



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 14, 2018 – 08:30 PM EDT

PDB ID : 6FXC
Title : The cryo-EM structure of hibernating 100S ribosome dimer from pathogenic *Staphylococcus aureus*
Authors : Matzov, D.; Aibara, S.; Zimmerman, E.; Bashan, A.; Kidmose, R.; Amunts, A.; Yonath, A.
Deposited on : 2018-03-08
Resolution : 6.76 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-20030736

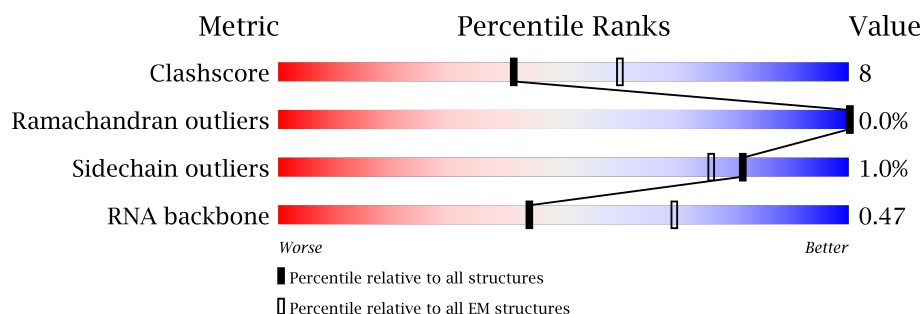
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.76 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.




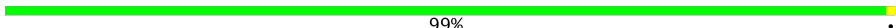
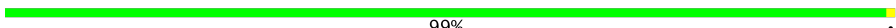
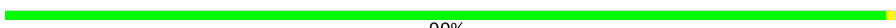









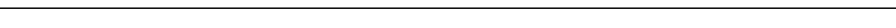

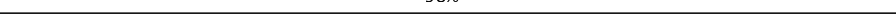
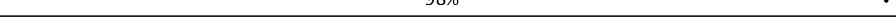


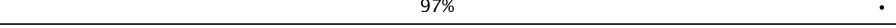
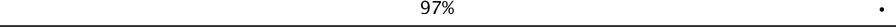
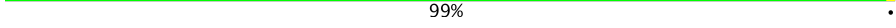
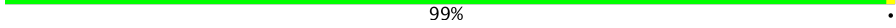
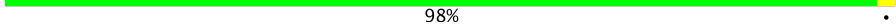
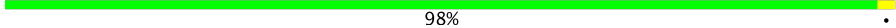
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	1539	68% 30% .
1	Ba	1539	68% 30% .
2	Ab	226	99% .
2	Bb	226	99% .
3	Ac	202	100%
3	Bc	202	100%
4	Ad	198	99% .
4	Bd	198	99% .

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Mol	Chain	Length	Quality of chain
5	Ae	156	 99% .
5	Be	156	 99% .
6	Af	95	 99% .
6	Bf	95	 99% .
7	Ag	152	 100%
7	Bg	152	 100%
8	Ah	131	 98% .
8	Bh	131	 98% .
9	Ai	127	 97% .
9	Bi	127	 97% .
10	Aj	97	 99% .
10	Bj	97	 99% .
11	Ak	114	 100%
11	Bk	114	 100%
12	Al	135	 98% .
12	Bl	135	 98% .
13	Am	121	 85% . 14%
13	Bm	121	 85% . 14%
14	An	60	 97% .
14	Bn	60	 97% .
15	Ao	88	 99% .
15	Bo	88	 99% .
16	Ap	89	 98% .
16	Bp	89	 98% .
17	Aq	80	 100%











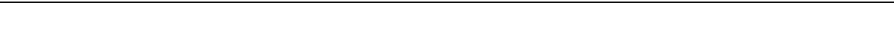

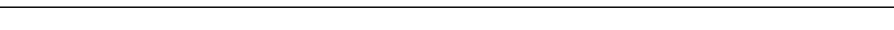
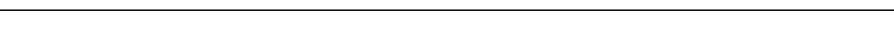











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Mol	Chain	Length	Quality of chain
17	Bq	80	100%
18	Ar	54	98%
18	Br	54	98%
19	As	80	99%
19	Bs	80	99%
20	At	81	99%
20	Bt	81	99%
21	Au	52	100%
21	Bu	52	100%
22	Av	190	82% 15%
22	Bv	190	82% 15%
23	AA	2923	55% 34% 10% ..
23	BA	2923	56% 33% 10% ..
24	AB	115	70% 24% ..
24	BB	115	71% 24% ..
25	AC	274	74% 25%
25	BC	274	76% 24%
26	AD	215	75% 25%
26	BD	215	74% 26%
27	AE	206	83% 17%
27	BE	206	83% 17%
28	AF	175	79% 21%
28	BF	175	81% 19%
29	AG	175	83% 16% .
29	BG	175	86% 14% .










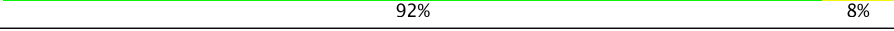



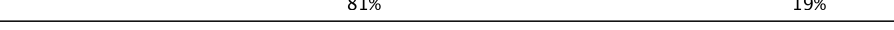







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Mol	Chain	Length	Quality of chain
30	AH	145	 90% 10%
30	BH	145	 90% 10%
31	AI	122	 68% 31% .
31	BI	122	 68% 31% .
32	AJ	146	 76% 24%
32	BJ	146	 76% 24%
33	AK	137	 77% 23% .
33	BK	137	 79% 20% .
34	AL	120	 87% 13%
34	BL	120	 87% 13%
35	AM	119	 76% 21% .
35	BM	119	 75% 23% .
36	AN	114	 81% 19%
36	BN	114	 80% 20%
37	AO	116	 84% 16% .
37	BO	116	 84% 16% .
38	AP	102	 87% 13%
38	BP	102	 87% 13%
39	AQ	112	 84% 15% .
39	BQ	112	 85% 14% .
40	AR	89	 81% 19%
40	BR	89	 81% 19%
41	AS	103	 81% 19%
41	BS	103	 81% 19%
42	AT	94	 91% 9%

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Mol	Chain	Length	Quality of chain
42	BT	94	 89% 11%
43	AU	82	 83% 16% .
43	BU	82	 80% 18% .
44	AV	58	 86% 12% .
44	BV	58	 86% 12% .
45	AW	67	 84% 16%
45	BW	67	 85% 15%
46	AX	58	 83% 17%
46	BX	58	 83% 17%
47	AY	59	 92% 8%
47	BY	59	 92% 8%
48	AZ	48	 79% 21%
48	BZ	48	 81% 19%
49	A1	47	 81% 19%
49	B1	47	 83% 17%
50	A2	43	 81% 19%
50	B2	43	 84% 16%
51	A3	64	 84% 16%
51	B3	64	 84% 16%
52	A4	37	 62% 35% .
52	B4	37	 65% 32% .

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 281510 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 Ribosomal RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	1539	Total	C	N	O	P	0	0
			32969	14719	6017	10694	1539		
1	Ba	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
			1813	1156	314	335	8		
2	Bb	226	Total	C	N	O	S	0	0
			1813	1156	314	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		
3	Bc	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		
4	Bd	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		
5	Be	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		
6	Bf	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		
7	Bg	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		
8	Bh	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		
9	Bi	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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bj	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		
11	Bk	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		
12	Bl	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	S	0	0
			727	453	139	135			
13	Bm	104	Total	C	N	O	S	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		
14	Bn	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		
15	Bo	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		
16	Bp	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	0	0
			621	392	112	117		
17	Bq	80	Total	C	N	O	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
			446	284	86	74	2		
18	Br	54	Total	C	N	O	S	0	0
			446	284	86	74	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		
19	Bs	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		
20	Bt	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		
21	Bu	52	Total	C	N	O	0	0
			400	249	79	72		

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

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

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

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

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

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	BD	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		
27	BE	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		
28	BF	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		
29	BG	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		
30	BH	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		
31	BI	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		
32	BJ	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		
33	BK	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		
34	BL	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		
35	BM	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	0	0
			889	563	175	151		
36	BN	114	Total	C	N	O	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		
37	BO	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		
38	BP	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		
39	BQ	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		
40	BR	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		
41	BS	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			

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Mol	Chain	Residues	Atoms				AltConf	Trace
42	BT	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		
43	BU	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		
44	BV	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		
45	BW	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		
46	BX	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		
47	BY	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		
48	BZ	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		
49	B1	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		
50	B2	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		
51	B3	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

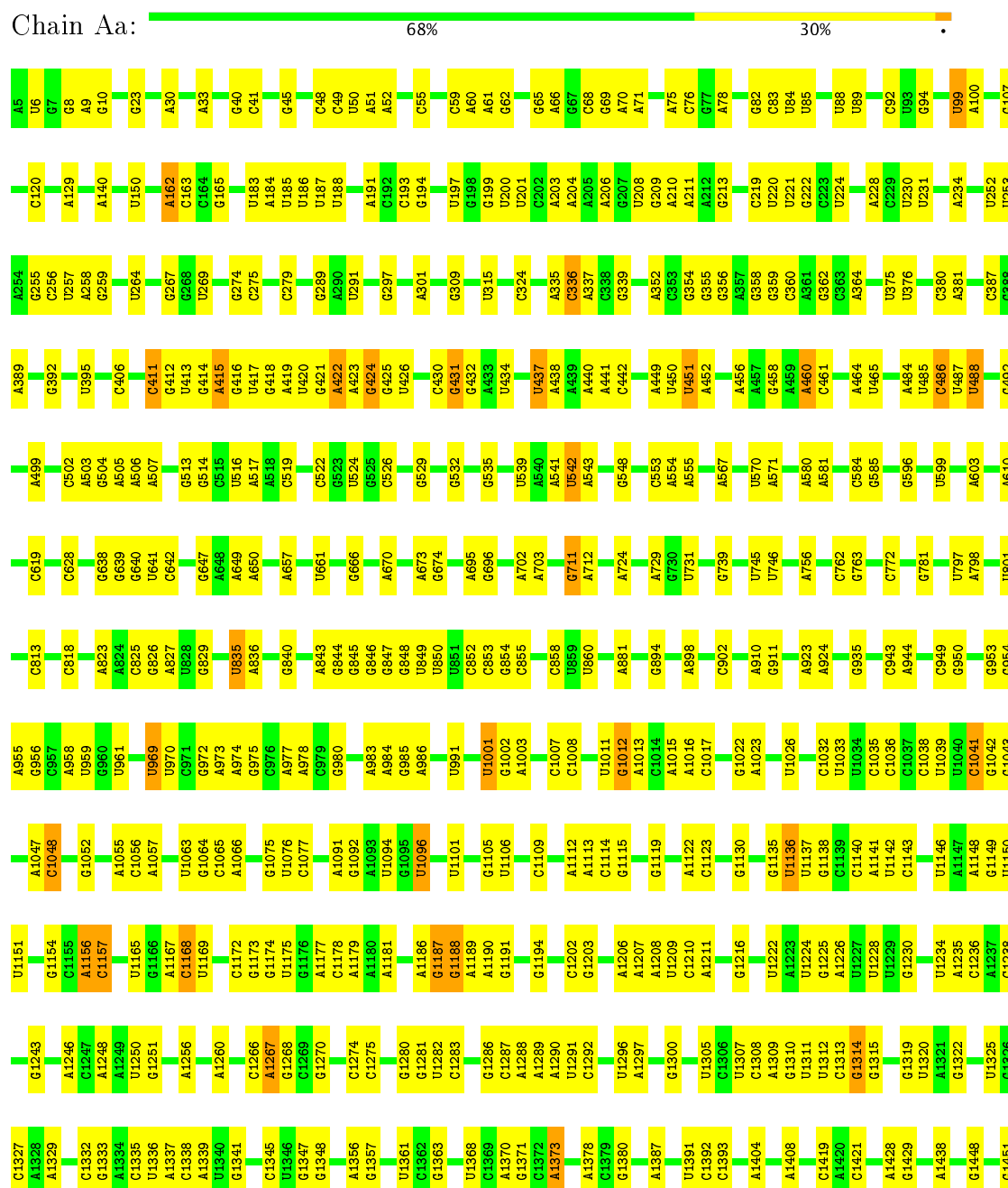
- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	A4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		
52	B4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

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.

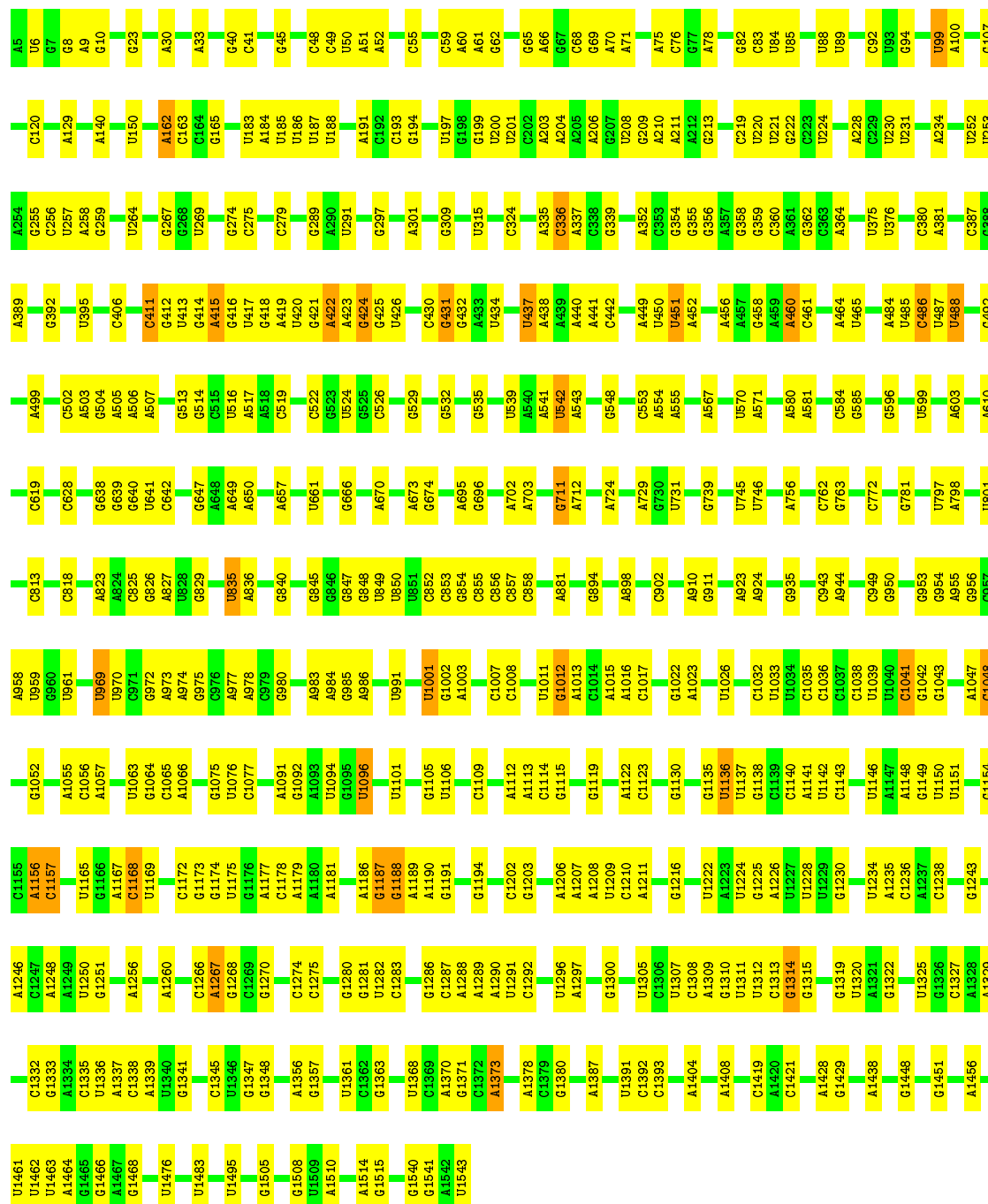
• Molecule 1: Ribosomal RNA 16S





• Molecule 1: Ribosomal RNA 16S

Chain Ba: 68% 30%



• Molecule 2: 30S ribosomal protein S2

Chain Ab: 99%



- Molecule 2: 30S ribosomal protein S2

Chain Bb:  99%



- Molecule 3: 30S ribosomal protein S3

Chain Ac:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: 30S ribosomal protein S3

Chain Bc:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: 30S ribosomal protein S4

Chain Ad:  99%



- Molecule 4: 30S ribosomal protein S4

Chain Bd:  99%



- Molecule 5: 30S ribosomal protein S5

Chain Ae:  99%



- Molecule 5: 30S ribosomal protein S5

Chain Be:  99%



- Molecule 6: 30S ribosomal protein S6

Chain Af:  99%



- Molecule 6: 30S ribosomal protein S6

Chain Bf:  99%



- Molecule 7: 30S ribosomal protein S7

Chain Ag:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: 30S ribosomal protein S7

Chain Bg:  100%

There are no outlier residues recorded for this chain.

- Molecule 8: 30S ribosomal protein S8

Chain Ah:  98%



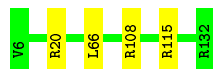
- Molecule 8: 30S ribosomal protein S8

Chain Bh:  98%



- Molecule 9: 30S ribosomal protein S9

Chain Ai:  97%



- Molecule 9: 30S ribosomal protein S9

Chain Bi:  97%

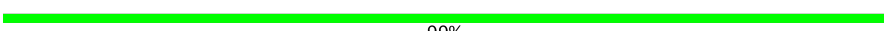


- Molecule 10: 30S ribosomal protein S10

Chain Aj:  99%



- Molecule 10: 30S ribosomal protein S10

Chain Bj:  99%



- Molecule 11: 30S ribosomal protein S11

Chain Ak:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: 30S ribosomal protein S11

Chain Bk:  100%

There are no outlier residues recorded for this chain.

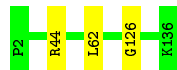
- Molecule 12: 30S ribosomal protein S12

Chain Al:  98%



- Molecule 12: 30S ribosomal protein S12

Chain Bl:  98%



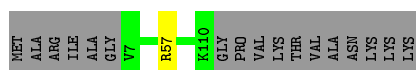
- Molecule 13: 30S ribosomal protein S13

Chain Am:  85% 14%



- Molecule 13: 30S ribosomal protein S13

Chain Bm:  85% 14%



- Molecule 14: 30S ribosomal protein S14 type Z

Chain An: 97%



- Molecule 14: 30S ribosomal protein S14 type Z

Chain Bn: 97%



- Molecule 15: 30S ribosomal protein S15

Chain Ao: 99%



- Molecule 15: 30S ribosomal protein S15

Chain Bo: 99%



- Molecule 16: 30S ribosomal protein S16

Chain Ap: 98%



- Molecule 16: 30S ribosomal protein S16

Chain Bp: 98%



- Molecule 17: 30S ribosomal protein S17

Chain Aq: 100%

There are no outlier residues recorded for this chain.

- Molecule 17: 30S ribosomal protein S17

Chain Bq:  100%

There are no outlier residues recorded for this chain.

- Molecule 18: 30S ribosomal protein S18

Chain Ar:  98%



- Molecule 18: 30S ribosomal protein S18

Chain Br:  98%



- Molecule 19: 30S ribosomal protein S19

Chain As:  99%



- Molecule 19: 30S ribosomal protein S19

Chain Bs:  99%



- Molecule 20: 30S ribosomal protein S20

Chain At:  99%



- Molecule 20: 30S ribosomal protein S20

Chain Bt:  99%



- Molecule 21: 30S ribosomal protein S21

Chain Au:  100%


There are no outlier residues recorded for this chain.

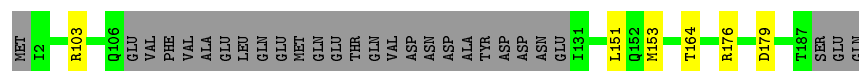
- Molecule 21: 30S ribosomal protein S21

Chain Bu: 100%


There are no outlier residues recorded for this chain.

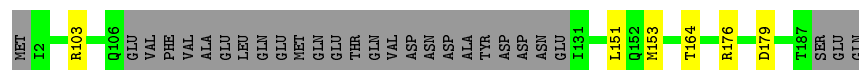
- Molecule 22: Ribosome hibernation promotion factor

Chain Av:  82% 15%



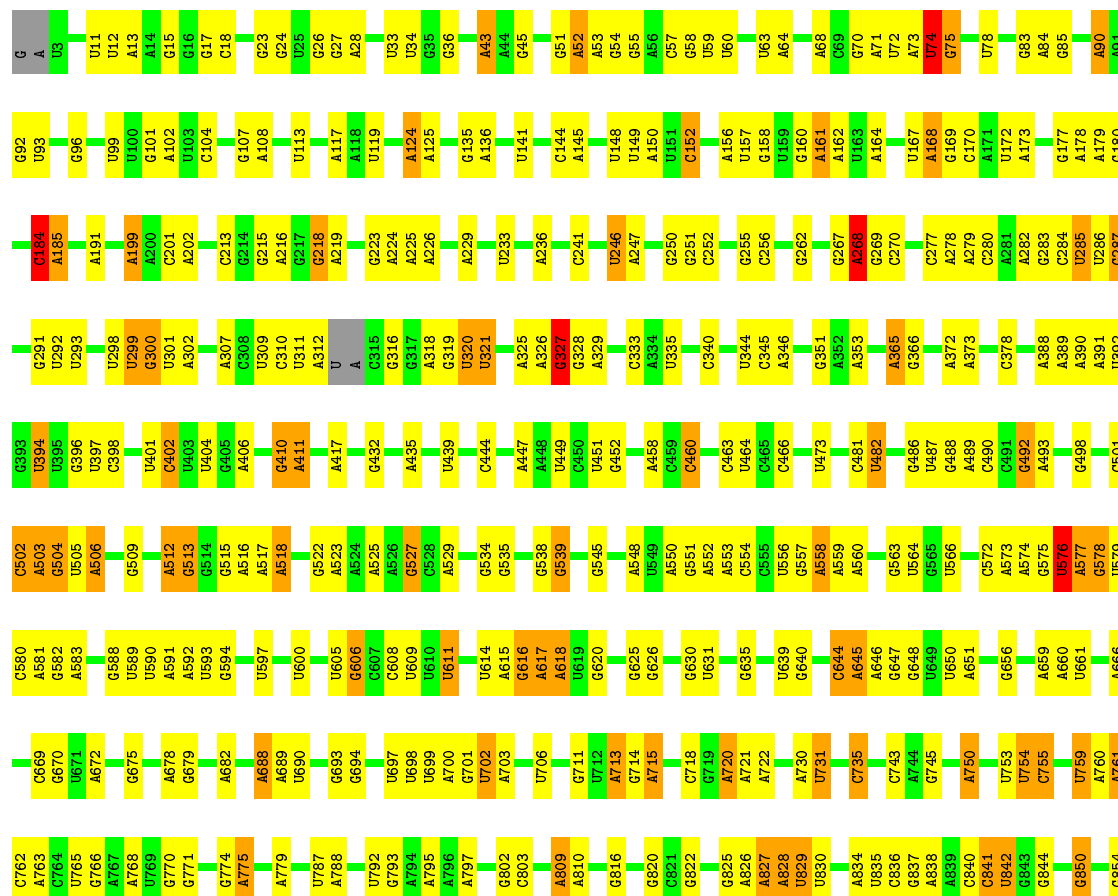
- Molecule 22: Ribosome hibernation promotion factor

Chain By:  82% • 15%

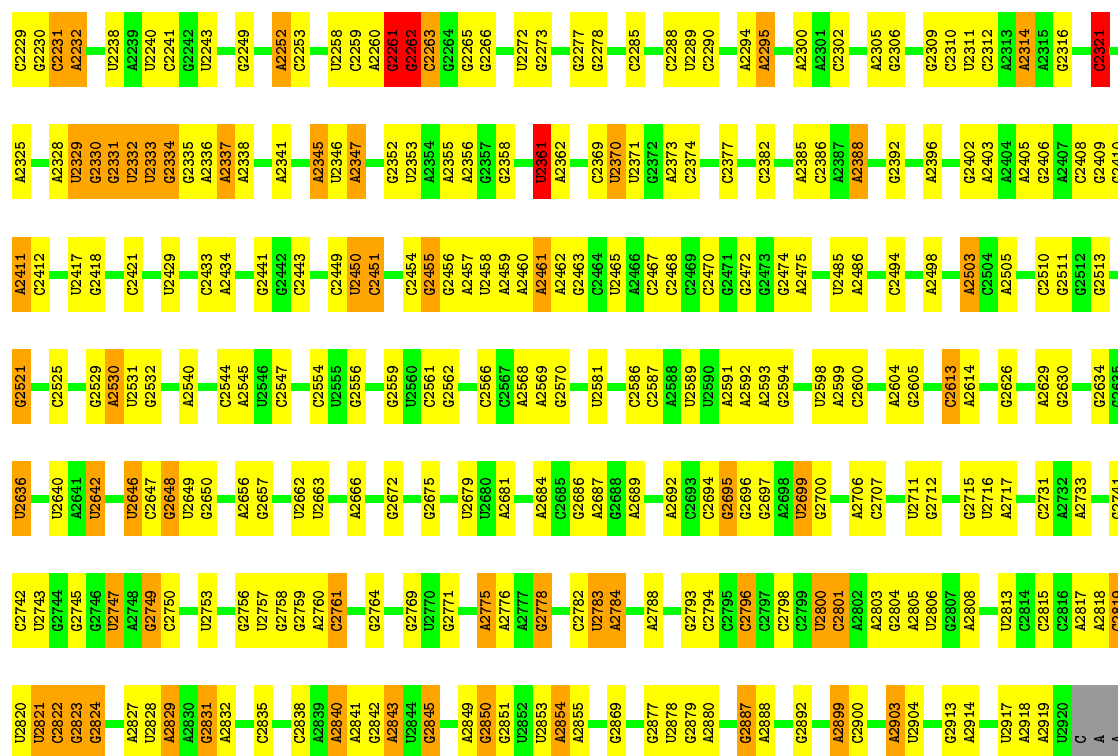


- Molecule 23: Ribosomal RNA 23S

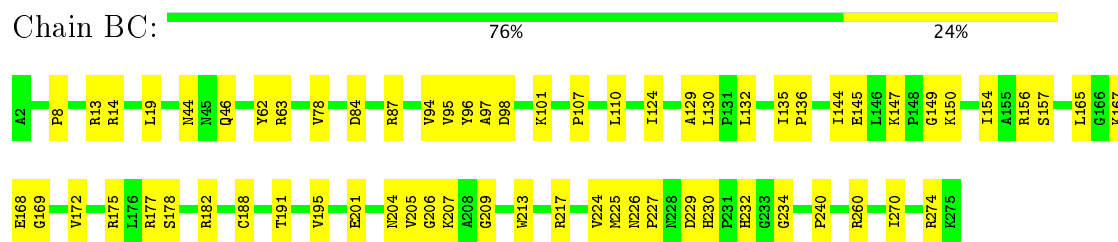
Chain AA:  55% 34% 10%



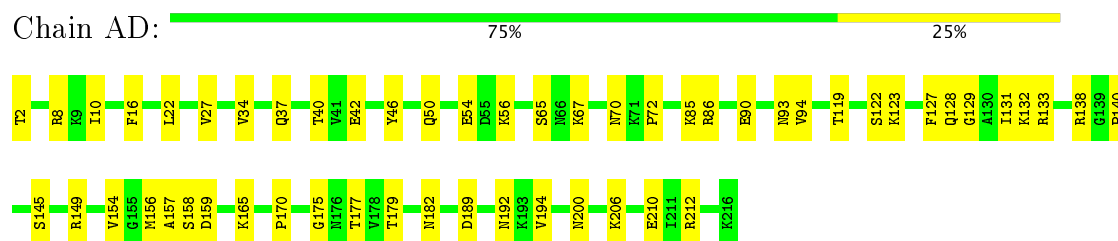
[illegible]



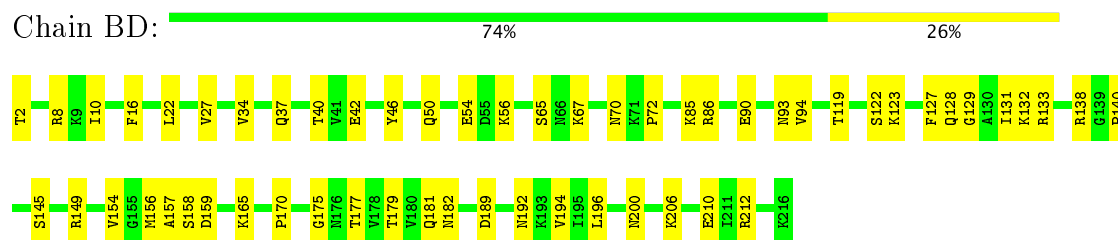
G2083	C1985	U1899	A1811	G1710	A1616	U1540	A1471	U1386	G1115	A1187	A955	C870	G774
G2084	G1986	G1900	A1812	A1710	A1617	U1540	C1472	C1387	C1116	A1190	A956	U871	A775
A2085	G1987	C1901	A1813	A1713	U1625	G1550	A1475	U1388	A1117	C1299	C957	U872	
A2086	G1988	G1902	A1814	G1718	A1626	U1551	G1476	U1389	G1118	C1197	C960	U873	A779
G2088	G1991	A1903	A1815	C1719	G1627	U1552	U1477	G1392	C1120	U1043	A961	A874	
A2089	G1992	A1904	A1816	G1719	A1628	A1553	A1478	U1393	G1198	U1044	A962	C878	A788
	G1993	U1907	G1817	A1726	A1629	A1554	G1479	G1394	A1121	A1045	A963	U879	
U2095	G1994	A1908	G1818	G1726	A1630	G1555	A1480	G1395	C1123	G1046	U964		
G2096	G1995	C1909	A1819	G1731	G1631	G1556	A1481	A1396	G1309	G1047	C882	G793	
G2097	A1996	G1910	U1732	U1732	A1632	C1557	U1482	G1397	A1311	U1048	C967	A794	
A2098	A1997	U1825	U1826	U1826	A1633	C1558	A1483		U1125	C1049	A968	G890	
	G1998	U1827	U1827	U1737	A1634	G1559	G1484	G1401	U1126		A969	A891	A795
U2103	G1999	U1913	U1828	C1738	A1635	A1560	G1485	A1402	U1127	U1055	U892	U890	A796
	G2000	C1914	A1829	G1739	U1636	G1561	C1486	C1403	A1128	A1056	A971	A891	A797
G2107	G2001	G1917	G1740	G1740		U1562	G1487	G1316	C1213	U1070	A972	U895	G802
U2108	U2002	C1918	G1743	G1743	G1639	U1563	A1488	G1320	U1214	A1130	A973	U896	C903
A2109	U2003	G1918	U1834	A1744	U1640	G1564	A1489	G1405	U1215	G1131	U974	U897	
G2110	U2018	G1930	U1835	A1745	G1641	U1565	G1490	A1407	U1216	U1063	A975	U901	
C2111	G2019	G1931	U1836	G1746	C1642	G1566	C1491	U1325	U1217	A1064	U976	A902	
C2112	U2020	U1932	G1746	G1746	C1643	G1492	G1499	C1326	G1133	U1065	A977	A902	
A2115	G2021	G1838	G1747	G1747	C1644	U1569	U1493	A1410	C1136	G1067	G903	G903	G816
U2116	U2022	G1839	G1750	U1750	A1647	G1570	G1494	U1337	U1224	G1137	A985	G904	
C2117	C2023	U1843	U1751	U1751	G1648	G1571	C1495	U1338	G1225	U1068	U986	U985	G820
U2118	A2024	G1844	A1752	A1752	C1649	U1572	G1496	U1339	G1226	G1069	U987	A906	G821
U2119	G2025	U1845	U1753	U1753	A1651	A1575	U1498	A1341	U1242	A1071	C988	G922	
G2120	G2026	U1846	U1754	A1754	A1653	A1576	G1500	U1421	A1243	G1075	G991	G914	
	A2030	U1847	G1759	G1759	A1654	A1578	G1501	A1422	G1245	A1076	A992	A921	
C2126	U2037	G1852	G1760	G1760		C1579	A1502	C1423	U1250	U1077	G997	G918	
	G2038	U	G1761	G1761	A1658	A1580	U1503	A1424	C1148	G1078	G919	U829	
C2129	G2039	A	U1581	U1762	U1581	U1581	U1504	U1349	U1149	A920	A920	U830	
C2134	U2043	A1855	U1763	G1763	C1661	U1582	G1508	U1431	G1257	G1086	G1000	C921	A833
U2135	U2043	A1856	U1764	A1764	A1662	G1583	A1432	U1432	A1258	C1087	A1001	G922	A834
U2136		C1857	A1765	A1765	G1663	U1584	G1509		U1152	C1088	U1002	A923	
	U2046	C1860				G1585	U1510	G1354	G1261	C1089	A1003		
A2139	A2047	U1861	C1768		A1666	U1586	C1511	A1440	A1264	A1090	G926	C936	
C2140	G2048	G1862	A1771	A1771	G1675	U1588	U1512	A1443	A1358	G1091	G927	A838	
U2049	U2049	C1863	G1772	G1772	U1675	U1589	A1514	C1445	G1265	A1004	G928	C937	
	G2056	A1864			A1679	C1590	G1515	U1446	G1266	U1011	C929	A839	
A2144	A2057	U1875	C1781	C1781		G1591	U1516	A1447	A1267	C	C	C940	
U2145	G1955	A1876	U1875	U1875	C1682	A1592	A1517	C1367	C1160	A1018	U	C941	
A2058	G2058	G1956	U1876	G1790	U1683	G1593	G1518	C1368	A1275	A1019	C	U	U842
G2147	G2059	G1957	U1877	G1791	A1684	U1594	U1519	G1369	G1276	G1020	U	U	G850
A2060	G2060	U1958	U1878	G1791		G1595	U1520	U1451	C1277	A1021			
U2061	U2061	A1959	U1879		C1596	C1596	A1521	C1370	G1278	U1011	G1022	C	
G2150	G2062	G1960	A1880	A1796	A1690	G1596	A1521	U1452	U102	U102	G1022	C	G854
				G1797	G1691	U1597	G1522	C1483	G1166	G103	A1023	G937	U855
G2152	C2070	A1963	U1885	A1800	C1692	U1598		U1454	U1104	U104	A1024		U856
G2154		A1886	A1886		G1693	G1599	U1525	G1376	U1174	U105	A1025	U940	C957
C2073	G2073	A1965				A1600	G1526	U1377	G1266	G106	C1026	A941	
G2074	G2074	U1966	G1803	G1803	G1697	U1601	A1527	U1378	U1287	G107	A1027	C942	C959
G2075	G2075	U1967	U1804	U1804				U1457	U1457	G107	C108	C943	U860
A2076	A2076	A1968	U1805	U1805	U1701	A1605	U1532	A1458	G1288	U1177	C1031		C861
U2159	U2159	C1969	U1806	U1806	C1702	C1606	A1533	A1459	G1380	C1178	U1110	G944	C962
G2079	G2079	G1894	A1807	A1807	U1703	G1534	U1534	U1381	G1290	C1179	A1111	C949	G863
A2161	G2080	U1970	U1808	U1808	G1613	G1535	A1292	G1383	A1291	A1112	A1034	C1035	
G2162	A2081	U1897	U1809	U1809	A1708	C1536	G1384	G1384	A1292	U1185	C1036	U1293	A868
		C1908	U1809	U1809	A1709	A1614	A1537	G1465	G1294	A1142	A952	A1037	



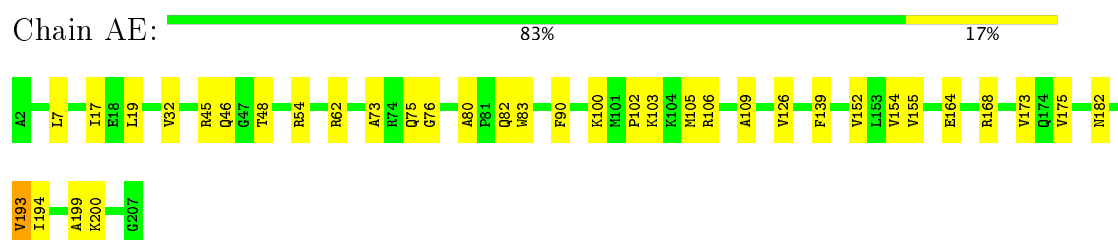
- Molecule 26: 50S ribosomal protein L3



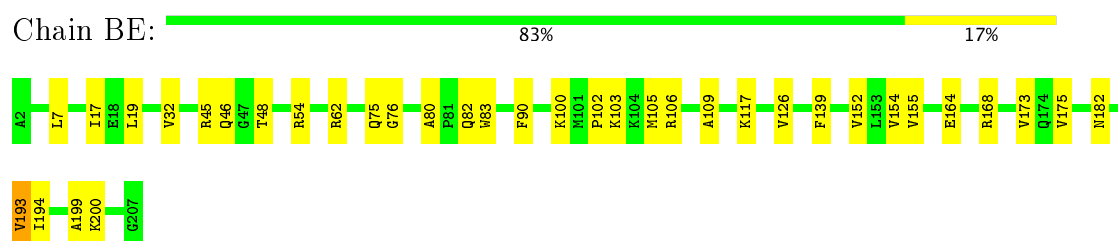
- Molecule 26: 50S ribosomal protein L3



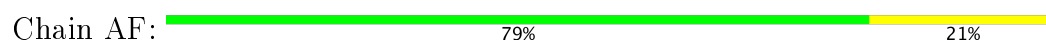
- Molecule 27: 50S ribosomal protein L4

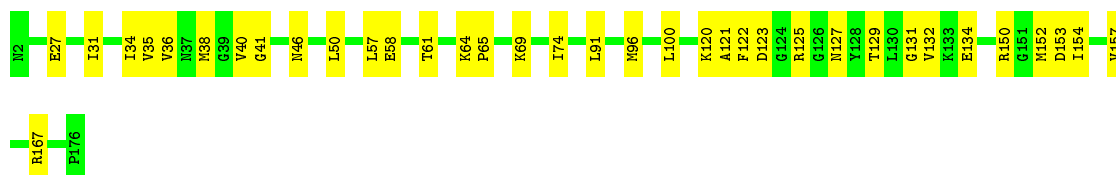


- Molecule 27: 50S ribosomal protein L4



- Molecule 28: 50S ribosomal protein L5





- Molecule 28: 50S ribosomal protein L5

Chain BF: 81% 19%



- Molecule 29: 50S ribosomal protein L6

Chain AG: 83% 16%



- Molecule 29: 50S ribosomal protein L6

Chain BG: 86% 14%



- Molecule 30: 50S ribosomal protein L13

Chain AH: 90% 10%



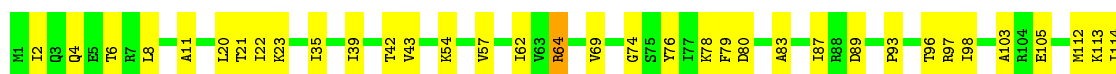
- Molecule 30: 50S ribosomal protein L13

Chain BH: 90% 10%

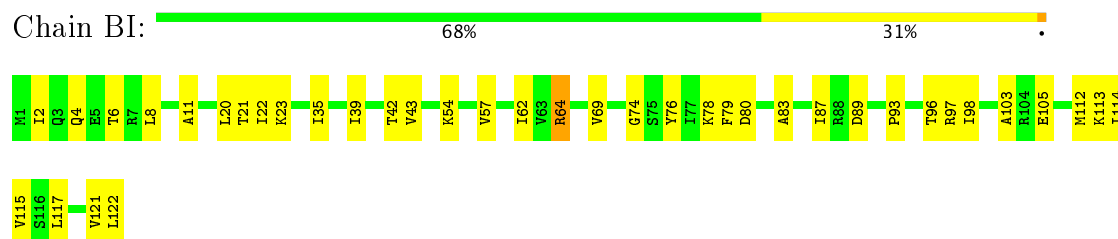


- Molecule 31: 50S ribosomal protein L14

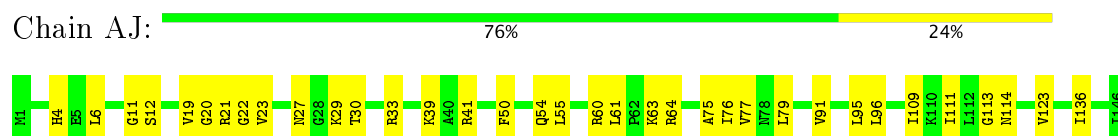
Chain AI: 68% 31%



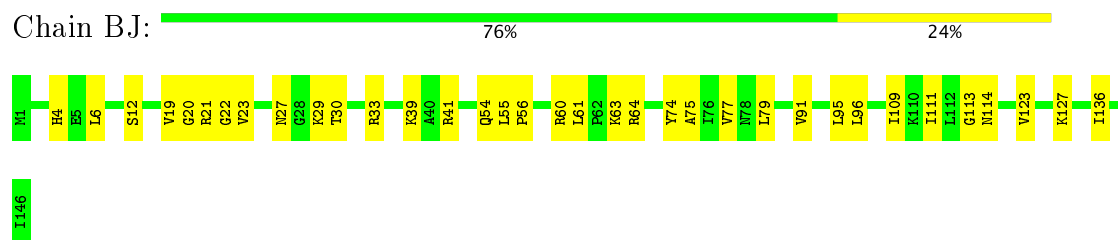
- Molecule 31: 50S ribosomal protein L14



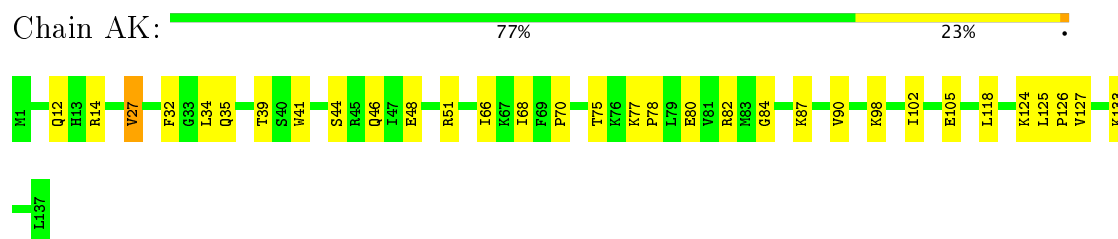
- Molecule 32: 50S ribosomal protein L15



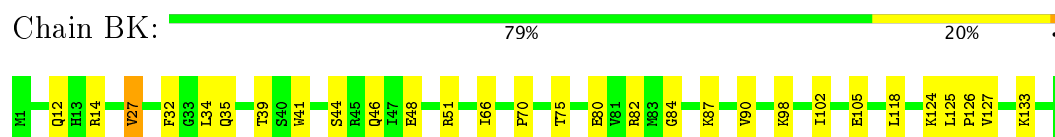
- Molecule 32: 50S ribosomal protein L15



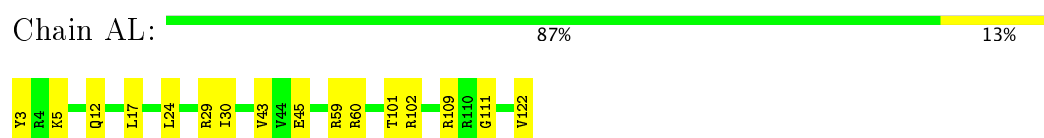
- Molecule 33: 50S ribosomal protein L16



- Molecule 33: 50S ribosomal protein L16

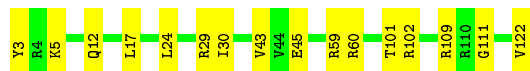


- Molecule 34: 50S ribosomal protein L17




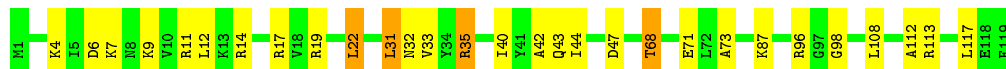
- Molecule 34: 50S ribosomal protein L17

Chain BL:  87% 13%




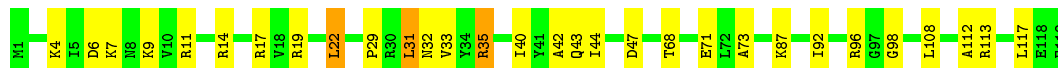
- Molecule 35: 50S ribosomal protein L18

Chain AM:  76% 21% .




- Molecule 35: 50S ribosomal protein L18

Chain BM:  75% 23% .




- Molecule 36: 50S ribosomal protein L19

Chain AN:  81% 19%




- Molecule 36: 50S ribosomal protein L19

Chain BN:  80% 20%




- Molecule 37: 50S ribosomal protein L20

Chain AO:  84% 16% .




- Molecule 37: 50S ribosomal protein L20

Chain BO:  84% 16% .



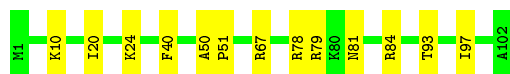
- Molecule 38: 50S ribosomal protein L21

Chain AP:  87% 13%




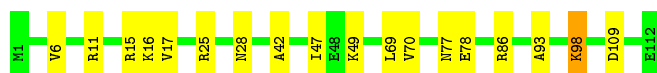
- Molecule 38: 50S ribosomal protein L21

Chain BP:  87% 13%




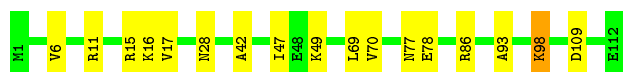
- Molecule 39: 50S ribosomal protein L22

Chain AQ:  84% 15%




- Molecule 39: 50S ribosomal protein L22

Chain BQ:  85% 14%




- Molecule 40: 50S ribosomal protein L23

Chain AR:  81% 19%




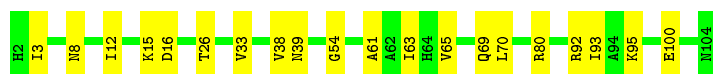
- Molecule 40: 50S ribosomal protein L23

Chain BR:  81% 19%




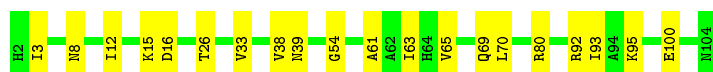
- Molecule 41: 50S ribosomal protein L24

Chain AS:  81% 19%



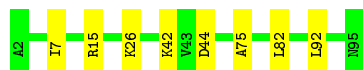
- Molecule 41: 50S ribosomal protein L24

Chain BS:  81% 19%



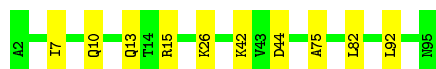
- Molecule 42: 50S ribosomal protein L25

Chain AT: 91% 9%



- Molecule 42: 50S ribosomal protein L25

Chain BT: 89% 11%



- Molecule 43: 50S ribosomal protein L27

Chain AU: 83% 16%



- Molecule 43: 50S ribosomal protein L27

Chain BU: 80% 18%



- Molecule 44: 50S ribosomal protein L28

Chain AV: 86% 12%



- Molecule 44: 50S ribosomal protein L28

Chain BV: 86% 12%



- Molecule 45: 50S ribosomal protein L29

Chain AW: 84% 16%




- Molecule 45: 50S ribosomal protein L29

Chain BW:  85% 15%




- Molecule 46: 50S ribosomal protein L30

Chain AX:  83% 17%



- Molecule 46: 50S ribosomal protein L30

Chain BX:  83% 17%



- Molecule 47: 50S ribosomal protein L31 type B

Chain AY:  92% 8%




- Molecule 47: 50S ribosomal protein L31 type B

Chain BY:  92% 8%




- Molecule 48: 50S ribosomal protein L32

Chain AZ:  79% 21%




- Molecule 48: 50S ribosomal protein L32

Chain BZ:  81% 19%



- Molecule 49: 50S ribosomal protein L33

Chain A1:  81% 19%



- Molecule 49: 50S ribosomal protein L33

Chain B1: 83% 17%



- Molecule 50: 50S ribosomal protein L34

Chain A2: 81% 19%



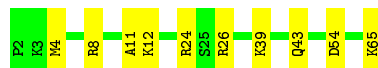
- Molecule 50: 50S ribosomal protein L34

Chain B2: 84% 16%



- Molecule 51: 50S ribosomal protein L35

Chain A3: 84% 16%



- Molecule 51: 50S ribosomal protein L35

Chain B3: 84% 16%



- Molecule 52: 50S ribosomal protein L36

Chain A4: 62% 35% .



- Molecule 52: 50S ribosomal protein L36

Chain B4: 65% 32% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	12570	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 ⓘ

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	101/57564 (0.2%)
1	Ba	0.38	0/36913	0.95	102/57564 (0.2%)
10	Aj	0.27	0/764	0.56	0/1034
10	Bj	0.27	0/764	0.56	0/1034
11	Ak	0.29	0/824	0.59	0/1119
11	Bk	0.29	0/824	0.59	0/1119
12	Al	0.30	0/1054	0.63	1/1415 (0.1%)
12	Bl	0.30	0/1054	0.63	1/1415 (0.1%)
13	Am	0.26	0/732	0.56	0/991
13	Bm	0.26	0/732	0.56	0/991
14	An	0.32	0/497	0.63	0/662
14	Bn	0.32	0/497	0.63	0/662
15	Ao	0.26	0/732	0.53	0/979
15	Bo	0.26	0/732	0.53	0/979
16	Ap	0.33	0/705	0.57	0/952
16	Bp	0.33	0/705	0.57	0/952
17	Aq	0.32	0/629	0.58	0/849
17	Bq	0.32	0/629	0.58	0/849
18	Ar	0.28	0/453	0.65	1/604 (0.2%)
18	Br	0.28	0/453	0.65	1/604 (0.2%)
19	As	0.31	0/654	0.58	0/879
19	Bs	0.31	0/654	0.58	0/879
2	Ab	0.26	0/1840	0.53	1/2470 (0.0%)
2	Bb	0.26	0/1840	0.53	1/2470 (0.0%)
20	At	0.23	0/591	0.50	0/793
20	Bt	0.23	0/591	0.50	0/793
21	Au	0.27	0/403	0.51	0/535
21	Bu	0.27	0/403	0.51	0/535
22	Av	0.49	0/1350	0.81	2/1812 (0.1%)
22	Bv	0.49	0/1350	0.81	2/1812 (0.1%)
23	AA	0.74	3/69738 (0.0%)	1.02	207/108747 (0.2%)
23	BA	0.74	3/69738 (0.0%)	1.02	208/108747 (0.2%)
24	AB	0.61	0/2732	1.16	21/4253 (0.5%)
24	BB	0.61	0/2732	1.16	21/4253 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
25	AC	0.48	0/2129	0.67	3/2858 (0.1%)
25	BC	0.48	0/2129	0.67	3/2858 (0.1%)
26	AD	0.49	0/1651	0.66	0/2215
26	BD	0.49	0/1651	0.66	0/2215
27	AE	0.47	0/1595	0.66	0/2154
27	BE	0.47	0/1595	0.66	0/2154
28	AF	0.31	0/1339	0.63	0/1805
28	BF	0.32	0/1339	0.63	0/1805
29	AG	0.35	0/1281	0.58	0/1736
29	BG	0.35	0/1281	0.58	0/1736
3	Ac	0.27	0/1523	0.59	0/2062
3	Bc	0.27	0/1523	0.59	0/2062
30	AH	0.48	0/1165	0.65	0/1570
30	BH	0.48	0/1165	0.65	0/1570
31	AI	0.47	0/925	0.73	3/1242 (0.2%)
31	BI	0.47	0/925	0.73	3/1242 (0.2%)
32	AJ	0.46	0/1100	0.71	2/1467 (0.1%)
32	BJ	0.45	0/1100	0.71	2/1467 (0.1%)
33	AK	0.46	0/1095	0.61	0/1472
33	BK	0.46	0/1095	0.61	0/1472
34	AL	0.43	0/936	0.71	0/1253
34	BL	0.43	0/936	0.71	0/1253
35	AM	0.43	0/900	0.69	3/1205 (0.2%)
35	BM	0.43	0/900	0.69	2/1205 (0.2%)
36	AN	0.44	0/901	0.65	1/1209 (0.1%)
36	BN	0.44	0/901	0.65	1/1209 (0.1%)
37	AO	0.52	0/954	0.64	0/1264
37	BO	0.52	0/954	0.64	0/1264
38	AP	0.47	0/800	0.67	0/1070
38	BP	0.47	0/800	0.67	0/1070
39	AQ	0.45	0/862	0.70	0/1161
39	BQ	0.45	0/862	0.70	0/1161
4	Ad	0.28	0/1526	0.62	1/2063 (0.0%)
4	Bd	0.28	0/1526	0.62	1/2063 (0.0%)
40	AR	0.43	0/723	0.63	0/966
40	BR	0.43	0/723	0.63	0/966
41	AS	0.39	0/779	0.67	0/1043
41	BS	0.39	0/779	0.67	0/1043
42	AT	0.37	0/730	0.66	1/981 (0.1%)
42	BT	0.37	0/730	0.66	1/981 (0.1%)
43	AU	0.55	0/628	0.68	1/833 (0.1%)
43	BU	0.55	0/628	0.68	1/833 (0.1%)
44	AV	0.38	0/451	0.66	0/603

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
44	BV	0.38	0/451	0.66	0/603
45	AW	0.39	0/542	0.69	0/722
45	BW	0.39	0/542	0.69	0/722
46	AX	0.40	0/451	0.61	0/606
46	BX	0.40	0/451	0.61	0/606
47	AY	0.25	0/378	0.53	0/521
47	BY	0.25	0/378	0.53	0/521
48	AZ	0.43	0/366	0.65	0/489
48	BZ	0.43	0/366	0.65	0/489
49	A1	0.34	0/395	0.60	0/530
49	B1	0.34	0/395	0.60	0/530
5	Ae	0.28	0/1159	0.59	0/1566
5	Be	0.28	0/1159	0.59	0/1566
50	A2	0.48	0/371	0.67	0/484
50	B2	0.47	0/371	0.67	0/484
51	A3	0.40	0/526	0.62	0/690
51	B3	0.40	0/526	0.61	0/690
52	A4	0.53	0/298	0.63	0/392
52	B4	0.52	0/298	0.63	0/392
6	Af	0.30	0/789	0.60	1/1060 (0.1%)
6	Bf	0.30	0/789	0.60	1/1060 (0.1%)
7	Ag	0.26	0/1176	0.54	0/1588
7	Bg	0.26	0/1176	0.54	0/1588
8	Ah	0.31	0/1038	0.63	0/1395
8	Bh	0.31	0/1038	0.63	0/1395
9	Ai	0.27	0/937	0.67	1/1269 (0.1%)
9	Bi	0.27	0/937	0.67	1/1269 (0.1%)
All	All	0.58	6/306060 (0.0%)	0.92	703/458404 (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
12	Bl	0	1
19	As	0	1
19	Bs	0	1
20	At	0	1
20	Bt	0	1
26	AD	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	BD	0	1
38	AP	0	1
38	BP	0	1
5	Ae	0	1
5	Be	0	1
9	Ai	0	1
9	Bi	0	1
All	All	0	14

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	BA	1065	A	N9-C4	-5.38	1.34	1.37
23	AA	1584	U	C1'-N1	5.31	1.56	1.48
23	BA	1584	U	C1'-N1	5.31	1.56	1.48
23	AA	1065	A	N9-C4	-5.26	1.34	1.37
23	BA	1186	A	N9-C4	-5.21	1.34	1.37

The worst 5 of 703 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	BB	87	C	N1-C2-O2	12.71	126.53	118.90
24	AB	87	C	N1-C2-O2	12.65	126.49	118.90
24	AB	87	C	C2-N1-C1'	12.14	132.15	118.80
24	BB	87	C	C2-N1-C1'	12.08	132.08	118.80
23	AA	576	U	C2-N1-C1'	12.02	132.13	117.70

There are no chirality outliers.

5 of 14 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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Aa	32969	0	16595	0	0
1	Ba	32969	0	16595	0	0
2	Ab	1813	0	1875	0	0
2	Bb	1813	0	1875	0	0
3	Ac	1501	0	1464	0	0
3	Bc	1501	0	1464	0	0
4	Ad	1497	0	1449	0	0
4	Bd	1497	0	1449	0	0
5	Ae	1145	0	1202	0	0
5	Be	1145	0	1202	0	0
6	Af	778	0	775	0	0
6	Bf	778	0	775	0	0
7	Ag	1161	0	1165	0	0
7	Bg	1161	0	1165	0	0
8	Ah	1026	0	1078	0	0
8	Bh	1026	0	1078	0	0
9	Ai	922	0	890	0	0
9	Bi	922	0	890	0	0
10	Aj	752	0	775	0	0
10	Bj	752	0	775	0	0
11	Ak	810	0	784	0	0
11	Bk	810	0	784	0	0
12	Al	1037	0	1091	0	0
12	Bl	1037	0	1091	0	0
13	Am	727	0	674	0	0
13	Bm	727	0	674	0	0
14	An	487	0	492	0	0
14	Bn	487	0	492	0	0
15	Ao	723	0	749	0	0
15	Bo	723	0	749	0	0
16	Ap	694	0	709	0	0
16	Bp	694	0	709	0	0
17	Aq	621	0	615	0	0
17	Bq	621	0	615	0	0
18	Ar	446	0	482	0	0
18	Br	446	0	482	0	0
19	As	636	0	626	0	0
19	Bs	636	0	626	0	0
20	At	591	0	616	0	0
20	Bt	591	0	616	0	0
21	Au	400	0	407	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	Bu	400	0	407	0	0
22	Av	1333	0	1349	0	0
22	Bv	1333	0	1349	0	0
23	AA	62277	0	31301	710	0
23	BA	62277	0	31301	692	0
24	AB	2445	0	1241	16	0
24	BB	2445	0	1241	14	0
25	AC	2094	0	2203	87	0
25	BC	2094	0	2203	84	0
26	AD	1627	0	1667	58	0
26	BD	1627	0	1667	58	0
27	AE	1572	0	1619	39	0
27	BE	1572	0	1619	40	0
28	AF	1325	0	1342	51	0
28	BF	1325	0	1342	52	0
29	AG	1263	0	1225	25	0
29	BG	1263	0	1225	24	0
30	AH	1143	0	1134	17	0
30	BH	1143	0	1134	16	0
31	AI	918	0	980	25	0
31	BI	918	0	980	24	0
32	AJ	1086	0	1125	28	0
32	BJ	1086	0	1125	27	0
33	AK	1071	0	1123	26	0
33	BK	1071	0	1123	23	0
34	AL	932	0	983	26	0
34	BL	932	0	983	26	0
35	AM	891	0	925	21	0
35	BM	891	0	925	21	0
36	AN	889	0	937	15	0
36	BN	889	0	937	16	0
37	AO	942	0	1014	31	0
37	BO	942	0	1014	31	0
38	AP	790	0	830	13	0
38	BP	790	0	830	12	0
39	AQ	854	0	914	17	0
39	BQ	854	0	914	16	0
40	AR	715	0	748	22	0
40	BR	715	0	748	21	0
41	AS	770	0	809	17	0
41	BS	770	0	809	17	0
42	AT	722	0	766	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BT	722	0	766	5	0
43	AU	622	0	643	9	0
43	BU	622	0	643	10	0
44	AV	445	0	466	6	0
44	BV	445	0	466	6	0
45	AW	541	0	563	9	0
45	BW	541	0	563	8	0
46	AX	449	0	491	9	0
46	BX	449	0	491	9	0
47	AY	370	0	243	3	0
47	BY	370	0	243	3	0
48	AZ	360	0	358	23	0
48	BZ	360	0	358	20	0
49	A1	390	0	394	8	0
49	B1	390	0	394	7	0
50	A2	367	0	415	10	0
50	B2	367	0	415	10	0
51	A3	521	0	586	10	0
51	B3	521	0	586	10	0
52	A4	295	0	340	14	0
52	B4	295	0	340	14	0
All	All	281510	0	186494	1864	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 1864 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:BA:2717:A:N7	34:BL:3:TYR:CD1	1.68	1.59
23:AA:2717:A:N7	34:AL:3:TYR:CD1	1.68	1.57
23:BA:581:A:OP1	30:BH:1:MET:CE	1.72	1.37
23:BA:1533:A:N7	25:BC:96:TYR:C	1.79	1.36
23:AA:581:A:OP1	30:AH:1:MET:CE	1.72	1.35

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	
2	Ab	224/226 (99%)	209 (93%)	14 (6%)	1 (0%)	38	77
2	Bb	224/226 (99%)	208 (93%)	14 (6%)	2 (1%)	20	63
3	Ac	200/202 (99%)	177 (88%)	23 (12%)	0	100	100
3	Bc	200/202 (99%)	177 (88%)	23 (12%)	0	100	100
4	Ad	196/198 (99%)	170 (87%)	26 (13%)	0	100	100
4	Bd	196/198 (99%)	170 (87%)	26 (13%)	0	100	100
5	Ae	154/156 (99%)	147 (96%)	7 (4%)	0	100	100
5	Be	154/156 (99%)	147 (96%)	7 (4%)	0	100	100
6	Af	93/95 (98%)	85 (91%)	8 (9%)	0	100	100
6	Bf	93/95 (98%)	85 (91%)	8 (9%)	0	100	100
7	Ag	150/152 (99%)	144 (96%)	6 (4%)	0	100	100
7	Bg	150/152 (99%)	144 (96%)	6 (4%)	0	100	100
8	Ah	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
8	Bh	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
9	Ai	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
9	Bi	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
10	Aj	95/97 (98%)	88 (93%)	7 (7%)	0	100	100
10	Bj	95/97 (98%)	88 (93%)	7 (7%)	0	100	100
11	Ak	112/114 (98%)	93 (83%)	19 (17%)	0	100	100
11	Bk	112/114 (98%)	93 (83%)	19 (17%)	0	100	100
12	Al	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
12	Bl	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
13	Am	100/121 (83%)	90 (90%)	10 (10%)	0	100	100
13	Bm	100/121 (83%)	90 (90%)	10 (10%)	0	100	100
14	An	58/60 (97%)	49 (84%)	9 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	Bn	58/60 (97%)	49 (84%)	9 (16%)	0	100	100
15	Ao	86/88 (98%)	85 (99%)	1 (1%)	0	100	100
15	Bo	86/88 (98%)	85 (99%)	1 (1%)	0	100	100
16	Ap	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
16	Bp	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
17	Aq	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
17	Bq	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
18	Ar	52/54 (96%)	51 (98%)	1 (2%)	0	100	100
18	Br	52/54 (96%)	51 (98%)	1 (2%)	0	100	100
19	As	78/80 (98%)	68 (87%)	10 (13%)	0	100	100
19	Bs	78/80 (98%)	69 (88%)	9 (12%)	0	100	100
20	At	79/81 (98%)	77 (98%)	2 (2%)	0	100	100
20	Bt	79/81 (98%)	77 (98%)	2 (2%)	0	100	100
21	Au	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
21	Bu	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
22	Av	158/190 (83%)	149 (94%)	9 (6%)	0	100	100
22	Bv	158/190 (83%)	149 (94%)	9 (6%)	0	100	100
25	AC	272/274 (99%)	257 (94%)	15 (6%)	0	100	100
25	BC	272/274 (99%)	257 (94%)	15 (6%)	0	100	100
26	AD	213/215 (99%)	194 (91%)	19 (9%)	0	100	100
26	BD	213/215 (99%)	194 (91%)	19 (9%)	0	100	100
27	AE	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
27	BE	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
28	AF	173/175 (99%)	142 (82%)	31 (18%)	0	100	100
28	BF	173/175 (99%)	142 (82%)	31 (18%)	0	100	100
29	AG	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
29	BG	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
30	AH	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
30	BH	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
31	AI	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
31	BI	120/122 (98%)	106 (88%)	14 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	AJ	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
32	BJ	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
33	AK	135/137 (98%)	127 (94%)	8 (6%)	0	100	100
33	BK	135/137 (98%)	127 (94%)	8 (6%)	0	100	100
34	AL	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
34	BL	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
35	AM	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
35	BM	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
36	AN	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
36	BN	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
37	AO	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
37	BO	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
38	AP	100/102 (98%)	93 (93%)	6 (6%)	1 (1%)	18	61
38	BP	100/102 (98%)	93 (93%)	6 (6%)	1 (1%)	18	61
39	AQ	110/112 (98%)	106 (96%)	4 (4%)	0	100	100
39	BQ	110/112 (98%)	106 (96%)	4 (4%)	0	100	100
40	AR	87/89 (98%)	81 (93%)	6 (7%)	0	100	100
40	BR	87/89 (98%)	81 (93%)	6 (7%)	0	100	100
41	AS	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
41	BS	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
42	AT	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
42	BT	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
43	AU	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
43	BU	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
44	AV	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	BV	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
45	AW	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
45	BW	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
46	AX	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
46	BX	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
47	AY	57/59 (97%)	45 (79%)	12 (21%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	BY	57/59 (97%)	45 (79%)	12 (21%)	0	100	100
48	AZ	46/48 (96%)	40 (87%)	6 (13%)	0	100	100
48	BZ	46/48 (96%)	40 (87%)	6 (13%)	0	100	100
49	A1	45/47 (96%)	44 (98%)	1 (2%)	0	100	100
49	B1	45/47 (96%)	44 (98%)	1 (2%)	0	100	100
50	A2	41/43 (95%)	39 (95%)	2 (5%)	0	100	100
50	B2	41/43 (95%)	39 (95%)	2 (5%)	0	100	100
51	A3	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
51	B3	62/64 (97%)	57 (92%)	5 (8%)	0	100	100
52	A4	35/37 (95%)	35 (100%)	0	0	100	100
52	B4	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11016/11310 (97%)	10097 (92%)	914 (8%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Ab	33	THR
38	AP	51	PRO
2	Bb	33	THR
38	BP	51	PRO
2	Bb	36	ASN

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	195/196 (100%)	194 (100%)	1 (0%)	91	95
2	Bb	195/196 (100%)	195 (100%)	0	100	100
3	Ac	138/164 (84%)	138 (100%)	0	100	100
3	Bc	138/164 (84%)	138 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Ad	147/174 (84%)	146 (99%)	1 (1%)	87	93
4	Bd	147/174 (84%)	146 (99%)	1 (1%)	87	93
5	Ae	118/122 (97%)	118 (100%)	0	100	100
5	Be	118/122 (97%)	118 (100%)	0	100	100
6	Af	80/83 (96%)	80 (100%)	0	100	100
6	Bf	80/83 (96%)	80 (100%)	0	100	100
7	Ag	118/128 (92%)	118 (100%)	0	100	100
7	Bg	118/128 (92%)	118 (100%)	0	100	100
8	Ah	111/112 (99%)	109 (98%)	2 (2%)	64	84
8	Bh	111/112 (99%)	109 (98%)	2 (2%)	64	84
9	Ai	86/105 (82%)	84 (98%)	2 (2%)	56	79
9	Bi	86/105 (82%)	84 (98%)	2 (2%)	56	79
10	Aj	81/87 (93%)	80 (99%)	1 (1%)	75	88
10	Bj	81/87 (93%)	80 (99%)	1 (1%)	75	88
11	Ak	82/90 (91%)	82 (100%)	0	100	100
11	Bk	82/90 (91%)	82 (100%)	0	100	100
12	Al	111/117 (95%)	110 (99%)	1 (1%)	82	91
12	Bl	111/117 (95%)	110 (99%)	1 (1%)	82	91
13	Am	62/104 (60%)	61 (98%)	1 (2%)	68	85
13	Bm	62/104 (60%)	61 (98%)	1 (2%)	68	85
14	An	48/52 (92%)	46 (96%)	2 (4%)	34	64
14	Bn	48/52 (92%)	46 (96%)	2 (4%)	34	64
15	Ao	77/80 (96%)	76 (99%)	1 (1%)	73	87
15	Bo	77/80 (96%)	76 (99%)	1 (1%)	73	87
16	Ap	73/75 (97%)	71 (97%)	2 (3%)	50	74
16	Bp	73/75 (97%)	71 (97%)	2 (3%)	50	74
17	Aq	65/75 (87%)	65 (100%)	0	100	100
17	Bq	65/75 (87%)	65 (100%)	0	100	100
18	Ar	48/49 (98%)	48 (100%)	0	100	100
18	Br	48/49 (98%)	48 (100%)	0	100	100
19	As	67/70 (96%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	Bs	67/70 (96%)	67 (100%)	0	100	100
20	At	61/67 (91%)	61 (100%)	0	100	100
20	Bt	61/67 (91%)	61 (100%)	0	100	100
21	Au	40/48 (83%)	40 (100%)	0	100	100
21	Bu	40/48 (83%)	40 (100%)	0	100	100
22	Av	147/173 (85%)	143 (97%)	4 (3%)	50	74
22	Bv	147/173 (85%)	143 (97%)	4 (3%)	50	74
25	AC	221/221 (100%)	221 (100%)	0	100	100
25	BC	221/221 (100%)	221 (100%)	0	100	100
26	AD	173/173 (100%)	172 (99%)	1 (1%)	89	94
26	BD	173/173 (100%)	172 (99%)	1 (1%)	89	94
27	AE	168/168 (100%)	167 (99%)	1 (1%)	89	94
27	BE	168/168 (100%)	167 (99%)	1 (1%)	89	94
28	AF	141/154 (92%)	139 (99%)	2 (1%)	71	86
28	BF	141/154 (92%)	139 (99%)	2 (1%)	71	86
29	AG	124/153 (81%)	122 (98%)	2 (2%)	68	85
29	BG	124/153 (81%)	122 (98%)	2 (2%)	68	85
30	AH	122/123 (99%)	121 (99%)	1 (1%)	85	92
30	BH	122/123 (99%)	121 (99%)	1 (1%)	85	92
31	AI	100/100 (100%)	99 (99%)	1 (1%)	80	90
31	BI	100/100 (100%)	99 (99%)	1 (1%)	80	90
32	AJ	109/112 (97%)	107 (98%)	2 (2%)	64	84
32	BJ	109/112 (97%)	107 (98%)	2 (2%)	64	84
33	AK	108/114 (95%)	107 (99%)	1 (1%)	82	91
33	BK	108/114 (95%)	107 (99%)	1 (1%)	82	91
34	AL	96/101 (95%)	95 (99%)	1 (1%)	80	90
34	BL	96/101 (95%)	95 (99%)	1 (1%)	80	90
35	AM	86/95 (90%)	83 (96%)	3 (4%)	41	69
35	BM	86/95 (90%)	83 (96%)	3 (4%)	41	69
36	AN	93/100 (93%)	92 (99%)	1 (1%)	78	89
36	BN	93/100 (93%)	92 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	AO	96/96 (100%)	95 (99%)	1 (1%)	80	90
37	BO	96/96 (100%)	95 (99%)	1 (1%)	80	90
38	AP	84/86 (98%)	84 (100%)	0	100	100
38	BP	84/86 (98%)	84 (100%)	0	100	100
39	AQ	89/91 (98%)	88 (99%)	1 (1%)	78	89
39	BQ	89/91 (98%)	88 (99%)	1 (1%)	78	89
40	AR	78/80 (98%)	76 (97%)	2 (3%)	51	75
40	BR	78/80 (98%)	76 (97%)	2 (3%)	51	75
41	AS	81/88 (92%)	80 (99%)	1 (1%)	75	88
41	BS	81/88 (92%)	80 (99%)	1 (1%)	75	88
42	AT	78/82 (95%)	78 (100%)	0	100	100
42	BT	78/82 (95%)	78 (100%)	0	100	100
43	AU	63/64 (98%)	60 (95%)	3 (5%)	30	61
43	BU	63/64 (98%)	60 (95%)	3 (5%)	30	61
44	AV	44/49 (90%)	43 (98%)	1 (2%)	56	79
44	BV	44/49 (90%)	43 (98%)	1 (2%)	56	79
45	AW	58/60 (97%)	58 (100%)	0	100	100
45	BW	58/60 (97%)	58 (100%)	0	100	100
46	AX	52/52 (100%)	52 (100%)	0	100	100
46	BX	52/52 (100%)	52 (100%)	0	100	100
47	AY	23/56 (41%)	23 (100%)	0	100	100
47	BY	23/56 (41%)	23 (100%)	0	100	100
48	AZ	35/44 (80%)	35 (100%)	0	100	100
48	BZ	35/44 (80%)	35 (100%)	0	100	100
49	A1	44/45 (98%)	44 (100%)	0	100	100
49	B1	44/45 (98%)	44 (100%)	0	100	100
50	A2	39/39 (100%)	39 (100%)	0	100	100
50	B2	39/39 (100%)	39 (100%)	0	100	100
51	A3	55/55 (100%)	55 (100%)	0	100	100
51	B3	55/55 (100%)	55 (100%)	0	100	100
52	A4	35/35 (100%)	34 (97%)	1 (3%)	48	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	B4	35/35 (100%)	34 (97%)	1 (3%)	48 73
All	All	8900/9614 (93%)	8813 (99%)	87 (1%)	81 90

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	AU	22	ARG
9	Bi	115	ARG
40	BR	56	MET
43	AU	61	ARG
4	Bd	115	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
43	AU	20	ASN
5	Be	83	HIS
41	BS	39	ASN
48	AZ	19	HIS
50	A2	17	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Aa	1537/1539 (99%)	470 (30%)	0
1	Ba	1537/1539 (99%)	468 (30%)	0
23	AA	2895/2923 (99%)	795 (27%)	27 (0%)
23	BA	2895/2923 (99%)	795 (27%)	28 (0%)
24	AB	113/115 (98%)	16 (14%)	0
24	BB	113/115 (98%)	16 (14%)	0
All	All	9090/9154 (99%)	2560 (28%)	55 (0%)

5 of 2560 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 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	AA	2568	A
23	BA	268	A
23	BA	2117	A
23	AA	2749	G
23	BA	99	U

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
23	BA	6
24	BB	1
1	Ba	1
13	Bm	1
24	AB	1
1	Aa	1
13	Am	1

The worst 5 of 18 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	BA	2207:U	O3'	2208:A	P	9.06
1	AA	2132:A	O3'	2133:G	P	8.44
1	BA	2132:A	O3'	2133:G	P	8.44
1	AA	1096:C	O3'	1097:U	P	6.77