wwPDB EM Validation Summary Report

Nov 7, 2023 – 06:00 am GMT

PDB ID	:	8PV7
EMDB ID	:	EMD-17956
Title	:	Chaetomium thermophilum pre-60S State 1 - pre-5S rotation (Arx1/Nog2 state) - Composite structure
Authors	:	Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2023-07-17
Resolution	:	2.12 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:

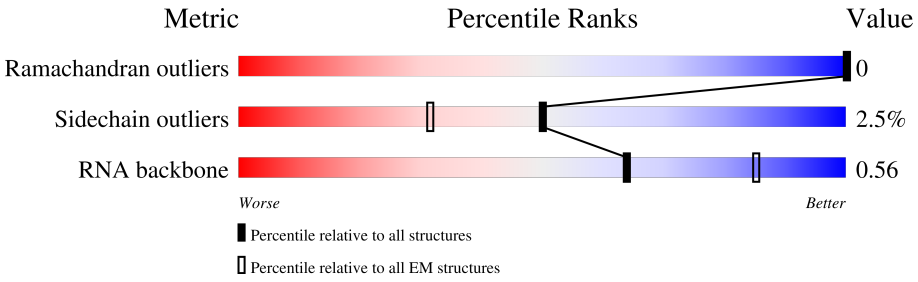
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.12 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=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	74% 17% 8%
2	C2	156	86% 13%
3	C3	162	6% 37% 12% 49%
4	C4	119	5% 80% 19%
5	CB	391	66% 32%
6	CF	270	89% 9%
7	CH	661	92% 5%
8	CI	414	36% 63%

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Mol	Chain	Length	Quality of chain
9	CJ	679	55% 44%
10	CK	261	89% 9%
11	CL	558	14% 86%
12	CM	249	86% 13%
12	LF	249	98%
13	CN	246	98%
14	CO	120	51% 48%
15	CQ	225	79% 19%
16	Lq	147	95% 5%
17	Cb	117	83% 14%
18	Cd	627	72% 26%
19	Ce	443	58% 41%
20	Cf	350	79% 19%
21	Cg	202	91% 7%
22	Ch	517	91% 6%
23	Cz	123	76% 6% 18%
24	LA	254	74% 25%
25	LB	392	98%
26	LC	365	98%
27	LD	304	92% 6%
28	LE	200	94%
29	LG	262	89% 10%
30	LH	229	81% 17%
31	LJ	173	91% 7%
32	LK	165	92%

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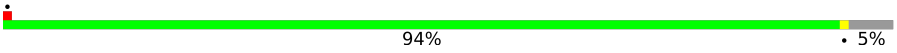
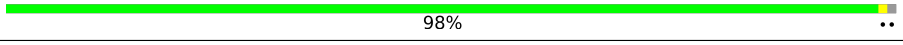
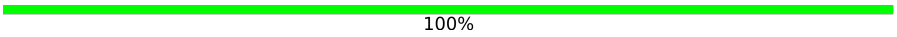
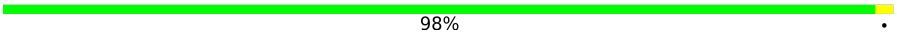
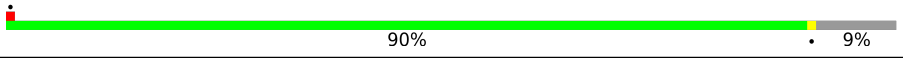
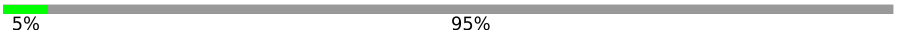
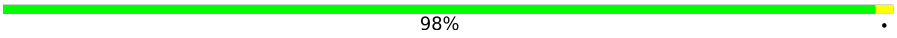
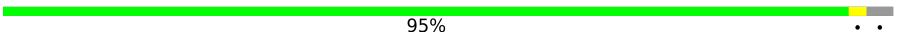
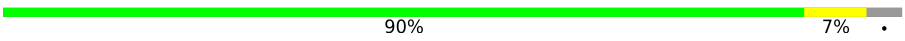
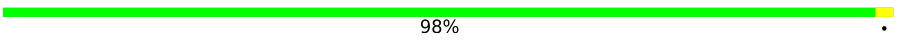
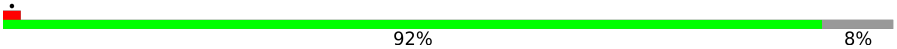
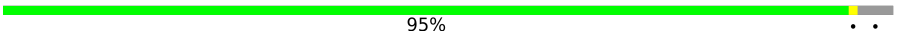
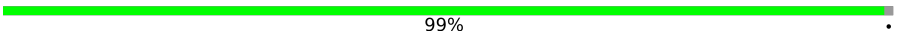
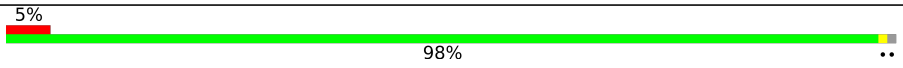
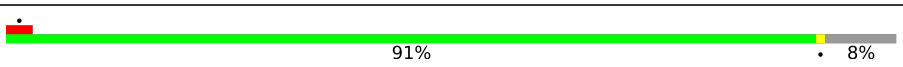
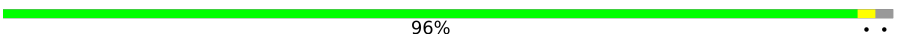
Mol	Chain	Length	Quality of chain
33	LL	213	
34	LM	142	
35	LN	203	
36	LO	204	
37	LP	187	
38	LQ	213	
39	LR	2898	
40	LS	174	
41	LT	160	
42	LU	127	
43	LV	139	
44	LX	156	
45	LY	138	
46	LZ	135	
47	La	149	
48	Lc	108	
49	Ld	120	
50	Le	131	
51	Lf	109	
52	Lg	119	
53	Lh	935	
54	Li	110	
55	Lj	95	
56	Lk	94	
57	Ll	51	

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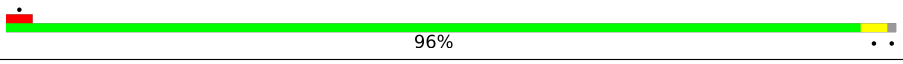
Mol	Chain	Length	Quality of chain
58	Lp	92	

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 157262 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
			Total	C	N	O	P		
1	C1	3078	65888	29429	11926	21455	3078	0	0

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

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

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C3	82	1754	780	316	576	82	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	C4	119	2536	1131	453	833	119	0	0

- Molecule 5 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	CB	267	2119	1359	373	384	3	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL10.

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

- Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CH	627	Total	C	N	O	S	0	0
			5063	3181	924	939	19		

- Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CI	152	Total	C	N	O	S	0	0
			1234	791	230	208	5		

- Molecule 9 is a protein called Pescadillo homolog.

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

- Molecule 10 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CK	237	Total	C	N	O	S	0	0
			1903	1198	368	333	4		

- Molecule 11 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	CL	79	Total	C	N	O	0	0
			622	389	125	108		

- Molecule 12 is a protein called 60S ribosomal protein l7-like protein.

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

- Molecule 13 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CN	246	Total	C	N	O	S	0	0
			1853	1156	322	368	7		

- Molecule 14 is a protein called DUF2423 domain-containing protein.

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

- Molecule 15 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CQ	183	Total	C	N	O	S	0	0
			1480	925	304	241	10		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Lq	139	Total	C	N	O	0	0
			1073	672	213	188		

- Molecule 17 is a protein called Zinc finger domain-containing protein.

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

- Molecule 18 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cd	462	Total	C	N	O	S	0	0
			3691	2350	671	659	11		

- Molecule 19 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ce	262	Total	C	N	O	S	0	0
			2148	1337	413	394	4		

- Molecule 20 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cf	285	Total	C	N	O	S	0	0
			2282	1443	417	401	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Cg	188	Total	C	N	O	S	0	0
			1478	924	283	270	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ch	485	Total	C	N	O	S	1	0
			3812	2396	696	710	10		

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	101	Total	C	N	O	S	0	0
			869	541	180	144	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LA	191	Total	C	N	O	S	0	0
			1454	917	278	256	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LB	389	Total	C	N	O	S	0	0
			3104	1973	579	539	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
			2751	1737	527	478	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LD	286	Total	C	N	O	S	0	0
			2266	1434	407	422	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
			1477	944	267	263	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
			1889	1210	350	324	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	169	Total	C	N	O	S	0	0
			1357	850	266	235	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	150	Total	C	N	O	S	0	0
			1200	759	239	200	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
			1426	917	266	238	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LT	129	Total	C	N	O	S	0	0
			1027	651	195	179	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
			846	548	146	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	0	0
			1133	723	211	199		

- 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
			1112	713	207	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 l30-like protein.

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

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

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

- Molecule 50 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 51 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 52 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lg	118	Total	C	N	O	S	0	0
			914	567	186	157	4		

- Molecule 53 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 54 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Li	101	Total	C	N	O	S	0	0
			827	509	181	136	1		

- Molecule 55 is a protein called Ribosomal protein L37.

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

- Molecule 56 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

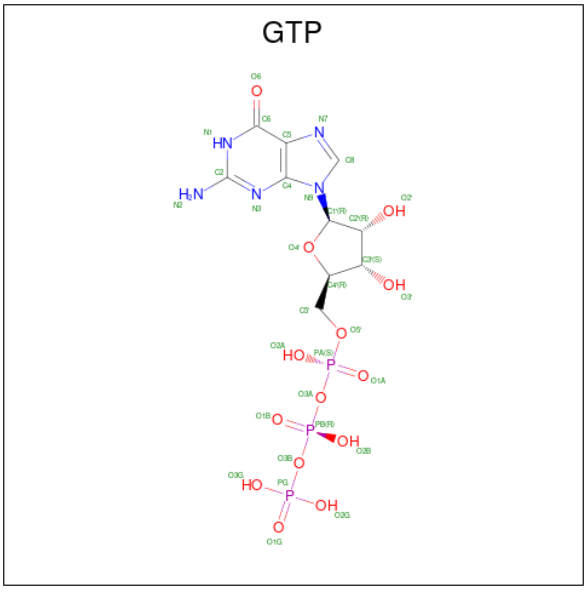
- Molecule 57 is a protein called Ribosomal protein eL39.

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

- Molecule 58 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lp	91	Total	C	N	O	S	0	0
			698	430	138	124	6		

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

Continued on next page...

Continued from previous page...

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

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 61 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	CQ	1	Total	Zn	0
			1	1	
61	Cb	1	Total	Zn	0
			1	1	
61	Lg	1	Total	Zn	0
			1	1	
61	Lj	1	Total	Zn	0
			1	1	
61	Lp	1	Total	Zn	0
			1	1	

- Molecule 62 is water.

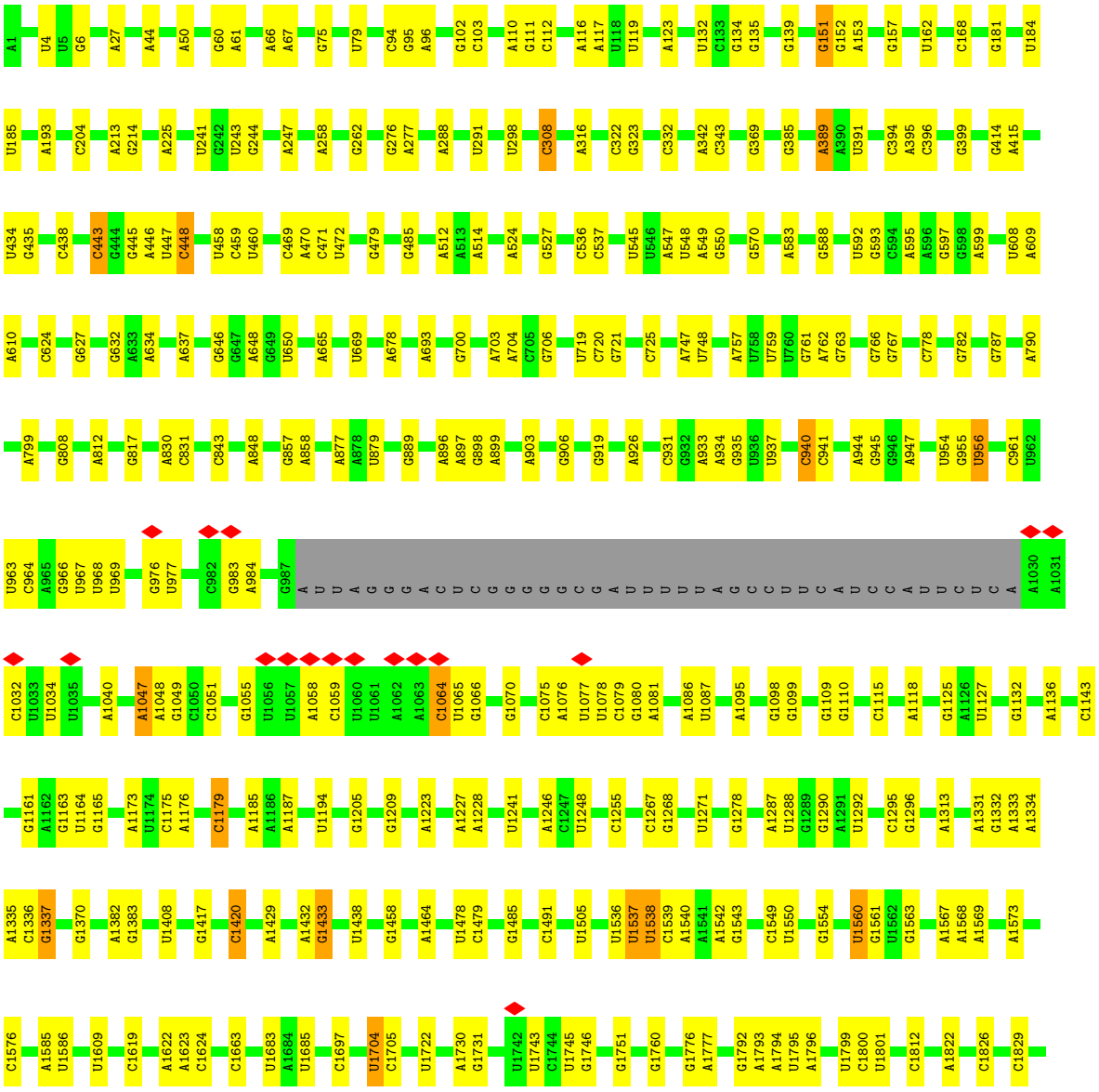
Mol	Chain	Residues	Atoms		AltConf
62	CH	1	Total	O	0
			1	1	
62	Cd	2	Total	O	0
			2	2	

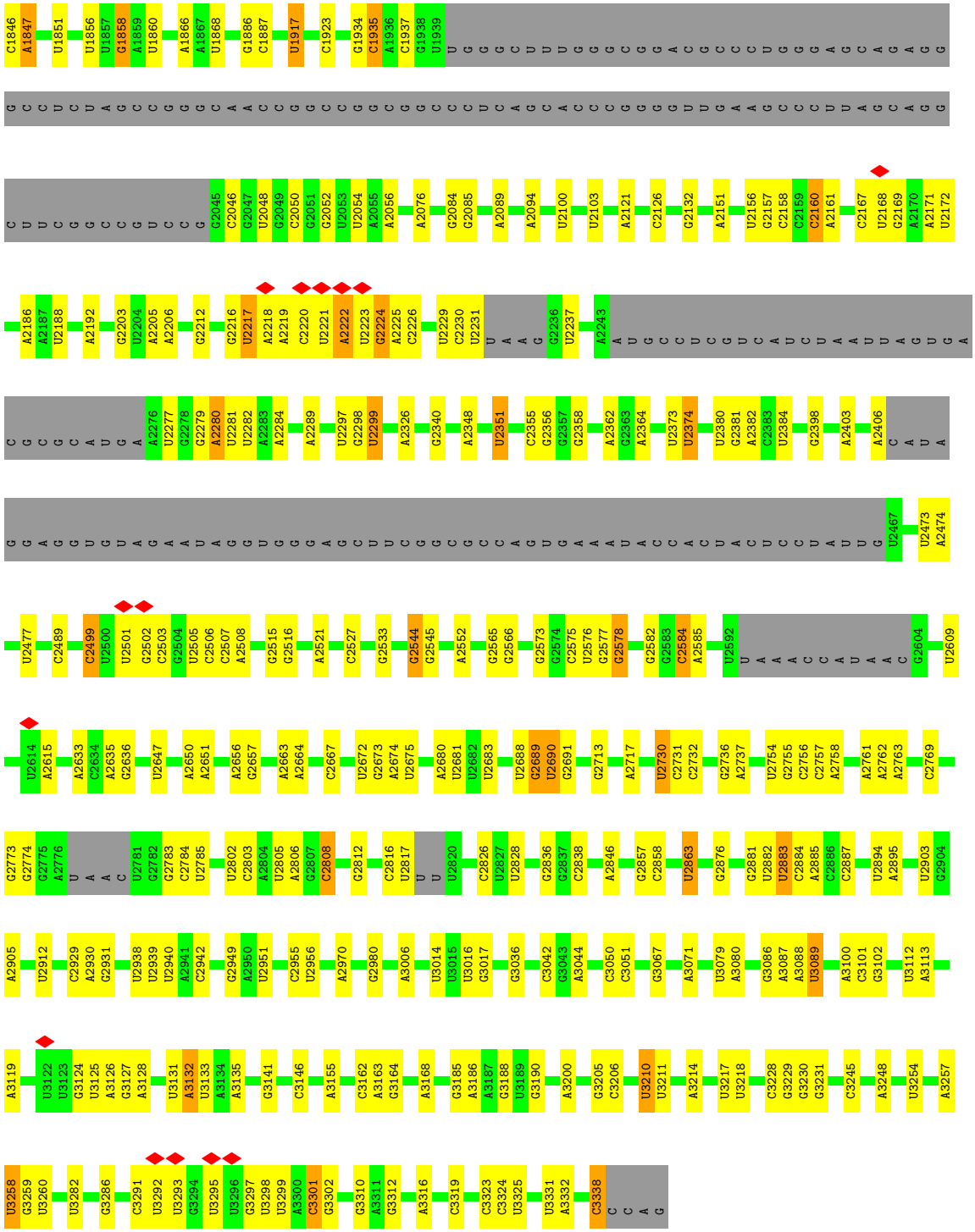
3 Residue-property plots (i)

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

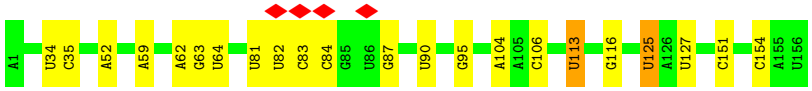
Chain C1:





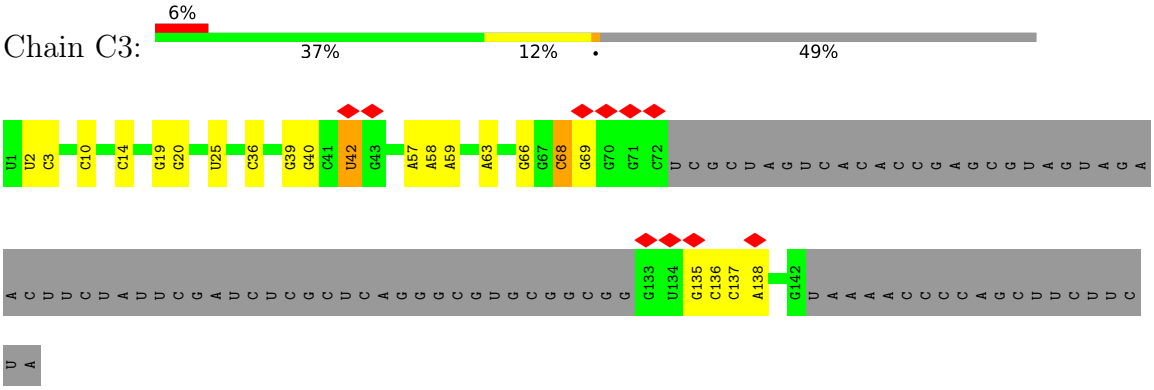
• Molecule 2: 5.8S rRNA

Chain C2:



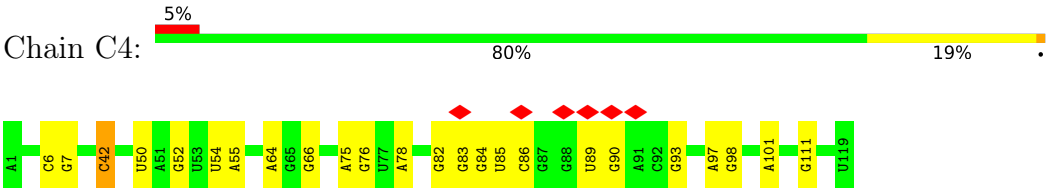
• Molecule 3: ITS2

Chain C3:



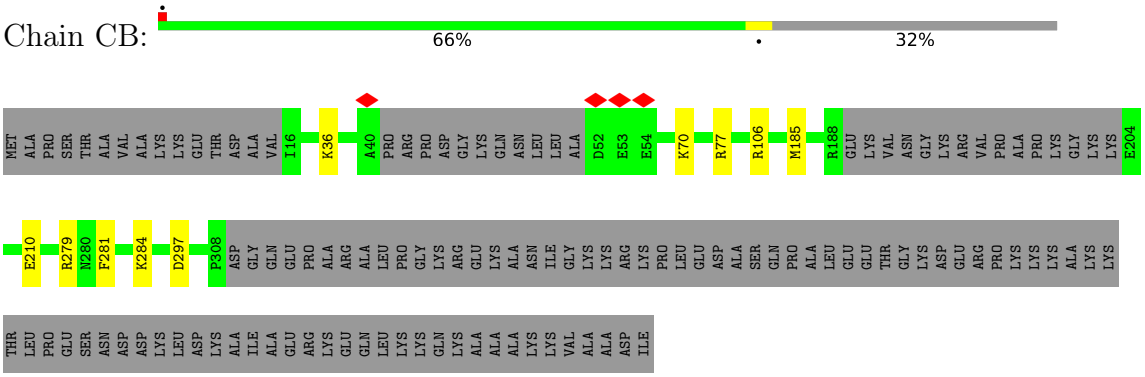
• Molecule 4: 5S rRNA

Chain C4:



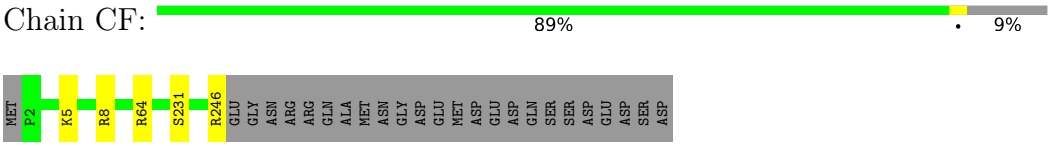
• Molecule 5: Utp30

Chain CB:



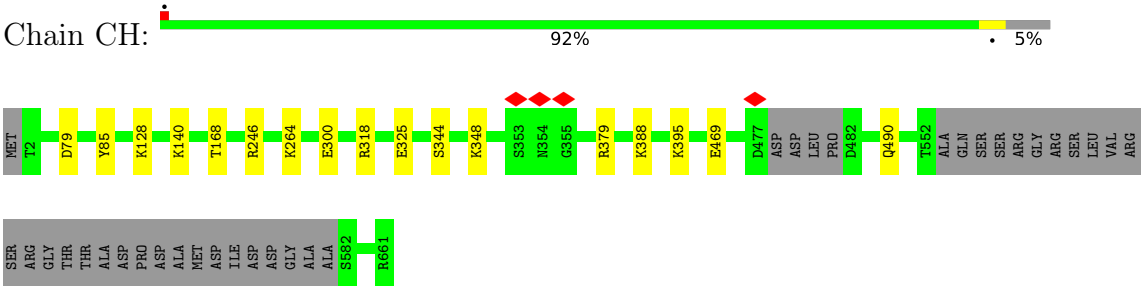
• Molecule 6: Large ribosomal subunit protein uL10

Chain CF:



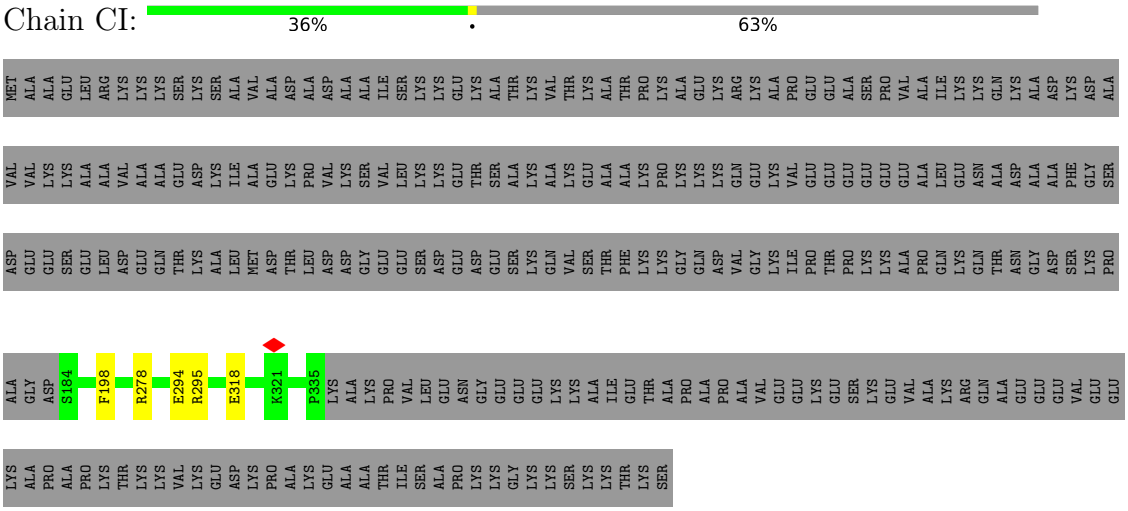
• Molecule 7: Nucleolar GTP-binding protein 1

Chain CH:



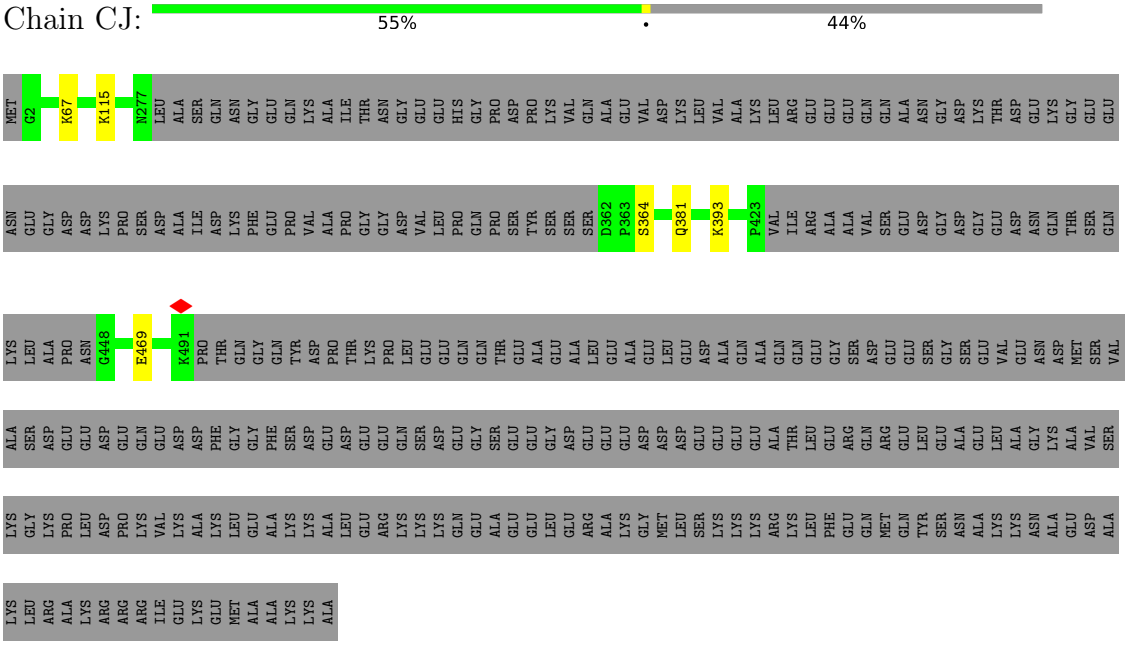
• Molecule 8: Putative RNA-binding protein

Chain CI:



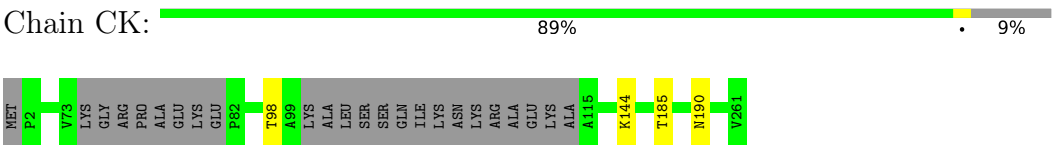
• Molecule 9: Pescadillo homolog

Chain CJ:



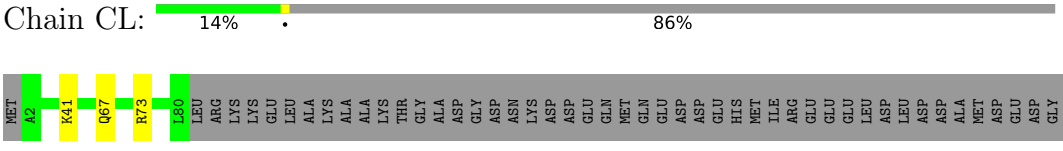
• Molecule 10: Ribosome biogenesis protein NSA2 homolog

Chain CK:



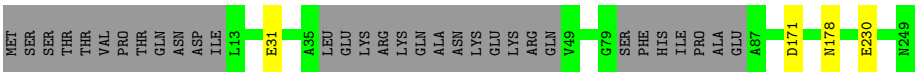
• Molecule 11: Putative GTP binding protein

Chain CL:



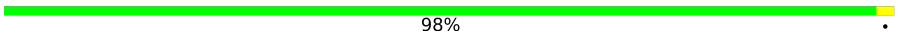
• Molecule 12: 60S ribosomal protein l7-like protein

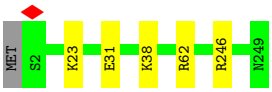
Chain CM:



• Molecule 12: 60S ribosomal protein l7-like protein

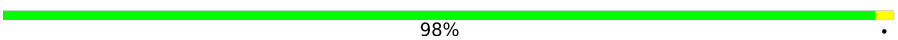
Chain LF:





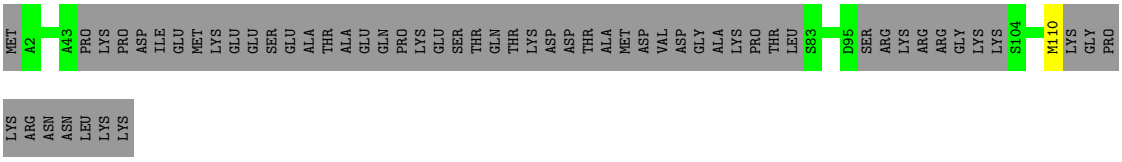
• Molecule 13: Eukaryotic translation initiation factor 6

Chain CN:



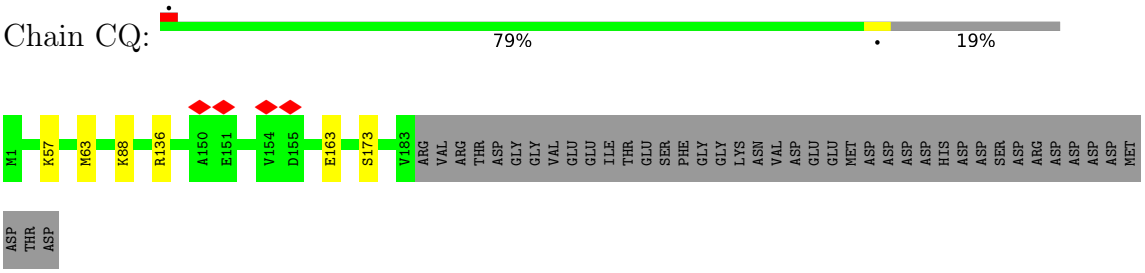
• Molecule 14: DUF2423 domain-containing protein

Chain CO:



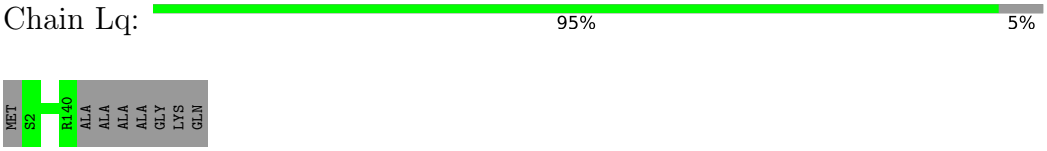
• Molecule 15: Ribosome biogenesis protein RLP24

Chain CQ:



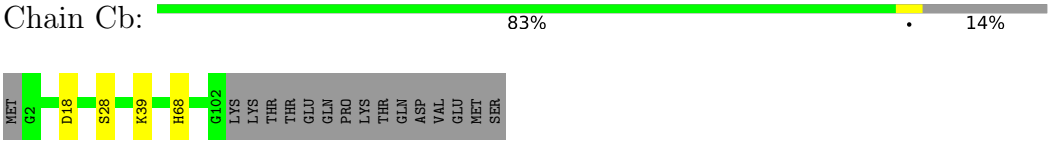
• Molecule 16: Putative 60S ribosomal protein

Chain Lq:



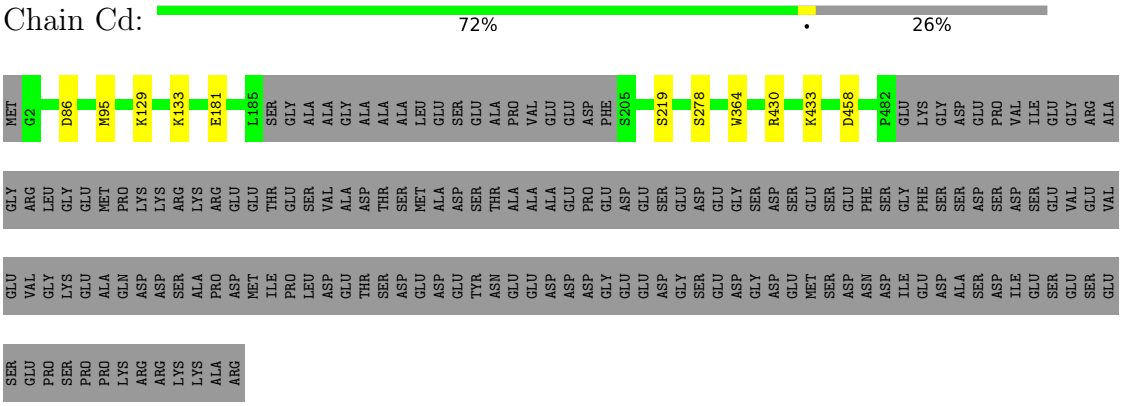
• Molecule 17: Zinc finger domain-containing protein

Chain Cb:



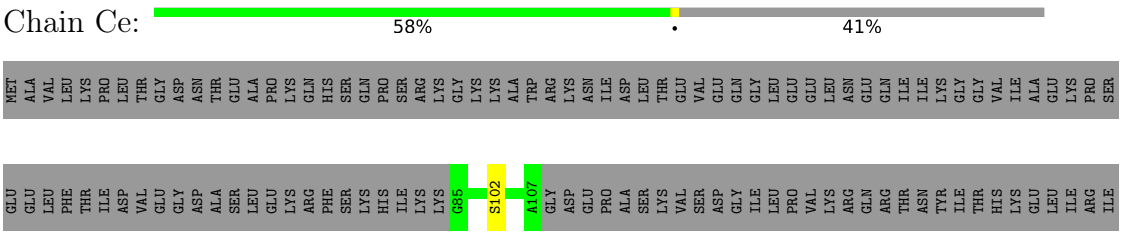
• Molecule 18: Nucleolar GTP-binding protein 2

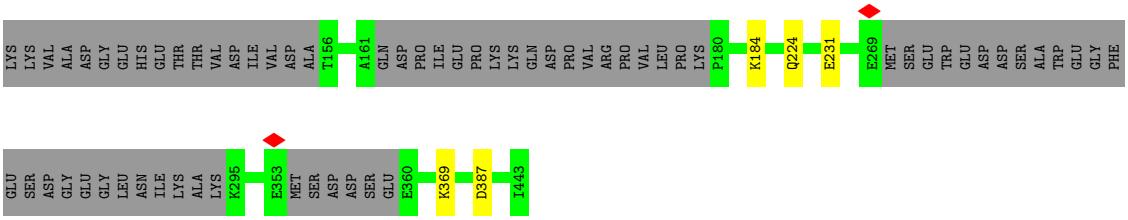
Chain Cd:



• Molecule 19: Ribosome biogenesis protein NOP53

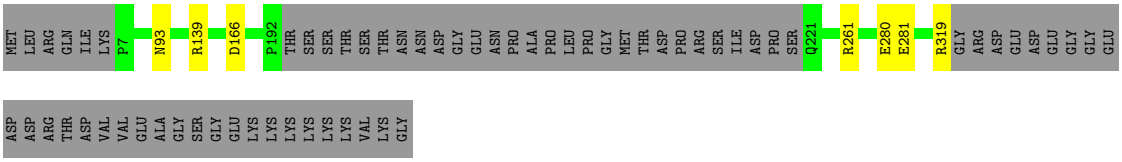
Chain Ce:





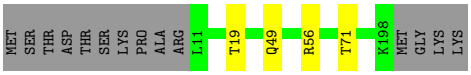
• Molecule 20: Ribosome production factor 2 homolog

Chain Cf:



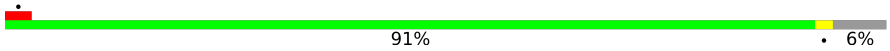
• Molecule 21: Ribosome biogenesis regulatory protein

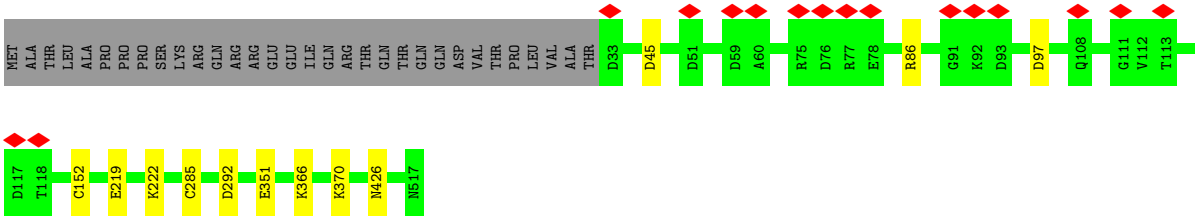
Chain Cg:



• Molecule 22: Ribosome assembly protein 4

Chain Ch:





• Molecule 23: rRNA-processing protein

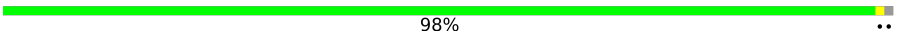
Chain Cz:

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

Chain LA:

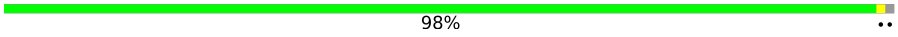
• Molecule 25: 60S ribosomal protein L3-like protein

Chain LB:



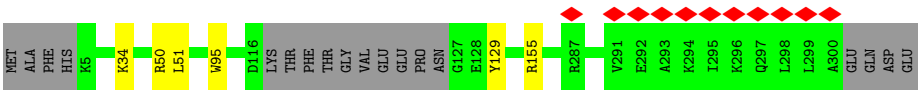
• Molecule 26: 60S ribosomal protein L4-like protein

Chain LC:



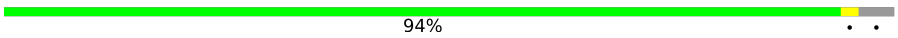
• Molecule 27: 60S ribosomal protein l5-like protein

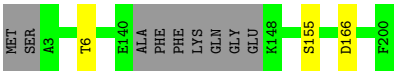
Chain LD:



• Molecule 28: 60S ribosomal protein L6

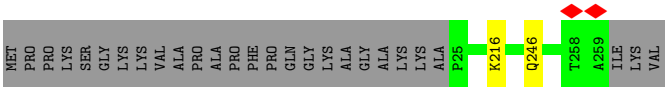
Chain LE:





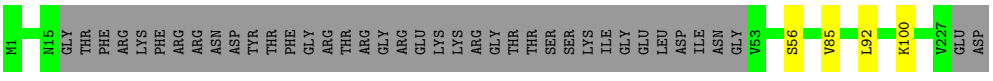
• Molecule 29: 60S ribosomal protein L8

Chain LG:



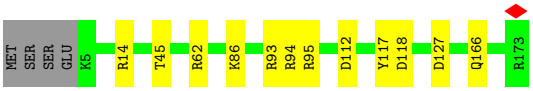
• Molecule 30: 60S ribosomal protein l9-like protein

Chain LH:



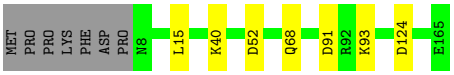
• Molecule 31: Putative ribosomal protein

Chain LJ:



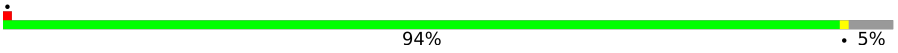
• Molecule 32: 60S ribosomal protein L12-like protein

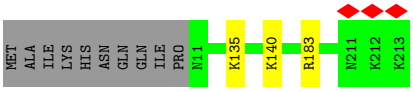
Chain LK:



• Molecule 33: 60S ribosomal protein L13

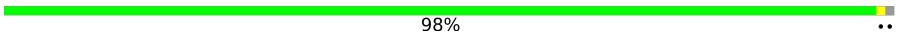
Chain LL:

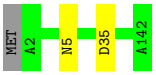




• Molecule 34: 60S ribosomal protein L14-like protein

Chain LM:



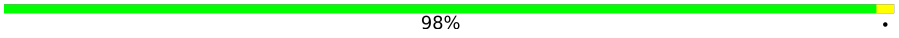


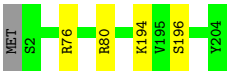
• Molecule 35: Ribosomal protein L15

Chain LN:

• Molecule 36: 60S ribosomal protein L16-like protein

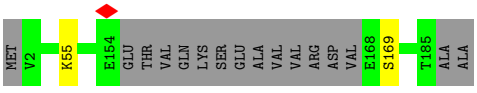
Chain LO:





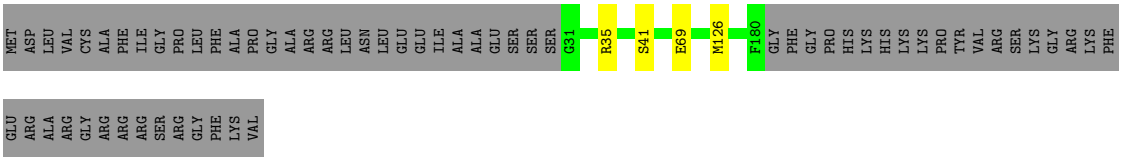
• Molecule 37: 60S ribosomal protein l17-like protein

Chain LP:



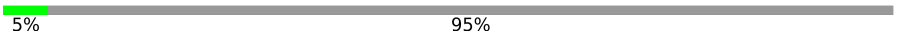
• Molecule 38: Ribosomal protein L18-like protein

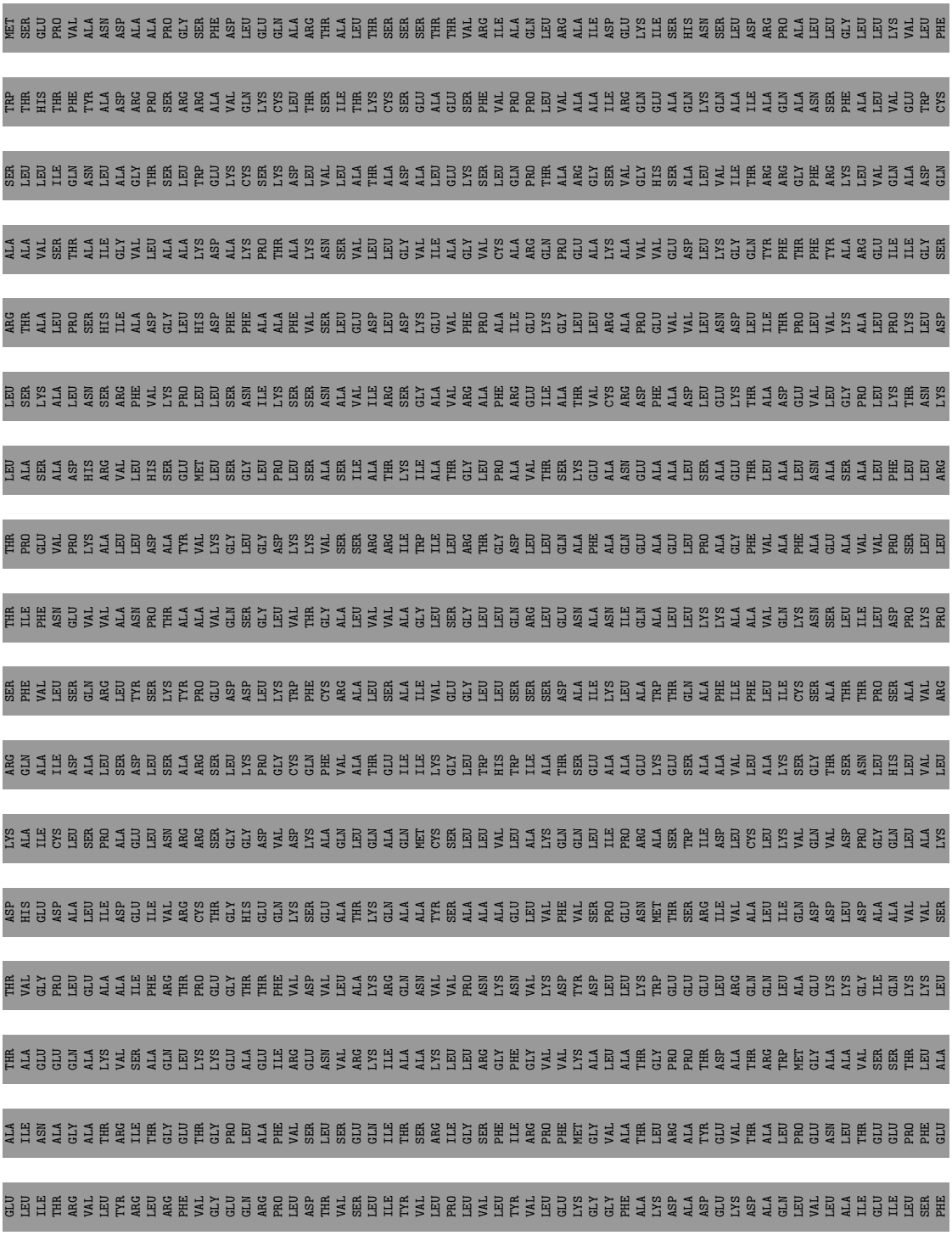
Chain LQ:



• Molecule 39: Ribosomal protein L19

Chain LR:





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

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

GLY HIS LYS MET ILE PRO TYR LEU GLU SER LYS ASP VAL GLN LEU ARG ARG ALA ALA ALA LYS SER LEU ALA GLU VAL ALA GLY GLN HIS PRO ASP VAL VAL ALA PRO ILE LEU GLU LYS LEU ARG GLU SER TYR VAL GLU LEU ALA LYS PRO ARG VAL GLN GLN LEU ASP GLU PHE GLY

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

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

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

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

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

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

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

GLY SER LEU ALA HIS LEU THR GLU ARG LYS ASP LEU ILE ALA HIS LEU PRO VAL LEU VAL ALA GLY LEU LYS VAL ALA VAL VAL ASP PRO VAL PRO THR THR ARG ALA THR ALA SER ARG ALA LEU GLY SER LEU VAL GLU LYS LEU GLY GLU ASP ALA LEU PRO ASP LEU ILE PRO ASN

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

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

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

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

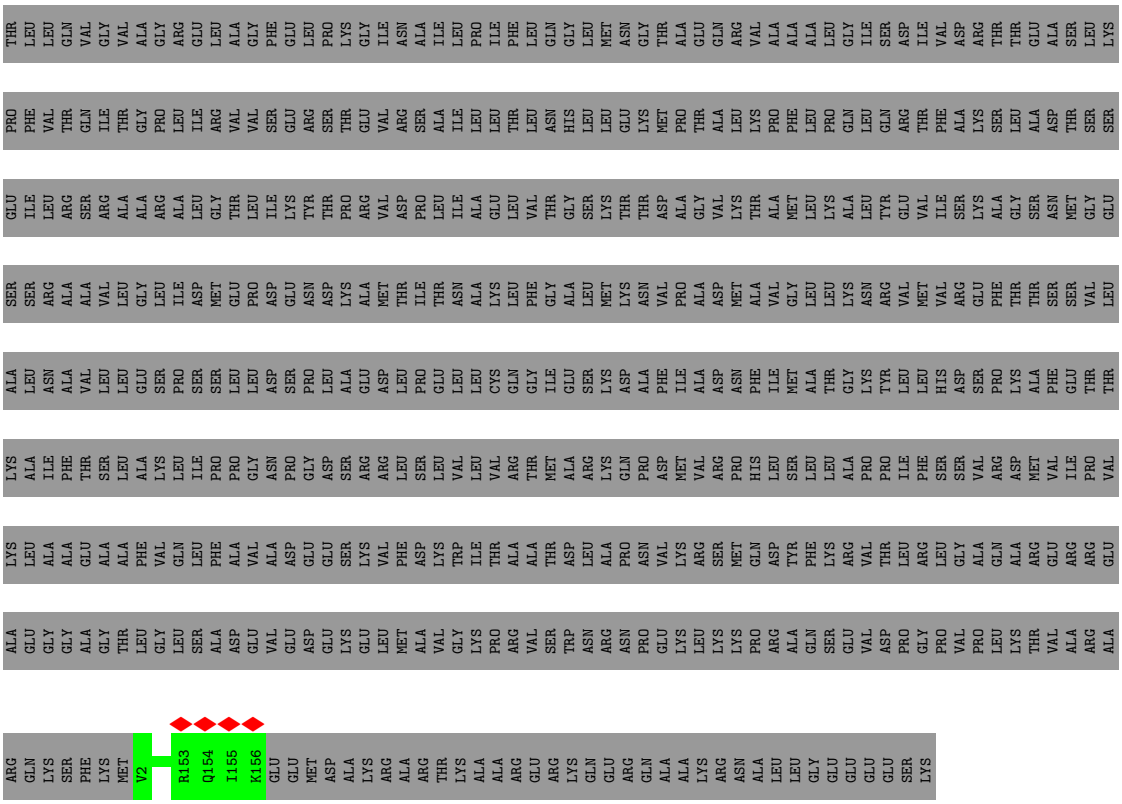
ILE ALA SER ASN ALA LEU GLY GLU LEU ILE LYS LYS ALA GLY ASP GLY VAL LEU ALA THR LEU LEU PRO THR LEU GLU GLU GLY LEU GLN THR SER ARG ASP VAL ASN ALA LYS GLN GLY ILE CYS LEU ALA LEU LYS GLU LEU ILE SER SER ALA SER PRO GLU ALA LEU GLU ASP HIS

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

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

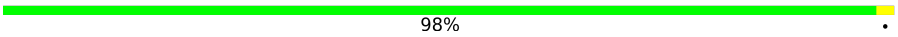
ASP ASN ILE VAL GLY CYS ALA ASP GLU THR LEU ARG GLU GLU LEU ASP THR SER PHE ASP THR VAL ILE LEU SER ILE ASP ASP THR ASP GLY LEU ASN VAL VAL MET ASN VAL LEU LEU GLN LEU ILE LYS HIS GLU ASP HIS ARG LYS ARG ALA ALA THR GLY ARG HIS LEU ALA LYS

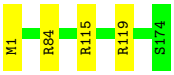
PHE PHE SER ALA ALA THR VAL ASN TYR SER ARG TYR ASN GLN ASP ILE ILE ARG ALA LEU LEU ILE SER PHE ASP ASP LYS ASP MET GLU VAL VAL LYS ALA SER TRP ASN ALA LEU ASN GLU PHE THR LYS ARG LEU LYS LYS GLU GLU MET GLU GLY LEU VAL ILE SER THR ARG GLN



• Molecule 40: 60S ribosomal protein L20

Chain LS:



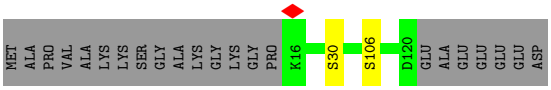


• Molecule 41: 60S ribosomal protein l21-like protein

Chain LT:

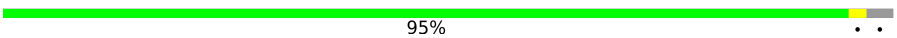
• Molecule 42: 60S ribosomal protein L22-like protein

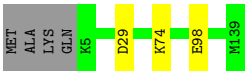
Chain LU:



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

Chain LV:





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

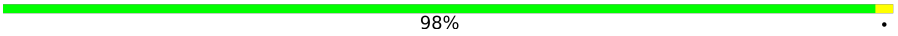
Chain LX:

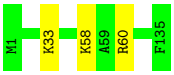
• Molecule 45: 60S ribosomal protein L26-like protein

Chain LY:

• Molecule 46: 60S ribosomal protein L27

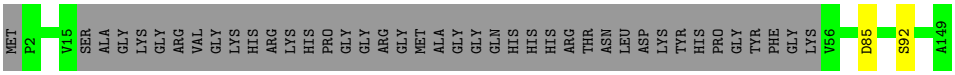
Chain LZ:





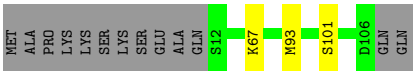
• Molecule 47: 60S ribosomal protein L28-like protein

Chain La:



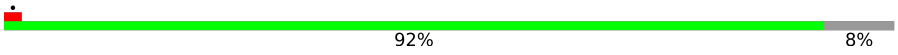
• Molecule 48: 60S ribosomal protein l30-like protein

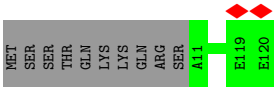
Chain Lc:



• Molecule 49: Putative 60S ribosomal protein

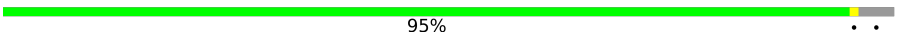
Chain Ld:

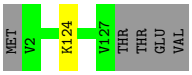




• Molecule 50: 60S ribosomal protein L32-like protein

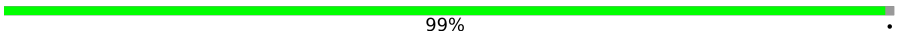
Chain Le:





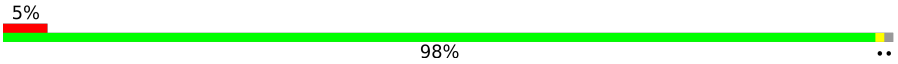
• Molecule 51: 60S ribosomal protein l33-like protein

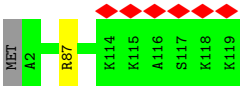
Chain Lf:



• Molecule 52: Ribosomal protein l34-like protein

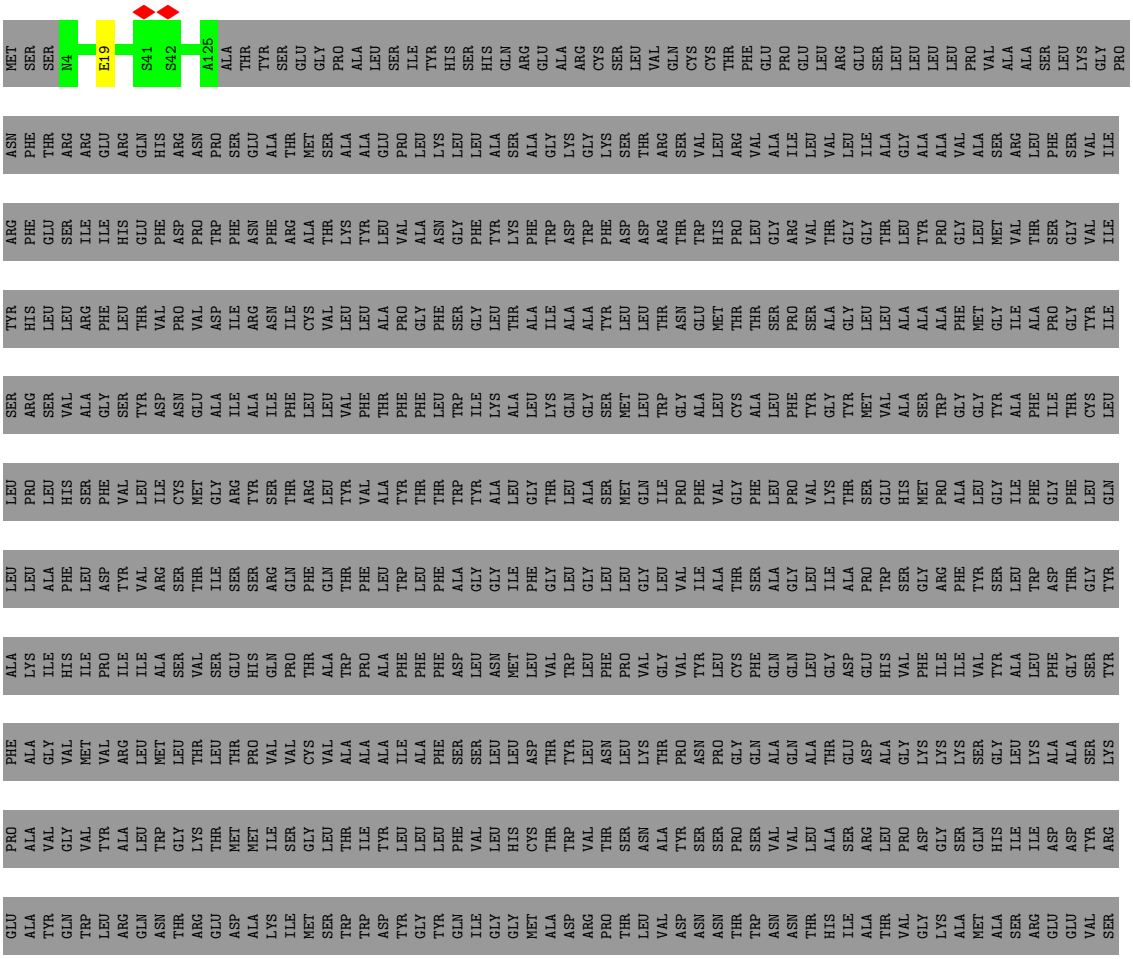
Chain Lg:

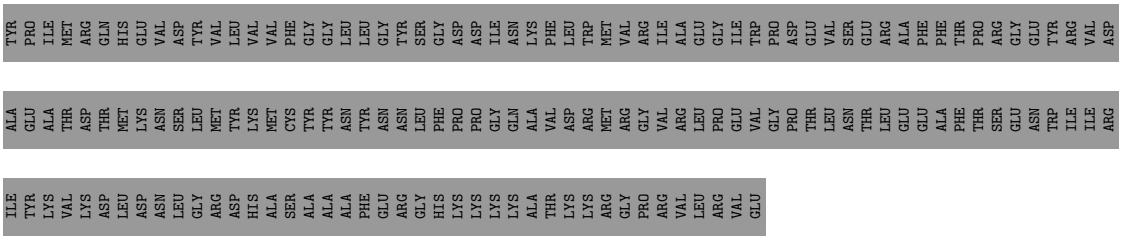




• Molecule 53: dolichyl-diphosphooligosaccharide--protein glycotransferase

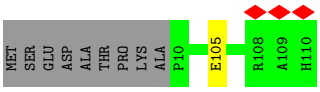
Chain Lh:





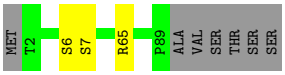
• Molecule 54: 60S ribosomal protein L36

Chain Li:



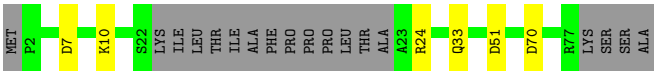
• Molecule 55: Ribosomal protein L37

Chain Lj:



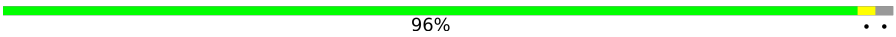
• Molecule 56: 60S ribosomal protein L38-like protein

Chain Lk:



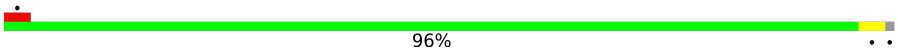
• Molecule 57: Ribosomal protein eL39

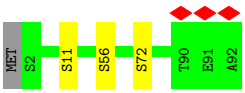
Chain Ll:



• Molecule 58: 60S ribosomal protein L43-like protein

Chain Lp:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	745895	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 ($e^-/Å^2$)	45.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	10.768	Depositor
Minimum map value	0.000	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.175	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 (i)

5.1 Standard geometry (i)

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

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	0.55	0/72882	0.95	123/113631 (0.1%)
2	C2	0.55	0/3710	0.90	5/5778 (0.1%)
3	C3	0.44	0/1958	0.98	4/3050 (0.1%)
4	C4	0.45	0/2833	0.98	3/4414 (0.1%)
5	CB	0.29	0/2166	0.52	0/2945
6	CF	0.32	0/1972	0.57	0/2660
7	CH	0.30	0/5147	0.56	0/6926
8	CI	0.37	0/1265	0.67	1/1702 (0.1%)
9	CJ	0.32	0/3196	0.53	0/4319
10	CK	0.31	0/1939	0.57	0/2608
11	CL	0.29	0/631	0.59	0/843
12	CM	0.34	0/1805	0.60	1/2417 (0.0%)
12	LF	0.34	0/2061	0.55	0/2765
13	CN	0.28	0/1878	0.56	0/2555
14	CO	0.31	0/470	0.53	0/619
15	CQ	0.32	0/1504	0.60	0/2000
16	Lq	0.30	0/1091	0.58	0/1468
17	Cb	0.29	0/845	0.59	0/1128
18	Cd	0.30	0/3770	0.54	1/5082 (0.0%)
19	Ce	0.30	0/2173	0.57	0/2890
20	Cf	0.29	0/2326	0.56	0/3113
21	Cg	0.31	0/1508	0.57	0/2051
22	Ch	0.30	0/3914	0.60	0/5319
23	Cz	0.33	0/877	0.65	1/1148 (0.1%)
24	LA	0.33	0/1488	0.61	1/2009 (0.0%)
25	LB	0.30	0/3172	0.56	0/4260
26	LC	0.30	0/2808	0.53	0/3785
27	LD	0.31	0/2308	0.54	0/3105
28	LE	0.30	0/1504	0.56	1/2027 (0.0%)
29	LG	0.34	0/1918	0.54	0/2565
30	LH	0.34	0/1515	0.58	1/2037 (0.0%)
31	LJ	0.30	0/1379	0.65	1/1844 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	LK	0.30	0/1198	0.61	2/1611 (0.1%)
33	LL	0.28	0/1614	0.57	0/2168
34	LM	0.31	0/1145	0.57	0/1539
35	LN	0.33	0/1741	0.62	0/2332
36	LO	0.33	0/1645	0.55	0/2205
37	LP	0.29	0/1364	0.58	0/1835
38	LQ	0.31	0/1218	0.59	0/1639
39	LR	0.29	0/1260	0.56	0/1683
40	LS	0.32	0/1461	0.58	0/1966
41	LT	0.33	0/1046	0.59	0/1409
42	LU	0.30	0/859	0.54	0/1151
43	LV	0.30	0/1009	0.57	1/1357 (0.1%)
44	LX	0.31	0/1151	0.59	2/1547 (0.1%)
45	LY	0.30	0/1070	0.61	0/1432
46	LZ	0.32	0/1135	0.60	0/1519
47	La	0.30	0/892	0.54	0/1200
48	Lc	0.30	0/714	0.49	0/960
49	Ld	0.28	0/889	0.55	0/1192
50	Le	0.29	0/1035	0.57	0/1379
51	Lf	0.31	0/883	0.56	0/1187
52	Lg	0.30	0/927	0.60	0/1244
53	Lh	0.31	0/1014	0.56	0/1349
54	Li	0.31	0/834	0.65	0/1099
55	Lj	0.30	0/712	0.63	0/944
56	Lk	0.29	0/640	0.53	0/850
57	Ll	0.27	0/446	0.57	0/593
58	Lp	0.31	0/706	0.67	0/940
All	All	0.44	0/166621	0.79	148/241393 (0.1%)

There are no bond length outliers.

The worst 5 of 148 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C1	1538	U	N3-C2-O2	-10.53	114.83	122.20
1	C1	1179	C	C2-N1-C1'	10.46	130.31	118.80
1	C1	1538	U	N1-C2-O2	10.06	129.84	122.80
1	C1	1179	C	N1-C2-O2	9.60	124.66	118.90
1	C1	1538	U	C2-N1-C1'	9.24	128.79	117.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CB	261/391 (67%)	256 (98%)	5 (2%)	0	100	100
6	CF	243/270 (90%)	238 (98%)	5 (2%)	0	100	100
7	CH	621/661 (94%)	614 (99%)	7 (1%)	0	100	100
8	CI	150/414 (36%)	149 (99%)	1 (1%)	0	100	100
9	CJ	376/679 (55%)	374 (100%)	2 (0%)	0	100	100
10	CK	231/261 (88%)	226 (98%)	5 (2%)	0	100	100
11	CL	77/558 (14%)	77 (100%)	0	0	100	100
12	CM	211/249 (85%)	207 (98%)	4 (2%)	0	100	100
12	LF	246/249 (99%)	240 (98%)	6 (2%)	0	100	100
13	CN	244/246 (99%)	238 (98%)	6 (2%)	0	100	100
14	CO	56/120 (47%)	56 (100%)	0	0	100	100
15	CQ	181/225 (80%)	179 (99%)	2 (1%)	0	100	100
16	Lq	137/147 (93%)	132 (96%)	5 (4%)	0	100	100
17	Cb	99/117 (85%)	98 (99%)	1 (1%)	0	100	100
18	Cd	458/627 (73%)	454 (99%)	4 (1%)	0	100	100
19	Ce	252/443 (57%)	251 (100%)	1 (0%)	0	100	100
20	Cf	281/350 (80%)	279 (99%)	2 (1%)	0	100	100
21	Cg	186/202 (92%)	186 (100%)	0	0	100	100
22	Ch	484/517 (94%)	471 (97%)	13 (3%)	0	100	100
23	Cz	99/123 (80%)	98 (99%)	1 (1%)	0	100	100
24	LA	189/254 (74%)	187 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	LB	387/392 (99%)	381 (98%)	6 (2%)	0	100	100
26	LC	361/365 (99%)	355 (98%)	6 (2%)	0	100	100
27	LD	282/304 (93%)	278 (99%)	4 (1%)	0	100	100
28	LE	187/200 (94%)	184 (98%)	3 (2%)	0	100	100
29	LG	233/262 (89%)	228 (98%)	5 (2%)	0	100	100
30	LH	188/229 (82%)	186 (99%)	2 (1%)	0	100	100
31	LJ	167/173 (96%)	166 (99%)	1 (1%)	0	100	100
32	LK	156/165 (94%)	155 (99%)	1 (1%)	0	100	100
33	LL	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
34	LM	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
35	LN	200/203 (98%)	196 (98%)	4 (2%)	0	100	100
36	LO	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
37	LP	167/187 (89%)	164 (98%)	3 (2%)	0	100	100
38	LQ	148/213 (70%)	147 (99%)	1 (1%)	0	100	100
39	LR	153/2898 (5%)	152 (99%)	1 (1%)	0	100	100
40	LS	172/174 (99%)	170 (99%)	2 (1%)	0	100	100
41	LT	127/160 (79%)	126 (99%)	1 (1%)	0	100	100
42	LU	103/127 (81%)	101 (98%)	2 (2%)	0	100	100
43	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
44	LX	143/156 (92%)	142 (99%)	1 (1%)	0	100	100
45	LY	131/138 (95%)	128 (98%)	3 (2%)	0	100	100
46	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
47	La	104/149 (70%)	104 (100%)	0	0	100	100
48	Lc	93/108 (86%)	93 (100%)	0	0	100	100
49	Ld	108/120 (90%)	108 (100%)	0	0	100	100
50	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
51	Lf	106/109 (97%)	106 (100%)	0	0	100	100
52	Lg	116/119 (98%)	115 (99%)	1 (1%)	0	100	100
53	Lh	120/935 (13%)	117 (98%)	3 (2%)	0	100	100
54	Li	99/110 (90%)	99 (100%)	0	0	100	100
55	Lj	86/95 (90%)	85 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	Lk	74/94 (79%)	74 (100%)	0	0	100	100
57	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
58	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
All	All	10361/16395 (63%)	10225 (99%)	136 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	CB	228/329 (69%)	218 (96%)	10 (4%)	28	27
6	CF	212/236 (90%)	207 (98%)	5 (2%)	49	52
7	CH	549/575 (96%)	532 (97%)	17 (3%)	40	42
8	CI	124/336 (37%)	120 (97%)	4 (3%)	39	40
9	CJ	331/579 (57%)	325 (98%)	6 (2%)	59	63
10	CK	206/225 (92%)	202 (98%)	4 (2%)	57	61
11	CL	61/458 (13%)	58 (95%)	3 (5%)	25	22
12	CM	185/215 (86%)	182 (98%)	3 (2%)	62	68
12	LF	213/215 (99%)	208 (98%)	5 (2%)	50	53
13	CN	205/206 (100%)	200 (98%)	5 (2%)	49	52
14	CO	48/99 (48%)	47 (98%)	1 (2%)	53	57
15	CQ	144/192 (75%)	138 (96%)	6 (4%)	30	29
16	Lq	109/112 (97%)	109 (100%)	0	100	100
17	Cb	85/101 (84%)	81 (95%)	4 (5%)	26	24
18	Cd	403/541 (74%)	393 (98%)	10 (2%)	47	50
19	Ce	223/383 (58%)	217 (97%)	6 (3%)	44	47
20	Cf	250/310 (81%)	243 (97%)	7 (3%)	43	46
21	Cg	158/176 (90%)	154 (98%)	4 (2%)	47	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
22	Ch	408/436 (94%)	396 (97%)	12 (3%)	42 44
23	Cz	89/107 (83%)	83 (93%)	6 (7%)	16 13
24	LA	150/198 (76%)	149 (99%)	1 (1%)	84 88
25	LB	329/331 (99%)	326 (99%)	3 (1%)	78 83
26	LC	282/285 (99%)	277 (98%)	5 (2%)	59 63
27	LD	221/253 (87%)	215 (97%)	6 (3%)	44 47
28	LE	157/166 (95%)	155 (99%)	2 (1%)	69 74
29	LG	200/222 (90%)	198 (99%)	2 (1%)	76 81
30	LH	167/200 (84%)	164 (98%)	3 (2%)	59 63
31	LJ	140/150 (93%)	129 (92%)	11 (8%)	12 8
32	LK	127/136 (93%)	122 (96%)	5 (4%)	32 32
33	LL	158/176 (90%)	155 (98%)	3 (2%)	57 61
34	LM	116/117 (99%)	114 (98%)	2 (2%)	60 66
35	LN	179/180 (99%)	179 (100%)	0	100 100
36	LO	162/163 (99%)	158 (98%)	4 (2%)	47 50
37	LP	133/152 (88%)	131 (98%)	2 (2%)	65 70
38	LQ	128/178 (72%)	124 (97%)	4 (3%)	40 42
39	LR	125/2396 (5%)	125 (100%)	0	100 100
40	LS	152/154 (99%)	148 (97%)	4 (3%)	46 49
41	LT	110/135 (82%)	107 (97%)	3 (3%)	44 47
42	LU	92/108 (85%)	90 (98%)	2 (2%)	52 55
43	LV	98/102 (96%)	96 (98%)	2 (2%)	55 59
44	LX	122/129 (95%)	117 (96%)	5 (4%)	30 30
45	LY	116/119 (98%)	107 (92%)	9 (8%)	12 9
46	LZ	121/121 (100%)	118 (98%)	3 (2%)	47 50
47	La	93/122 (76%)	91 (98%)	2 (2%)	52 55
48	Lc	76/88 (86%)	73 (96%)	3 (4%)	32 32
49	Ld	90/105 (86%)	90 (100%)	0	100 100
50	Le	109/114 (96%)	108 (99%)	1 (1%)	78 83
51	Lf	89/90 (99%)	89 (100%)	0	100 100
52	Lg	95/102 (93%)	94 (99%)	1 (1%)	73 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
53	Lh	109/781 (14%)	108 (99%)	1 (1%)	78 83
54	Li	85/93 (91%)	84 (99%)	1 (1%)	71 77
55	Lj	72/78 (92%)	69 (96%)	3 (4%)	30 29
56	Lk	73/88 (83%)	67 (92%)	6 (8%)	11 7
57	Ll	45/46 (98%)	44 (98%)	1 (2%)	52 55
58	Lp	73/74 (99%)	70 (96%)	3 (4%)	30 30
All	All	8825/13783 (64%)	8604 (98%)	221 (2%)	50 50

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	LB	168	ARG
31	LJ	86	LYS
58	Lp	56	SER
47	La	85	ASP
26	LC	270	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
32	LK	65	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3069/3342 (91%)	550 (17%)	23 (0%)
2	C2	155/156 (99%)	21 (13%)	0
3	C3	80/162 (49%)	21 (26%)	0
4	C4	118/119 (99%)	23 (19%)	0
All	All	3422/3779 (90%)	615 (17%)	23 (0%)

5 of 615 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	4	U
1	C1	6	G
1	C1	27	A
1	C1	44	A

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Mol	Chain	Res	Type
1	C1	50	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3079	U
1	C1	3210	U
1	C1	3205	G
1	C1	3230	G
1	C1	1267	C

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

34 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	OMG	C1	646	1	18,26,27	1.22	2 (11%)	19,38,41	0.87	2 (10%)
1	A2M	C1	637	1	18,25,26	4.30	7 (38%)	18,36,39	3.94	4 (22%)
1	OMG	C1	627	1	18,26,27	1.24	3 (16%)	19,38,41	0.99	1 (5%)
1	OMC	C1	778	1	19,22,23	0.59	0	26,31,34	0.85	1 (3%)
1	A2M	C1	858	1	18,25,26	4.38	8 (44%)	18,36,39	3.98	4 (22%)
1	A2M	C1	1223	1	18,25,26	4.28	8 (44%)	18,36,39	3.88	5 (27%)
1	OMU	C1	2277	1	19,22,23	2.99	6 (31%)	26,31,34	1.69	4 (15%)
1	OMG	C1	2774	1	18,26,27	1.21	2 (11%)	19,38,41	0.86	1 (5%)
1	OMG	C1	2881	1	18,26,27	1.16	2 (11%)	19,38,41	0.84	1 (5%)
1	OMC	C1	1836	1	19,22,23	0.63	0	26,31,34	0.70	0
1	OMU	C1	2688	1	19,22,23	2.99	6 (31%)	26,31,34	1.67	4 (15%)
1	OMU	C1	1868	1	19,22,23	2.98	7 (36%)	26,31,34	1.88	5 (19%)
1	A2M	C1	389	1	18,25,26	4.33	8 (44%)	18,36,39	3.87	4 (22%)
1	OMC	C1	1491	1	19,22,23	0.62	0	26,31,34	0.70	0
1	OMU	C1	2690	1	19,22,23	2.98	7 (36%)	26,31,34	1.74	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	OMC	C1	2918	1	19,22,23	0.64	0	26,31,34	0.78	0
1	OMG	C1	385	1	18,26,27	1.19	2 (11%)	19,38,41	0.80	1 (5%)
1	OMG	C1	1433	1	18,26,27	1.24	2 (11%)	19,38,41	0.86	1 (5%)
1	OMG	C1	2876	1	18,26,27	1.16	2 (11%)	19,38,41	0.88	1 (5%)
1	A2M	C1	1432	1	18,25,26	4.33	8 (44%)	18,36,39	3.94	4 (22%)
1	OMU	C1	1917	1	19,22,23	3.01	6 (31%)	26,31,34	1.75	6 (23%)
1	OMC	C1	2838	1	19,22,23	0.77	1 (5%)	26,31,34	1.54	4 (15%)
1	OMC	C1	1812	1	19,22,23	0.64	0	26,31,34	1.38	2 (7%)
1	OMU	C1	2380	1	19,22,23	2.96	7 (36%)	26,31,34	1.69	5 (19%)
1	OMC	C1	1420	1	19,22,23	0.71	0	26,31,34	1.24	3 (11%)
1	OMC	C1	2300	1	19,22,23	0.62	0	26,31,34	0.66	0
1	A2M	C1	2289	1	18,25,26	4.37	7 (38%)	18,36,39	3.77	4 (22%)
1	A2M	C1	1847	1	18,25,26	4.33	8 (44%)	18,36,39	4.01	5 (27%)
1	OMG	C1	2578	1	18,26,27	1.20	2 (11%)	19,38,41	0.99	1 (5%)
1	OMG	C1	787	1	18,26,27	1.20	2 (11%)	19,38,41	0.92	1 (5%)
1	OMU	C1	2683	1	19,22,23	2.96	7 (36%)	26,31,34	1.73	5 (19%)
1	OMU	C1	2384	1	19,22,23	3.02	7 (36%)	26,31,34	1.71	5 (19%)
1	A2M	C1	848	1	18,25,26	4.34	9 (50%)	18,36,39	3.83	5 (27%)
1	OMG	C1	2358	1	18,26,27	1.21	2 (11%)	19,38,41	0.85	1 (5%)

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	OMG	C1	646	1	-	0/5/27/28	0/3/3/3
1	A2M	C1	637	1	-	1/5/27/28	0/3/3/3
1	OMG	C1	627	1	-	0/5/27/28	0/3/3/3
1	OMC	C1	778	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	858	1	-	0/5/27/28	0/3/3/3
1	A2M	C1	1223	1	-	1/5/27/28	0/3/3/3
1	OMU	C1	2277	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2774	1	-	0/5/27/28	0/3/3/3
1	OMG	C1	2881	1	-	0/5/27/28	0/3/3/3
1	OMC	C1	1836	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2688	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	389	1	-	3/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	C1	1491	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2690	1	-	2/9/27/28	0/2/2/2
1	OMC	C1	2918	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	385	1	-	2/5/27/28	0/3/3/3
1	OMG	C1	1433	1	-	3/5/27/28	0/3/3/3
1	OMG	C1	2876	1	-	0/5/27/28	0/3/3/3
1	A2M	C1	1432	1	-	0/5/27/28	0/3/3/3
1	OMU	C1	1917	1	-	2/9/27/28	0/2/2/2
1	OMC	C1	2838	1	-	2/9/27/28	0/2/2/2
1	OMC	C1	1812	1	-	2/9/27/28	0/2/2/2
1	OMU	C1	2380	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1420	1	-	4/9/27/28	0/2/2/2
1	OMC	C1	2300	1	-	1/9/27/28	0/2/2/2
1	A2M	C1	2289	1	-	0/5/27/28	0/3/3/3
1	A2M	C1	1847	1	-	3/5/27/28	0/3/3/3
1	OMG	C1	2578	1	-	3/5/27/28	0/3/3/3
1	OMG	C1	787	1	-	0/5/27/28	0/3/3/3
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2384	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	848	1	-	0/5/27/28	0/3/3/3
1	OMG	C1	2358	1	-	0/5/27/28	0/3/3/3

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2289	A2M	C3'-C2'	-12.93	1.24	1.52
1	C1	858	A2M	C3'-C2'	-12.83	1.24	1.52
1	C1	637	A2M	C3'-C2'	-12.72	1.24	1.52
1	C1	1223	A2M	C3'-C2'	-12.71	1.24	1.52
1	C1	1432	A2M	C3'-C2'	-12.66	1.24	1.52

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C1	1847	A2M	C1'-N9-C4	10.82	145.66	126.64
1	C1	389	A2M	C1'-N9-C4	10.53	145.13	126.64
1	C1	1432	A2M	C1'-N9-C4	10.36	144.85	126.64
1	C1	637	A2M	C1'-N9-C4	10.28	144.70	126.64
1	C1	858	A2M	C1'-N9-C4	10.08	144.35	126.64

There are no chirality outliers.

5 of 31 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	1433	OMG	O4'-C4'-C5'-O5'
1	C1	1812	OMC	C1'-C2'-O2'-CM2
1	C1	1847	A2M	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 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	$\#\|Z\| > 2$
59	GTP	Cd	1000	60	26,34,34	1.22	1 (3%)	32,54,54	1.49	7 (21%)
59	GTP	CH	701	60	26,34,34	1.22	1 (3%)	32,54,54	1.48	7 (21%)

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
59	GTP	Cd	1000	60	-	3/18/38/38	0/3/3/3
59	GTP	CH	701	60	-	6/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	CH	701	GTP	C5-C6	-4.35	1.38	1.47
59	Cd	1000	GTP	C5-C6	-4.30	1.38	1.47

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	Cd	1000	GTP	PB-O3B-PG	-3.35	121.33	132.83
59	CH	701	GTP	C5-C6-N1	3.15	119.52	113.95
59	Cd	1000	GTP	C5-C6-N1	3.11	119.45	113.95
59	CH	701	GTP	O2G-PG-O3B	3.10	115.02	104.64
59	CH	701	GTP	C8-N7-C5	3.03	108.77	102.99

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

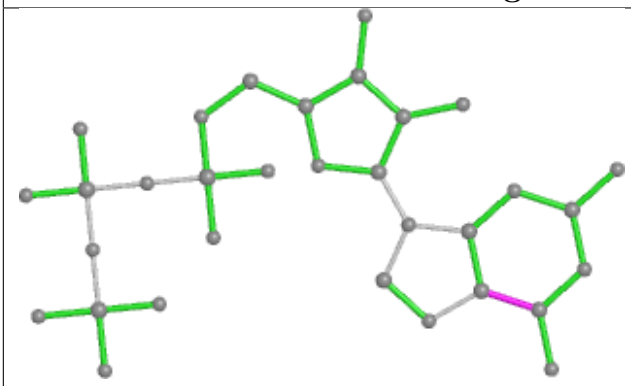
Mol	Chain	Res	Type	Atoms
59	CH	701	GTP	C5'-O5'-PA-O3A
59	CH	701	GTP	O4'-C4'-C5'-O5'
59	CH	701	GTP	C3'-C4'-C5'-O5'
59	CH	701	GTP	C5'-O5'-PA-O1A
59	CH	701	GTP	C5'-O5'-PA-O2A

There are no ring outliers.

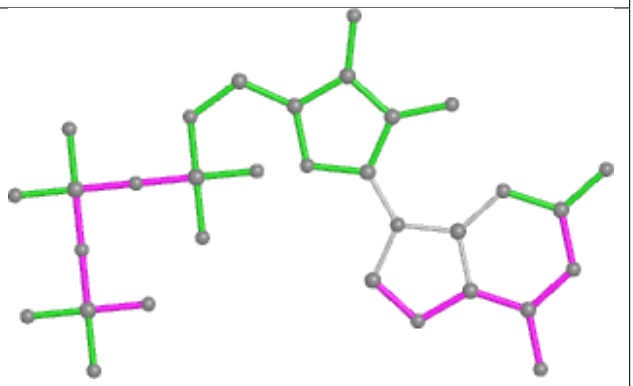
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

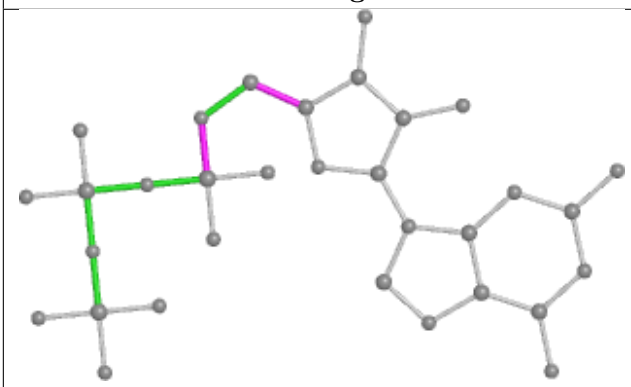
Ligand GTP Cd 1000



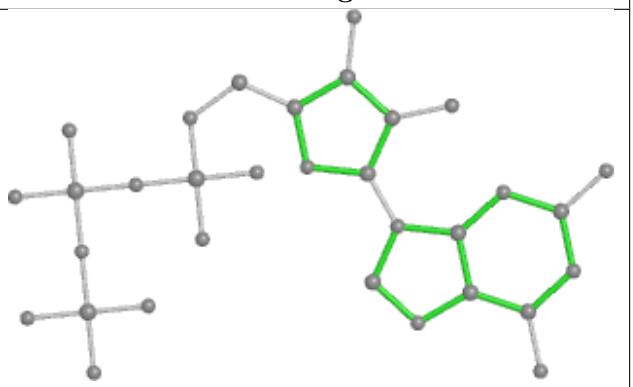
Bond lengths



Bond angles

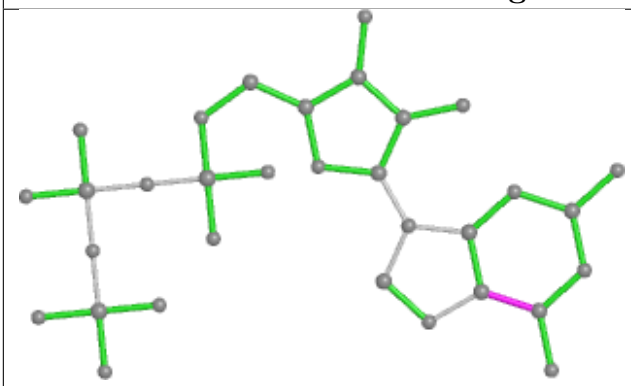


Torsions

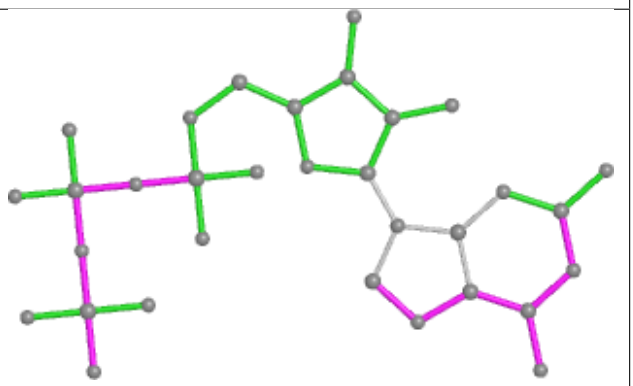


Rings

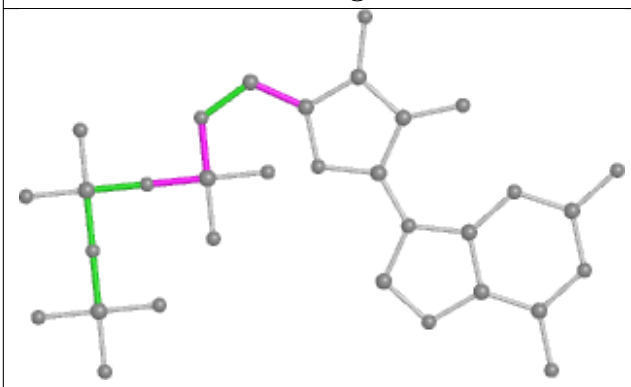
Ligand GTP CH 701



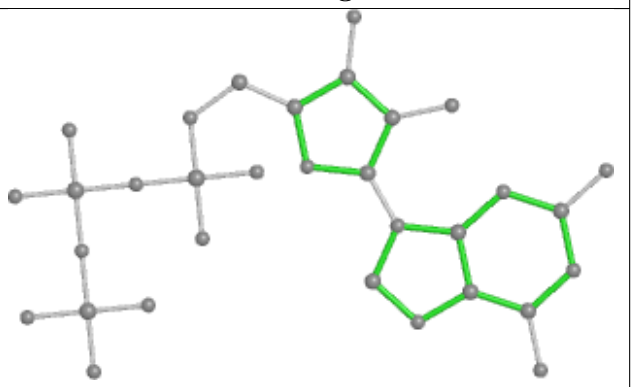
Bond lengths



Bond angles



Torsions



Rings

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.

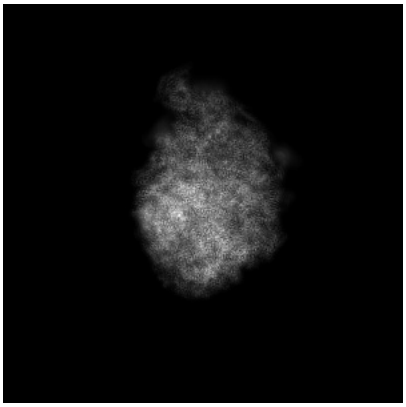
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17956. These allow visual inspection of the internal detail of the map and identification of artifacts.

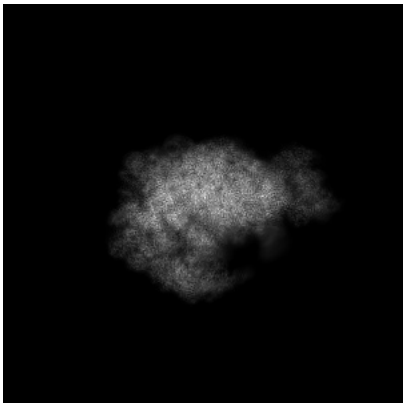
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

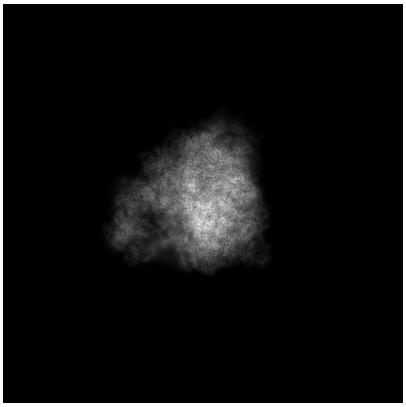
6.1.1 Primary map



X



Y

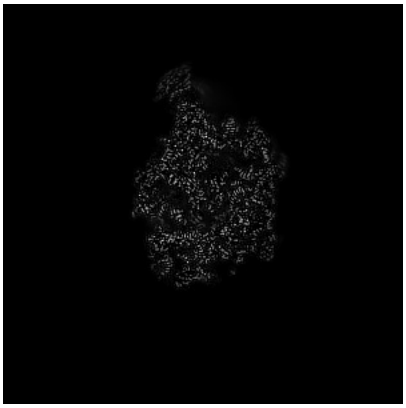


Z

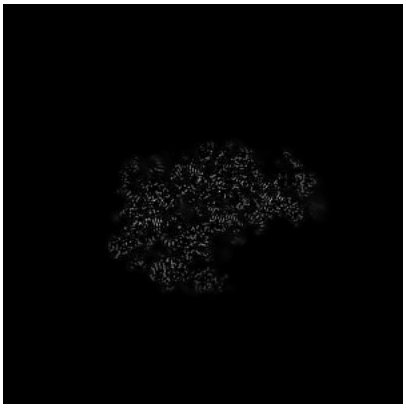
The images above show the map projected in three orthogonal directions.

6.2 Central slices

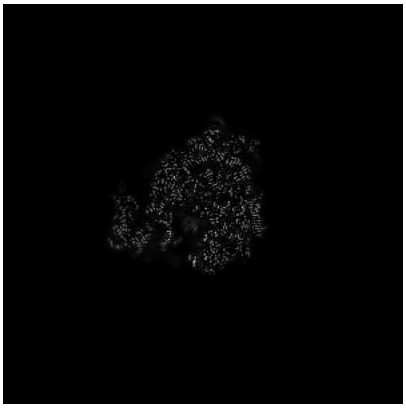
6.2.1 Primary map



X Index: 250



Y Index: 250

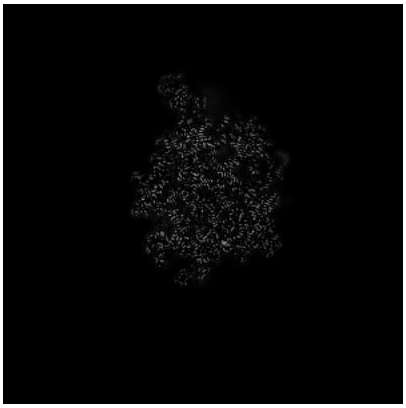


Z Index: 250

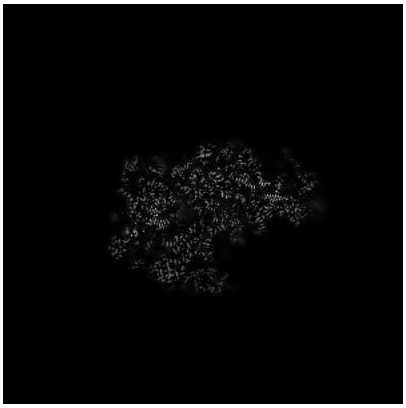
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

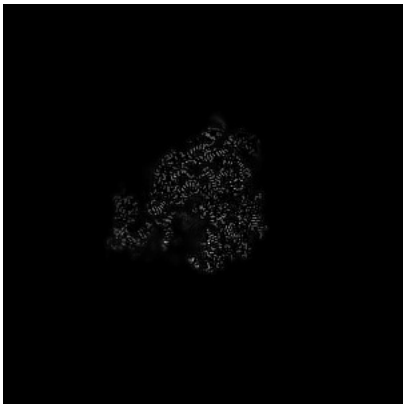
6.3.1 Primary map



X Index: 259



Y Index: 248

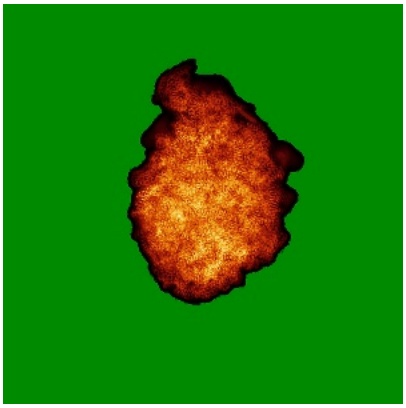


Z Index: 252

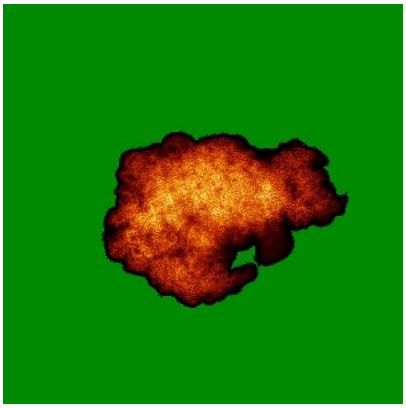
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

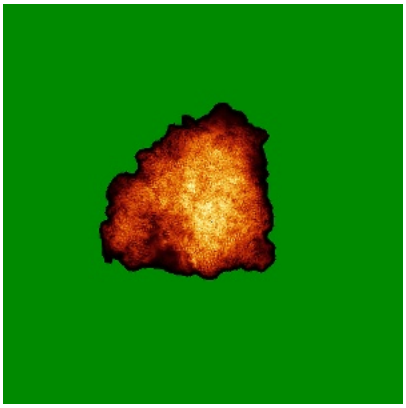
6.4.1 Primary map



X



Y

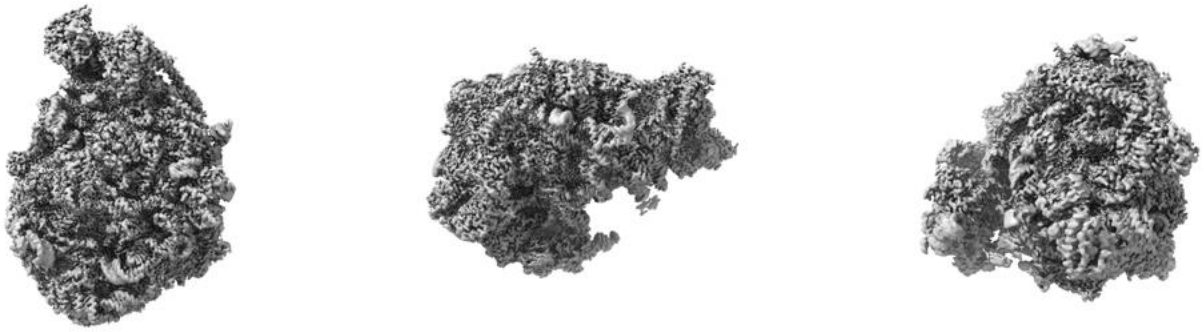


Z

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



X Y Z

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.

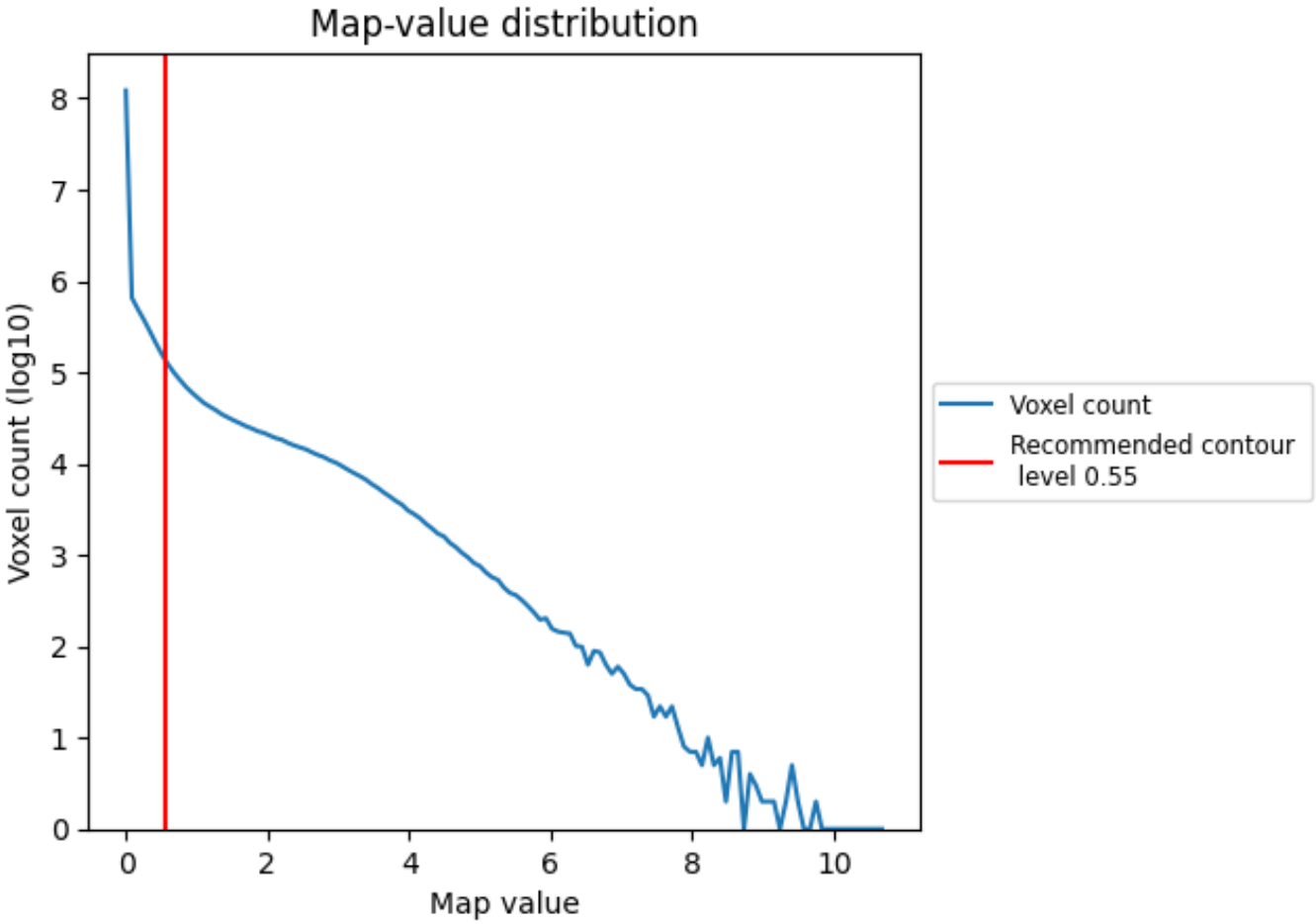
6.6 Mask visualisation (i)

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

7 Map analysis

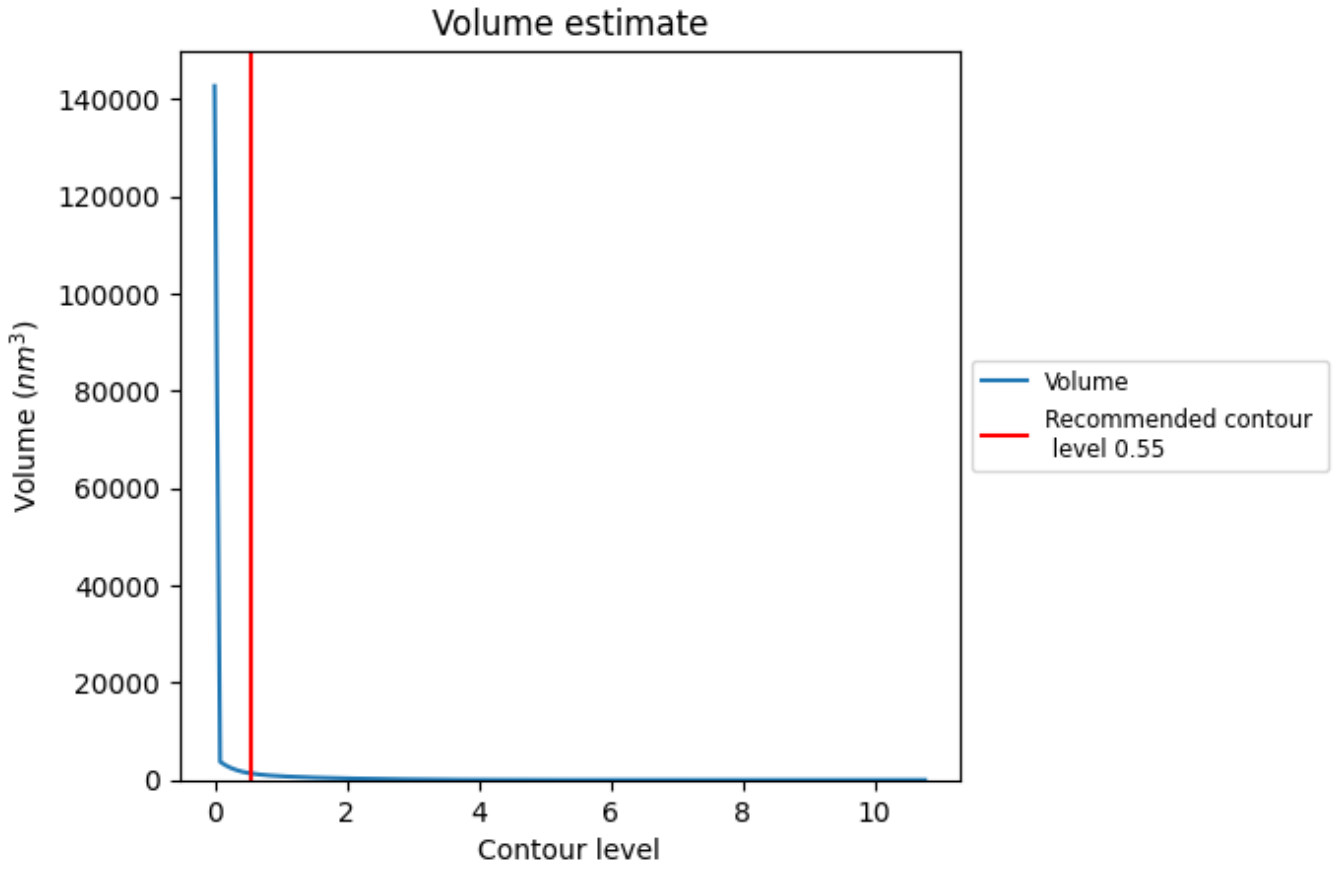
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

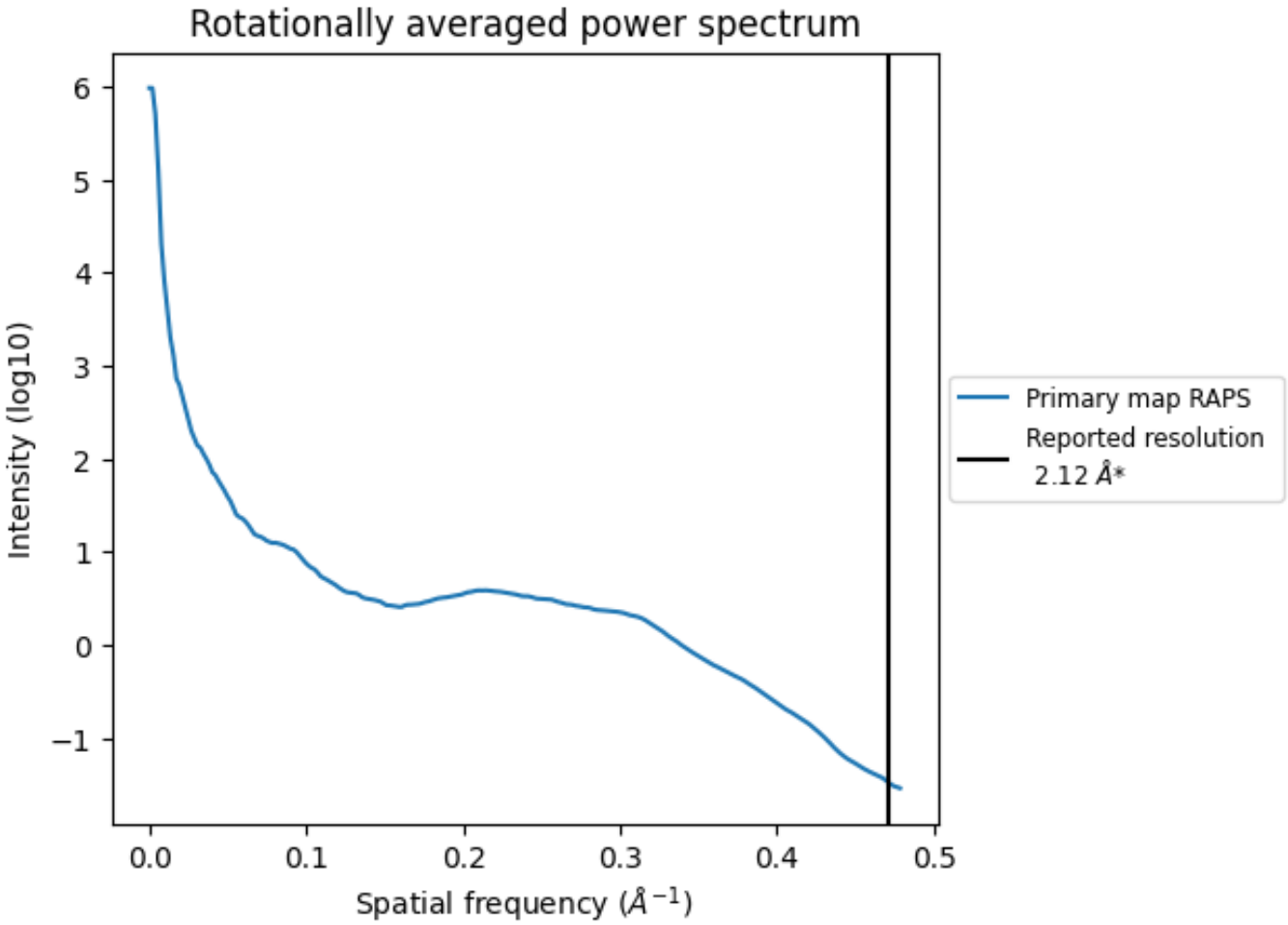
7.2 Volume estimate (i)



The volume at the recommended contour level is 1355 nm^3; this corresponds to an approximate mass of 1224 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 (i)



*Reported resolution corresponds to spatial frequency of 0.472 Å^{-1}

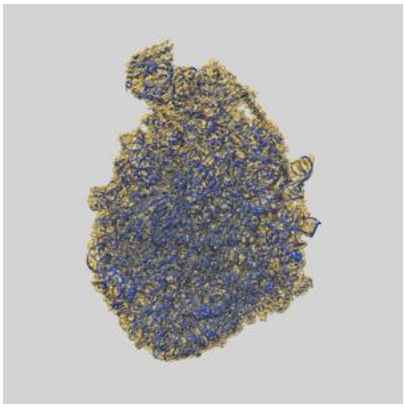
8 Fourier-Shell correlation (i)

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

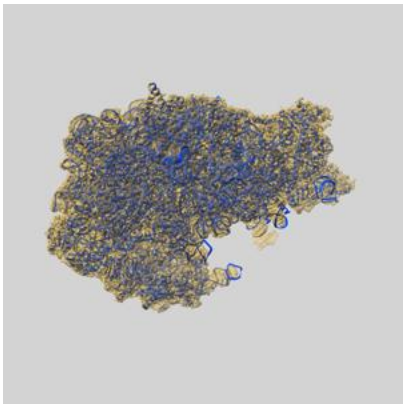
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17956 and PDB model 8PV7. Per-residue inclusion information can be found in section 3 on page 16.

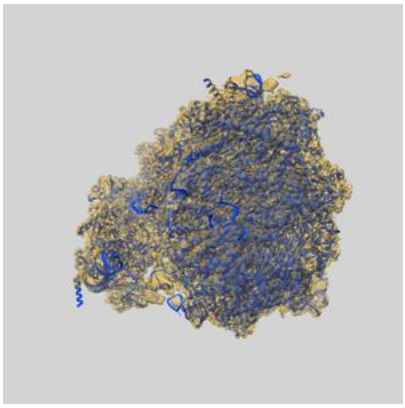
9.1 Map-model overlay



X



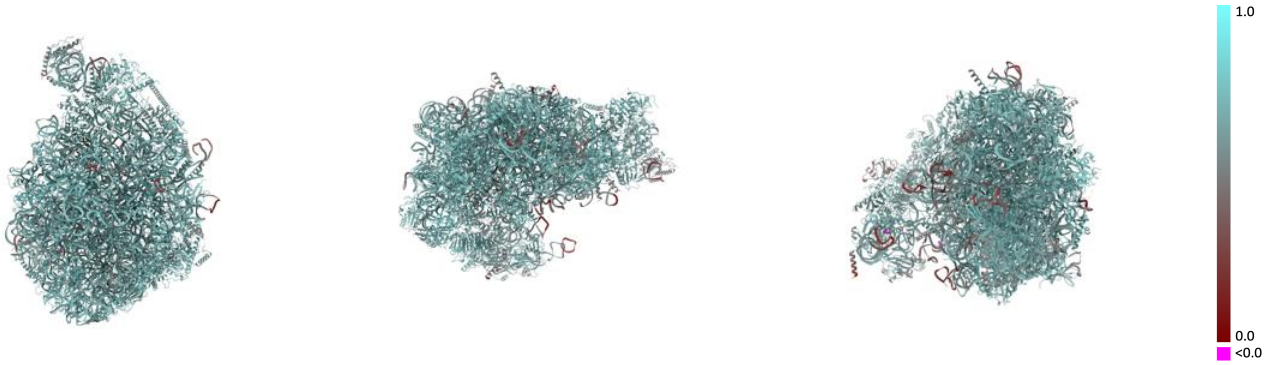
Y



Z

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.

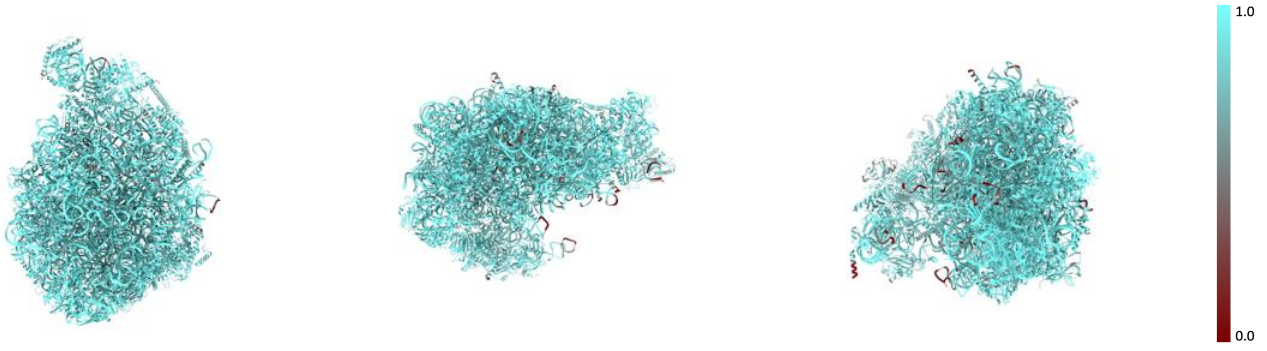
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

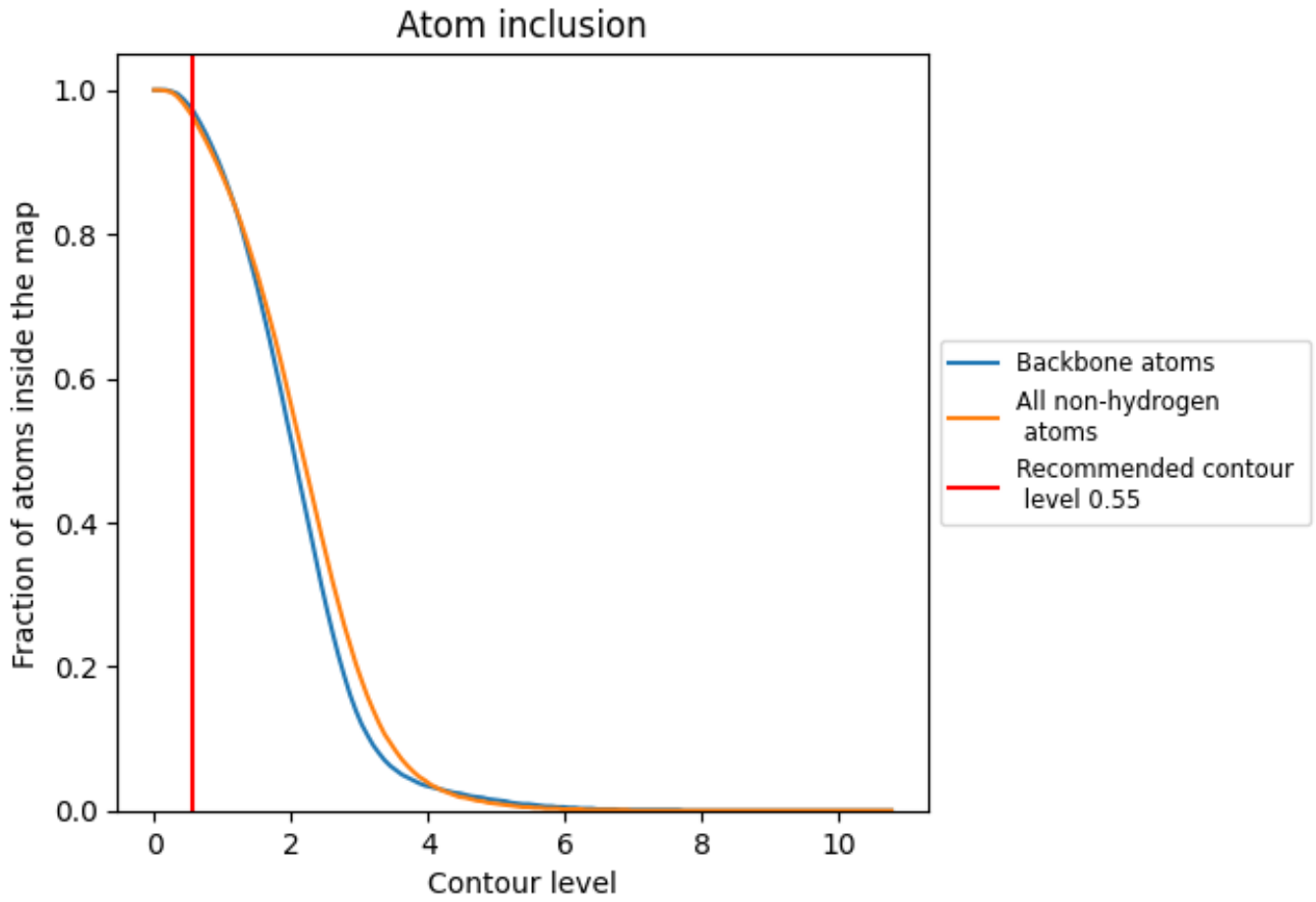
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.55).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.9650	0.6760
C1	0.9770	0.6650
C2	0.9770	0.6890
C3	0.8300	0.5370
C4	0.9280	0.5990
CB	0.9290	0.6250
CF	0.9670	0.6860
CH	0.9490	0.6920
CI	0.9200	0.6380
CJ	0.9840	0.6940
CK	0.9860	0.7230
CL	0.9440	0.6420
CM	0.9520	0.6590
CN	0.9730	0.7110
CO	0.9520	0.7060
CQ	0.9210	0.6770
Cb	0.9750	0.7070
Cd	0.9690	0.7000
Ce	0.8940	0.6380
Cf	0.9640	0.6740
Cg	0.9650	0.6590
Ch	0.9210	0.6570
Cz	0.8810	0.5970
LA	0.9870	0.7100
LB	0.9850	0.7300
LC	0.9810	0.7230
LD	0.9300	0.6620
LE	0.9440	0.6810
LF	0.9770	0.7050
LG	0.9720	0.6990
LH	0.9730	0.7150
LJ	0.9290	0.5920
LK	0.9410	0.6470
LL	0.9610	0.7030
LM	0.9730	0.7060

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Chain	Atom inclusion	Q-score
LN	0.9960	0.7310
LO	0.9890	0.7290
LP	0.9870	0.7210
LQ	0.9860	0.7000
LR	0.9620	0.7080
LS	0.9880	0.7080
LT	0.9490	0.6280
LU	0.9410	0.6620
LV	0.9910	0.7310
LX	0.9730	0.6940
LY	0.9770	0.7080
LZ	0.9670	0.7020
La	0.9730	0.7060
Lc	0.9600	0.6890
Ld	0.9660	0.7160
Le	0.9880	0.7310
Lf	0.9960	0.7380
Lg	0.9340	0.6940
Lh	0.9460	0.6620
Li	0.9500	0.6780
Lj	0.9930	0.7380
Lk	0.9170	0.6740
Ll	0.9980	0.7390
Lp	0.9480	0.6910
Lq	0.9690	0.6970