



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Oct 2, 2017 – 04:52 AM EDT

PDB ID : 5NGM
EMDB ID: : EMD-3637
Title : 2.9S structure of the 70S ribosome composing the S. aureus 100S complex
Authors : Matzov, D.; Aibara, S.; Zimmerman, E.; Bashan, A.; Amunts, A.; Yonath, A.
Deposited on : unknown
Resolution : 2.90 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

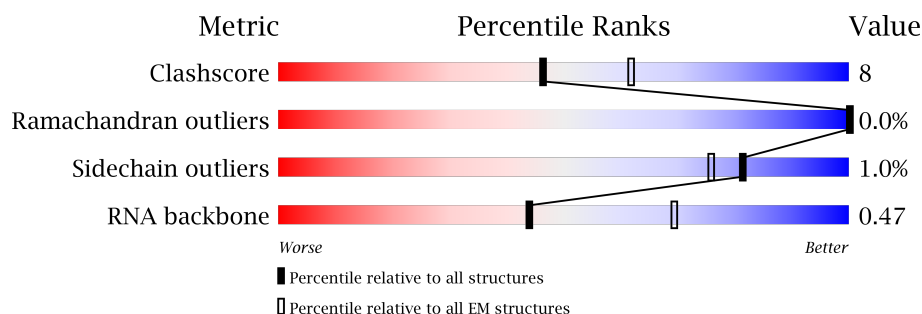
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.




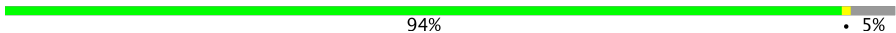

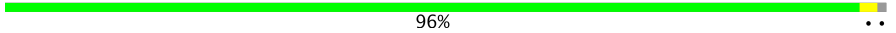

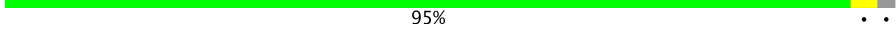
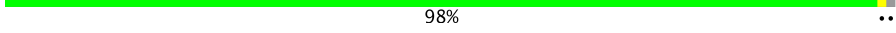
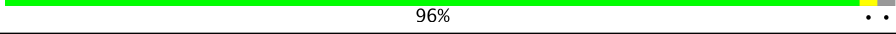



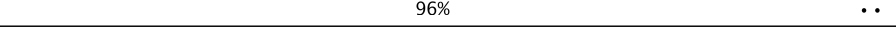

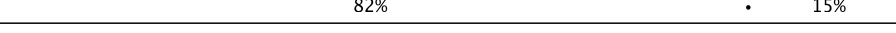
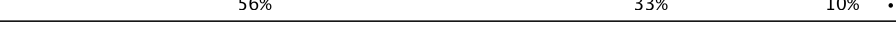


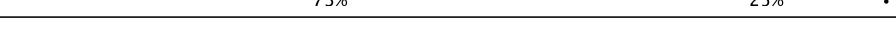


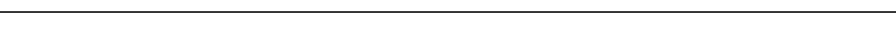




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	Aa	1555	68% 29% ..
2	Ab	255	88% 11%
3	Ac	217	93% 7%
4	Ad	200	98% ..
5	Ae	166	93% 6%
6	Af	98	96% ..
7	Ag	156	97% .
8	Ah	132	98% ..









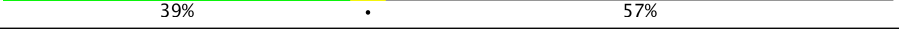


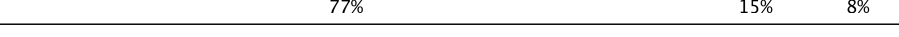

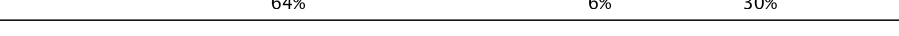


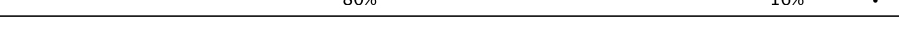

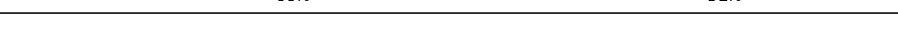
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Mol	Chain	Length	Quality of chain
9	Ai	132	 93% . .
10	Aj	102	 94% . 5%
11	Ak	129	 88% 12%
12	Al	137	 96% . .
13	Am	121	 85% . 14%
14	An	61	 95% . .
15	Ao	89	 98% . .
16	Ap	91	 96% . .
17	Aq	87	 92% 8%
18	Ar	80	 66% . 33%
19	As	92	 86% . 13%
20	At	83	 96% . .
21	Au	58	 90% 10%
22	Av	190	 82% . 15%
23	AA	2923	 56% 33% 10% . .
24	AB	115	 72% 23% . .
25	AC	277	 75% 24% .
26	AD	220	 73% 25% .
27	AE	207	 83% 16%
28	AF	179	 78% 20% .
29	AG	178	 83% 15% . .
30	AH	145	 90% 10%
31	AI	122	 67% 32% .
32	AJ	146	 76% 24%
33	AK	144	 76% 18% . 5%

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Mol	Chain	Length	Quality of chain
34	AL	122	
35	AM	119	
36	AN	116	
37	AO	118	
38	AP	102	
39	AQ	117	
40	AR	91	
41	AS	105	
42	AT	217	
43	AU	94	
44	AV	62	
45	AW	73	
46	AX	59	
47	AY	84	
48	AZ	57	
49	A1	49	
50	A2	45	
51	A3	66	
52	A4	37	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 140965 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	1539	Total	C	N	O	P	0	0
			32969	14719	6017	10694	1539		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	226	Total	C	N	O	S	0	0
			1819	1159	317	335	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ac	202	Total	C	N	O	S	0	0
			1501	945	284	271	1		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ad	198	Total	C	N	O	S	0	0
			1497	952	275	268	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ae	156	Total	C	N	O	S	0	0
			1145	723	211	209	2		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Af	95	Total	C	N	O	S	0	0
			778	493	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ag	152	Total	C	N	O	S	0	0
			1161	722	218	217	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Ah	131	Total	C	N	O	S	0	0
			1026	650	183	189	4		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ai	127	Total	C	N	O	S	0	0
			922	576	179	166	1		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Aj	97	Total	C	N	O	S	0	0
			752	475	140	136	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ak	114	Total	C	N	O	S	0	0
			810	498	151	159	2		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Al	135	Total	C	N	O	S	0	0
			1037	646	211	178	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Am	104	Total	C	N	O	0	0
			727	453	139	135		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	An	60	Total	C	N	O	S	0	0
			487	307	98	77	5		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ao	88	Total	C	N	O	S	0	0
			723	448	150	124	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ap	89	Total	C	N	O	S	0	0
			694	436	128	129	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Aq	80	Total	C	N	O	S	0	0
			621	392	112	117			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ar	54	Total	C	N	O	S	0	0
			445	284	86	73	2		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	As	80	Total	C	N	O	S	0	0
			636	410	113	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	At	81	Total	C	N	O	S	0	0
			591	358	117	115	1		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Au	52	Total	C	N	O	0	0
			400	249	79	72		

- Molecule 22 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Av	162	Total	C	N	O	S	0	0
			1333	835	242	254	2		

- Molecule 23 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AA	2905	Total	C	N	O	P	0	0
			62277	27803	11387	20182	2905		

- Molecule 24 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AB	115	Total	C	N	O	P	0	0
			2445	1094	436	801	114		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AC	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AD	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AE	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AF	175	Total	C	N	O	S	0	0
			1325	837	227	255	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AG	175	Total	C	N	O	S	0	0
			1263	790	239	231	3		

- Molecule 30 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AH	145	Total	C	N	O	S	0	0
			1143	714	208	218	3		

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AI	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AJ	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AK	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AL	120	Total	C	N	O	S	0	0
			932	576	182	173	1		

- Molecule 35 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AM	119	Total	C	N	O	S	0	0
			891	557	174	159	1		

- Molecule 36 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AN	114	Total	C	N	O	S	0	0
			889	563	175	151			

- Molecule 37 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AO	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 38 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AP	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 39 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AQ	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AR	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AS	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 42 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	AT	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	AU	82	Total	C	N	O	0	0
			622	385	122	115		

- Molecule 44 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	AV	58	Total	C	N	O	0	0
			445	277	96	72		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	AW	67	Total	C	N	O	0	0
			541	333	102	106		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	AX	58	Total	C	N	O	0	0
			449	280	85	84		

- Molecule 47 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AY	59	Total	C	N	O	S	0	0
			370	225	68	76	1		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AZ	48	Total	C	N	O	S	0	0
			360	222	77	59	2		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	A1	47	Total	C	N	O	S	0	0
			390	238	78	70	4		

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	A2	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	A3	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	A4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

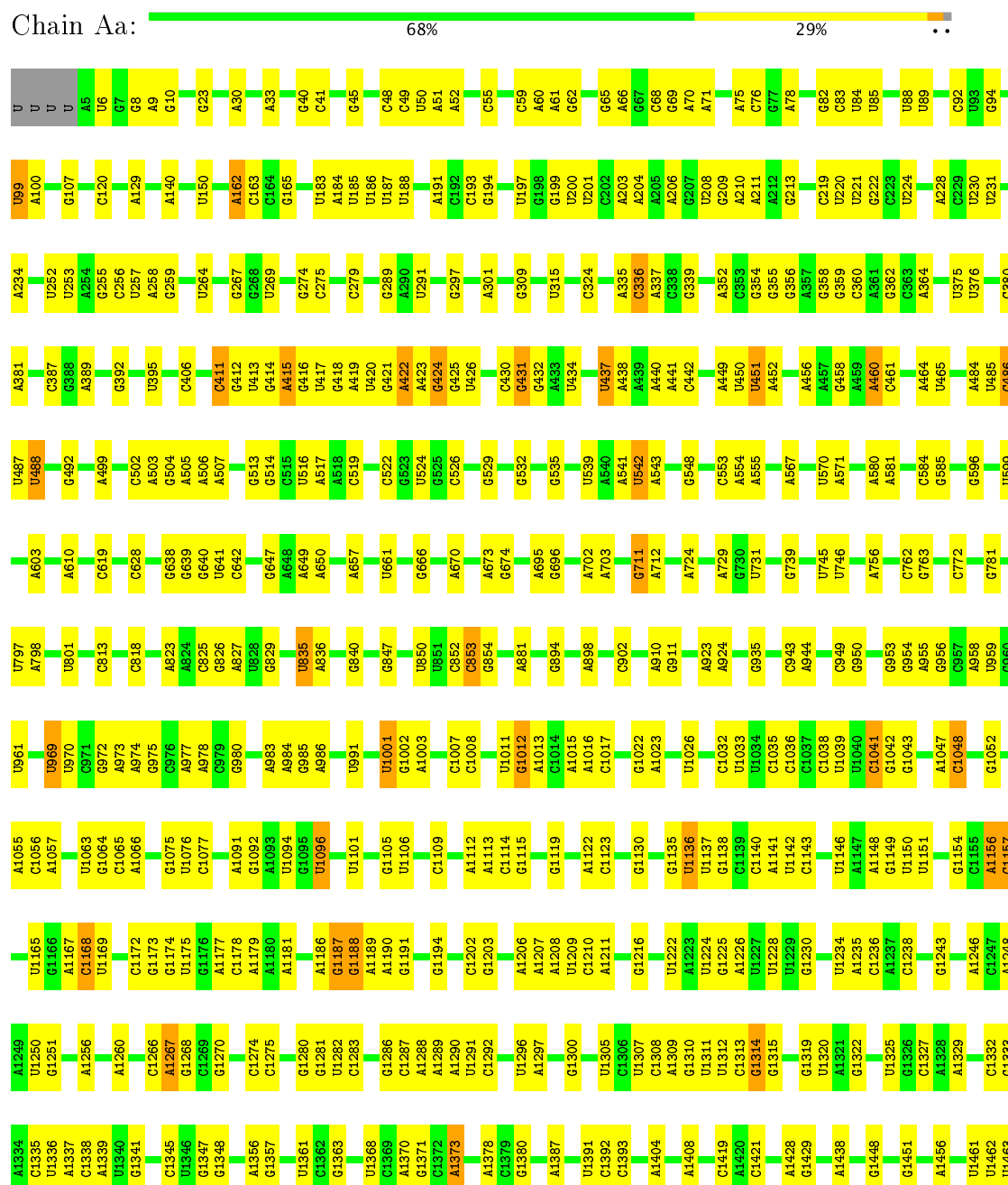
- Molecule 53 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	AB	2	Total	Mg	0
			2	2	
53	AA	199	Total	Mg	0
			199	199	
53	AZ	1	Total	Mg	0
			1	1	
53	AC	2	Total	Mg	0
			2	2	
53	AU	1	Total	Mg	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

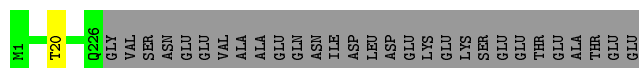
• Molecule 1: 16S ribosomal RNA





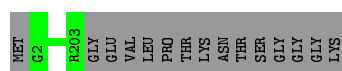
- Molecule 2: 30S ribosomal protein S2

Chain Ab: 88% 11%



- Molecule 3: 30S ribosomal protein S3

Chain Ac: 93% 7%



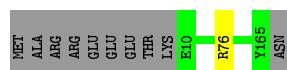
- Molecule 4: 30S ribosomal protein S4

Chain Ad: 98% ..



- Molecule 5: 30S ribosomal protein S5

Chain Ae: 93% • 6%



- Molecule 6: 30S ribosomal protein S6

Chain Af: 96% ..



- Molecule 7: 30S ribosomal protein S7

Chain Ag: 97% •



- Molecule 8: 30S ribosomal protein S8

Chain Ah: 98% ..



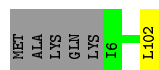
- Molecule 9: 30S ribosomal protein S9

Chain Ai:  93%



- Molecule 10: 30S ribosomal protein S10

Chain Aj:  94%



- Molecule 11: 30S ribosomal protein S11

Chain Ak:  88%



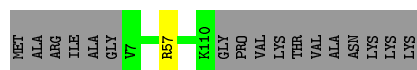
- Molecule 12: 30S ribosomal protein S12

Chain Al:  96%



- Molecule 13: 30S ribosomal protein S13

Chain Am:  85%



- Molecule 14: 30S ribosomal protein S14 type Z

Chain An:  95%



- Molecule 15: 30S ribosomal protein S15

Chain Ao:  98%



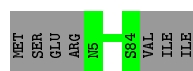
- Molecule 16: 30S ribosomal protein S16

Chain Ap:  96% ..



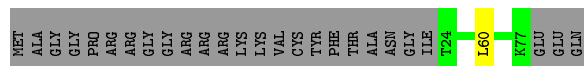
- Molecule 17: 30S ribosomal protein S17

Chain Aq:  92% 8%




- Molecule 18: 30S ribosomal protein S18

Chain Ar:  66% 33%



- Molecule 19: 30S ribosomal protein S19

Chain As:  86% 13%



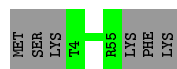
- Molecule 20: 30S ribosomal protein S20

Chain At:  96% ..




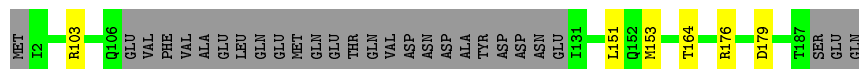
- Molecule 21: 30S ribosomal protein S21

Chain Au:  90% 10%



- Molecule 22: Ribosome hibernation promoting factor

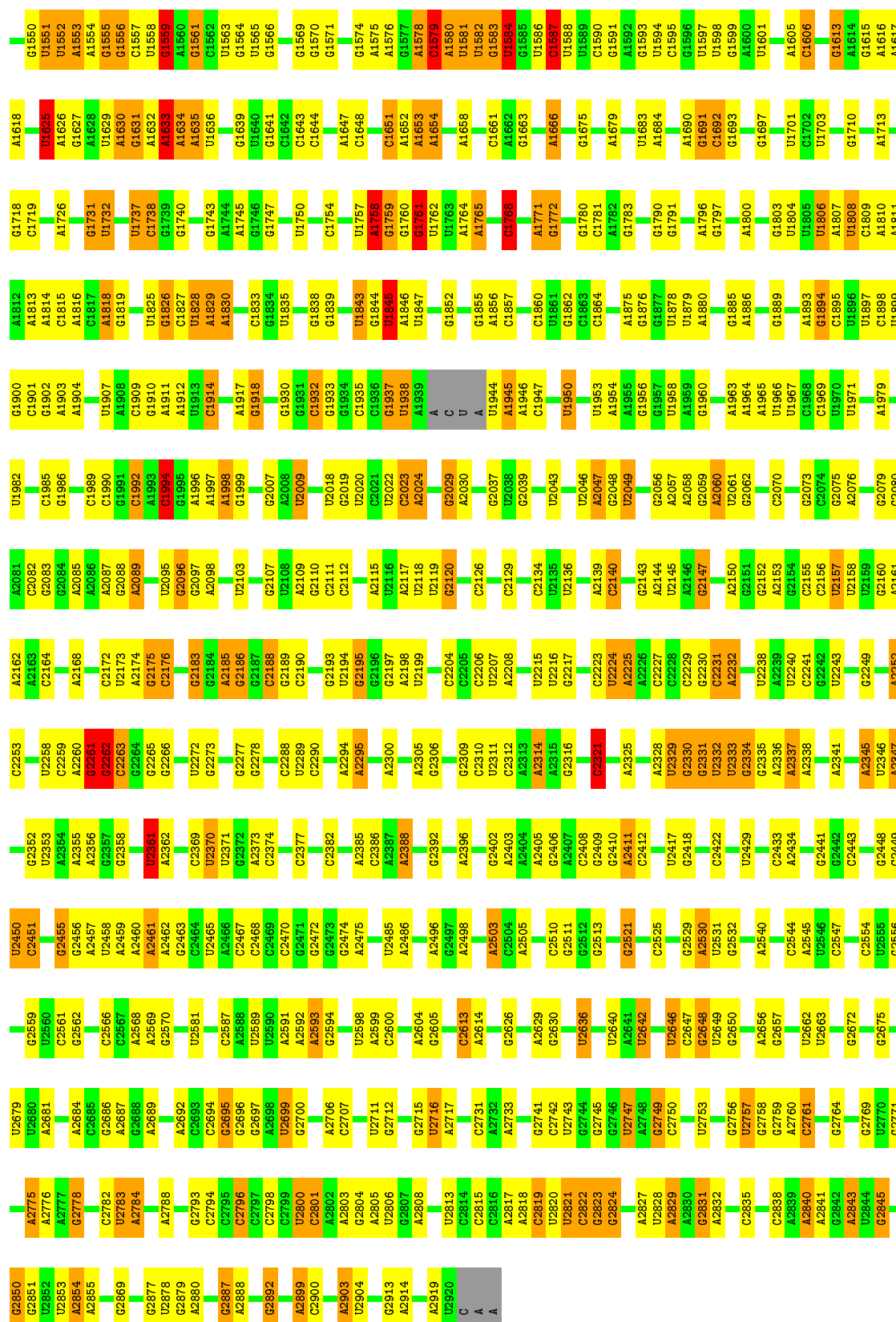
Chain Av:  82% 15%

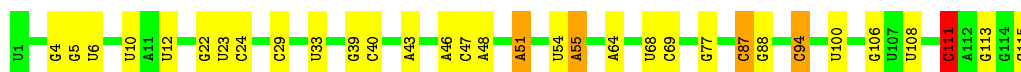


- Molecule 23: 23S Ribosomal RNA

Chain AA:  56% 33% 10% ..

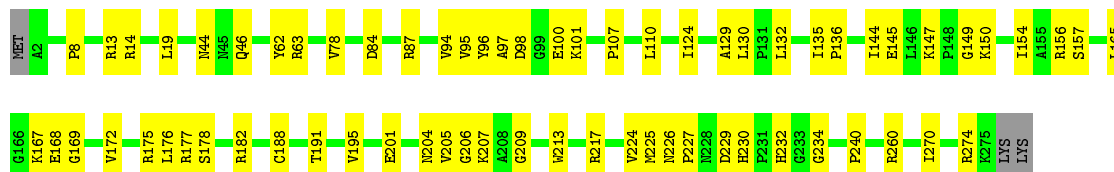
U1389	U1299	A1190	G1118	G1041	C980	A874	A775	A682	G588	G509	C402	U301	C184	U93	G
G1392	G1300	G1197	C1119	C1042	G961	C878	A779	A688	U589	A512	U403	A302	A185	G96	A
G1477	G1304	G1198	A1120	U1043	A962	U879		A689	U590	A513	G405	A307	A191	U99	U3
G1479	U1305	A1199	A1121	A1044	U964		U787	U690	A591	G514	A406	U308	A199	U100	U11
G1395	A1200	G1046	G1122	A1045		C882	A788	U690	A592	G515	G410	C310	A200	G101	U12
A1396	G1201	A1124	A1123	A1047	C967			G693	U593	A516	A411	C311	A201	A102	A13
	A1310	U1125	U1048	U1049	A968	G890	U792	G694	G594	A517	A417	A312	C202	G104	A14
A1312	A1311	U1126	C1049		A969	A891	A794		U597	A518		U	C213	G107	G16
A1316		U1127	A1055	U1056	A972	U895	A796	U697	U600	G522	G432	C315	G214	G108	C18
G1315	G1316	A1128	U1057	A1057	A973	U896	A797	U699	U605	A523	A435	G317	G215	A108	
		A1129						A700	G606	A524	A436	A318	G217	U113	G23
		G1131	U1063	U1064	U975	G901	G802	G701	C607	A525	A437	G319	G218	U114	G24
		G1133	A1065	A1070	U976	A902	C903	U702	C608	A526	U438	G320	G219	U115	U25
		G1136	G1066	A1072	A977	G903	A809	A703	C609	G527	U439	U321	A219	A117	G26
		G1137	U1067			G904	A810	U706	U610	A529			A224	U119	G27
		U1138	G1068		A985	U985			U611	C530	C444	A325	A225	A28	
		A1139	G1069	U987	G986	A906	G816	G711	U614	G534	A447	A326	A226	U33	
		U1140	A1070	C988	C988			U712	A615	G535	A448	C327	A227	U34	
		U1141	A1071	A989	A989	A911	G820	U713	A616		U449	A328	U233	U35	
		G1142	A1072		G990	G914	G822	G714	G617	G538	C450	A329	G135	G36	
		G1143			A981			A715	A618	G539	U451		C241	A136	
		G1144	G1075		A992		G825	G718	U619	G545	G452	C333	U246	U141	A43
		U1145	A1076	U1077	G997	G918	A826	G719	G620			A334	A247	A44	
		G1148	G1078			G919	A827	A720	G630	A548	G456	C340	G250	C144	G51
		U1149			G1000	A921	A828	A721	U631	U549			C251	A145	A52
		A1150	U1091		A1001	G922	U829	A722	G635	A550	C460	U344	C252	U148	A53
		G1151	G1086	C1087	U1002	A923	U830		U639	A552	C463	C345	C255	U149	G54
		G1152	C1088	C1089	A1003			A730	U639	C554		A346	C256	A150	G55
		C1153	A1090	G1005	G1005	G926	U835	U731	C644	C555	C466	G351	C257	C152	G57
		G1154	G1091	C1092	C1008	C928	C336	C735	A645	U556		A352	G267	G58	
		A1155	A1092	C1093		C929	G837	C743	A646	G557	U473	A353	A268	U59	
		U1157	C1094	A1095	G1012	C	A839		G647	A558		A365	G269	U157	
		G1158	A1094			U	C941	A750	G648	A559	C481	G366	C270	G158	U63
		C1160	A1095			C	U842	U753	U649	A560	U482		C277	U159	A64
		U1161	G1099	G1099	A1018			U754	U650			A372	C278	G160	A68
		C1162	G1100	A1101	A1019	U		C755	A651	G563	G486	A373	A279	A161	G69
		U1163	U1102	G1021	G1021	C	G850			U564	U487		C280	A162	G70
		G1166	G1103	G1022	G1022	G937		U759	G656	G565	G488	C378	A281	A164	
		U1174	U1104	A1024	A1024	U940	U856	A760		U566	A489		A282	A167	A71
		A1284	U1105	A1025	A941		U858	A761	A660	A567	C490	A388	G283	U167	U72
		A1285	G1106	C1026	C942	C942	C859	C762	A661	C572	C491	A389	C284	A168	U74
		U1286	G1107	A1027	A1027	C943	U860	A763	U661	A573	G492	A390	U285	G169	G75
		U1287	C1108			G944	C861	C764		A574	A493	A391	U286	C170	
		C1177	U1109		C1031		C862	U765	C669	U575	G498	U392	G287	A171	U78
		U1178	U1110			C949	G863	U766	G670	U576		G393	U172	U172	
		C1179	A1111	A1034	A1034	A952	A868	A767	U671	A577		U394	G291	A173	G83
		G1183	G1112	C1035	C1035		G869	U769	A672	G578	C501	U395	U292	A177	A84
		A1184	A1113	A1037	A1037	A985	C870		G675	U579	C502	G396	U293	G177	G85
		U1185	G1114	A1037	A1037		U871	G770		C580	A503	U397	U298	A178	
		A1186	G1115	C1038	C1038	A956	U872	G771	A678	A581	U505	C398	U299	A179	A90
			C1116	C1039	C1039	C957	U873	G774	G679	A583	A506	U401	G300	G180	G92
			A1117	A1117	A1040										





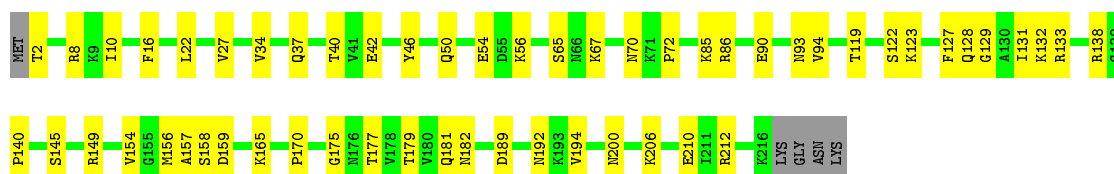
- Molecule 25: 50S ribosomal protein L2

Chain AC: 75% 24%



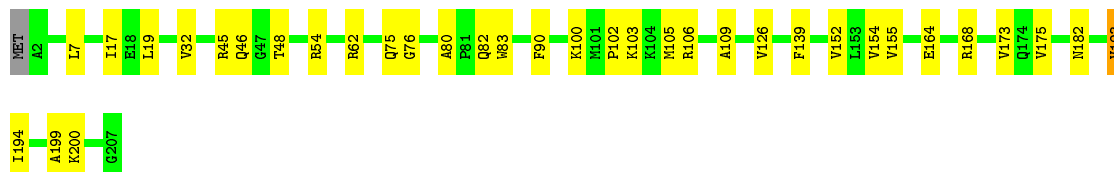
- Molecule 26: 50S ribosomal protein L3

Chain AD: 73% 25%



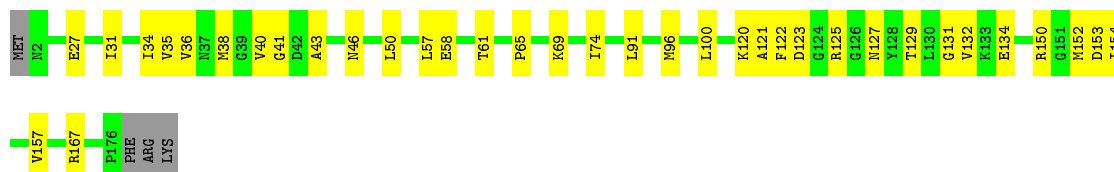
- Molecule 27: 50S ribosomal protein L4

Chain AE: 83% 16%



- Molecule 28: 50S ribosomal protein L5

Chain AF: 78% 20%



- Molecule 29: 50S ribosomal protein L6

Chain AG: 83% 15%



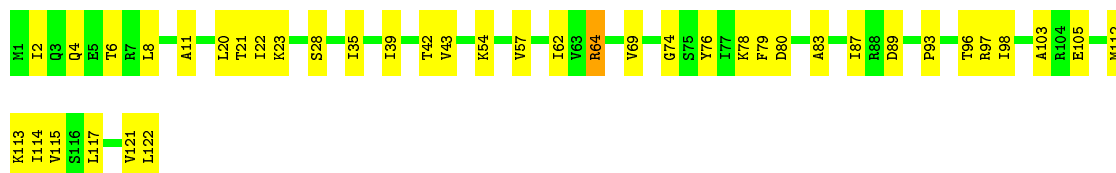
- Molecule 30: 50S ribosomal protein L13

Chain AH:  90% 10%




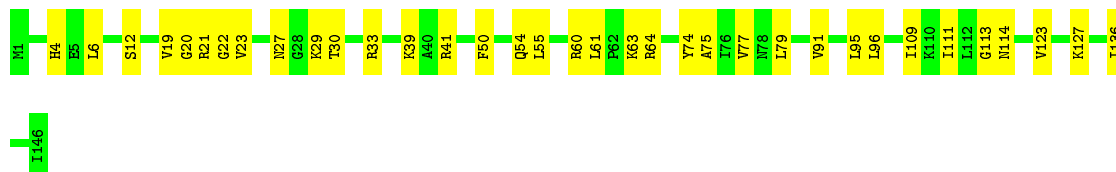
- Molecule 31: 50S ribosomal protein L14

Chain AI:  67% 32%




- Molecule 32: 50S ribosomal protein L15

Chain AJ:  76% 24%




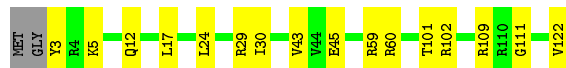
- Molecule 33: 50S ribosomal protein L16

Chain AK:  76% 18% 5%




- Molecule 34: 50S ribosomal protein L17

Chain AL:  85% 13%





- Molecule 35: 50S ribosomal protein L18

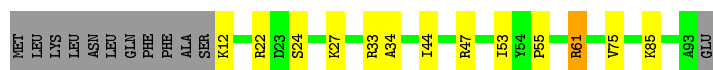
Chain AM:  76% 22%




- Molecule 36: 50S ribosomal protein L19

Chain AN:  79% 19%

Chain AU:  73% 13% • 13%




- Molecule 44: 50S ribosomal protein L28

Chain AV:  81% 11% • 6%




- Molecule 45: 50S ribosomal protein L29

Chain AW:  77% 15% 8%



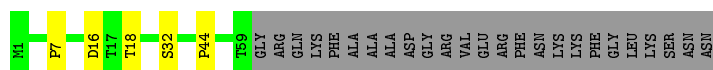
- Molecule 46: 50S ribosomal protein L30

Chain AX:  81% 17% •



- Molecule 47: 50S ribosomal protein L31 type B

Chain AY:  64% 6% 30%




- Molecule 48: 50S ribosomal protein L32

Chain AZ:  67% 18% 16%




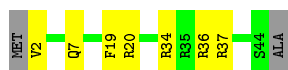
- Molecule 49: 50S ribosomal protein L33

Chain A1:  80% 16% •

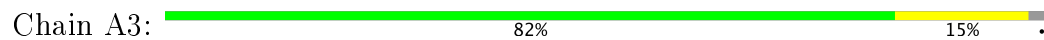


- Molecule 50: 50S ribosomal protein L34

Chain A2:  80% 16% •



- Molecule 51: 50S ribosomal protein L35



- Molecule 52: 50S ribosomal protein L36



4 Experimental information ⓘ

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	224554	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.3	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (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: MG

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 > 2$	RMSZ	# $ Z > 2$
1	Aa	0.38	0/36913	0.95	102/57564 (0.2%)
10	Aj	0.27	0/764	0.56	0/1034
11	Ak	0.29	0/824	0.59	0/1119
12	Al	0.30	0/1054	0.63	1/1415 (0.1%)
13	Am	0.26	0/732	0.56	0/991
14	An	0.32	0/497	0.63	0/662
15	Ao	0.26	0/732	0.53	0/979
16	Ap	0.33	0/705	0.57	0/952
17	Aq	0.31	0/629	0.58	0/849
18	Ar	0.28	0/452	0.65	1/604 (0.2%)
19	As	0.31	0/654	0.58	0/879
2	Ab	0.26	0/1846	0.54	1/2477 (0.0%)
20	At	0.23	0/591	0.50	0/793
21	Au	0.27	0/403	0.51	0/535
22	Av	0.49	0/1350	0.81	2/1812 (0.1%)
23	AA	0.74	3/69738 (0.0%)	1.02	202/108747 (0.2%)
24	AB	0.61	0/2732	1.16	20/4253 (0.5%)
25	AC	0.48	0/2129	0.67	3/2858 (0.1%)
26	AD	0.49	0/1651	0.66	0/2215
27	AE	0.47	0/1595	0.66	0/2154
28	AF	0.31	0/1339	0.63	0/1805
29	AG	0.35	0/1281	0.58	0/1736
3	Ac	0.27	0/1523	0.59	0/2062
30	AH	0.48	0/1165	0.65	0/1570
31	AI	0.47	0/925	0.73	3/1242 (0.2%)
32	AJ	0.45	0/1100	0.71	2/1467 (0.1%)
33	AK	0.46	0/1095	0.61	0/1472
34	AL	0.43	0/936	0.71	0/1253
35	AM	0.43	0/900	0.68	2/1205 (0.2%)
36	AN	0.43	0/901	0.65	1/1209 (0.1%)
37	AO	0.52	0/954	0.64	0/1264
38	AP	0.47	0/800	0.67	0/1070

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	AQ	0.45	0/862	0.70	0/1161
4	Ad	0.28	0/1526	0.62	1/2063 (0.0%)
40	AR	0.43	0/723	0.63	0/966
41	AS	0.39	0/779	0.67	0/1043
42	AT	0.37	0/730	0.66	1/981 (0.1%)
43	AU	0.54	0/628	0.68	1/833 (0.1%)
44	AV	0.38	0/451	0.66	0/603
45	AW	0.39	0/542	0.69	0/722
46	AX	0.40	0/451	0.61	0/606
47	AY	0.25	0/378	0.53	0/521
48	AZ	0.43	0/366	0.65	0/489
49	A1	0.34	0/395	0.60	0/530
5	Ae	0.28	0/1159	0.59	0/1566
50	A2	0.48	0/371	0.67	0/484
51	A3	0.40	0/526	0.61	0/690
52	A4	0.52	0/298	0.63	0/392
6	Af	0.30	0/789	0.60	1/1060 (0.1%)
7	Ag	0.26	0/1176	0.54	0/1588
8	Ah	0.31	0/1038	0.63	0/1395
9	Ai	0.27	0/937	0.67	1/1269 (0.1%)
All	All	0.58	3/153035 (0.0%)	0.92	345/229209 (0.2%)

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
12	Al	0	1
19	As	0	1
20	At	0	1
26	AD	0	1
38	AP	0	1
5	Ae	0	1
9	Ai	0	1
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AA	1584	U	C1'-N1	5.36	1.56	1.48
23	AA	1065	A	N9-C4	-5.35	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AA	1186	A	N9-C4	-5.08	1.34	1.37

The worst 5 of 345 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AB	87	C	N1-C2-O2	12.65	126.49	118.90
24	AB	87	C	C2-N1-C1'	12.12	132.13	118.80
23	AA	576	U	C2-N1-C1'	11.98	132.08	117.70
1	Aa	745	U	OP1-P-O3'	-11.40	80.13	105.20
23	AA	2150	A	N7-C8-N9	10.80	119.20	113.80

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	Ae	76	ARG	Peptide
9	Ai	108	ARG	Peptide
12	Al	126	GLY	Peptide
19	As	80	PHE	Peptide
20	At	58	ASP	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	Aa	32969	0	16595	0	0
2	Ab	1819	0	1886	0	0
3	Ac	1501	0	1464	0	0
4	Ad	1497	0	1449	0	0
5	Ae	1145	0	1202	0	0
6	Af	778	0	775	0	0
7	Ag	1161	0	1165	0	0
8	Ah	1026	0	1078	0	0
9	Ai	922	0	890	0	0
10	Aj	752	0	775	0	0
11	Ak	810	0	784	0	0
12	Al	1037	0	1091	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	Am	727	0	674	0	0
14	An	487	0	492	0	0
15	Ao	723	0	749	0	0
16	Ap	694	0	709	0	0
17	Aq	621	0	615	0	0
18	Ar	445	0	482	0	0
19	As	636	0	626	0	0
20	At	591	0	616	0	0
21	Au	400	0	407	0	0
22	Av	1333	0	1349	0	0
23	AA	62277	0	31301	700	0
24	AB	2445	0	1241	14	0
25	AC	2094	0	2203	86	0
26	AD	1627	0	1667	56	0
27	AE	1572	0	1619	39	0
28	AF	1325	0	1342	52	0
29	AG	1263	0	1225	24	0
30	AH	1143	0	1134	16	0
31	AI	918	0	980	25	0
32	AJ	1086	0	1125	27	0
33	AK	1071	0	1123	23	0
34	AL	932	0	983	26	0
35	AM	891	0	925	21	0
36	AN	889	0	937	15	0
37	AO	942	0	1014	31	0
38	AP	790	0	830	12	0
39	AQ	854	0	914	17	0
40	AR	715	0	748	21	0
41	AS	770	0	809	17	0
42	AT	722	0	766	5	0
43	AU	622	0	643	8	0
44	AV	445	0	466	6	0
45	AW	541	0	563	8	0
46	AX	449	0	491	8	0
47	AY	370	0	243	3	0
48	AZ	360	0	358	22	0
49	A1	390	0	394	7	0
50	A2	367	0	415	10	0
51	A3	521	0	586	10	0
52	A4	295	0	340	14	0
53	AA	199	0	0	2	0
53	AB	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	AC	2	0	0	0	0
53	AU	1	0	0	0	0
53	AZ	1	0	0	0	0
All	All	140965	0	93258	923	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 8.

The worst 5 of 923 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)
23:AA:2717:A:N7	34:AL:3:TYR:CD1	1.68	1.60
23:AA:1533:A:N7	25:AC:96:TYR:C	1.79	1.36
23:AA:2717:A:N7	34:AL:3:TYR:CE1	1.94	1.36
23:AA:581:A:OP1	30:AH:1:MET:CE	1.72	1.35
23:AA:581:A:OP1	30:AH:1:MET:HE1	1.18	1.25

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Ab	224/255 (88%)	213 (95%)	11 (5%)	0	100	100
3	Ac	200/217 (92%)	177 (88%)	23 (12%)	0	100	100
4	Ad	196/200 (98%)	170 (87%)	26 (13%)	0	100	100
5	Ae	154/166 (93%)	147 (96%)	7 (4%)	0	100	100
6	Af	93/98 (95%)	85 (91%)	8 (9%)	0	100	100
7	Ag	150/156 (96%)	144 (96%)	6 (4%)	0	100	100
8	Ah	129/132 (98%)	121 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	Ai	125/132 (95%)	112 (90%)	13 (10%)	0	100	100
10	Aj	95/102 (93%)	88 (93%)	7 (7%)	0	100	100
11	Ak	112/129 (87%)	93 (83%)	19 (17%)	0	100	100
12	Al	133/137 (97%)	118 (89%)	15 (11%)	0	100	100
13	Am	100/121 (83%)	90 (90%)	10 (10%)	0	100	100
14	An	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
15	Ao	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
16	Ap	87/91 (96%)	78 (90%)	9 (10%)	0	100	100
17	Aq	78/87 (90%)	72 (92%)	6 (8%)	0	100	100
18	Ar	52/80 (65%)	51 (98%)	1 (2%)	0	100	100
19	As	78/92 (85%)	69 (88%)	9 (12%)	0	100	100
20	At	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
21	Au	50/58 (86%)	48 (96%)	2 (4%)	0	100	100
22	Av	158/190 (83%)	149 (94%)	9 (6%)	0	100	100
25	AC	272/277 (98%)	257 (94%)	15 (6%)	0	100	100
26	AD	213/220 (97%)	194 (91%)	19 (9%)	0	100	100
27	AE	204/207 (99%)	192 (94%)	12 (6%)	0	100	100
28	AF	173/179 (97%)	142 (82%)	31 (18%)	0	100	100
29	AG	173/178 (97%)	155 (90%)	18 (10%)	0	100	100
30	AH	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
31	AI	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
32	AJ	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
33	AK	135/144 (94%)	127 (94%)	8 (6%)	0	100	100
34	AL	118/122 (97%)	114 (97%)	4 (3%)	0	100	100
35	AM	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
36	AN	112/116 (97%)	99 (88%)	13 (12%)	0	100	100
37	AO	114/118 (97%)	109 (96%)	5 (4%)	0	100	100
38	AP	100/102 (98%)	93 (93%)	6 (6%)	1 (1%)	18	51
39	AQ	110/117 (94%)	106 (96%)	4 (4%)	0	100	100
40	AR	87/91 (96%)	81 (93%)	6 (7%)	0	100	100
41	AS	101/105 (96%)	89 (88%)	12 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	AT	92/217 (42%)	87 (95%)	5 (5%)	0	100	100
43	AU	80/94 (85%)	72 (90%)	8 (10%)	0	100	100
44	AV	56/62 (90%)	53 (95%)	3 (5%)	0	100	100
45	AW	65/73 (89%)	58 (89%)	7 (11%)	0	100	100
46	AX	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	AY	57/84 (68%)	45 (79%)	12 (21%)	0	100	100
48	AZ	46/57 (81%)	40 (87%)	6 (13%)	0	100	100
49	A1	45/49 (92%)	44 (98%)	1 (2%)	0	100	100
50	A2	41/45 (91%)	39 (95%)	2 (5%)	0	100	100
51	A3	62/66 (94%)	57 (92%)	5 (8%)	0	100	100
52	A4	35/37 (95%)	35 (100%)	0	0	100	100
All	All	5508/6027 (91%)	5052 (92%)	455 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	AP	51	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	
2	Ab	196/221 (89%)	196 (100%)	0	100	100
3	Ac	138/175 (79%)	138 (100%)	0	100	100
4	Ad	147/175 (84%)	146 (99%)	1 (1%)	87	97
5	Ae	118/131 (90%)	118 (100%)	0	100	100
6	Af	80/86 (93%)	80 (100%)	0	100	100
7	Ag	118/132 (89%)	118 (100%)	0	100	100
8	Ah	111/113 (98%)	109 (98%)	2 (2%)	64	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Ai	86/109 (79%)	84 (98%)	2 (2%)	56	85
10	Aj	81/91 (89%)	80 (99%)	1 (1%)	75	93
11	Ak	82/104 (79%)	82 (100%)	0	100	100
12	Al	111/119 (93%)	110 (99%)	1 (1%)	82	95
13	Am	62/104 (60%)	61 (98%)	1 (2%)	68	90
14	An	48/53 (91%)	46 (96%)	2 (4%)	34	69
15	Ao	77/81 (95%)	76 (99%)	1 (1%)	73	93
16	Ap	73/77 (95%)	71 (97%)	2 (3%)	50	82
17	Aq	65/82 (79%)	65 (100%)	0	100	100
18	Ar	48/68 (71%)	48 (100%)	0	100	100
19	As	67/80 (84%)	67 (100%)	0	100	100
20	At	61/69 (88%)	61 (100%)	0	100	100
21	Au	40/54 (74%)	40 (100%)	0	100	100
22	Av	147/173 (85%)	143 (97%)	4 (3%)	50	82
25	AC	221/224 (99%)	221 (100%)	0	100	100
26	AD	173/177 (98%)	172 (99%)	1 (1%)	89	97
27	AE	168/169 (99%)	167 (99%)	1 (1%)	89	97
28	AF	141/158 (89%)	139 (99%)	2 (1%)	71	91
29	AG	124/155 (80%)	122 (98%)	2 (2%)	68	90
30	AH	122/123 (99%)	121 (99%)	1 (1%)	85	96
31	AI	100/100 (100%)	99 (99%)	1 (1%)	80	95
32	AJ	109/112 (97%)	107 (98%)	2 (2%)	64	89
33	AK	108/119 (91%)	107 (99%)	1 (1%)	82	95
34	AL	96/102 (94%)	95 (99%)	1 (1%)	80	95
35	AM	86/95 (90%)	83 (96%)	3 (4%)	41	75
36	AN	93/102 (91%)	92 (99%)	1 (1%)	78	94
37	AO	96/98 (98%)	95 (99%)	1 (1%)	80	95
38	AP	84/86 (98%)	84 (100%)	0	100	100
39	AQ	89/94 (95%)	88 (99%)	1 (1%)	78	94
40	AR	78/82 (95%)	76 (97%)	2 (3%)	51	83
41	AS	81/90 (90%)	80 (99%)	1 (1%)	75	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	AT	78/190 (41%)	78 (100%)	0	100	100
43	AU	63/75 (84%)	60 (95%)	3 (5%)	30	64
44	AV	44/52 (85%)	43 (98%)	1 (2%)	56	85
45	AW	58/66 (88%)	58 (100%)	0	100	100
46	AX	52/53 (98%)	52 (100%)	0	100	100
47	AY	23/75 (31%)	23 (100%)	0	100	100
48	AZ	35/50 (70%)	35 (100%)	0	100	100
49	A1	44/47 (94%)	44 (100%)	0	100	100
50	A2	39/40 (98%)	39 (100%)	0	100	100
51	A3	55/57 (96%)	55 (100%)	0	100	100
52	A4	35/35 (100%)	34 (97%)	1 (3%)	48	81
All	All	4451/5123 (87%)	4408 (99%)	43 (1%)	81	95

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	AF	69	LYS
31	AI	122	LEU
43	AU	61	ARG
28	AF	125	ARG
29	AG	41	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
25	AC	230	HIS
28	AF	127	ASN
48	AZ	19	HIS
26	AD	128	GLN
26	AD	167	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Aa	1537/1555 (98%)	461 (29%)	0
23	AA	2895/2923 (99%)	794 (27%)	28 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	AB	113/115 (98%)	16 (14%)	0
All	All	4545/4593 (98%)	1271 (27%)	28 (0%)

5 of 1271 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Aa	6	U
1	Aa	8	G
1	Aa	9	A
1	Aa	10	G
1	Aa	23	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	AA	711	G
23	AA	1024	A
23	AA	2568	A
23	AA	840	C
23	AA	987	U

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 205 ligands modelled in this entry, 205 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	AA	6
24	AB	1
1	Aa	1
13	Am	1

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	2207:U	O3'	2208:A	P	9.06
1	AA	2132:A	O3'	2133:G	P	8.44
1	AA	1096:C	O3'	1097:U	P	6.77
1	Aa	465:U	O3'	466:G	P	3.97
1	AA	1153:C	O3'	1154:G	P	3.61