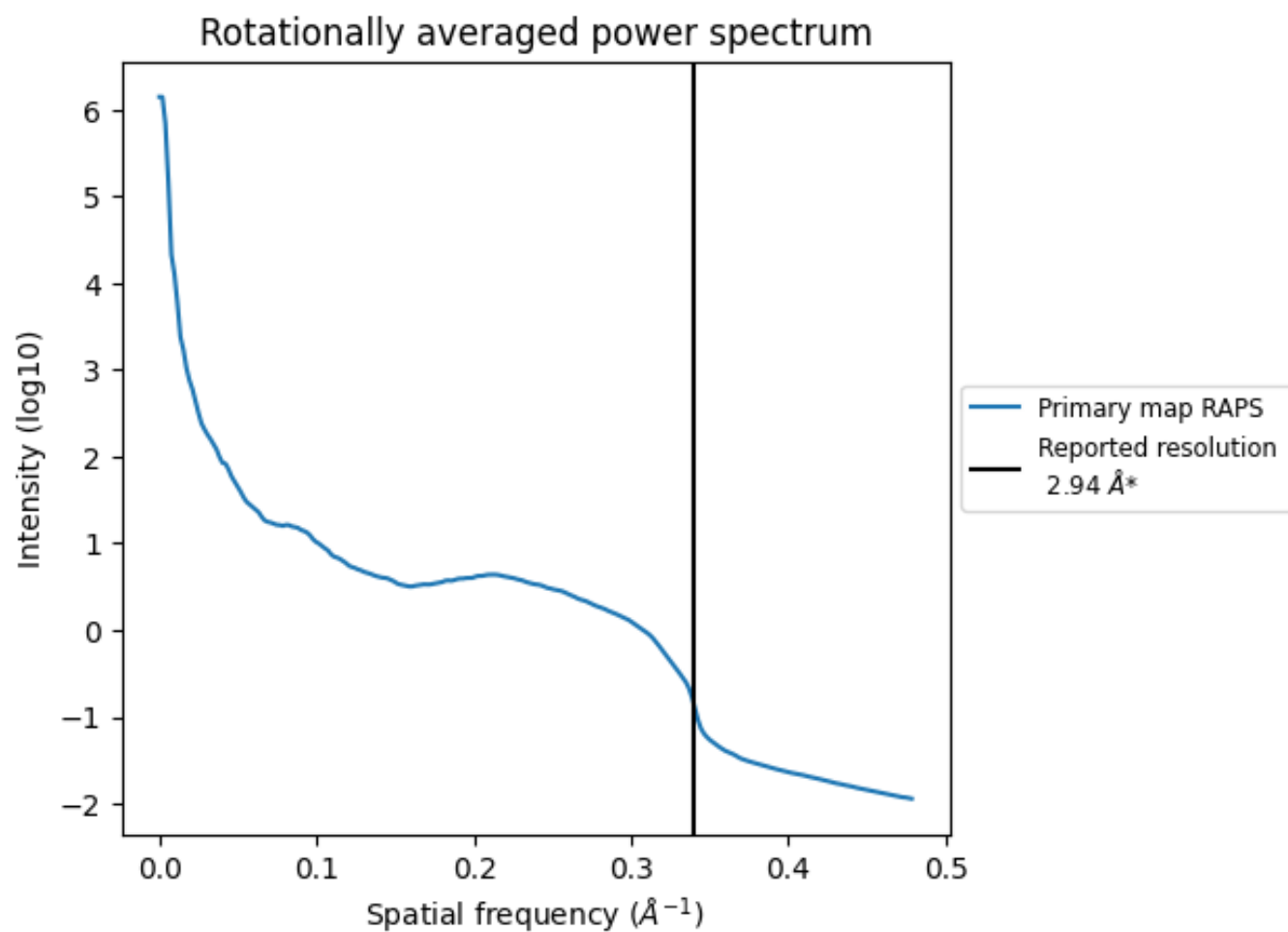
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1418 nm^3 ; this corresponds to an approximate mass of 1281 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 0.340 Å⁻¹

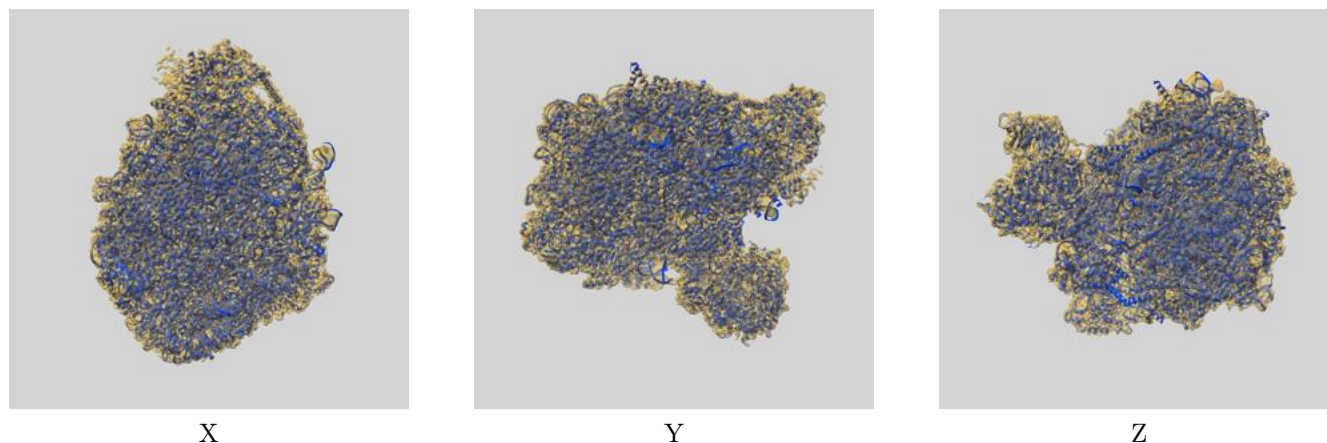
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

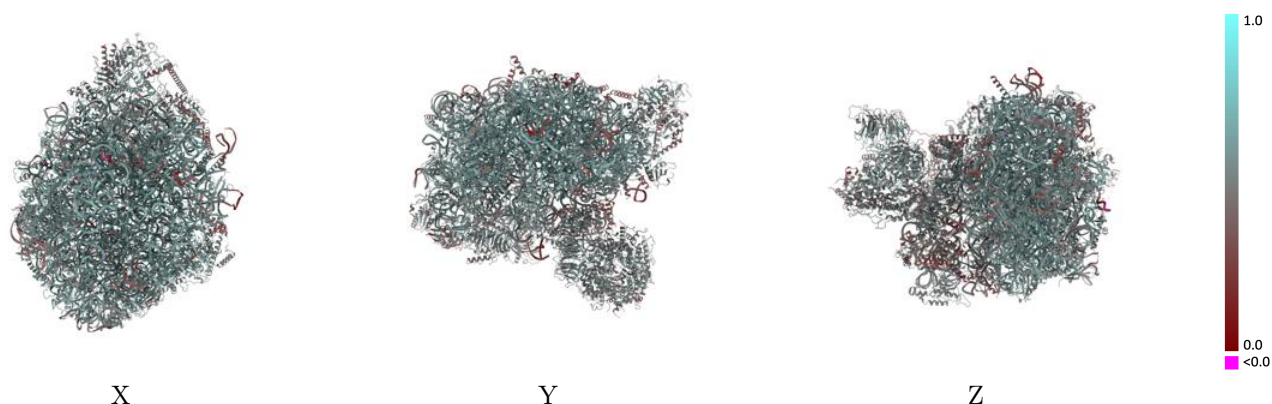
This section contains information regarding the fit between EMDB map EMD-17955 and PDB model 8PV6. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

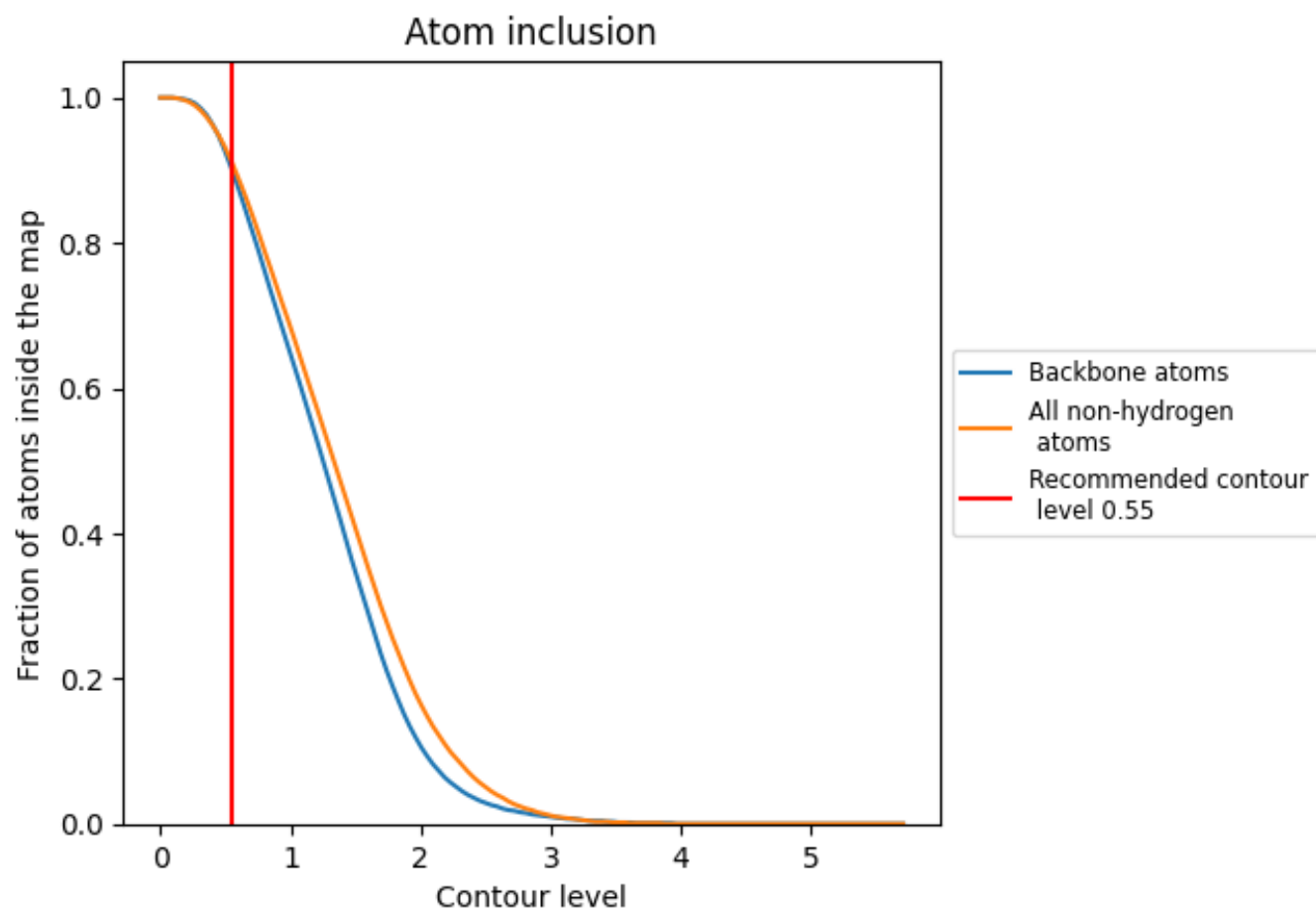


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 91% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.5470
C1	 0.9730	 0.5650
C2	 0.9650	 0.5840
C3	 0.7830	 0.4850
C4	 0.9910	 0.5130
CF	 0.8150	 0.5010
CH	 0.8540	 0.5350
CI	 0.7360	 0.4770
CJ	 0.8890	 0.5370
CK	 0.9190	 0.5800
CL	 0.5890	 0.4240
CM	 0.7900	 0.4600
CN	 0.9200	 0.5660
CO	 0.8470	 0.5430
CQ	 0.8550	 0.5330
CR	 0.7820	 0.4910
CS	 0.6840	 0.4670
CT	 0.8430	 0.4930
CU	 0.8490	 0.5120
CV	 0.8310	 0.4910
CW	 0.8550	 0.4970
Cb	 0.9090	 0.5610
Cd	 0.8710	 0.5560
Ce	 0.7550	 0.4740
Ch	 0.8490	 0.5090
Cz	 0.7980	 0.4710
LA	 0.9700	 0.6120
LB	 0.9610	 0.6020
LC	 0.9410	 0.5920
LD	 0.8980	 0.4940
LE	 0.8840	 0.5500
LF	 0.9210	 0.5670
LG	 0.9160	 0.5630
LH	 0.8920	 0.5670
LJ	 0.9350	 0.5140



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Chain	Atom inclusion	Q-score
LK	 0.7190	 0.4370
LL	 0.9070	 0.5690
LM	 0.9040	 0.5690
LN	 0.9900	 0.6170
LO	 0.9480	 0.5970
LP	 0.9550	 0.5920
LQ	 0.9470	 0.5870
LR	 0.9320	 0.5800
LS	 0.9300	 0.5750
LT	 0.8690	 0.4840
LU	 0.8710	 0.5320
LV	 0.9550	 0.5910
LX	 0.9200	 0.5650
LY	 0.9140	 0.5690
LZ	 0.9310	 0.5550
La	 0.9280	 0.5810
Lb	 0.5310	 0.3630
Lc	 0.8850	 0.5530
Ld	 0.9190	 0.5820
Le	 0.9420	 0.5920
Lf	 0.9760	 0.6190
Lg	 0.9080	 0.5770
Lh	 0.8800	 0.5300
Li	 0.9350	 0.5590
Lj	 0.9780	 0.6190
Lk	 0.8410	 0.5310
Ll	 0.9810	 0.6210
Lp	 0.8880	 0.5630
Lq	 0.9410	 0.5790
Lr	 0.6770	 0.3720