



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 01:05 AM UTC

PDB ID : 7TOO / pdb_00007too
EMDB ID : EMD-26033
Title : Yeast 80S ribosome bound with the ALS/FTD-associated dipeptide repeat protein GR20
Authors : Loveland, A.B.; Svidritskiy, E.; Susorov, D.; Lee, S.; Park, A.; Zvornicanin, S.; Demo, G.; Gao, F.B.; Korostelev, A.A.
Deposited on : 2022-01-24
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

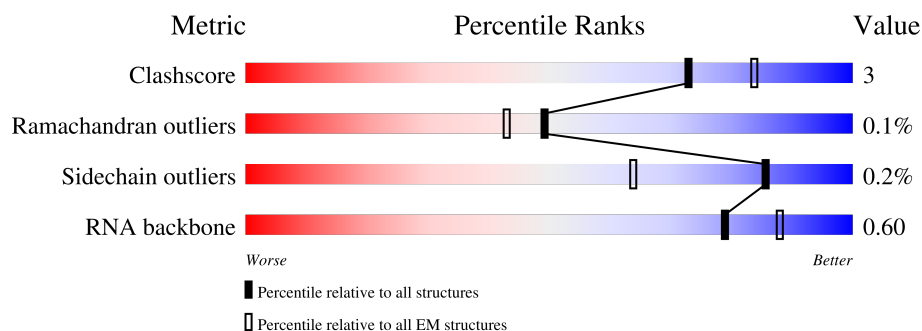
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.



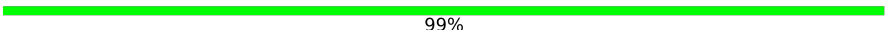
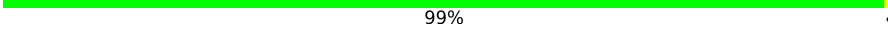
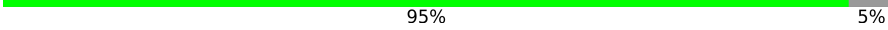
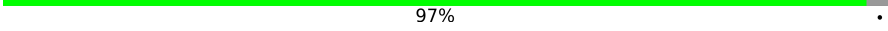
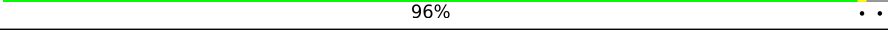
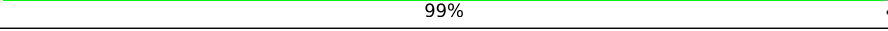
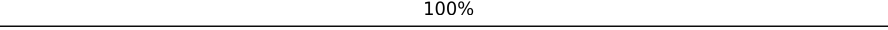
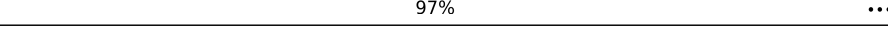
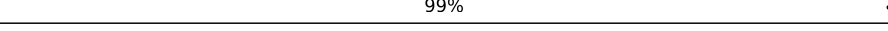
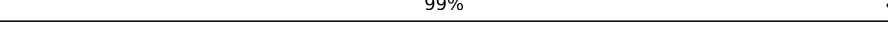
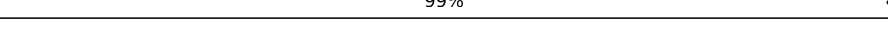
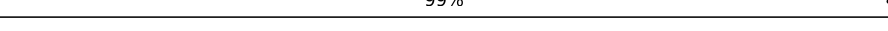
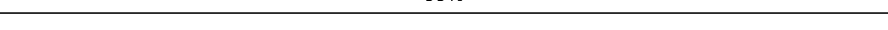
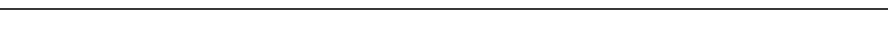
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A25S	3396	80% 14% 6%
2	A58S	158	82% 18%
3	A5S	121	88% 12%
4	AGR	40	32% 10% 58%
5	AL02	254	99% .
6	AL03	387	99% .
7	AL04	362	99% .

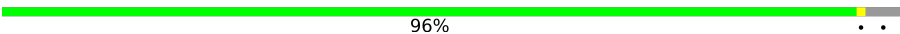
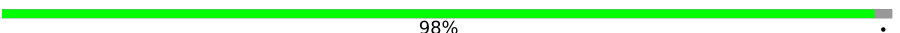
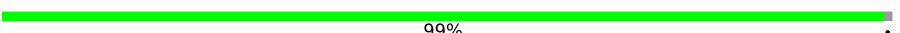
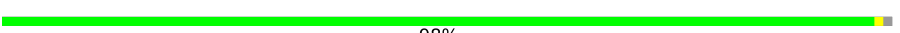
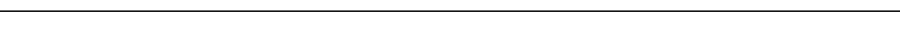
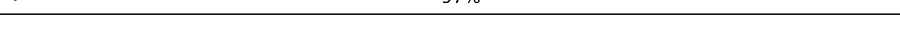
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Mol	Chain	Length	Quality of chain
8	AL05	297	 99%
9	AL06	176	 89% 11%
10	AL07	244	 90% 9%
11	AL08	256	 89% 9%
12	AL09	191	 99%
13	AL10	221	 95% 5%
14	AL11	174	 97%
15	AL12	155	 8% 92%
16	AL13	199	 96%
17	AL14	138	 99%
18	AL15	204	 100%
19	AL16	199	 97%
20	AL17	184	 99%
21	AL18	186	 99%
22	AL19	189	 82% 18%
23	AL20	172	 99%
24	AL21	160	 99%
25	AL22	121	 83% 17%
26	AL23	137	 99%
27	AL24	155	 41% 59%
28	AL25	142	 85% 15%
29	AL26	127	 99%
30	AL27	136	 99%
31	AL28	149	 99%
32	AL29	59	 98%

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Mol	Chain	Length	Quality of chain
33	AL30	105	 92% 8%
34	AL31	113	 96% ..
35	AL32	130	 98% .
36	AL33	107	 99% .
37	AL34	121	 93% 7%
38	AL35	120	 98% ..
39	AL36	100	 98% ..
40	AL37	88	 99% .
41	AL38	78	 99% .
42	AL39	51	 98% .
43	AL40	128	 40% . 59%
44	AL41	25	 92% 8%
45	AL42	106	 99% .
46	AL43	92	 99% .
47	ALP0	221	 . 97%
48	APTN	77	 90% 10%

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 125395 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A25S	3194	Total	C	N	O	P	0	0
			68318	30516	12315	22293	3194		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A58S	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A5S	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

- Molecule 4 is a protein called ALS-FTD-associated dipeptide repeat protein, GR20.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	AGR	17	Total	C	N	O	0	0
			131	70	44	17		

- Molecule 5 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AL02	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 6 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AL03	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 7 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AL04	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 8 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AL05	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AL06	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AL07	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL08	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL09	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 13 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL10	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 14 is a protein called RPL11A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL11	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 15 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AL12	12	Total	C	N	O	0	0
			60	36	12	12		

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AL13	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL14	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AL15	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AL16	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AL17	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AL18	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AL19	155	Total	C	N	O		0	0
			1249	776	264	209			

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AL20	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AL21	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AL22	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AL23	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 27 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AL24	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 28 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AL25	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AL26	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AL27	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AL28	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 32 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AL29	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AL30	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AL31	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 35 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AL32	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AL33	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL34	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AL35	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AL36	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AL37	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 41 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	AL38	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AL39	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AL40	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 44 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AL41	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AL42	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AL43	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

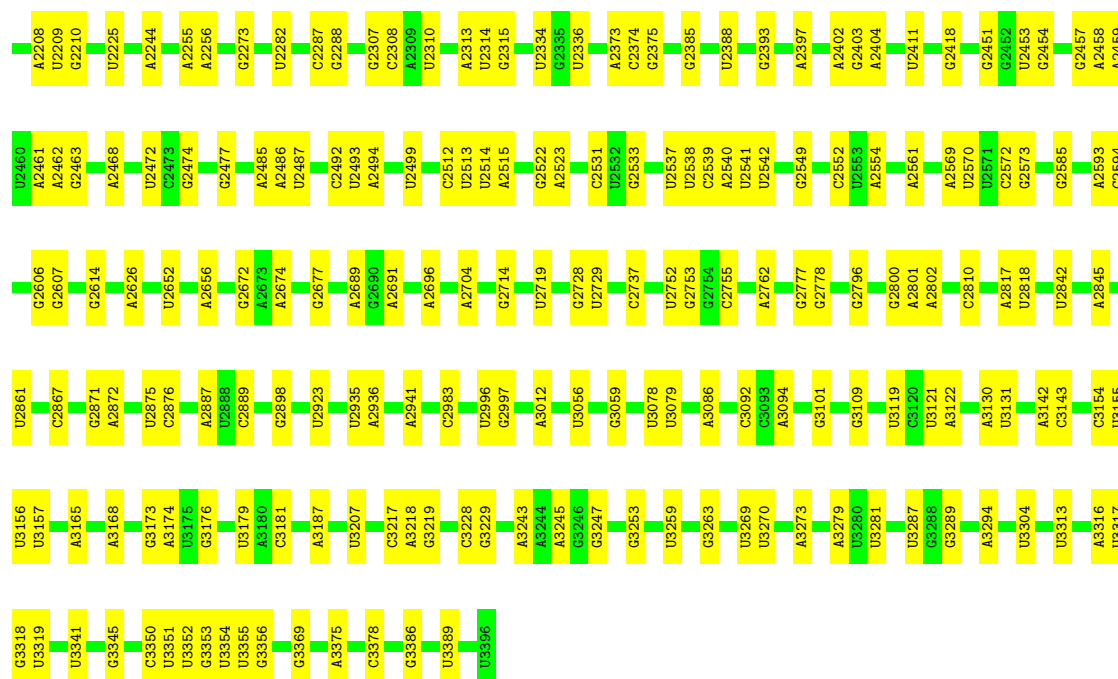
Mol	Chain	Residues	Atoms					AltConf	Trace
47	ALP0	7	Total	C	N	O	S	0	0
			54	32	12	9	1		

- Molecule 48 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	APT ^N	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	AL37	1	Total 1	Zn 1	0
49	AL40	1	Total 1	Zn 1	0
49	AL42	1	Total 1	Zn 1	0
49	AL43	1	Total 1	Zn 1	0



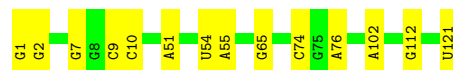
• Molecule 2: 5.8S rRNA

Chain A58S: 82% 18%



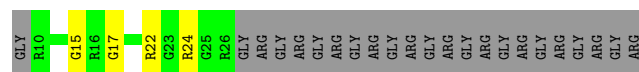
• Molecule 3: 5S rRNA

Chain A5S: 88% 12%



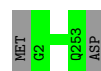
• Molecule 4: ALS-FTD-associated dipeptide repeat protein, GR20

Chain AGR: 32% 10% 58%

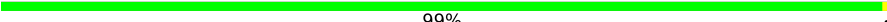


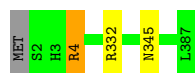
• Molecule 5: 60S ribosomal protein L2-A

Chain AL02: 99% 1%

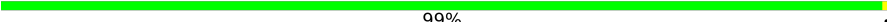


• Molecule 6: RPL3 isoform 1

Chain AL03:  99%



- Molecule 7: RPL4A isoform 1

Chain AL04:  99%



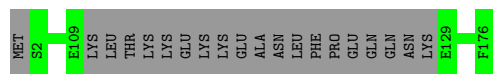
- Molecule 8: RPL5 isoform 1

Chain AL05:  99%



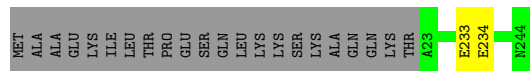
- Molecule 9: 60S ribosomal protein L6-A

Chain AL06:  89%  11%



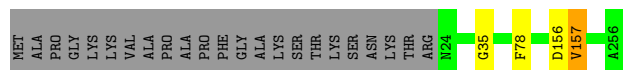
- Molecule 10: 60S ribosomal protein L7-A

Chain AL07:  90%  9%

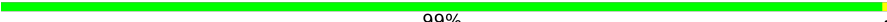


- Molecule 11: 60S ribosomal protein L8-A

Chain AL08:  89%  9%

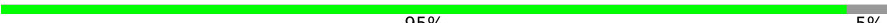


- Molecule 12: 60S ribosomal protein L9-A

Chain AL09:  99%



- Molecule 13: RPL10 isoform 1

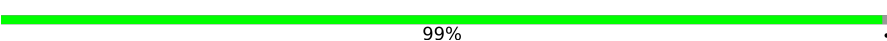
Chain AL10:  95%  5%

- Molecule 20: 60S ribosomal protein L17-A

Chain AL17:  99%

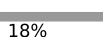


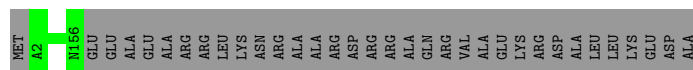
- Molecule 21: 60S ribosomal protein L18-A

Chain AL18:  99%



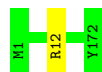
- Molecule 22: 60S ribosomal protein L19-A

Chain AL19:  82%  18%

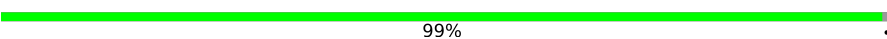


- Molecule 23: 60S ribosomal protein L20-A

Chain AL20:  99%



- Molecule 24: 60S ribosomal protein L21-A

Chain AL21:  99%

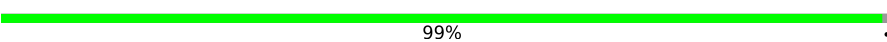


- Molecule 25: 60S ribosomal protein L22-A

Chain AL22:  83%  17%



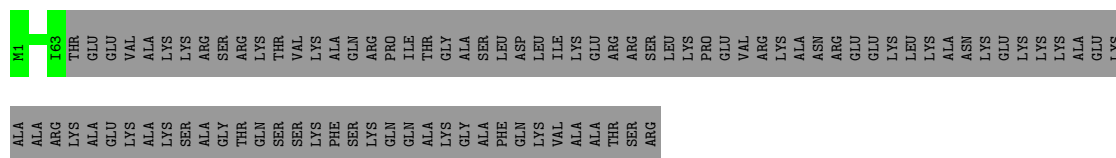
- Molecule 26: 60S ribosomal protein L23-A

Chain AL23:  99%



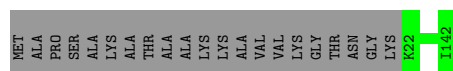
- Molecule 27: RPL24A isoform 1

Chain AL24:  41% 59%



- Molecule 28: 60S ribosomal protein L25

Chain AL25:  85% 15%



- Molecule 29: 60S ribosomal protein L26-A

Chain AL26:  99% .



- Molecule 30: 60S ribosomal protein L27-A

Chain AL27:  99% .



- Molecule 31: 60S ribosomal protein L28

Chain AL28:  99% .



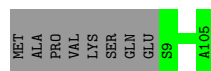
- Molecule 32: RPL29 isoform 1

Chain AL29:  98% .

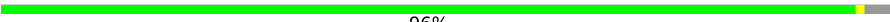


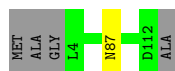
- Molecule 33: 60S ribosomal protein L30

Chain AL30:  92% 8%

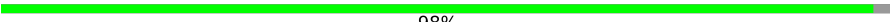


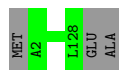
- Molecule 34: 60S ribosomal protein L31-A

Chain AL31:  96% ..

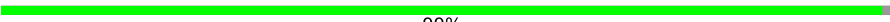


- Molecule 35: RPL32 isoform 1

Chain AL32:  98% .



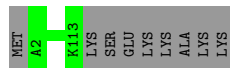
- Molecule 36: 60S ribosomal protein L33-A

Chain AL33:  99% .

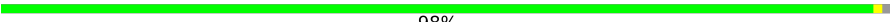


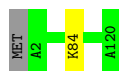
- Molecule 37: 60S ribosomal protein L34-A

Chain AL34:  93% 7%

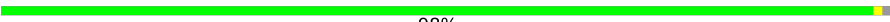


- Molecule 38: 60S ribosomal protein L35-A

Chain AL35:  98% ..

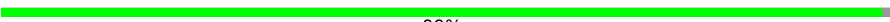


- Molecule 39: 60S ribosomal protein L36-A

Chain AL36:  98% ..

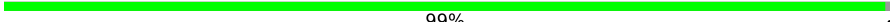


- Molecule 40: 60S ribosomal protein L37-A

Chain AL37:  99% .

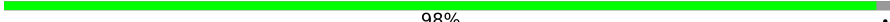


- Molecule 41: RPL38 isoform 1

Chain AL38:  99%



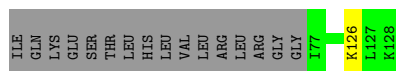
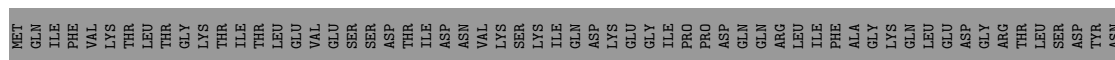
- Molecule 42: 60S ribosomal protein L39

Chain AL39:  98%



- Molecule 43: Ubiquitin-60S ribosomal protein L40

Chain AL40:  40%

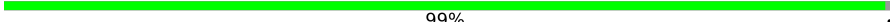


- Molecule 44: 60S ribosomal protein L41-A

Chain AL41:  92%

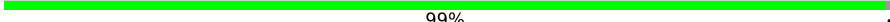


- Molecule 45: 60S ribosomal protein L42-A

Chain AL42:  99%



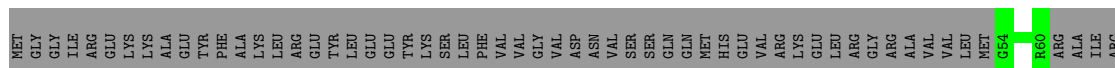
- Molecule 46: 60S ribosomal protein L43-A

Chain AL43:  99%



- Molecule 47: 60S acidic ribosomal protein P0

Chain ALP0:  97%

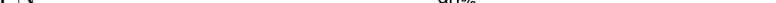


[illegible]

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

- Molecule 48: tRNA^{fMet}

Chain APTN:  90% 10%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	467615	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A25S	0.07	0/76471	0.18	0/119222
2	A58S	0.07	0/3747	0.15	0/5832
3	A5S	0.06	0/2884	0.12	0/4491
4	AGR	0.18	0/130	0.59	0/163
5	AL02	0.12	0/1948	0.36	0/2617
6	AL03	0.12	0/3146	0.37	0/4228
7	AL04	0.13	0/2800	0.41	0/3790
8	AL05	0.13	0/2425	0.40	0/3271
9	AL06	0.13	0/1260	0.35	0/1694
10	AL07	0.14	0/1821	0.38	0/2451
11	AL08	0.13	0/1836	0.52	4/2481 (0.2%)
12	AL09	0.15	0/1539	0.45	0/2073
13	AL10	0.13	0/1741	0.36	0/2335
14	AL11	0.16	0/1374	0.45	0/1842
16	AL13	0.15	0/1568	0.48	0/2106
17	AL14	0.11	0/1068	0.39	0/1438
18	AL15	0.12	0/1757	0.38	0/2354
19	AL16	0.12	0/1585	0.34	0/2128
20	AL17	0.11	0/1443	0.36	0/1944
21	AL18	0.12	0/1465	0.36	0/1965
22	AL19	0.10	0/1266	0.34	0/1690
23	AL20	0.13	0/1481	0.38	0/1990
24	AL21	0.13	0/1300	0.41	0/1743
25	AL22	0.13	0/812	0.34	0/1099
26	AL23	0.11	0/1018	0.33	0/1369
27	AL24	0.11	0/533	0.36	0/707
28	AL25	0.10	0/979	0.30	0/1321
29	AL26	0.11	0/1004	0.33	0/1341
30	AL27	0.12	0/1118	0.37	0/1497
31	AL28	0.13	0/1204	0.41	0/1612
32	AL29	0.13	0/473	0.37	0/629
33	AL30	0.10	0/751	0.31	0/1008

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	AL31	0.15	0/890	0.42	0/1196
35	AL32	0.10	0/1041	0.33	0/1394
36	AL33	0.11	0/868	0.33	0/1168
37	AL34	0.12	0/890	0.40	0/1189
38	AL35	0.11	0/978	0.44	2/1301 (0.2%)
39	AL36	0.14	0/778	0.40	0/1034
40	AL37	0.13	0/696	0.41	0/923
41	AL38	0.12	0/618	0.36	0/826
42	AL39	0.11	0/443	0.38	0/588
43	AL40	0.14	0/423	0.39	0/562
44	AL41	0.13	0/234	0.40	0/300
45	AL42	0.14	0/860	0.41	0/1136
46	AL43	0.14	0/701	0.44	0/934
47	ALP0	0.11	0/53	0.43	0/68
48	APTN	0.06	0/1836	0.14	0/2859
All	All	0.10	0/135256	0.27	6/199909 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	AL03	0	1
10	AL07	0	1
11	AL08	0	2
12	AL09	0	1
19	AL16	0	1
23	AL20	0	1
All	All	0	7

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AL08	157	VAL	CA-C-N	6.50	129.16	120.58
11	AL08	157	VAL	C-N-CA	6.50	129.16	120.58
11	AL08	78	PHE	CA-C-N	5.43	131.92	121.54
11	AL08	78	PHE	C-N-CA	5.43	131.92	121.54
38	AL35	84	LYS	CA-C-N	5.23	131.52	121.54
38	AL35	84	LYS	C-N-CA	5.23	131.52	121.54

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AL03	4	ARG	Peptide
10	AL07	233	GLU	Peptide
11	AL08	156	ASP	Peptide
11	AL08	35	GLY	Peptide
12	AL09	22	SER	Peptide
19	AL16	110	PRO	Peptide
23	AL20	12	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A25S	68318	0	0	0	0
2	A58S	3354	0	0	0	0
3	A5S	2580	0	1304	2	0
4	AGR	131	0	140	2	0
5	AL02	1914	0	0	0	0
6	AL03	3075	0	0	0	0
7	AL04	2748	0	0	0	0
8	AL05	2375	0	0	0	0
9	AL06	1239	0	0	0	0
10	AL07	1784	0	0	0	0
11	AL08	1804	0	0	0	0
12	AL09	1518	0	0	0	0
13	AL10	1705	0	0	0	0
14	AL11	1353	0	0	0	0
15	AL12	60	0	0	0	0
16	AL13	1543	0	0	0	0
17	AL14	1053	0	0	0	0
18	AL15	1720	0	0	0	0
19	AL16	1555	0	0	0	0
20	AL17	1420	0	0	0	0
21	AL18	1441	0	0	0	0
22	AL19	1249	0	0	0	0
23	AL20	1445	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	AL21	1276	0	0	0	0
25	AL22	796	0	0	0	0
26	AL23	1003	0	0	0	0
27	AL24	521	0	0	0	0
28	AL25	964	0	0	0	0
29	AL26	993	0	0	0	0
30	AL27	1092	0	0	0	0
31	AL28	1173	0	0	0	0
32	AL29	462	0	0	0	0
33	AL30	743	0	0	0	0
34	AL31	876	0	0	0	0
35	AL32	1020	0	0	0	0
36	AL33	850	0	0	0	0
37	AL34	880	0	0	0	0
38	AL35	969	0	0	0	0
39	AL36	771	0	0	0	0
40	AL37	681	0	0	0	0
41	AL38	612	0	0	0	0
42	AL39	436	0	0	0	0
43	AL40	417	0	0	0	0
44	AL41	233	0	0	0	0
45	AL42	847	0	0	0	0
46	AL43	694	0	0	0	0
47	ALP0	54	0	0	0	0
48	APTN	1644	0	0	0	0
49	AL37	1	0	0	0	0
49	AL40	1	0	0	0	0
49	AL42	1	0	0	0	0
49	AL43	1	0	0	0	0
All	All	125395	0	1444	4	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (4) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AGR:17:GLY:HA2	4:AGR:24:ARG:HD2	1.68	0.73
3:A5S:1:G:H2'	3:A5S:2:G:H8	1.80	0.45
3:A5S:9:C:OP2	3:A5S:10:C:N4	2.50	0.45
4:AGR:15:GLY:O	4:AGR:22:ARG:NH1	2.52	0.42

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AGR	15/40 (38%)	10 (67%)	5 (33%)	0	100	100
5	AL02	250/254 (98%)	245 (98%)	5 (2%)	0	100	100
6	AL03	384/387 (99%)	367 (96%)	16 (4%)	1 (0%)	36	60
7	AL04	359/362 (99%)	335 (93%)	23 (6%)	1 (0%)	36	60
8	AL05	294/297 (99%)	279 (95%)	15 (5%)	0	100	100
9	AL06	152/176 (86%)	148 (97%)	4 (3%)	0	100	100
10	AL07	220/244 (90%)	206 (94%)	13 (6%)	1 (0%)	24	48
11	AL08	231/256 (90%)	213 (92%)	17 (7%)	1 (0%)	30	54
12	AL09	189/191 (99%)	170 (90%)	19 (10%)	0	100	100
13	AL10	207/221 (94%)	200 (97%)	7 (3%)	0	100	100
14	AL11	167/174 (96%)	154 (92%)	13 (8%)	0	100	100
16	AL13	191/199 (96%)	176 (92%)	14 (7%)	1 (0%)	24	48
17	AL14	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
18	AL15	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
19	AL16	195/199 (98%)	189 (97%)	4 (2%)	2 (1%)	12	32
20	AL17	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
21	AL18	183/186 (98%)	178 (97%)	5 (3%)	0	100	100
22	AL19	153/189 (81%)	147 (96%)	6 (4%)	0	100	100
23	AL20	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
24	AL21	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
25	AL22	98/121 (81%)	96 (98%)	2 (2%)	0	100	100
26	AL23	134/137 (98%)	132 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	AL24	61/155 (39%)	59 (97%)	2 (3%)	0	100	100
28	AL25	119/142 (84%)	117 (98%)	2 (2%)	0	100	100
29	AL26	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
30	AL27	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
31	AL28	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
32	AL29	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
33	AL30	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
34	AL31	107/113 (95%)	99 (92%)	8 (8%)	0	100	100
35	AL32	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
36	AL33	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
37	AL34	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
38	AL35	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
39	AL36	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
40	AL37	85/88 (97%)	83 (98%)	2 (2%)	0	100	100
41	AL38	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	AL39	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
43	AL40	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
44	AL41	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
45	AL42	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
46	AL43	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
47	ALP0	5/221 (2%)	5 (100%)	0	0	100	100
All	All	6137/6844 (90%)	5839 (95%)	291 (5%)	7 (0%)	49	73

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	AL04	339	LEU
10	AL07	234	GLU
19	AL16	111	PRO
6	AL03	4	ARG
16	AL13	77	LEU
11	AL08	157	VAL
19	AL16	110	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AGR	9/20 (45%)	9 (100%)	0	100	100
5	AL02	193/196 (98%)	193 (100%)	0	100	100
6	AL03	320/323 (99%)	318 (99%)	2 (1%)	78	91
7	AL04	288/289 (100%)	287 (100%)	1 (0%)	86	94
8	AL05	244/245 (100%)	243 (100%)	1 (0%)	84	93
9	AL06	134/153 (88%)	134 (100%)	0	100	100
10	AL07	186/205 (91%)	186 (100%)	0	100	100
11	AL08	187/208 (90%)	187 (100%)	0	100	100
12	AL09	171/171 (100%)	171 (100%)	0	100	100
13	AL10	177/187 (95%)	177 (100%)	0	100	100
14	AL11	147/150 (98%)	147 (100%)	0	100	100
16	AL13	154/159 (97%)	154 (100%)	0	100	100
17	AL14	107/109 (98%)	107 (100%)	0	100	100
18	AL15	175/176 (99%)	175 (100%)	0	100	100
19	AL16	160/162 (99%)	159 (99%)	1 (1%)	78	91
20	AL17	140/146 (96%)	140 (100%)	0	100	100
21	AL18	150/151 (99%)	150 (100%)	0	100	100
22	AL19	128/154 (83%)	128 (100%)	0	100	100
23	AL20	156/156 (100%)	156 (100%)	0	100	100
24	AL21	136/137 (99%)	136 (100%)	0	100	100
25	AL22	87/107 (81%)	87 (100%)	0	100	100
26	AL23	104/105 (99%)	104 (100%)	0	100	100
27	AL24	55/129 (43%)	55 (100%)	0	100	100
28	AL25	104/118 (88%)	104 (100%)	0	100	100
29	AL26	109/110 (99%)	109 (100%)	0	100	100
30	AL27	115/116 (99%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	AL28	118/119 (99%)	118 (100%)	0	100	100
32	AL29	46/47 (98%)	46 (100%)	0	100	100
33	AL30	81/88 (92%)	81 (100%)	0	100	100
34	AL31	92/97 (95%)	91 (99%)	1 (1%)	65	85
35	AL32	109/111 (98%)	109 (100%)	0	100	100
36	AL33	90/91 (99%)	90 (100%)	0	100	100
37	AL34	95/103 (92%)	95 (100%)	0	100	100
38	AL35	104/105 (99%)	104 (100%)	0	100	100
39	AL36	81/82 (99%)	80 (99%)	1 (1%)	63	84
40	AL37	70/71 (99%)	70 (100%)	0	100	100
41	AL38	68/69 (99%)	68 (100%)	0	100	100
42	AL39	45/46 (98%)	45 (100%)	0	100	100
43	AL40	47/116 (40%)	46 (98%)	1 (2%)	47	75
44	AL41	23/23 (100%)	21 (91%)	2 (9%)	9	24
45	AL42	90/91 (99%)	90 (100%)	0	100	100
46	AL43	71/72 (99%)	71 (100%)	0	100	100
47	ALP0	6/166 (4%)	6 (100%)	0	100	100
All	All	5172/5679 (91%)	5162 (100%)	10 (0%)	85	95

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	AL03	332	ARG
6	AL03	345	ASN
7	AL04	138	ARG
8	AL05	196	ARG
19	AL16	117	ARG
34	AL31	87	ASN
39	AL36	99	ARG
43	AL40	126	LYS
44	AL41	9	ARG
44	AL41	12	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A25S	3191/3396 (93%)	455 (14%)	31 (0%)
2	A58S	157/158 (99%)	28 (17%)	1 (0%)
3	A5S	120/121 (99%)	10 (8%)	0
48	APTN	76/77 (98%)	8 (10%)	0
All	All	3544/3752 (94%)	501 (14%)	32 (0%)

All (501) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A25S	40	A
1	A25S	43	A
1	A25S	49	A
1	A25S	59	G
1	A25S	60	A
1	A25S	65	A
1	A25S	66	A
1	A25S	92	G
1	A25S	109	A
1	A25S	110	G
1	A25S	111	C
1	A25S	116	A
1	A25S	121	A
1	A25S	122	A
1	A25S	133	U
1	A25S	136	G
1	A25S	148	G
1	A25S	154	U
1	A25S	156	G
1	A25S	157	A
1	A25S	161	G
1	A25S	166	C
1	A25S	170	G
1	A25S	187	A
1	A25S	190	U
1	A25S	191	U
1	A25S	200	C
1	A25S	210	U
1	A25S	218	G
1	A25S	219	A
1	A25S	234	G
1	A25S	240	U

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Mol	Chain	Res	Type
1	A25S	243	G
1	A25S	249	U
1	A25S	251	G
1	A25S	252	U
1	A25S	269	G
1	A25S	283	G
1	A25S	286	U
1	A25S	295	A
1	A25S	298	U
1	A25S	305	U
1	A25S	323	A
1	A25S	329	U
1	A25S	339	C
1	A25S	350	C
1	A25S	376	G
1	A25S	398	A
1	A25S	401	U
1	A25S	402	A
1	A25S	403	C
1	A25S	421	G
1	A25S	422	A
1	A25S	439	C
1	A25S	440	A
1	A25S	521	A
1	A25S	535	G
1	A25S	543	C
1	A25S	545	U
1	A25S	546	C
1	A25S	547	G
1	A25S	548	G
1	A25S	552	G
1	A25S	555	U
1	A25S	556	U
1	A25S	557	A
1	A25S	559	A
1	A25S	579	G
1	A25S	589	A
1	A25S	604	G
1	A25S	609	G
1	A25S	611	A
1	A25S	612	U
1	A25S	620	U

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Mol	Chain	Res	Type
1	A25S	621	A
1	A25S	622	A
1	A25S	637	C
1	A25S	638	C
1	A25S	649	A
1	A25S	677	A
1	A25S	681	U
1	A25S	691	A
1	A25S	705	A
1	A25S	712	G
1	A25S	715	A
1	A25S	716	A
1	A25S	719	U
1	A25S	758	C
1	A25S	766	U
1	A25S	767	U
1	A25S	776	U
1	A25S	777	U
1	A25S	780	A
1	A25S	781	G
1	A25S	785	G
1	A25S	786	A
1	A25S	806	A
1	A25S	817	A
1	A25S	830	A
1	A25S	849	C
1	A25S	857	G
1	A25S	861	C
1	A25S	874	U
1	A25S	879	U
1	A25S	896	A
1	A25S	907	G
1	A25S	908	G
1	A25S	914	A
1	A25S	916	G
1	A25S	917	A
1	A25S	921	A
1	A25S	937	G
1	A25S	944	C
1	A25S	959	C
1	A25S	960	U
1	A25S	974	G

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Mol	Chain	Res	Type
1	A25S	979	U
1	A25S	980	A
1	A25S	981	U
1	A25S	982	C
1	A25S	1001	G
1	A25S	1002	A
1	A25S	1006	A
1	A25S	1010	G
1	A25S	1021	G
1	A25S	1022	U
1	A25S	1033	U
1	A25S	1037	C
1	A25S	1047	A
1	A25S	1049	C
1	A25S	1063	G
1	A25S	1064	A
1	A25S	1065	A
1	A25S	1072	G
1	A25S	1081	U
1	A25S	1082	U
1	A25S	1093	A
1	A25S	1094	U
1	A25S	1095	U
1	A25S	1096	U
1	A25S	1097	G
1	A25S	1098	A
1	A25S	1103	A
1	A25S	1104	G
1	A25S	1117	G
1	A25S	1131	G
1	A25S	1144	U
1	A25S	1153	A
1	A25S	1155	C
1	A25S	1159	A
1	A25S	1180	A
1	A25S	1181	U
1	A25S	1191	U
1	A25S	1196	C
1	A25S	1201	C
1	A25S	1209	G
1	A25S	1221	A
1	A25S	1222	G

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Mol	Chain	Res	Type
1	A25S	1235	U
1	A25S	1236	G
1	A25S	1237	G
1	A25S	1239	C
1	A25S	1242	G
1	A25S	1244	A
1	A25S	1245	A
1	A25S	1246	G
1	A25S	1258	U
1	A25S	1262	G
1	A25S	1263	A
1	A25S	1264	G
1	A25S	1286	A
1	A25S	1287	A
1	A25S	1307	G
1	A25S	1308	A
1	A25S	1309	U
1	A25S	1313	G
1	A25S	1330	A
1	A25S	1331	U
1	A25S	1348	U
1	A25S	1349	G
1	A25S	1351	U
1	A25S	1352	A
1	A25S	1355	A
1	A25S	1356	U
1	A25S	1357	G
1	A25S	1386	A
1	A25S	1392	G
1	A25S	1399	A
1	A25S	1400	G
1	A25S	1419	A
1	A25S	1434	G
1	A25S	1437	C
1	A25S	1446	A
1	A25S	1481	A
1	A25S	1487	G
1	A25S	1496	C
1	A25S	1508	C
1	A25S	1536	G
1	A25S	1555	U
1	A25S	1556	C

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Mol	Chain	Res	Type
1	A25S	1557	A
1	A25S	1560	G
1	A25S	1562	C
1	A25S	1563	C
1	A25S	1564	U
1	A25S	1569	U
1	A25S	1576	G
1	A25S	1581	C
1	A25S	1583	A
1	A25S	1589	A
1	A25S	1593	A
1	A25S	1607	U
1	A25S	1620	U
1	A25S	1629	U
1	A25S	1639	C
1	A25S	1642	A
1	A25S	1643	A
1	A25S	1645	U
1	A25S	1657	C
1	A25S	1717	U
1	A25S	1724	U
1	A25S	1725	C
1	A25S	1730	G
1	A25S	1741	A
1	A25S	1750	A
1	A25S	1751	G
1	A25S	1760	A
1	A25S	1765	U
1	A25S	1766	G
1	A25S	1770	G
1	A25S	1775	G
1	A25S	1780	G
1	A25S	1797	A
1	A25S	1808	G
1	A25S	1814	A
1	A25S	1816	A
1	A25S	1817	G
1	A25S	1820	U
1	A25S	1821	U
1	A25S	1839	A
1	A25S	1840	U
1	A25S	1841	A

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Mol	Chain	Res	Type
1	A25S	1842	A
1	A25S	1849	C
1	A25S	1850	A
1	A25S	1866	C
1	A25S	1880	U
1	A25S	1881	A
1	A25S	1893	A
1	A25S	1906	G
1	A25S	1952	G
1	A25S	2091	U
1	A25S	2093	A
1	A25S	2101	C
1	A25S	2102	U
1	A25S	2112	U
1	A25S	2113	A
1	A25S	2114	C
1	A25S	2121	G
1	A25S	2122	G
1	A25S	2131	A
1	A25S	2144	A
1	A25S	2158	A
1	A25S	2160	G
1	A25S	2169	G
1	A25S	2205	U
1	A25S	2208	A
1	A25S	2209	U
1	A25S	2210	G
1	A25S	2225	U
1	A25S	2244	A
1	A25S	2255	A
1	A25S	2256	A
1	A25S	2273	G
1	A25S	2282	U
1	A25S	2287	C
1	A25S	2288	G
1	A25S	2307	G
1	A25S	2308	C
1	A25S	2310	U
1	A25S	2313	A
1	A25S	2314	U
1	A25S	2315	G
1	A25S	2334	U

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Mol	Chain	Res	Type
1	A25S	2336	U
1	A25S	2373	A
1	A25S	2374	C
1	A25S	2375	G
1	A25S	2385	G
1	A25S	2388	U
1	A25S	2393	G
1	A25S	2397	A
1	A25S	2402	A
1	A25S	2403	G
1	A25S	2404	A
1	A25S	2411	U
1	A25S	2418	G
1	A25S	2451	G
1	A25S	2453	U
1	A25S	2454	G
1	A25S	2457	G
1	A25S	2458	A
1	A25S	2459	A
1	A25S	2461	A
1	A25S	2462	A
1	A25S	2463	G
1	A25S	2468	A
1	A25S	2472	U
1	A25S	2474	G
1	A25S	2477	G
1	A25S	2485	A
1	A25S	2486	A
1	A25S	2487	U
1	A25S	2492	C
1	A25S	2493	U
1	A25S	2494	A
1	A25S	2499	U
1	A25S	2513	U
1	A25S	2514	U
1	A25S	2515	A
1	A25S	2522	G
1	A25S	2523	A
1	A25S	2531	C
1	A25S	2533	G
1	A25S	2537	U
1	A25S	2538	U

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Mol	Chain	Res	Type
1	A25S	2539	C
1	A25S	2540	A
1	A25S	2541	U
1	A25S	2542	U
1	A25S	2549	G
1	A25S	2552	C
1	A25S	2554	A
1	A25S	2561	A
1	A25S	2569	A
1	A25S	2570	U
1	A25S	2572	C
1	A25S	2573	G
1	A25S	2585	G
1	A25S	2593	A
1	A25S	2594	C
1	A25S	2606	G
1	A25S	2607	G
1	A25S	2614	G
1	A25S	2626	A
1	A25S	2652	U
1	A25S	2656	A
1	A25S	2672	G
1	A25S	2674	A
1	A25S	2677	G
1	A25S	2689	A
1	A25S	2691	A
1	A25S	2696	A
1	A25S	2704	A
1	A25S	2714	G
1	A25S	2719	U
1	A25S	2728	G
1	A25S	2729	U
1	A25S	2737	C
1	A25S	2752	U
1	A25S	2753	G
1	A25S	2755	C
1	A25S	2762	A
1	A25S	2777	G
1	A25S	2778	G
1	A25S	2796	G
1	A25S	2800	G
1	A25S	2801	A

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Mol	Chain	Res	Type
1	A25S	2802	A
1	A25S	2810	C
1	A25S	2817	A
1	A25S	2818	U
1	A25S	2842	U
1	A25S	2845	A
1	A25S	2861	U
1	A25S	2867	C
1	A25S	2871	G
1	A25S	2872	A
1	A25S	2875	U
1	A25S	2876	C
1	A25S	2887	A
1	A25S	2889	C
1	A25S	2898	G
1	A25S	2923	U
1	A25S	2935	U
1	A25S	2936	A
1	A25S	2941	A
1	A25S	2983	C
1	A25S	2996	U
1	A25S	2997	G
1	A25S	3012	A
1	A25S	3056	U
1	A25S	3059	G
1	A25S	3078	U
1	A25S	3079	U
1	A25S	3086	A
1	A25S	3092	C
1	A25S	3094	A
1	A25S	3101	G
1	A25S	3109	G
1	A25S	3119	U
1	A25S	3122	A
1	A25S	3130	A
1	A25S	3131	U
1	A25S	3142	A
1	A25S	3143	C
1	A25S	3154	C
1	A25S	3155	U
1	A25S	3156	U
1	A25S	3157	U

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Mol	Chain	Res	Type
1	A25S	3165	A
1	A25S	3168	A
1	A25S	3173	G
1	A25S	3174	A
1	A25S	3176	G
1	A25S	3179	U
1	A25S	3181	C
1	A25S	3187	A
1	A25S	3207	U
1	A25S	3217	C
1	A25S	3218	A
1	A25S	3219	G
1	A25S	3229	G
1	A25S	3243	A
1	A25S	3245	A
1	A25S	3247	G
1	A25S	3253	G
1	A25S	3259	U
1	A25S	3263	G
1	A25S	3269	U
1	A25S	3270	U
1	A25S	3273	A
1	A25S	3279	A
1	A25S	3281	U
1	A25S	3287	U
1	A25S	3289	G
1	A25S	3294	A
1	A25S	3304	U
1	A25S	3313	U
1	A25S	3316	A
1	A25S	3318	G
1	A25S	3319	U
1	A25S	3341	U
1	A25S	3345	G
1	A25S	3350	C
1	A25S	3352	U
1	A25S	3353	G
1	A25S	3354	U
1	A25S	3355	U
1	A25S	3356	G
1	A25S	3369	G
1	A25S	3375	A

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Mol	Chain	Res	Type
1	A25S	3378	C
1	A25S	3386	G
1	A25S	3389	U
2	A58S	23	U
2	A58S	34	U
2	A58S	35	C
2	A58S	39	G
2	A58S	51	G
2	A58S	59	A
2	A58S	62	C
2	A58S	63	G
2	A58S	80	A
2	A58S	81	U
2	A58S	82	U
2	A58S	84	C
2	A58S	85	G
2	A58S	86	U
2	A58S	87	G
2	A58S	90	U
2	A58S	95	G
2	A58S	104	A
2	A58S	106	C
2	A58S	111	A
2	A58S	113	U
2	A58S	125	U
2	A58S	126	A
2	A58S	127	U
2	A58S	138	A
2	A58S	148	G
2	A58S	151	C
2	A58S	155	A
3	A5S	7	G
3	A5S	51	A
3	A5S	54	U
3	A5S	55	A
3	A5S	65	G
3	A5S	74	C
3	A5S	76	A
3	A5S	102	A
3	A5S	112	G
3	A5S	121	U
48	APTN	9	G

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Mol	Chain	Res	Type
48	APTN	18	G
48	APTN	19	G
48	APTN	20	U
48	APTN	47	U
48	APTN	48	C
48	APTN	59	A
48	APTN	76	A

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A25S	65	A
1	A25S	169	U
1	A25S	282	G
1	A25S	547	G
1	A25S	637	C
1	A25S	916	G
1	A25S	979	U
1	A25S	1064	A
1	A25S	1097	G
1	A25S	1103	A
1	A25S	1241	U
1	A25S	1307	G
1	A25S	1329	U
1	A25S	1355	A
1	A25S	1554	U
1	A25S	1562	C
1	A25S	1815	U
1	A25S	2101	C
1	A25S	2112	U
1	A25S	2209	U
1	A25S	2512	C
1	A25S	2514	U
1	A25S	2537	U
1	A25S	2541	U
1	A25S	2593	A
1	A25S	3121	U
1	A25S	3218	A
1	A25S	3228	C
1	A25S	3269	U
1	A25S	3317	U
1	A25S	3351	U

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Mol	Chain	Res	Type
2	A58S	85	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [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-26033. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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 ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.