wwPDB EM Validation Summary Report ⓘ

Dec 14, 2023 – 04:24 pm GMT

PDB ID	:	8PV1
EMDB ID	:	EMD-17950
Title	:	Chaetomium thermophilum pre-60S State 6 - pre-5S rotation - L1 intermediate - composite structure
Authors	:	Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2023-07-17
Resolution	:	2.56 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:

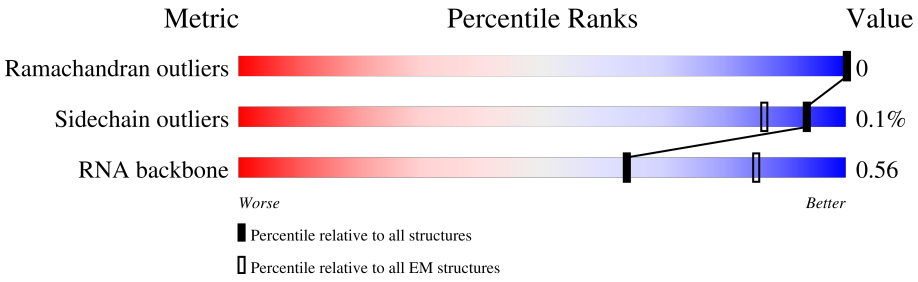
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.56 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	9% 36% 14% 49%
4	C4	119	7% 78% 22%
5	CB	391	5% 67% 32%
6	CF	270	90% 9%
7	CH	661	95% 5%
8	CI	414	36% 63%

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Mol	Chain	Length	Quality of chain
9	CJ	679	56% 44%
10	CK	261	91% 9%
11	CL	558	14% 86%
12	CM	249	87% 13%
12	LF	249	100%
13	CN	246	100%
14	CO	120	52% 48%
15	CQ	225	6% 81% 19%
16	Cb	117	86% 14%
17	Cd	627	74% 26%
18	Ce	443	59% 41%
19	Cf	350	81% 19%
20	Cg	202	93% 7%
21	Ch	517	6% 94% 6%
22	Cz	123	82% 18%
23	LA	254	75% 25%
24	LB	392	99%
25	LC	365	99%
26	LD	304	5% 94% 6%
27	LE	200	95%
28	LG	262	90% 10%
29	LH	229	83% 17%
30	LJ	173	98%
31	LK	165	95%
32	LL	213	95% 5%

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Mol	Chain	Length	Quality of chain
33	LM	142	99%
34	LN	203	100%
35	LO	204	100%
36	LP	187	91% 9%
37	LQ	213	70% 30%
38	LR	2898	5% 95%
39	LS	174	100%
40	LT	160	81% 19%
41	LU	127	83% 17%
42	LV	139	97%
43	LX	156	93% 7%
44	LY	138	96%
45	LZ	135	100%
46	La	149	72% 28%
47	Lc	108	88% 12%
48	Ld	120	92% 8%
49	Le	131	96%
50	Lf	109	99%
51	Lg	119	8% 99%
52	Lh	935	13% 87%
53	Li	110	92% 8%
54	Lj	95	93% 7%
55	Lk	94	81% 19%
56	Ll	51	98%
57	Lp	92	99%

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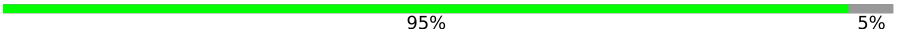
Mol	Chain	Length	Quality of chain
58	Lq	147	

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 157250 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	265	2107	1351	371	382	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 Zinc finger domain-containing protein.

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

- Molecule 17 is a protein called Nucleolar GTP-binding protein 2.

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

- Molecule 18 is a protein called Ribosome biogenesis protein NOP53.

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

- Molecule 19 is a protein called Ribosome production factor 2 homolog.

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

- Molecule 20 is a protein called Ribosome biogenesis regulatory protein.

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

- Molecule 21 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	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 22 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Cz	101	Total	C	N	O	S	0	0
			869	541	180	144	4		

- Molecule 23 is a protein called 60S ribosomal protein L2-like protein.

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

- Molecule 24 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LB	389	Total	C	N	O	S	0	0
			3104	1973	579	539	13		

- Molecule 25 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LC	363	Total	C	N	O	S	0	0
			2751	1737	527	478	9		

- Molecule 26 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LD	286	Total	C	N	O	S	0	0
			2266	1434	407	422	3		

- Molecule 27 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LE	191	Total	C	N	O	S	0	0
			1477	944	267	263	3		

- Molecule 28 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LG	235	Total	C	N	O	S	0	0
			1889	1210	350	324	5		

- Molecule 29 is a protein called 60S ribosomal protein l9-like protein.

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

- Molecule 30 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LJ	169	Total	C	N	O	S	0	0
			1357	850	266	235	6		

- Molecule 31 is a protein called 60S ribosomal protein L12-like protein.

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

- Molecule 32 is a protein called 60S ribosomal protein L13.

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

- Molecule 33 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 34 is a protein called Ribosomal protein L15.

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

- Molecule 35 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 36 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 37 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LQ	150	Total	C	N	O	S	0	0
			1200	759	239	200	2		

- Molecule 38 is a protein called Ribosomal protein L19.

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

- Molecule 39 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LS	174	Total	C	N	O	S	0	0
			1426	917	266	238	5		

- Molecule 40 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LT	129	Total	C	N	O	S	0	0
			1027	651	195	179	2		

- Molecule 41 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LU	105	Total	C	N	O	S	0	0
			846	548	146	151	1		

- Molecule 42 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 43 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	LX	145	Total	C	N	O	0	0
			1133	723	211	199		

- Molecule 44 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 45 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LZ	135	Total	C	N	O	S	0	0
			1112	713	207	188	4		

- Molecule 46 is a protein called 60S ribosomal protein L28-like protein.

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

- Molecule 47 is a protein called 60S ribosomal protein l30-like protein.

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

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

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

- Molecule 49 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 50 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 51 is a protein called Ribosomal protein l34-like protein.

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

- Molecule 52 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 53 is a protein called 60S ribosomal protein L36.

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

- Molecule 54 is a protein called Ribosomal protein L37.

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

- Molecule 55 is a protein called 60S ribosomal protein L38-like protein.

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

- Molecule 56 is a protein called Ribosomal protein eL39.

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

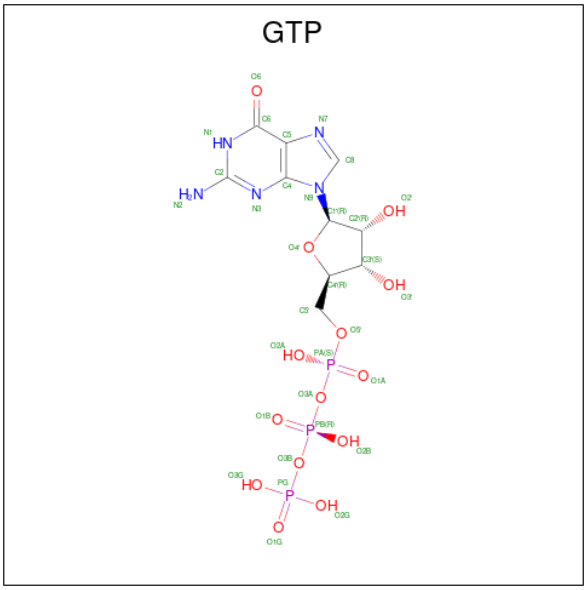
- Molecule 57 is a protein called 60S ribosomal protein L43-like protein.

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

- Molecule 58 is a protein called Putative 60S ribosomal protein.

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

- 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	

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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.

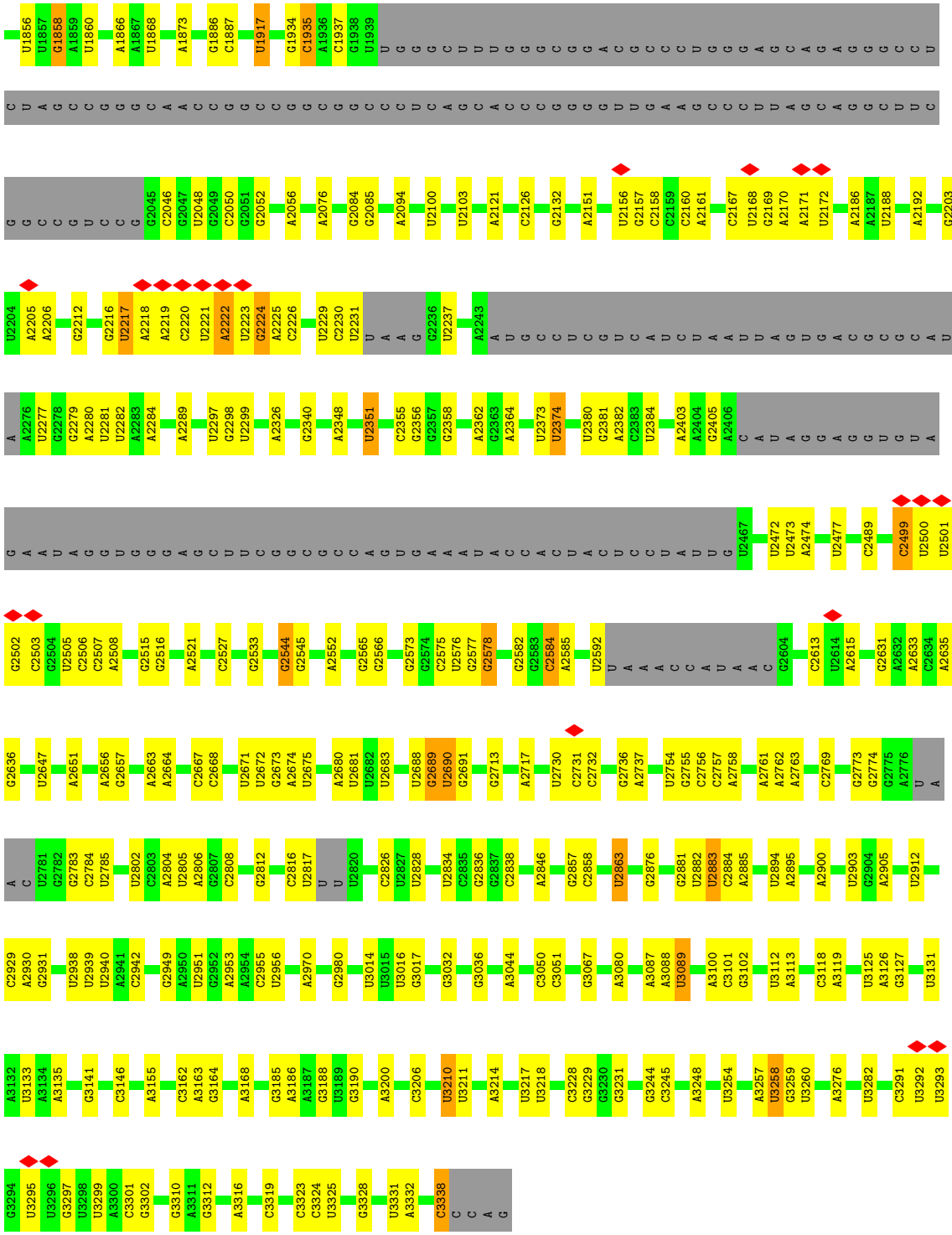
Mol	Chain	Residues	Atoms		AltConf
62	CH	1	Total	O	0
			1	1	
62	Cd	2	Total	O	0
			2	2	

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.

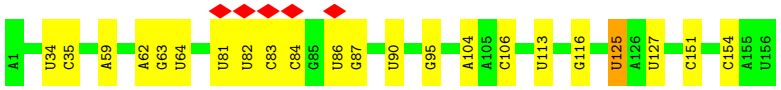
- Molecule 1: 26S rRNA

Chain C1:



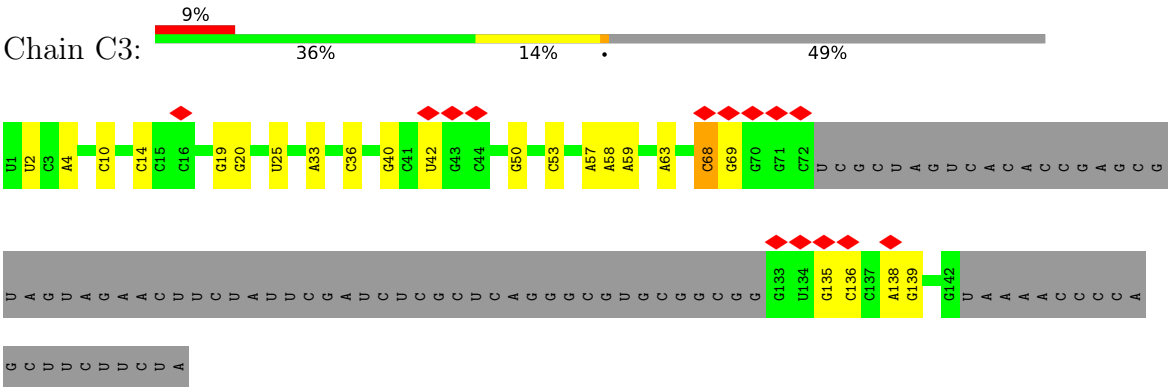
• Molecule 2: 5.8S rRNA

Chain C2:



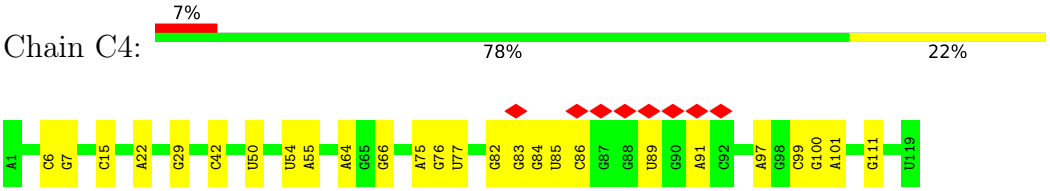
• Molecule 3: ITS2

Chain C3:



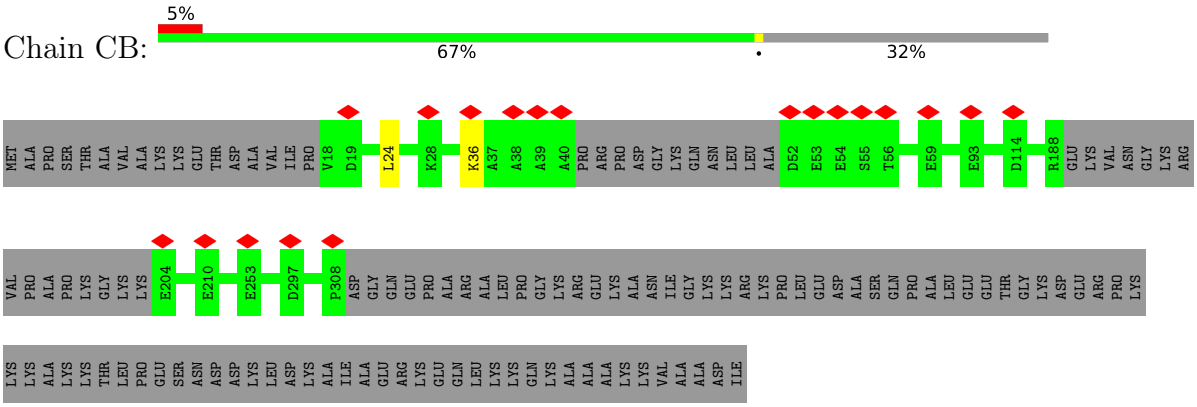
• Molecule 4: 5S rRNA

Chain C4:



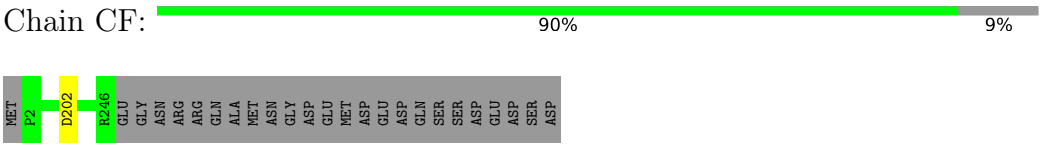
• Molecule 5: Utp30

Chain CB:



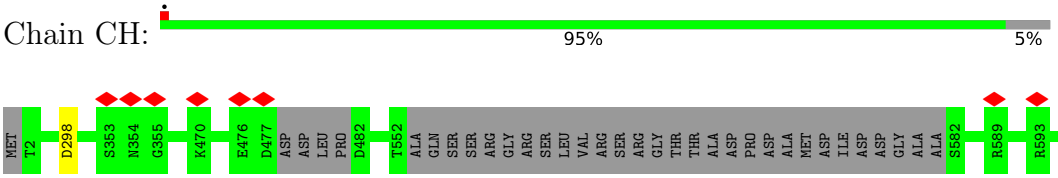
• Molecule 6: Large ribosomal subunit protein uL10

Chain CF:



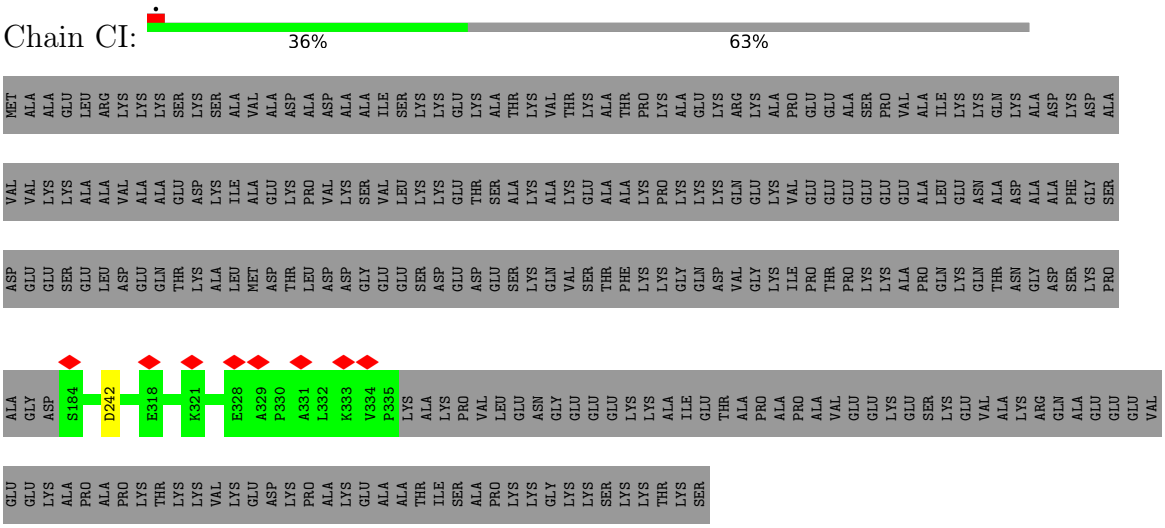
• Molecule 7: Nucleolar GTP-binding protein 1

Chain CH:



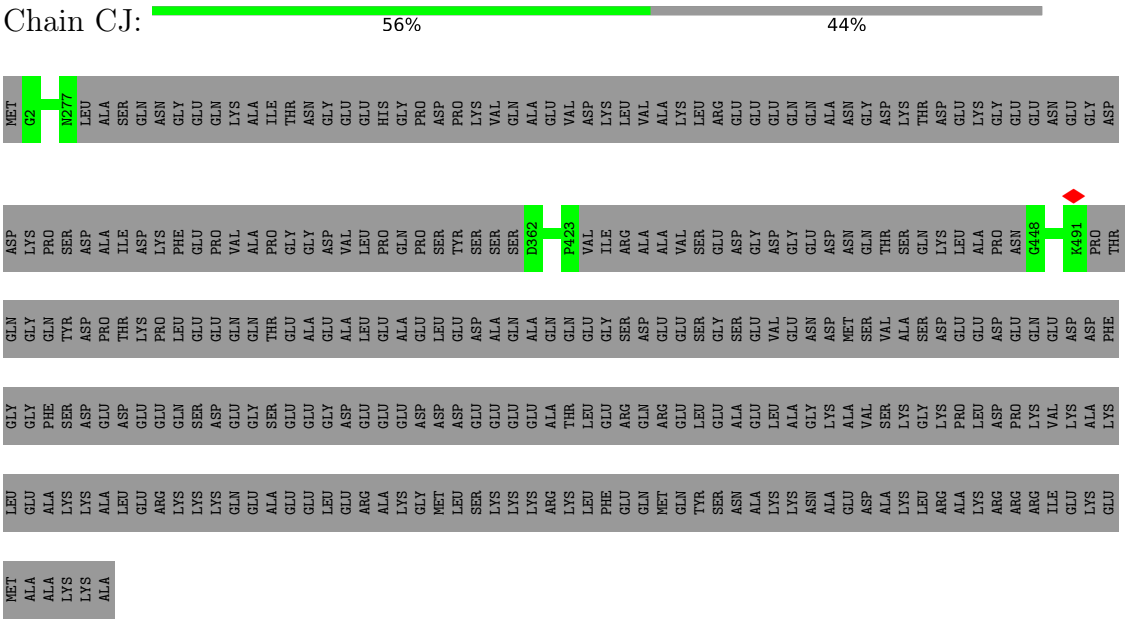
• Molecule 8: Putative RNA-binding protein

Chain CI:



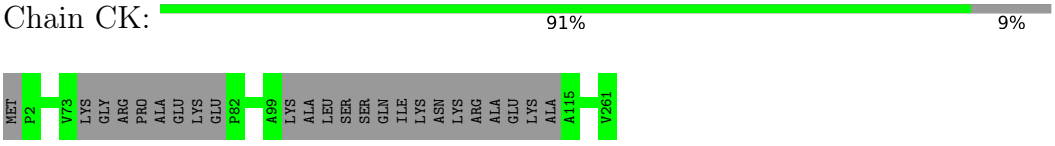
• Molecule 9: Pescadillo homolog

Chain CJ:



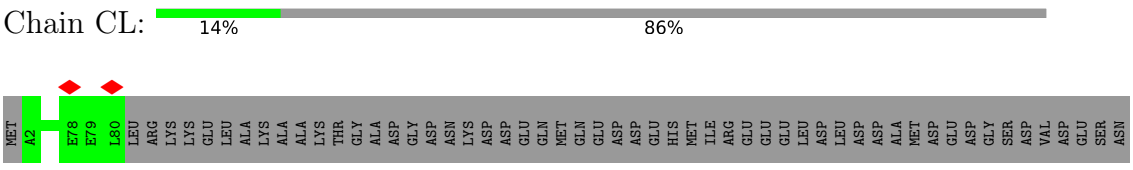
• Molecule 10: Ribosome biogenesis protein NSA2 homolog

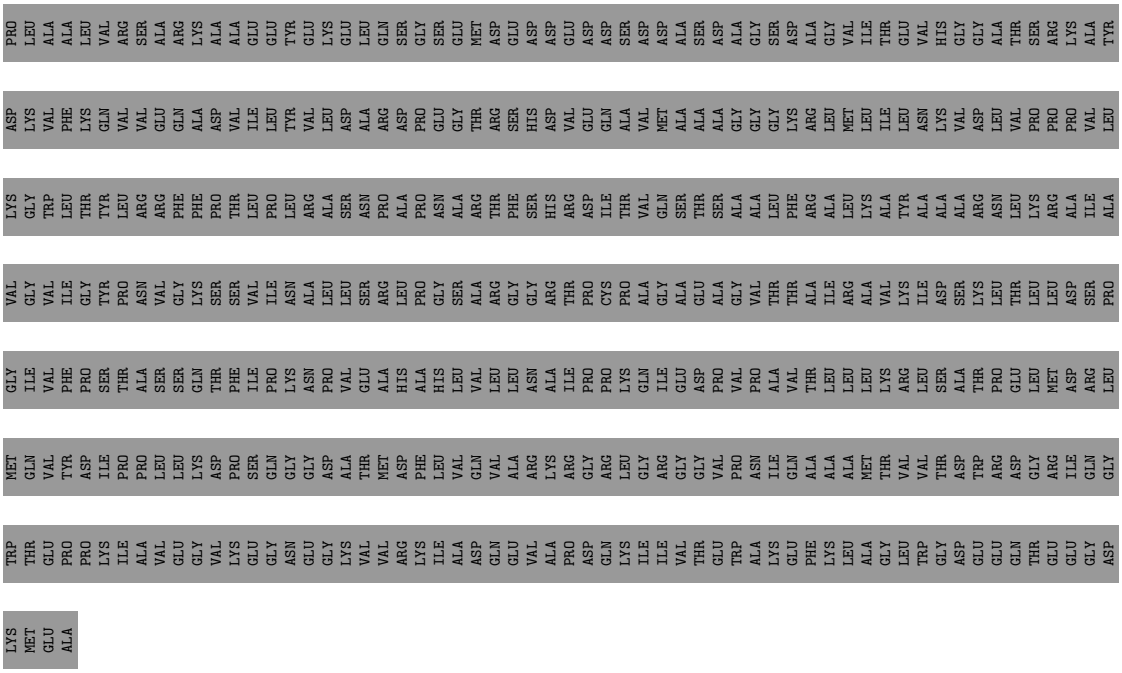
Chain CK:



• Molecule 11: Putative GTP binding protein

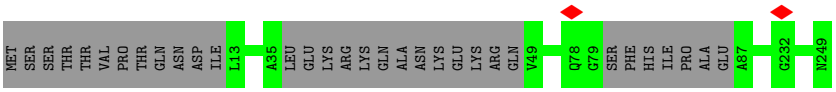
Chain CL:





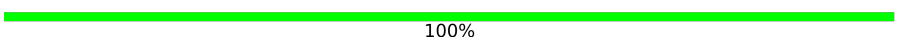
• Molecule 12: 60S ribosomal protein l7-like protein

Chain CM:



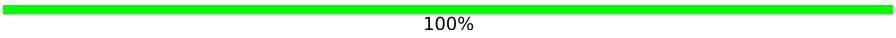
• Molecule 12: 60S ribosomal protein l7-like protein

Chain LF:



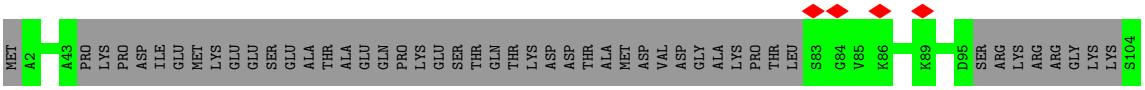
• Molecule 13: Eukaryotic translation initiation factor 6

Chain CN:



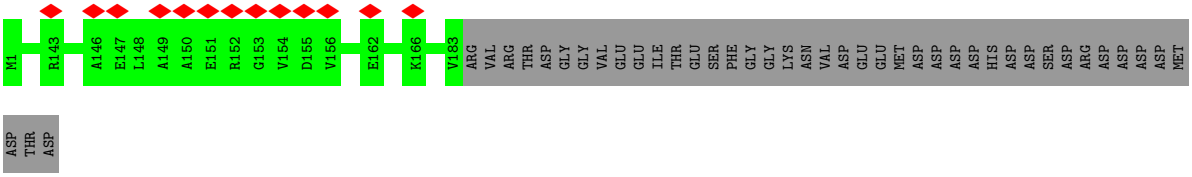
• Molecule 14: DUF2423 domain-containing protein

Chain CO:



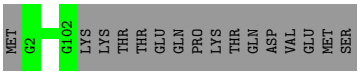
• Molecule 15: Ribosome biogenesis protein RLP24

Chain CQ:



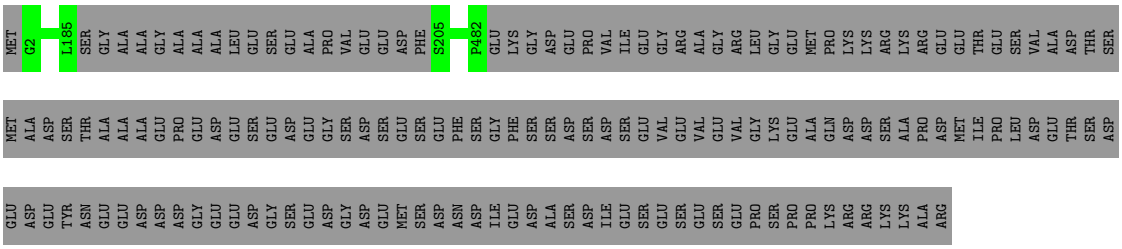
• Molecule 16: Zinc finger domain-containing protein

Chain Cb:



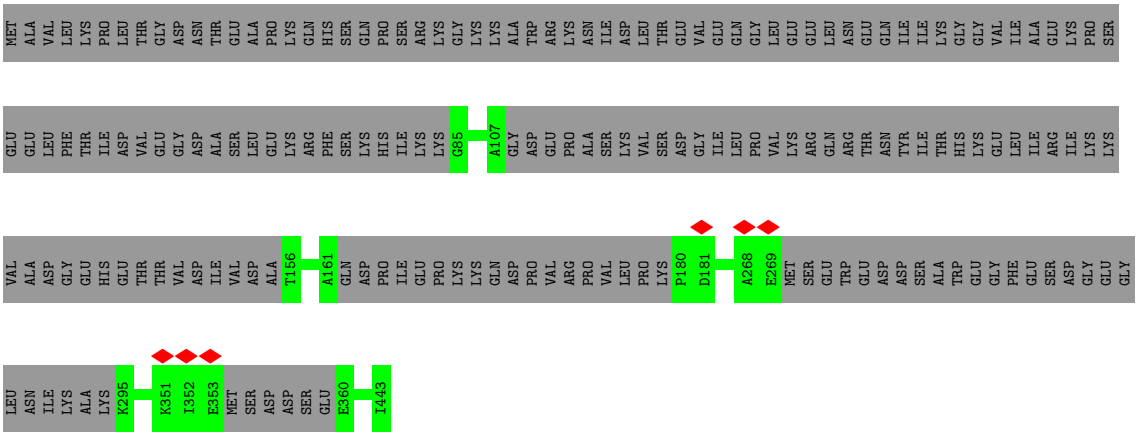
• Molecule 17: Nucleolar GTP-binding protein 2

Chain Cd:



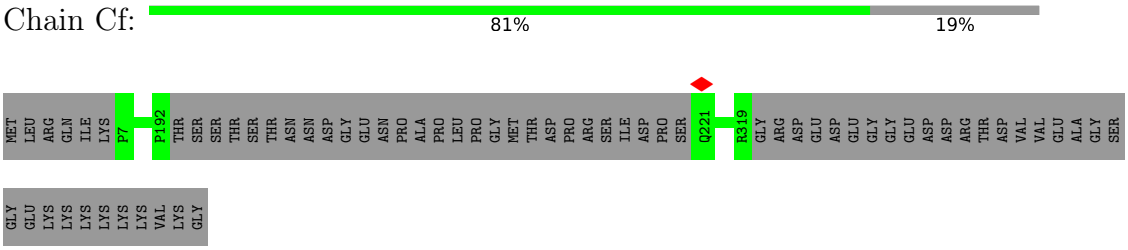
• Molecule 18: Ribosome biogenesis protein NOP53

Chain Ce:



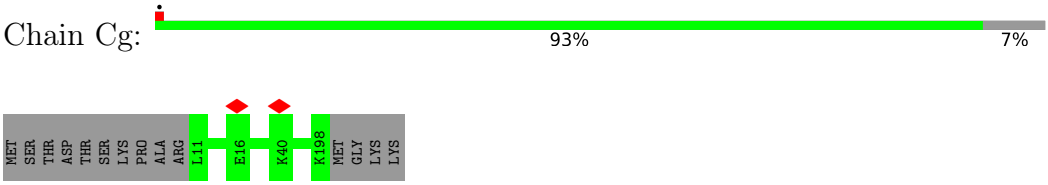
• Molecule 19: Ribosome production factor 2 homolog

Chain Cf:



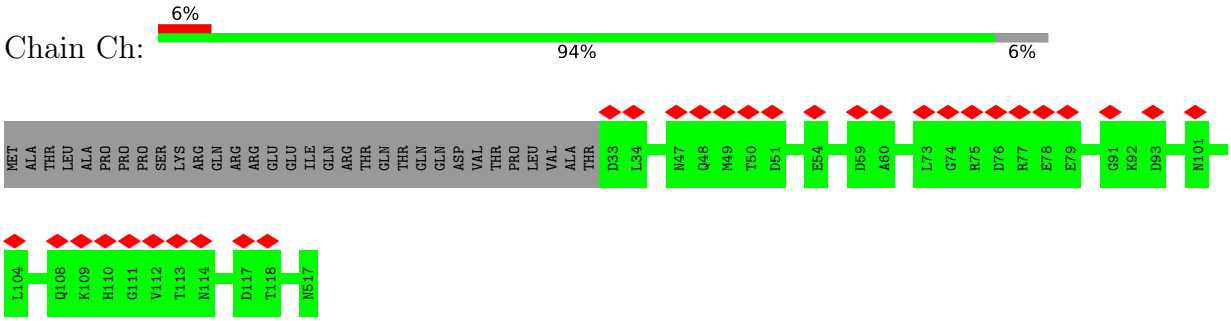
• Molecule 20: Ribosome biogenesis regulatory protein

Chain Cg:



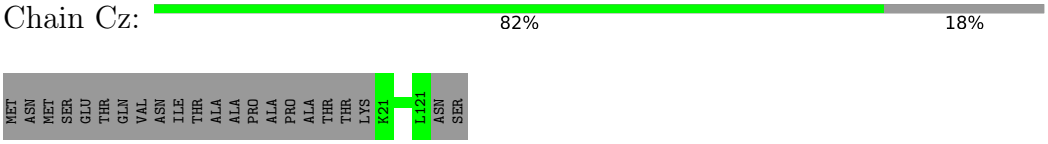
• Molecule 21: Ribosome assembly protein 4

Chain Ch:



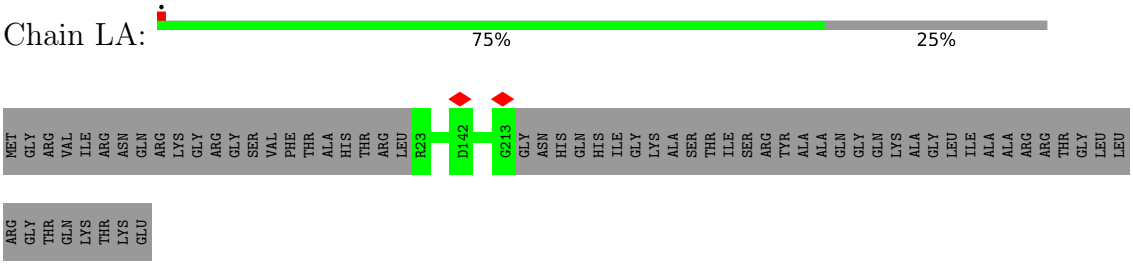
• Molecule 22: rRNA-processing protein

Chain Cz:



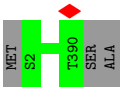
• Molecule 23: 60S ribosomal protein L2-like protein

Chain LA:



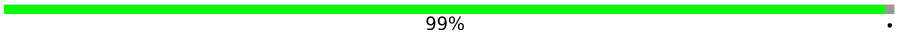
• Molecule 24: 60S ribosomal protein L3-like protein

Chain LB:



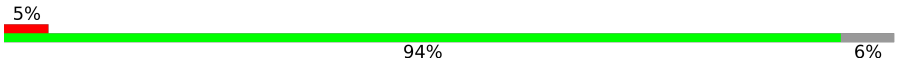
• Molecule 25: 60S ribosomal protein L4-like protein

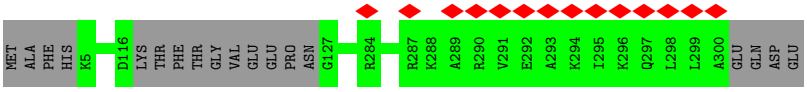
Chain LC:



• Molecule 26: 60S ribosomal protein l5-like protein

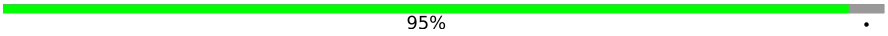
Chain LD:

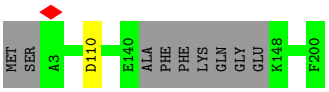




• Molecule 27: 60S ribosomal protein L6

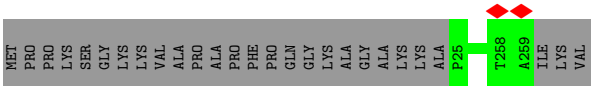
Chain LE:





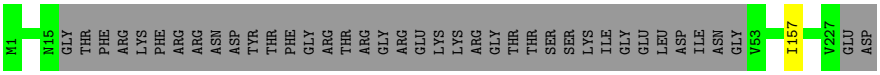
• Molecule 28: 60S ribosomal protein L8

Chain LG:



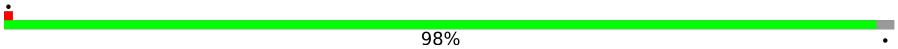
• Molecule 29: 60S ribosomal protein l9-like protein

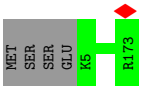
Chain LH:



• Molecule 30: Putative ribosomal protein

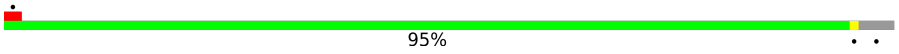
Chain LJ:

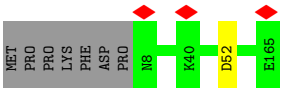




• Molecule 31: 60S ribosomal protein L12-like protein

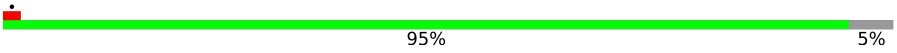
Chain LK:

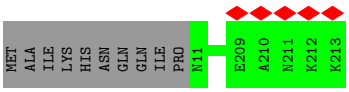




• Molecule 32: 60S ribosomal protein L13

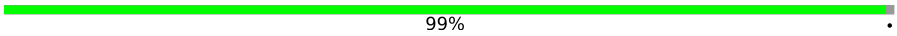
Chain LL:





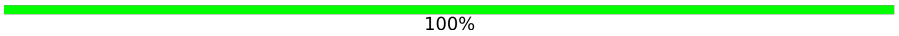
• Molecule 33: 60S ribosomal protein L14-like protein

Chain LM:



• Molecule 34: Ribosomal protein L15

Chain LN:

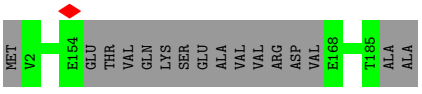


• Molecule 35: 60S ribosomal protein L16-like protein

Chain LO:

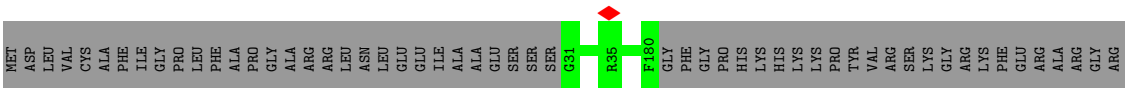
• Molecule 36: 60S ribosomal protein l17-like protein

Chain LP:



• Molecule 37: Ribosomal protein L18-like protein

Chain LQ:



ARG ARG SER ARG GLY PHE LYS VAL

- Molecule 38: Ribosomal protein L19

Chain LR: 5% 95%

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

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

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

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

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

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

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

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

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

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

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

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

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

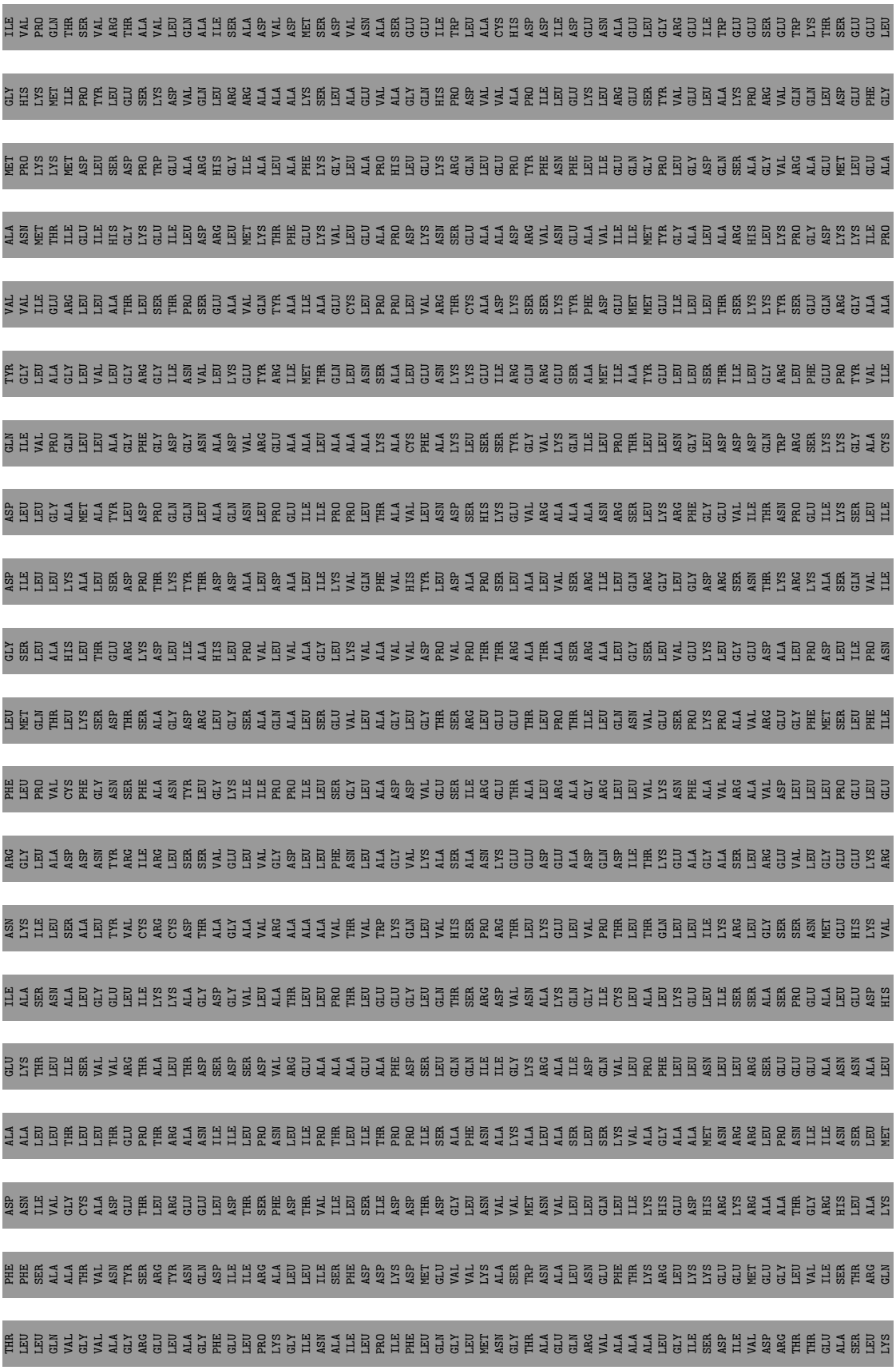
THR VAL GLY PRO LEU GLU PHE ARG THR PRO GLU GLY GLY THR THR PHE VAL ASP VAL LEU ALA LYS ARG GLN ASN VAL VAL PRO ASN LYS ASN VAL LYS ASP TYR ASP LEU LEU LYS TRP GLU GLU GLU LEU ARG GLN GLN LEU ALA GLU GLU LYS LYS LEU

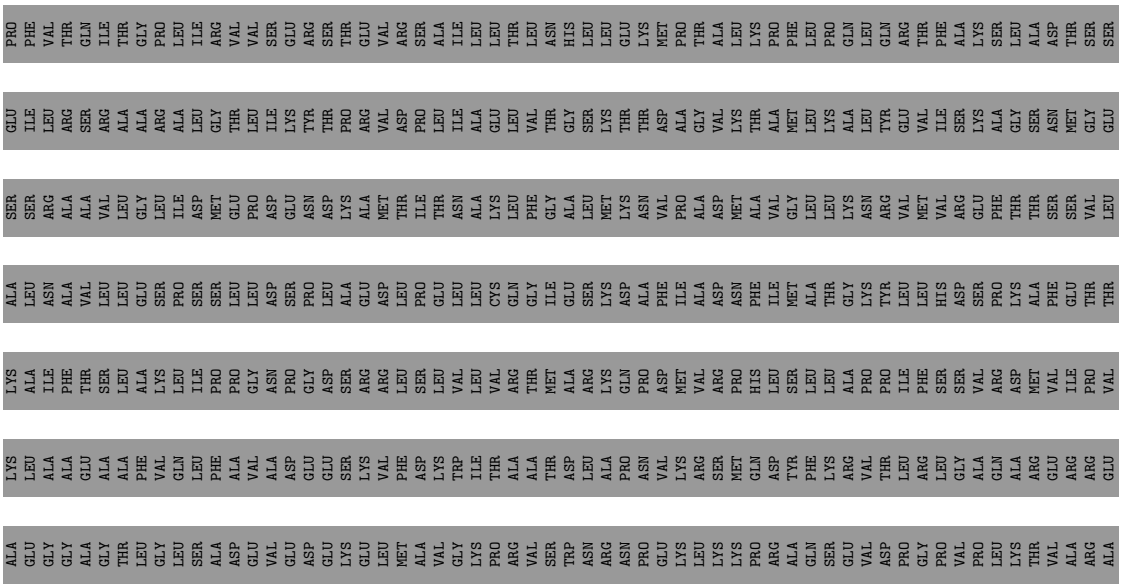
THR ALA GLU GLU GLN ALA LYS VAL SER ALA GLN LEU ILE ARG GLU ASN VAL ARG LYS ILE ALA ALA LYS LEU LEU ARG GLY PHE ILE GLY VAL VAL LYS ALA LEU ALA THR GLY PRO PRO THR ASP ALA THR ARG TRP MET GLY ALA ALA VAL ALA SER SER THR LEU ALA

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

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

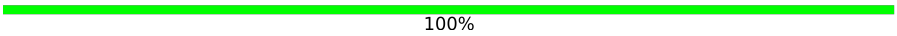
HIS THR ASP VAL ALA PHE ASP GLU ALA GLU ILE LEU SER SER LEU ILE SER SER MET GLN LYS TYR SER GLN HIS TYR LYS ILE LEU LYS ASP CYS PHE SER ASP MET VAL ARG CYS ILE ALA PRO ASN ILE SER PRO ALA GLU ILE GLY VAL LEU ALA ARG GLY ALA


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



• Molecule 39: 60S ribosomal protein L20

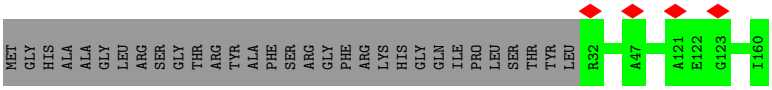
Chain LS:



There are no outlier residues recorded for this chain.

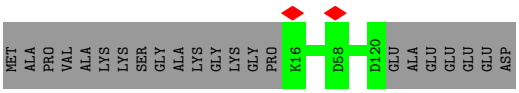
• Molecule 40: 60S ribosomal protein l21-like protein

Chain LT:



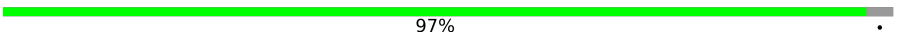
• Molecule 41: 60S ribosomal protein L22-like protein

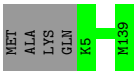
Chain LU:



• Molecule 42: 60S ribosomal protein l23-like protein

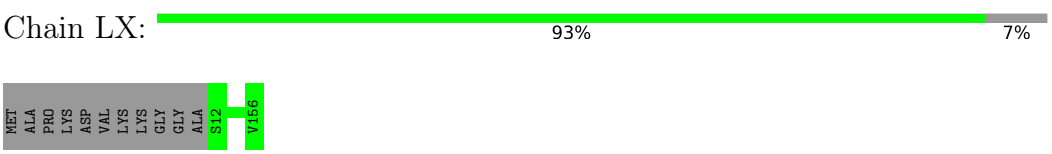
Chain LV:





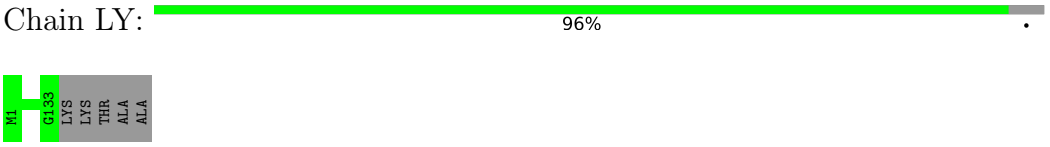
• Molecule 43: 60S ribosomal protein L25-like protein

Chain LX:



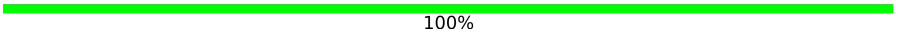
• Molecule 44: 60S ribosomal protein L26-like protein

Chain LY:



• Molecule 45: 60S ribosomal protein L27

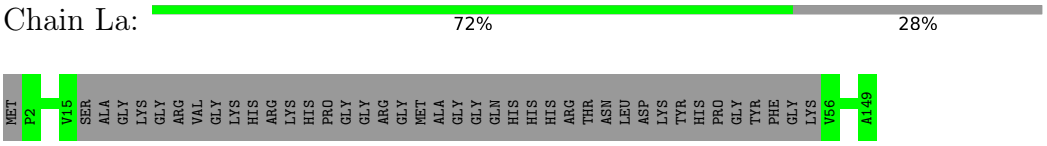
Chain LZ:



There are no outlier residues recorded for this chain.

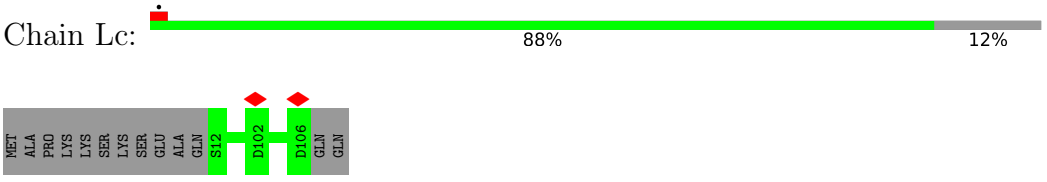
• Molecule 46: 60S ribosomal protein L28-like protein

Chain La:



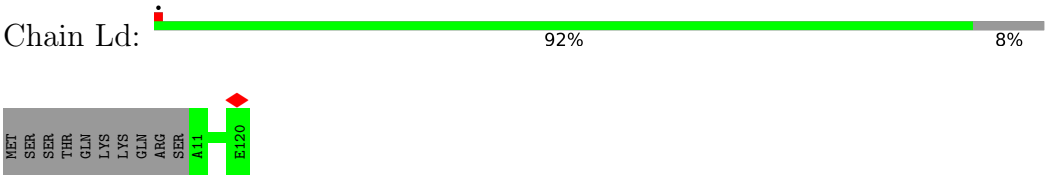
• Molecule 47: 60S ribosomal protein l30-like protein

Chain Lc:



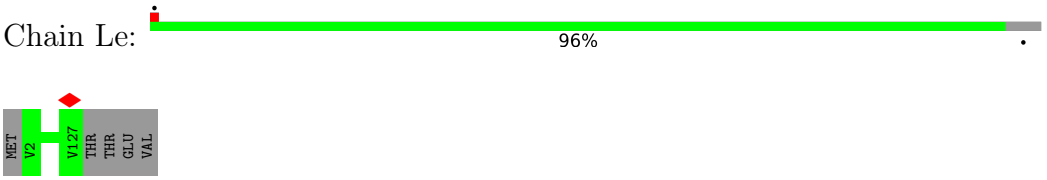
• Molecule 48: Putative 60S ribosomal protein

Chain Ld:



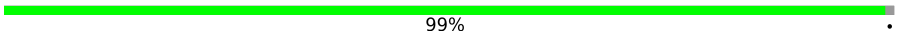
• Molecule 49: 60S ribosomal protein L32-like protein

Chain Le:



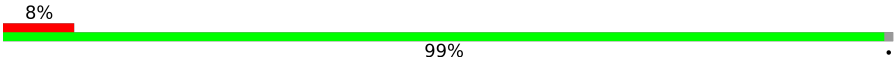
• Molecule 50: 60S ribosomal protein l33-like protein

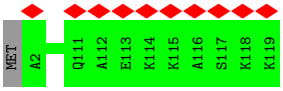
Chain Lf:



• Molecule 51: Ribosomal protein l34-like protein

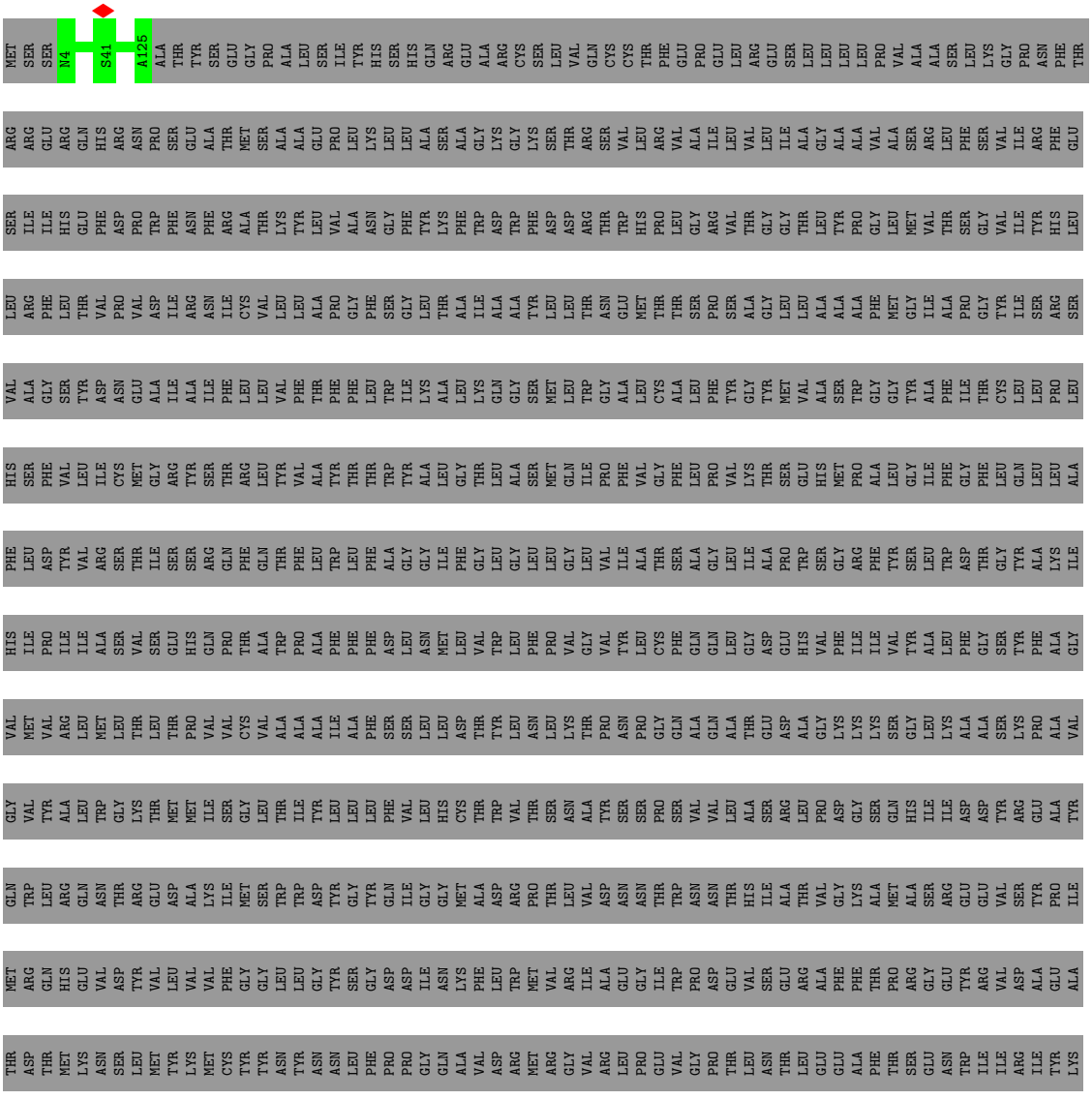
Chain Lg:





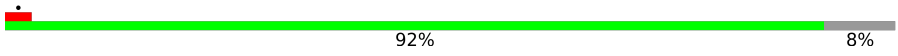
• Molecule 52: dolichyl-diphosphooligosaccharide--protein glycotransferase

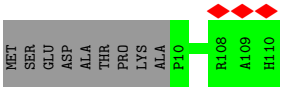
Chain Lh:



• Molecule 53: 60S ribosomal protein L36

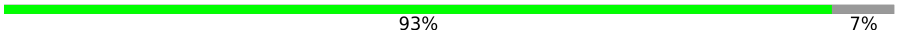
Chain Li:





• Molecule 54: Ribosomal protein L37

Chain Lj:

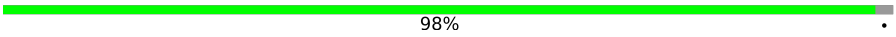


• Molecule 55: 60S ribosomal protein L38-like protein

Chain Lk:

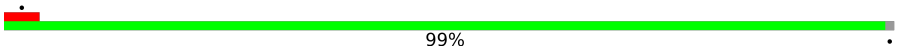
• Molecule 56: Ribosomal protein eL39

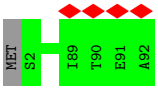
Chain Ll:



• Molecule 57: 60S ribosomal protein L43-like protein

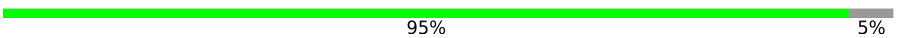
Chain Lp:

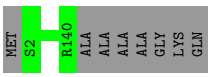




• Molecule 58: Putative 60S ribosomal protein

Chain Lq:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74642	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	9.056	Depositor
Minimum map value	0.000	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.169	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: ZN, OMU, MG, OMG, GTP, OMC, A2M

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	0.33	0/72882	0.92	107/113631 (0.1%)
2	C2	0.32	0/3710	0.88	4/5778 (0.1%)
3	C3	0.26	0/1958	0.94	5/3050 (0.2%)
4	C4	0.30	0/2833	0.95	5/4414 (0.1%)
5	CB	0.26	0/2153	0.55	1/2926 (0.0%)
6	CF	0.26	0/1972	0.56	1/2660 (0.0%)
7	CH	0.27	0/5147	0.55	1/6926 (0.0%)
8	CI	0.34	0/1265	0.67	1/1702 (0.1%)
9	CJ	0.27	0/3196	0.51	0/4319
10	CK	0.27	0/1939	0.55	0/2608
11	CL	0.29	0/631	0.57	0/843
12	CM	0.28	0/1805	0.53	0/2417
12	LF	0.29	0/2061	0.53	0/2765
13	CN	0.26	0/1878	0.55	0/2555
14	CO	0.26	0/470	0.51	0/619
15	CQ	0.30	0/1504	0.60	0/2000
16	Cb	0.27	0/845	0.58	0/1128
17	Cd	0.26	0/3770	0.51	0/5082
18	Ce	0.27	0/2173	0.55	0/2890
19	Cf	0.26	0/2326	0.54	0/3113
20	Cg	0.26	0/1508	0.54	0/2051
21	Ch	0.26	0/3914	0.56	0/5319
22	Cz	0.30	0/877	0.62	0/1148
23	LA	0.28	0/1488	0.57	0/2009
24	LB	0.28	0/3172	0.56	0/4260
25	LC	0.27	0/2808	0.53	0/3785
26	LD	0.27	0/2308	0.52	0/3105
27	LE	0.26	0/1504	0.53	1/2027 (0.0%)
28	LG	0.27	0/1918	0.51	0/2565
29	LH	0.27	0/1515	0.55	1/2037 (0.0%)
30	LJ	0.26	0/1379	0.61	0/1844
31	LK	0.26	0/1198	0.58	1/1611 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	LL	0.25	0/1614	0.56	0/2168
33	LM	0.28	0/1145	0.56	0/1539
34	LN	0.27	0/1741	0.61	0/2332
35	LO	0.31	0/1645	0.58	0/2205
36	LP	0.26	0/1364	0.57	0/1835
37	LQ	0.26	0/1218	0.56	0/1639
38	LR	0.26	0/1260	0.56	0/1683
39	LS	0.26	0/1461	0.55	0/1966
40	LT	0.28	0/1046	0.58	0/1409
41	LU	0.27	0/859	0.50	0/1151
42	LV	0.28	0/1009	0.56	0/1357
43	LX	0.26	0/1151	0.51	0/1547
44	LY	0.27	0/1070	0.61	0/1432
45	LZ	0.27	0/1135	0.55	0/1519
46	La	0.25	0/892	0.52	0/1200
47	Lc	0.26	0/714	0.51	0/960
48	Ld	0.27	0/889	0.54	0/1192
49	Le	0.25	0/1035	0.54	0/1379
50	Lf	0.28	0/883	0.58	0/1187
51	Lg	0.27	0/927	0.59	0/1244
52	Lh	0.30	0/1014	0.58	0/1349
53	Li	0.28	0/834	0.62	0/1099
54	Lj	0.28	0/712	0.61	0/944
55	Lk	0.28	0/640	0.59	0/850
56	Ll	0.25	0/446	0.57	0/593
57	Lp	0.26	0/706	0.60	0/940
58	Lq	0.29	0/1091	0.57	0/1468
All	All	0.30	0/166608	0.77	128/241374 (0.1%)

There are no bond length outliers.

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C1	1179	C	C2-N1-C1'	9.55	129.30	118.80
1	C1	1179	C	N1-C2-O2	9.46	124.57	118.90
5	CB	24	LEU	CA-CB-CG	9.42	136.96	115.30
1	C1	1538	U	N1-C2-O2	9.36	129.35	122.80
1	C1	1538	U	N3-C2-O2	-9.14	115.80	122.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

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	CB	259/391 (66%)	254 (98%)	5 (2%)	0	100	100
6	CF	243/270 (90%)	240 (99%)	3 (1%)	0	100	100
7	CH	621/661 (94%)	613 (99%)	8 (1%)	0	100	100
8	CI	150/414 (36%)	149 (99%)	1 (1%)	0	100	100
9	CJ	376/679 (55%)	371 (99%)	5 (1%)	0	100	100
10	CK	231/261 (88%)	225 (97%)	6 (3%)	0	100	100
11	CL	38/558 (7%)	38 (100%)	0	0	100	100
All	All	1918/3234 (59%)	1890 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CB	227/329 (69%)	226 (100%)	1 (0%)	91	95
6	CF	212/236 (90%)	212 (100%)	0	100	100
7	CH	549/575 (96%)	549 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	CI	124/336 (37%)	124 (100%)	0	100	100
9	CJ	331/579 (57%)	331 (100%)	0	100	100
10	CK	206/225 (92%)	206 (100%)	0	100	100
11	CL	33/458 (7%)	33 (100%)	0	100	100
All	All	1682/2738 (61%)	1681 (100%)	1 (0%)	93	97

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

Mol	Chain	Res	Type
5	CB	36	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
7	CH	302	GLN
10	CK	60	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3069/3342 (91%)	556 (18%)	0
2	C2	155/156 (99%)	21 (13%)	0
3	C3	80/162 (49%)	20 (25%)	0
4	C4	118/119 (99%)	22 (18%)	0
All	All	3422/3779 (90%)	619 (18%)	0

5 of 619 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
1	C1	50	A

There are no RNA pucker outliers to report.

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	OMU	C1	2690	1	19,22,23	3.06	6 (31%)	26,31,34	1.68	4 (15%)
1	A2M	C1	2289	1	18,25,26	4.37	9 (50%)	18,36,39	3.76	4 (22%)
1	OMC	C1	1420	1	19,22,23	0.65	0	26,31,34	1.35	4 (15%)
1	OMU	C1	2380	1	19,22,23	3.01	6 (31%)	26,31,34	1.65	5 (19%)
1	OMG	C1	2774	1	18,26,27	1.16	2 (11%)	19,38,41	0.86	1 (5%)
1	OMG	C1	2358	1	18,26,27	1.16	2 (11%)	19,38,41	0.90	1 (5%)
1	A2M	C1	848	1	18,25,26	4.34	9 (50%)	18,36,39	3.83	4 (22%)
1	A2M	C1	389	1	18,25,26	4.33	9 (50%)	18,36,39	3.83	4 (22%)
1	OMG	C1	646	1	18,26,27	1.14	2 (11%)	19,38,41	0.89	1 (5%)
1	OMC	C1	778	1	19,22,23	0.58	0	26,31,34	0.92	1 (3%)
1	OMU	C1	1868	1	19,22,23	3.07	6 (31%)	26,31,34	1.72	4 (15%)
1	OMU	C1	2384	1	19,22,23	3.07	6 (31%)	26,31,34	1.65	5 (19%)
1	OMC	C1	1836	1	19,22,23	0.58	0	26,31,34	0.83	1 (3%)
1	OMU	C1	1917	1	19,22,23	3.10	6 (31%)	26,31,34	1.78	5 (19%)
1	A2M	C1	1847	1	18,25,26	4.35	8 (44%)	18,36,39	3.90	4 (22%)
1	OMG	C1	627	1	18,26,27	1.17	2 (11%)	19,38,41	0.92	1 (5%)
1	OMG	C1	787	1	18,26,27	1.17	2 (11%)	19,38,41	0.89	1 (5%)
1	OMC	C1	2918	1	19,22,23	0.60	0	26,31,34	0.80	0
1	OMC	C1	1491	1	19,22,23	0.54	0	26,31,34	0.70	0
1	OMU	C1	2683	1	19,22,23	3.03	6 (31%)	26,31,34	1.64	4 (15%)
1	OMG	C1	2881	1	18,26,27	1.12	2 (11%)	19,38,41	0.84	1 (5%)
1	OMC	C1	1812	1	19,22,23	0.59	0	26,31,34	1.23	2 (7%)
1	OMG	C1	2578	1	18,26,27	1.14	2 (11%)	19,38,41	0.90	1 (5%)
1	A2M	C1	1432	1	18,25,26	4.34	9 (50%)	18,36,39	3.87	4 (22%)
1	A2M	C1	637	1	18,25,26	4.33	9 (50%)	18,36,39	3.88	4 (22%)
1	A2M	C1	858	1	18,25,26	4.38	9 (50%)	18,36,39	3.88	4 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	A2M	C1	1223	1	18,25,26	4.31	9 (50%)	18,36,39	3.85	4 (22%)
1	OMU	C1	2688	1	19,22,23	3.05	6 (31%)	26,31,34	1.67	5 (19%)
1	OMG	C1	2876	1	18,26,27	1.13	2 (11%)	19,38,41	0.84	1 (5%)
1	OMG	C1	385	1	18,26,27	1.14	2 (11%)	19,38,41	0.82	1 (5%)
1	OMU	C1	2277	1	19,22,23	3.06	6 (31%)	26,31,34	1.67	5 (19%)
1	OMC	C1	2300	1	19,22,23	0.55	0	26,31,34	0.70	0
1	OMC	C1	2838	1	19,22,23	0.70	0	26,31,34	1.55	4 (15%)
1	OMG	C1	1433	1	18,26,27	1.16	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	OMU	C1	2690	1	-	2/9/27/28	0/2/2/2
1	A2M	C1	2289	1	-	0/5/27/28	0/3/3/3
1	OMC	C1	1420	1	-	3/9/27/28	0/2/2/2
1	OMU	C1	2380	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	2358	1	-	0/5/27/28	0/3/3/3
1	A2M	C1	848	1	-	1/5/27/28	0/3/3/3
1	A2M	C1	389	1	-	3/5/27/28	0/3/3/3
1	OMG	C1	646	1	-	0/5/27/28	0/3/3/3
1	OMC	C1	778	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	2384	1	-	1/9/27/28	0/2/2/2
1	OMC	C1	1836	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	1917	1	-	3/9/27/28	0/2/2/2
1	A2M	C1	1847	1	-	3/5/27/28	0/3/3/3
1	OMG	C1	627	1	-	0/5/27/28	0/3/3/3
1	OMG	C1	787	1	-	0/5/27/28	0/3/3/3
1	OMC	C1	2918	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1491	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	2881	1	-	0/5/27/28	0/3/3/3
1	OMC	C1	1812	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	2578	1	-	3/5/27/28	0/3/3/3
1	A2M	C1	1432	1	-	0/5/27/28	0/3/3/3
1	A2M	C1	637	1	-	1/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	C1	858	1	-	1/5/27/28	0/3/3/3
1	A2M	C1	1223	1	-	1/5/27/28	0/3/3/3
1	OMU	C1	2688	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2876	1	-	0/5/27/28	0/3/3/3
1	OMG	C1	385	1	-	2/5/27/28	0/3/3/3
1	OMU	C1	2277	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	2300	1	-	1/9/27/28	0/2/2/2
1	OMC	C1	2838	1	-	2/9/27/28	0/2/2/2
1	OMG	C1	1433	1	-	3/5/27/28	0/3/3/3

The worst 5 of 139 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	858	A2M	C3'-C2'	-12.77	1.24	1.52
1	C1	637	A2M	C3'-C2'	-12.74	1.24	1.52
1	C1	2289	A2M	C3'-C2'	-12.73	1.24	1.52
1	C1	1432	A2M	C3'-C2'	-12.70	1.24	1.52
1	C1	1223	A2M	C3'-C2'	-12.67	1.24	1.52

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C1	1432	A2M	C1'-N9-C4	10.64	145.33	126.64
1	C1	389	A2M	C1'-N9-C4	10.54	145.16	126.64
1	C1	1847	A2M	C1'-N9-C4	10.49	145.08	126.64
1	C1	637	A2M	C1'-N9-C4	10.47	145.04	126.64
1	C1	858	A2M	C1'-N9-C4	10.33	144.79	126.64

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

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

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	CH	701	60	26,34,34	1.14	2 (7%)	32,54,54	1.61	7 (21%)
59	GTP	Cd	1000	60	26,34,34	1.15	2 (7%)	32,54,54	1.53	6 (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
59	GTP	CH	701	60	-	4/18/38/38	0/3/3/3
59	GTP	Cd	1000	60	-	3/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	CH	701	GTP	C5-C6	-4.05	1.39	1.47
59	Cd	1000	GTP	C5-C6	-4.00	1.39	1.47
59	CH	701	GTP	C2-N3	2.13	1.38	1.33
59	Cd	1000	GTP	C2-N3	2.05	1.38	1.33

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	Cd	1000	GTP	PB-O3B-PG	-3.61	120.44	132.83
59	CH	701	GTP	PB-O3B-PG	-3.46	120.97	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	CH	701	GTP	PA-O3A-PB	-3.31	121.47	132.83
59	CH	701	GTP	C5-C6-N1	3.22	119.63	113.95
59	Cd	1000	GTP	C5-C6-N1	3.14	119.50	113.95

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

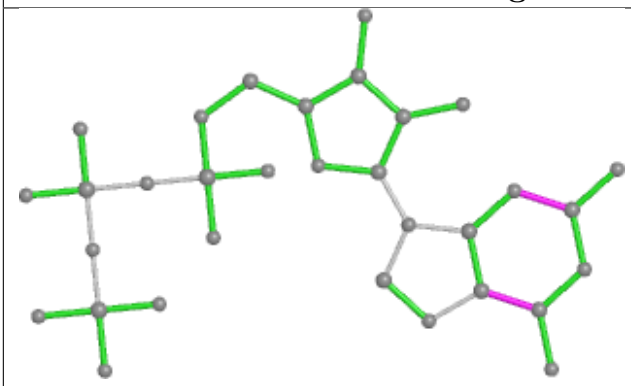
Mol	Chain	Res	Type	Atoms
59	Cd	1000	GTP	O4'-C4'-C5'-O5'
59	CH	701	GTP	PB-O3B-PG-O2G
59	Cd	1000	GTP	C3'-C4'-C5'-O5'
59	CH	701	GTP	PB-O3A-PA-O2A
59	CH	701	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

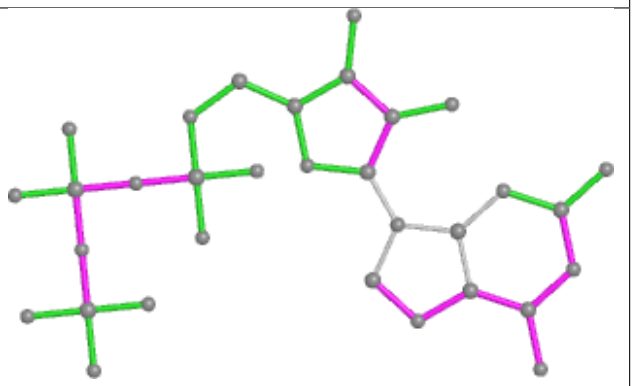
No monomer is involved in short contacts.

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.

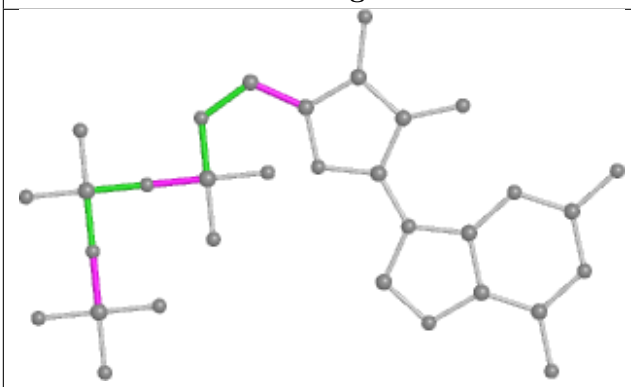
Ligand GTP CH 701



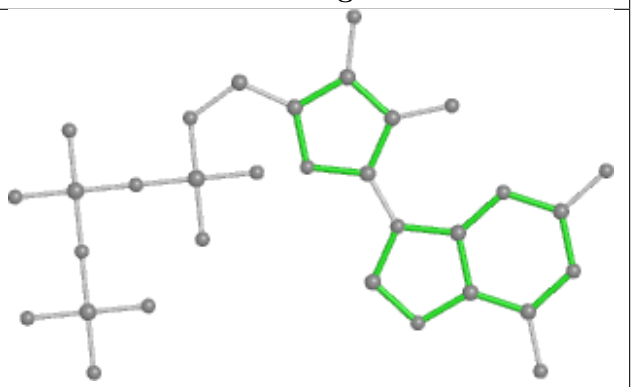
Bond lengths



Bond angles

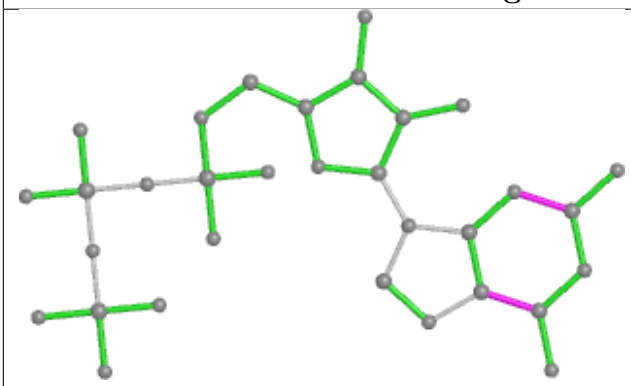


Torsions

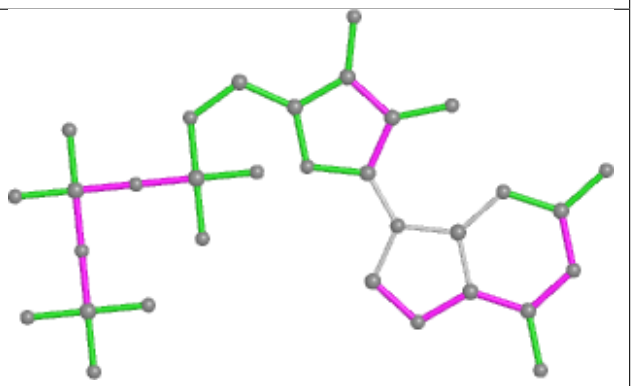


Rings

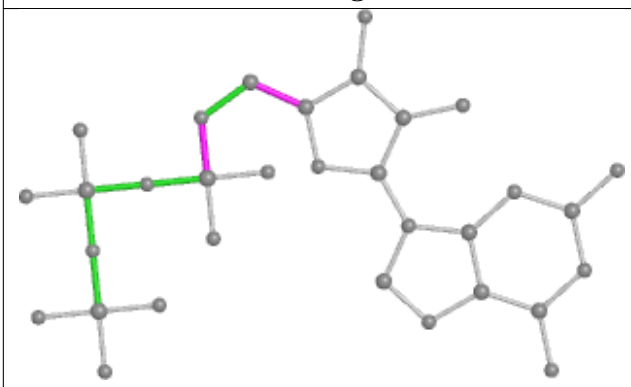
Ligand GTP Cd 1000



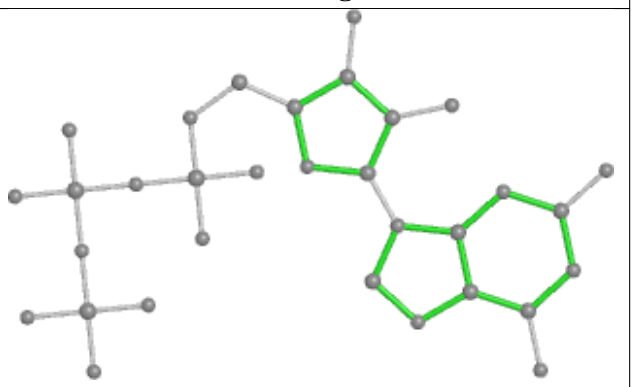
Bond lengths



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.

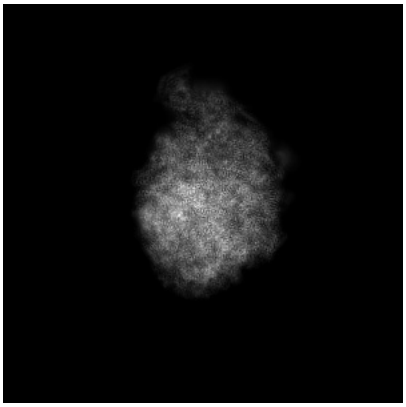
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17950. These allow visual inspection of the internal detail of the map and identification of artifacts.

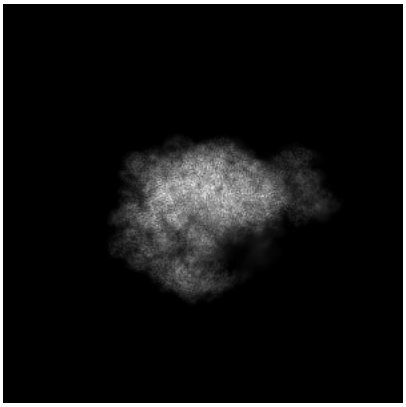
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

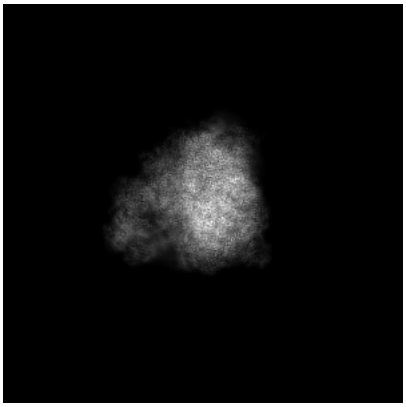
6.1.1 Primary map



X



Y

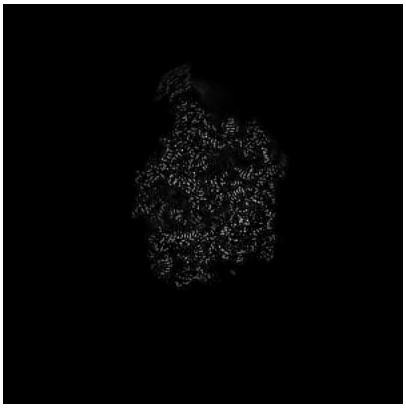


Z

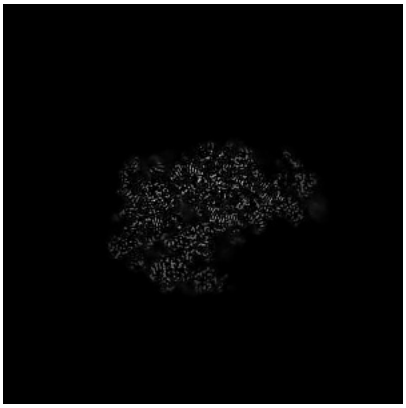
The images above show the map projected in three orthogonal directions.

6.2 Central slices

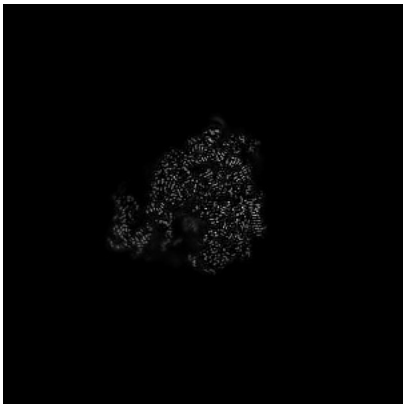
6.2.1 Primary map



X Index: 250



Y Index: 250

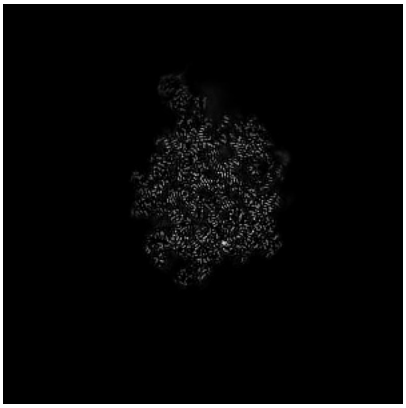


Z Index: 250

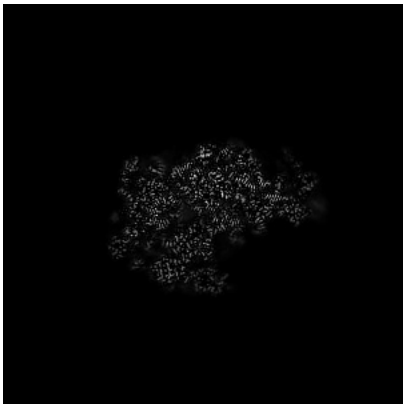
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

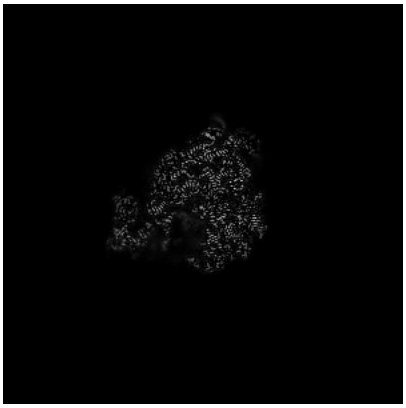
6.3.1 Primary map



X Index: 259



Y Index: 248

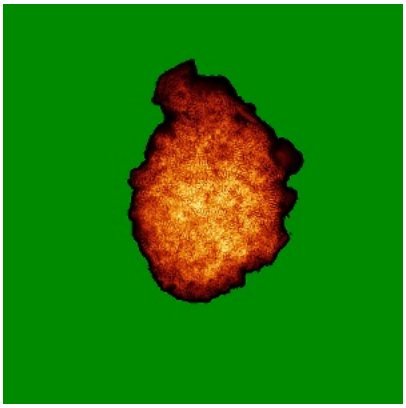


Z Index: 252

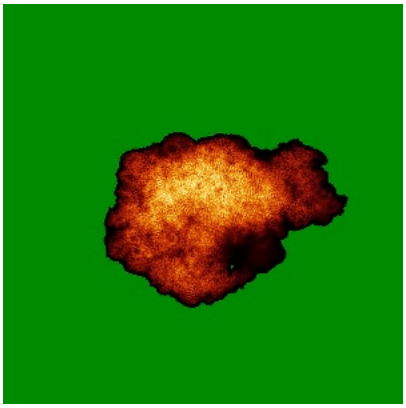
The images above show the largest variance slices of the map in three orthogonal directions.

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

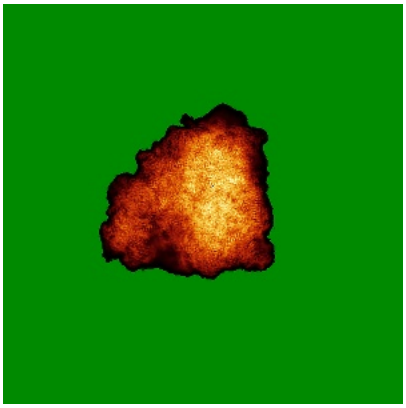
6.4.1 Primary map



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.

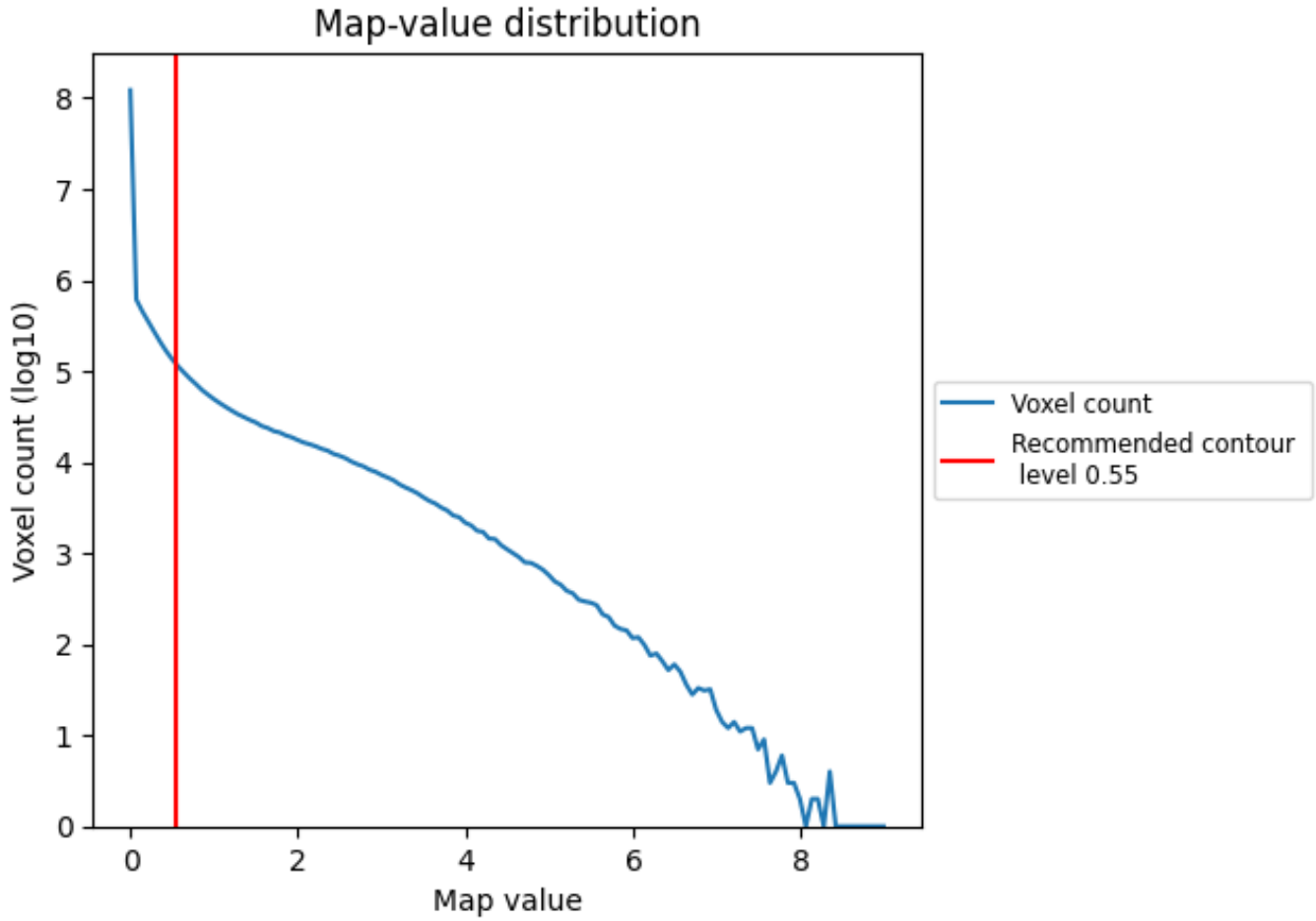
6.6 Mask visualisation (i)

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

7 Map analysis

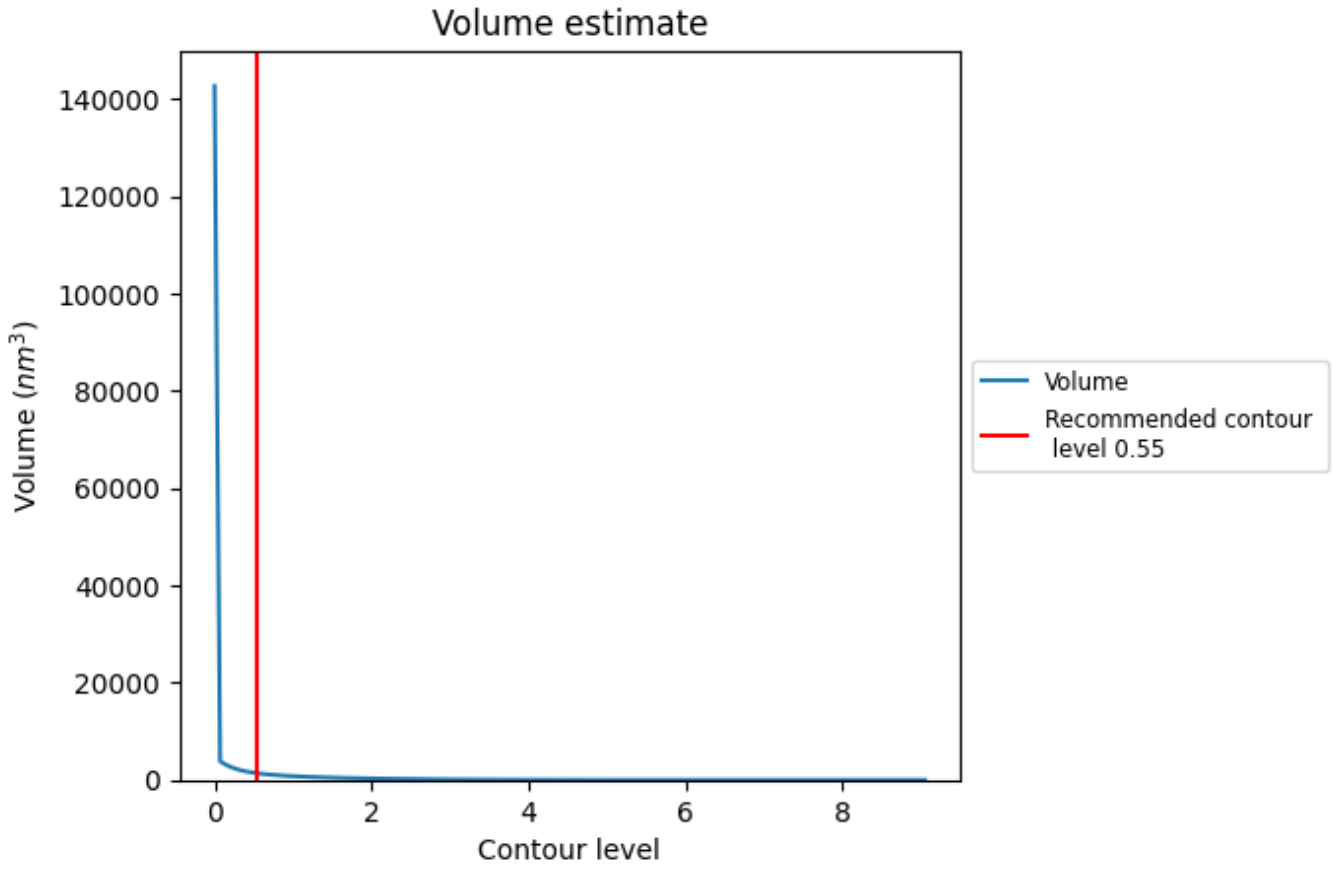
This section contains the results of statistical analysis of the map.

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.

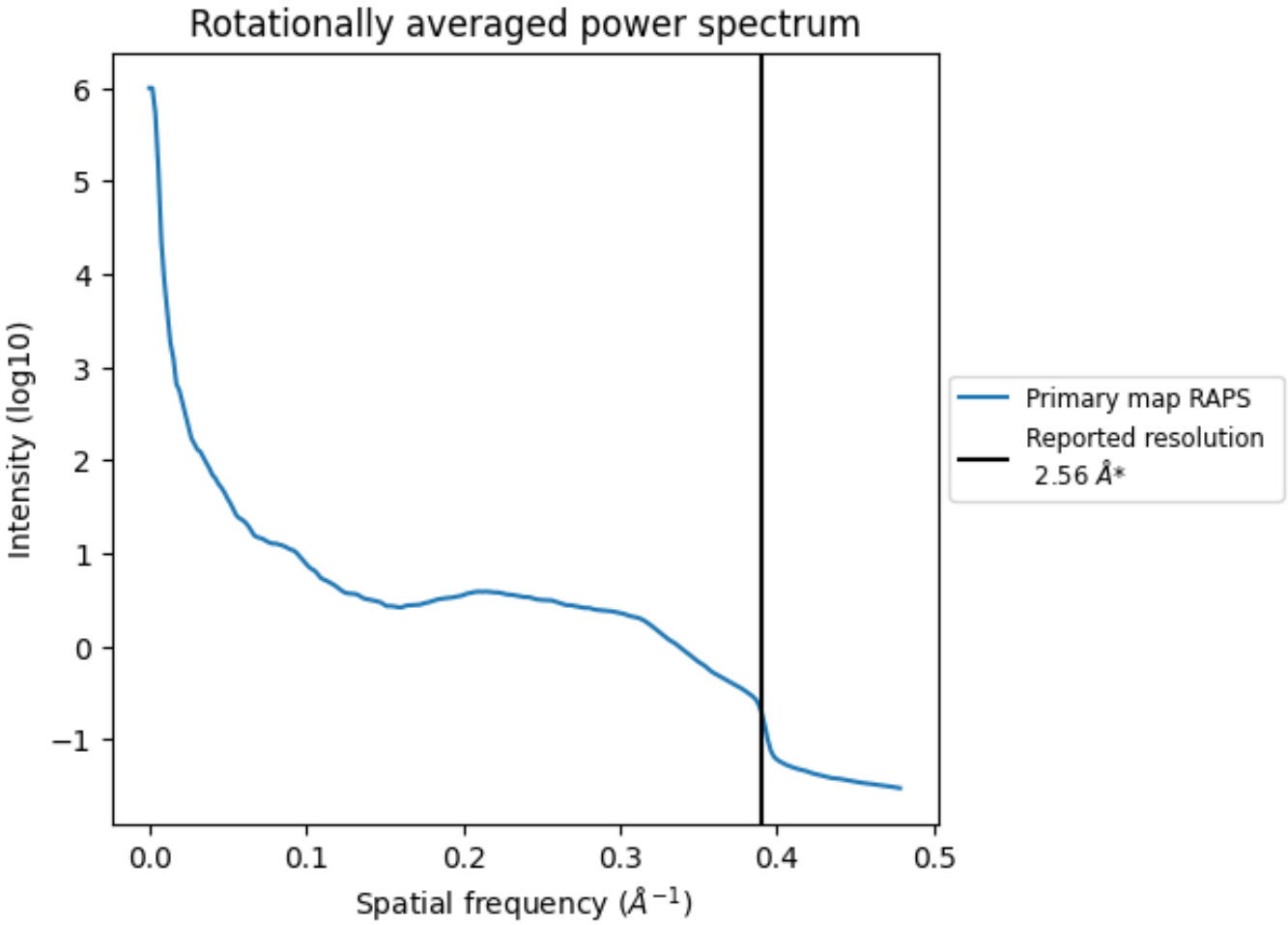
7.2 Volume estimate (i)



The volume at the recommended contour level is 1366 nm^3; this corresponds to an approximate mass of 1234 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 0.391 Å^{-1}

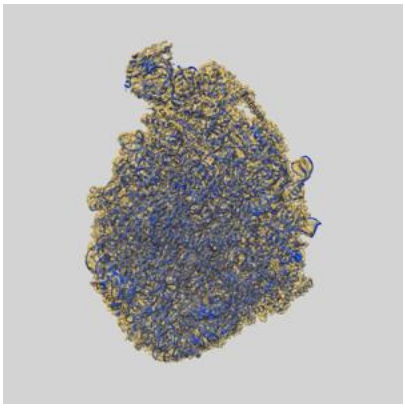
8 Fourier-Shell correlation

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

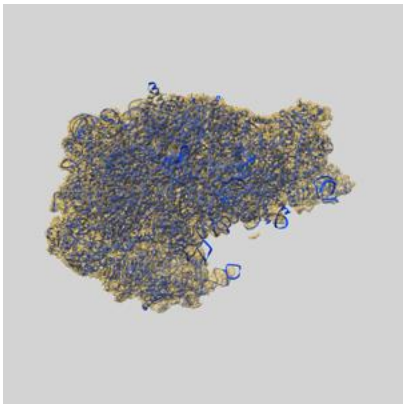
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17950 and PDB model 8PV1. Per-residue inclusion information can be found in section 3 on page 16.

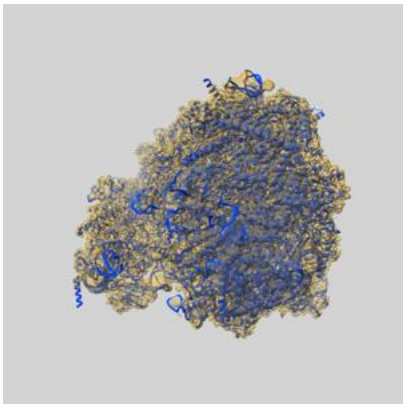
9.1 Map-model overlay



X



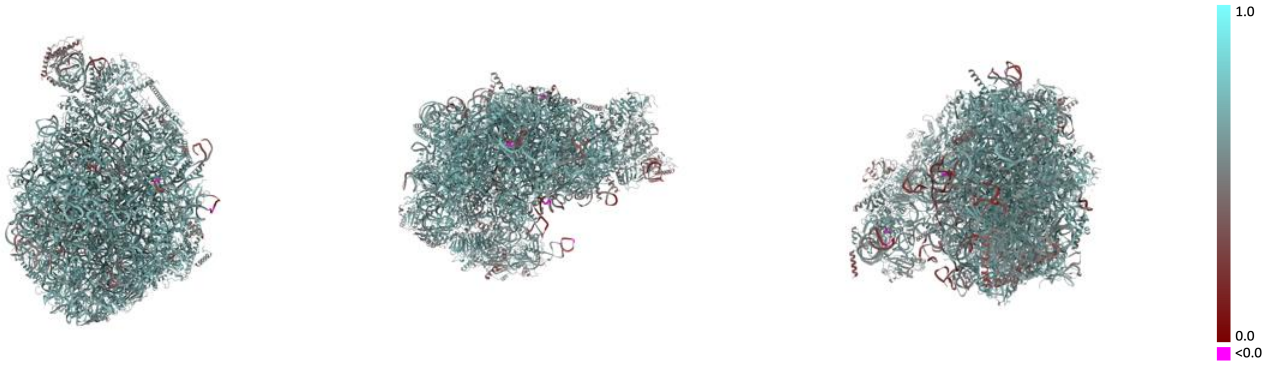
Y



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.

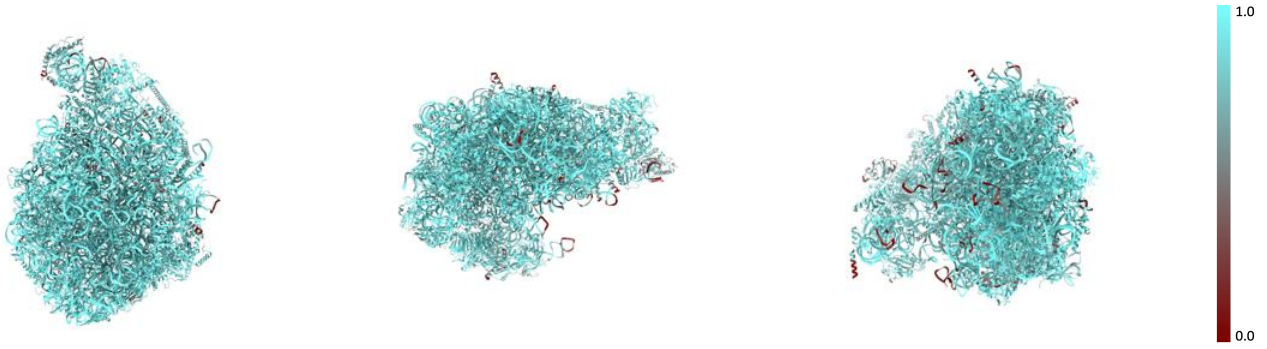
9.2 Q-score mapped to coordinate model



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.

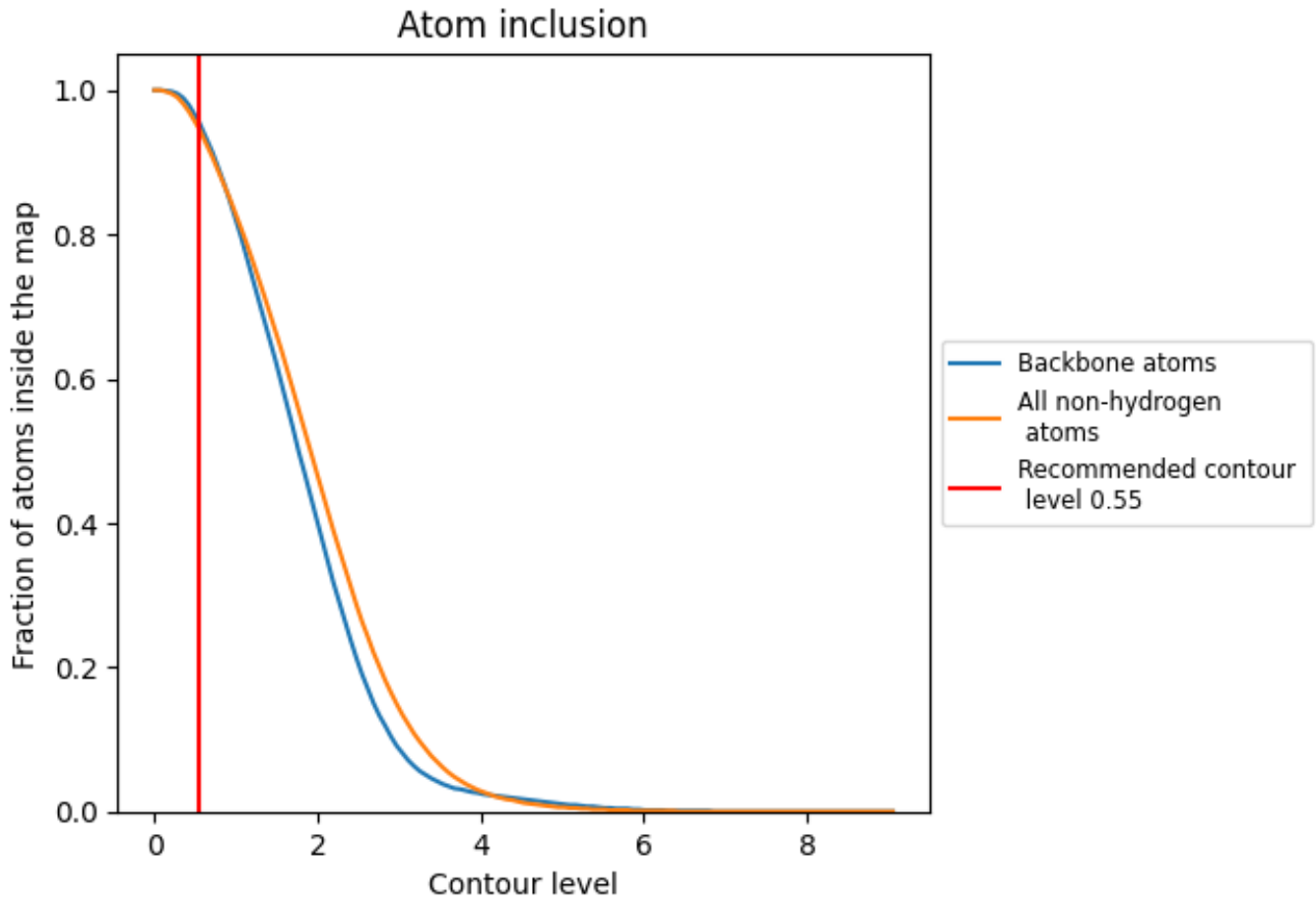
9.3 Atom inclusion mapped to coordinate model



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, 96% of all backbone atoms, 95% 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	0.9460	0.6180
C1	0.9700	0.6200
C2	0.9720	0.6490
C3	0.7660	0.4470
C4	0.9080	0.5310
CB	0.7780	0.4950
CF	0.9210	0.5950
CH	0.9190	0.6190
CI	0.8300	0.5240
CJ	0.9600	0.6200
CK	0.9710	0.6530
CL	0.8890	0.5630
CM	0.9060	0.5750
CN	0.9630	0.6520
CO	0.9100	0.6370
CQ	0.8810	0.6140
Cb	0.9560	0.6450
Cd	0.9580	0.6340
Ce	0.8510	0.5650
Cf	0.9350	0.5990
Cg	0.9280	0.5810
Ch	0.8870	0.5910
Cz	0.8380	0.5240
LA	0.9690	0.6540
LB	0.9810	0.6850
LC	0.9770	0.6680
LD	0.9090	0.5860
LE	0.9260	0.6220
LF	0.9590	0.6480
LG	0.9480	0.6270
LH	0.9520	0.6460
LJ	0.8900	0.5120
LK	0.8580	0.5450
LL	0.9390	0.6360
LM	0.9580	0.6450

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Chain	Atom inclusion	Q-score
LN	0.9900	0.6750
LO	0.9830	0.6790
LP	0.9810	0.6790
LQ	0.9600	0.6390
LR	0.9510	0.6580
LS	0.9670	0.6470
LT	0.8620	0.5280
LU	0.9250	0.6050
LV	0.9890	0.6820
LX	0.9530	0.6370
LY	0.9590	0.6440
LZ	0.9550	0.6370
La	0.9550	0.6410
Lc	0.9320	0.6220
Ld	0.9730	0.6770
Le	0.9810	0.6750
Lf	0.9920	0.6930
Lg	0.9150	0.6400
Lh	0.9270	0.6000
Li	0.9240	0.6060
Lj	0.9880	0.6900
Lk	0.8950	0.6060
Ll	0.9950	0.6980
Lp	0.9200	0.6340
Lq	0.9580	0.6410