



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:21 PM BST

PDB ID : 4V5Z
EMDB ID: : EMD-1480
Title : Structure of a mammalian 80S ribosome obtained by docking homology models of the RNA and proteins into an 8.7 Å cryo-EM map
Authors : Chandramouli, P.; Akey, C.W.
Deposited on : 2008-03-27
Resolution : 8.70 Å (reported)
Based on PDB ID : 1J5E, 1Vi6, 1fjg, 1iGV, 1i6U, 2AVY, 1G1X, 1RQ6, 1K7K

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

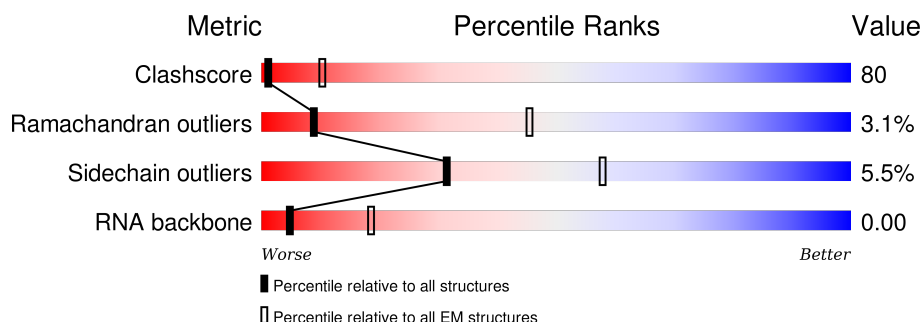
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.70 Å.

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









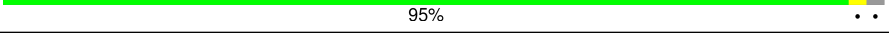

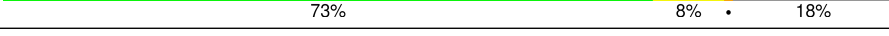

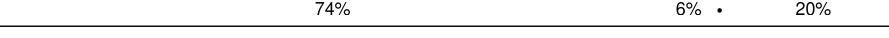
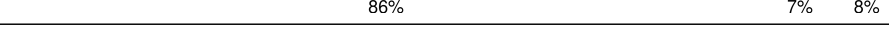

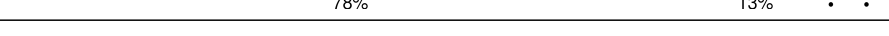


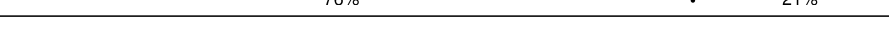

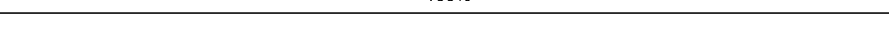






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	1563	89% 11%
2	AB	35	91% 9%
3	AC	32	91% 9%
4	AD	42	100%
5	AE	32	100%
6	AF	31	100%
7	AG	14	100%
8	AH	41	100%

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Mol	Chain	Length	Quality of chain
9	Aa	317	
10	Ab	295	
11	Ac	243	
12	Ad	209	
13	Ae	179	
14	Ag	204	
15	Ah	130	
16	Ai	146	
17	Aj	119	
18	Ak	151	
19	Al	143	
20	Am	152	
21	An	56	
22	Ao	89	
23	Aq	158	
24	As	145	
25	B1	123	
26	B0	2903	
27	BA	21	
28	BB	27	
29	BC	17	
30	BD	16	
31	BE	54	
32	BF	120	
33	BG	48	


















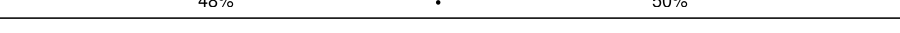
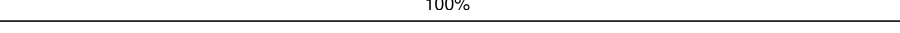
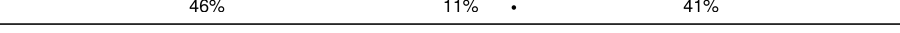





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Mol	Chain	Length	Quality of chain
34	BH	25	100%
35	BI	72	100%
36	BJ	30	100%
37	BK	26	96% .
38	BL	20	100%
39	BM	19	100%
40	BN	78	100%
41	BO	20	100%
42	BP	15	100%
43	BQ	30	100%
44	BR	30	100%
45	BS	38	100%
46	BT	30	100%
47	BU	16	100%
48	BV	22	100%
49	BW	16	100%
50	BX	113	100%
51	BY	115	100%
52	BZ	72	99% .
53	Ba	257	88% 6% . 5%
54	Bb	403	64% 20% . 14%
55	Bc	421	51% 9% . 39%
56	Bd	178	75% 15% . . 7%
57	Be	192	78% 11% . 9%
58	Bf	266	34% 9% . . 55%

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Mol	Chain	Length	Quality of chain
59	Bg	317	
60	Bh	214	
61	Bi	165	
62	Bj	203	
63	Bk	140	
64	Bl	148	
65	Bm	204	
66	Bn	297	
67	Bo	188	
68	Bp	196	
69	B7	13	
70	Bq	160	
71	Br	184	
72	Bs	156	
73	Bt	145	
74	Bu	157	
75	Bv	123	
76	B8	10	
77	Bw	270	
78	Bx	125	
79	By	135	
80	B9	58	
81	Bz	92	
82	B2	97	
83	B3	51	

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Mol	Chain	Length	Quality of chain
84	B4	106	<div><div></div><div>26%</div><div>56%</div><div>5%</div><div>13%</div></div>
85	B5	212	<div><div></div><div>36%</div><div>62%</div><div></div><div>..</div></div>
86	B6	115	<div><div></div><div>26%</div><div>69%</div><div></div><div>..</div></div>

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 55531 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 18S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	AA	1391	Total	P	0	1391
			1391	1391		

- Molecule 2 is a RNA chain called RNA Expansion segment ES3.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	AB	32	Total	P	0	32
			32	32		

- Molecule 3 is a RNA chain called RNA Expansion segment ES4.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	AC	29	Total	P	0	29
			29	29		

- Molecule 4 is a RNA chain called RNA Expansion segment ES6 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	AD	42	Total	P	0	42
			42	42		

- Molecule 5 is a RNA chain called RNA Expansion segment ES6 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	AE	32	Total	P	0	32
			32	32		

- Molecule 6 is a RNA chain called RNA Expansion segment ES9.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	AF	31	Total	P	0	31
			31	31		

- Molecule 7 is a RNA chain called RNA helix.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	AG	14	Total	P	0	14
			14	14		

- Molecule 8 is a RNA chain called RNA helix.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	AH	41	Total	P	0	41
			41	41		

- Molecule 9 is a protein called 40S Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aa	306	Total	C	N	O	S	0	0
			2380	1501	414	453	12		

- Molecule 10 is a protein called 40S Ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ab	192	Total	C	N	O	S	0	0
			1521	972	271	271	7		

- Molecule 11 is a protein called 40S Ribosomal protein S3e.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ac	192	Total	C	N	O	S	0	0
			1498	953	274	264	7		

- Molecule 12 is a protein called 40S Ribosomal protein S9e.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Ad	103	Total	C	N	O	0	0
			845	527	172	146		

- Molecule 13 is a protein called 40S Ribosomal protein S2e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Ae	148	Total	C	N	O	S	0	0
			1096	697	202	191	6		

- Molecule 14 is a protein called 40S Ribosomal protein S5e.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Ag	163	Total	C	N	O	S	0	0
			1277	795	241	234	7		

- Molecule 15 is a protein called 40S Ribosomal protein S15ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ah	127	Total	C	N	O	S	0	0
			1016	648	188	174	6		

- Molecule 16 is a protein called 40S Ribosomal protein S16e.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ai	138	Total	C	N	O	S	0	0
			1102	699	209	191	3		

- Molecule 17 is a protein called 40S Ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Aj	97	Total	C	N	O	S	0	0
			772	483	147	138	4		

- Molecule 18 is a protein called 40S Ribosomal protein S14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ak	125	Total	C	N	O	S	0	0
			935	572	181	176	6		

- Molecule 19 is a protein called 40S Ribosomal protein S23e.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Al	115	Total	C	N	O	S	0	0
			871	557	162	150	2		

- Molecule 20 is a protein called 40S Ribosomal protein S18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Am	140	Total	C	N	O	S	0	0
			1150	717	236	196	1		

- Molecule 21 is a protein called 40S Ribosomal protein S29e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	An	49	Total	C	N	O	S	0	0
			410	258	84	63	5		

- Molecule 22 is a protein called 40S Ribosomal protein S13e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ao	85	Total	C	N	O	S	0	0
			710	445	141	122	2		

- Molecule 23 is a protein called 40S Ribosomal protein S11e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Aq	76	Total	C	N	O	S	0	0
			629	401	121	102	5		

- Molecule 24 is a protein called 40S Ribosomal protein S15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	As	88	Total	C	N	O	S	0	0
			721	459	139	118	5		

- Molecule 25 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
25	B1	97	Total	P	0	97
			97	97		

- Molecule 26 is a RNA chain called 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
26	B0	2407	Total	P	0	2407
			2407	2407		

- Molecule 27 is a RNA chain called RNA Expansion segment ES3.

Mol	Chain	Residues	Atoms		AltConf	Trace
27	BA	21	Total	P	0	21
			21	21		

- Molecule 28 is a RNA chain called RNA Expansion segment ES4.

Mol	Chain	Residues	Atoms	AltConf	Trace
28	BB	27	Total P 27 27	0	27

- Molecule 29 is a RNA chain called RNA Expansion segment ES5.

Mol	Chain	Residues	Atoms	AltConf	Trace
29	BC	17	Total P 17 17	0	17

- Molecule 30 is a RNA chain called RNA Expansion segment ES7 part I.

Mol	Chain	Residues	Atoms	AltConf	Trace
30	BD	16	Total P 16 16	0	16

- Molecule 31 is a RNA chain called RNA Expansion segment ES7 part II.

Mol	Chain	Residues	Atoms	AltConf	Trace
31	BE	54	Total P 54 54	0	54

- Molecule 32 is a RNA chain called RNA Expansion segment ES7 part III.

Mol	Chain	Residues	Atoms	AltConf	Trace
32	BF	120	Total P 120 120	0	120

- Molecule 33 is a RNA chain called RNA Expansion segment ES9.

Mol	Chain	Residues	Atoms	AltConf	Trace
33	BG	48	Total P 48 48	0	48

- Molecule 34 is a RNA chain called RNA Expansion segment ES12.

Mol	Chain	Residues	Atoms	AltConf	Trace
34	BH	25	Total P 25 25	0	25

- Molecule 35 is a RNA chain called RNA Expansion segment ES15 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
35	BI	72	Total	P	0	72
			72	72		

- Molecule 36 is a RNA chain called RNA Expansion segment ES15 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
36	BJ	30	Total	P	0	30
			30	30		

- Molecule 37 is a RNA chain called RNA Expansion segment ES19.

Mol	Chain	Residues	Atoms		AltConf	Trace
37	BK	25	Total	P	0	25
			25	25		

- Molecule 38 is a RNA chain called RNA Expansion segment ES20.

Mol	Chain	Residues	Atoms		AltConf	Trace
38	BL	20	Total	P	0	20
			20	20		

- Molecule 39 is a RNA chain called RNA Expansion segment ES24.

Mol	Chain	Residues	Atoms		AltConf	Trace
39	BM	19	Total	P	0	19
			19	19		

- Molecule 40 is a RNA chain called RNA Expansion segment ES27.

Mol	Chain	Residues	Atoms		AltConf	Trace
40	BN	78	Total	P	0	78
			78	78		

- Molecule 41 is a RNA chain called RNA Expansion segment ES30.

Mol	Chain	Residues	Atoms		AltConf	Trace
41	BO	20	Total	P	0	20
			20	20		

- Molecule 42 is a RNA chain called RNA Expansion segment ES31 part I.

Mol	Chain	Residues	Atoms	AltConf	Trace
42	BP	15	Total P 15 15	0	15

- Molecule 43 is a RNA chain called RNA Expansion segment ES31 part II.

Mol	Chain	Residues	Atoms	AltConf	Trace
43	BQ	30	Total P 30 30	0	30

- Molecule 44 is a RNA chain called RNA Expansion segment ES39 part I.

Mol	Chain	Residues	Atoms	AltConf	Trace
44	BR	30	Total P 30 30	0	30

- Molecule 45 is a RNA chain called RNA Expansion segment ES39 part II.

Mol	Chain	Residues	Atoms	AltConf	Trace
45	BS	38	Total P 38 38	0	38

- Molecule 46 is a RNA chain called RNA Expansion segment ES39 part III.

Mol	Chain	Residues	Atoms	AltConf	Trace
46	BT	30	Total P 30 30	0	30

- Molecule 47 is a RNA chain called RNA Expansion segment ES41.

Mol	Chain	Residues	Atoms	AltConf	Trace
47	BU	16	Total P 16 16	0	16

- Molecule 48 is a RNA chain called RNA Expansion segment ES9 part2.

Mol	Chain	Residues	Atoms	AltConf	Trace
48	BV	22	Total P 22 22	0	22

- Molecule 49 is a RNA chain called RNA Expansion segment ES10.

Mol	Chain	Residues	Atoms		AltConf	Trace
49	BW	16	Total	P	0	16
			16	16		

- Molecule 50 is a RNA chain called RNA helices.

Mol	Chain	Residues	Atoms		AltConf	Trace
50	BX	113	Total	P	0	113
			113	113		

- Molecule 51 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
51	BY	115	Total	P	0	115
			115	115		

- Molecule 52 is a RNA chain called E site t-RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
52	BZ	72	Total	P	0	72
			72	72		

- Molecule 53 is a protein called 60S Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ba	244	Total	C	N	O	S	0	0
			1867	1172	382	307	6		

- Molecule 54 is a protein called 60S Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bb	345	Total	C	N	O	S	0	0
			2765	1758	521	474	12		

- Molecule 55 is a protein called 60S Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Bc	257	Total	C	N	O	S	0	0
			2035	1282	399	344	10		

- Molecule 56 is a protein called 60S Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Bd	165	Total	C	N	O	S	0	0
			1325	837	248	234	6		

- Molecule 57 is a protein called 60S Ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Be	175	Total	C	N	O	S	0	0
			1407	889	264	249	5		

- Molecule 58 is a protein called 60S Ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Bf	120	Total	C	N	O	S	0	0
			920	584	172	160	4		

- Molecule 59 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	Bg	48	Total	C	N	O	0	0
			327	206	52	69		

- Molecule 60 is a protein called 60S Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Bh	166	Total	C	N	O	S	0	0
			1331	841	260	218	12		

- Molecule 61 is a protein called 60S Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bi	74	Total	C	N	O	S	0	0
			573	355	110	106	2		

- Molecule 62 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bj	136	Total	C	N	O	S	0	0
			1095	707	216	168	4		

- Molecule 63 is a protein called 60S Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bk	124	Total	C	N	O	S	0	0
			927	586	173	163	5		

- Molecule 64 is a protein called 60S Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bl	122	Total	C	N	O	S	0	0
			951	601	193	154	3		

- Molecule 65 is a protein called 60S Ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bm	175	Total	C	N	O	S	0	0
			1454	921	298	231	4		

- Molecule 66 is a protein called 60S Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bn	236	Total	C	N	O	S	0	0
			1912	1209	340	350	13		

- Molecule 67 is a protein called 60S Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bo	120	Total	C	N	O	S	0	0
			956	607	185	160	4		

- Molecule 68 is a protein called 60S Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bp	159	Total	C	N	O	S	0	0
			1329	817	285	220	7		

- Molecule 69 is a protein called 60S Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	B7	13	Total	C	N	O	S	0	0
			129	80	34	14	1		

- Molecule 70 is a protein called 60S Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bq	96	Total	C	N	O	S	0	0
			773	492	155	121	5		

- Molecule 71 is a protein called 60S Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Br	150	Total	C	N	O	S	0	0
			1217	760	237	211	9		

- Molecule 72 is a protein called 60S Ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bs	78	Total	C	N	O	S	0	0
			622	401	105	115	1		

- Molecule 73 is a protein called 60S Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bt	110	Total	C	N	O	S	0	0
			916	570	188	156	2		

- Molecule 74 is a protein called 60S Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bu	53	Total	C	N	O	S	0	0
			443	284	83	74	2		

- Molecule 75 is a protein called 60S Ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	Bv	61	Total	C	N	O	0	0
			477	300	93	84		

- Molecule 76 is a protein called 60S Ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	B8	10	Total	C	N	O	0	0
			78	48	15	15		

- Molecule 77 is a protein called 60S Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bw	158	Total	C	N	O	S	0	0
			1281	823	240	213	5		

- Molecule 78 is a protein called 60S Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bx	80	Total	C	N	O	S	0	0
			670	418	139	111	2		

- Molecule 79 is a protein called 60S Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	By	60	Total	C	N	O	S	0	0
			514	324	114	75	1		

- Molecule 80 is a protein called 60S Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	B9	58	Total	C	N	O	S	0	0
			460	290	87	79	4		

- Molecule 81 is a protein called 60S Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bz	72	Total	C	N	O	S	0	0
			548	345	102	94	7		

- Molecule 82 is a protein called 60S Ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	B2	51	Total	C	N	O	S	0	0
			407	250	87	66	4		

- Molecule 83 is a protein called 60S Ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	B3	48	Total	C	N	O	S	0	0
			429	272	96	60	1		

- Molecule 84 is a protein called 60S Ribosomal protein L44e.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	B4	92	Total	C	N	O	S	0	0
			760	478	154	122	6		

- Molecule 85 is a protein called 60S Ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	B5	210	Total	C	N	O	S	0	0
			1621	990	278	347	6		

- Molecule 86 is a protein called 60S Ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	B6	113	Total	C	N	O	S	0	0
			874	552	154	161	7		

There are no outlier residues recorded for this chain.

- Molecule 5: RNA Expansion segment ES6 part II

Chain AE:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: RNA Expansion segment ES9

Chain AF:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: RNA helix

Chain AG:  100%


There are no outlier residues recorded for this chain.

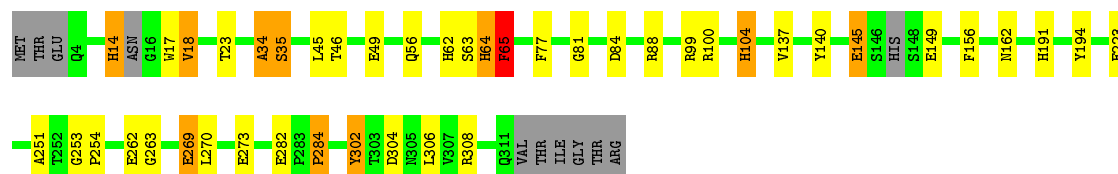
- Molecule 8: RNA helix

Chain AH:  100%

There are no outlier residues recorded for this chain.

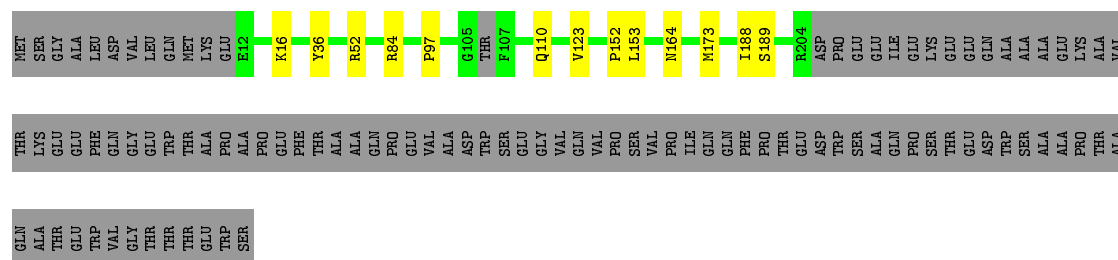
- Molecule 9: 40S Ribosomal protein RACK1

Chain Aa:  83% 10% • •



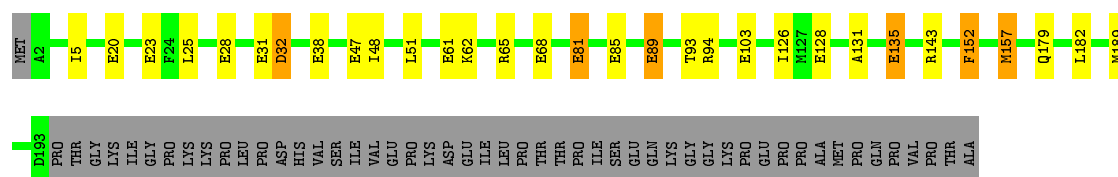
- Molecule 10: 40S Ribosomal protein SA

Chain Ab:  61% 35%

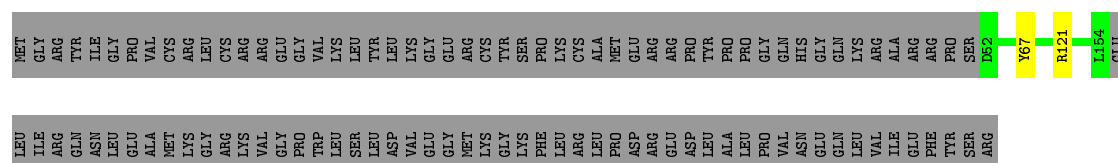


- Molecule 11: 40S Ribosomal protein S3e

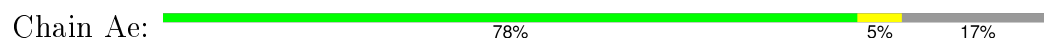
Chain Ac:  66% 10% 21%



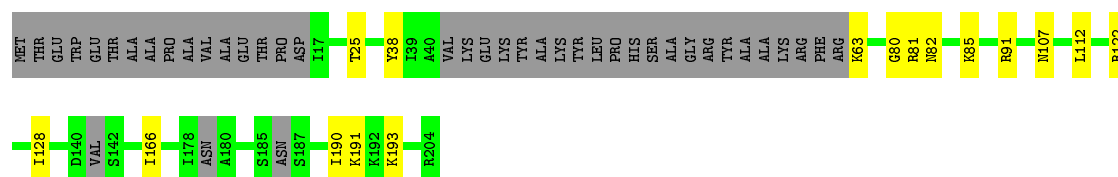
- Molecule 12: 40S Ribosomal protein S9e



- Molecule 13: 40S Ribosomal protein S2e



- Molecule 14: 40S Ribosomal protein S5e



- Molecule 15: 40S Ribosomal protein S15ae

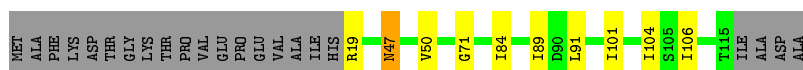


- Molecule 16: 40S Ribosomal protein S16e



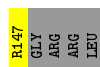
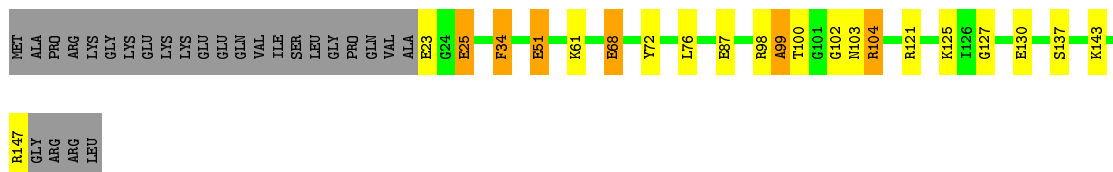
- Molecule 17: 40S Ribosomal protein S20e





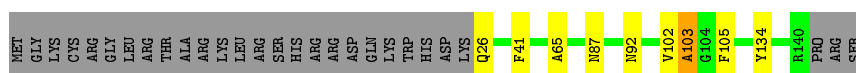
- Molecule 18: 40S Ribosomal protein S14e

Chain Ak: 68% 11% 17%



- Molecule 19: 40S Ribosomal protein S23e

Chain Al: 74% 6% 20%



- Molecule 20: 40S Ribosomal protein S18e

Chain Am: 86% 7% 8%



- Molecule 21: 40S Ribosomal protein S29e

Chain An: 82% 5% 13%



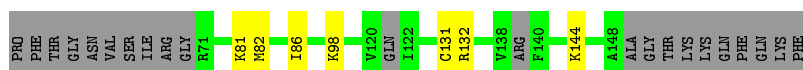
- Molecule 22: 40S Ribosomal protein S13e

Chain Ao: 78% 13% 9%



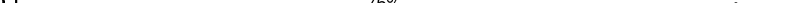
- Molecule 23: 40S Ribosomal protein S11e

Chain Aq: 44% 52% 4%




- Molecule 24: 40S Ribosomal protein S15e

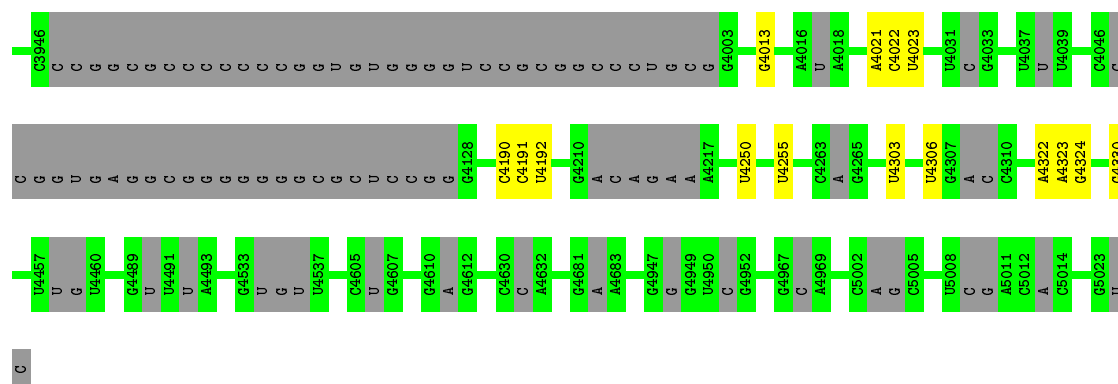
[illegible]

- Chain B1:  76% 21%

C
G
A3
G31
C
G33
C45
A48
G
G
G51
A54
G55
U71
A
A
A
U
U
U
G
G
C
C
A
A
G
G
C
A
A
C
C
A
A
C
C
C
C
U
U
U
U
G
G
A
A
U
U
C92
G96
A
G98
A105
U104

- Chain B0:  82% 17%

[illegible]



- Molecule 27: RNA Expansion segment ES3

Chain BA:  100%

There are no outlier residues recorded for this chain.

- Molecule 28: RNA Expansion segment ES4

Chain BB:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: RNA Expansion segment ES5

Chain BC:  100%

There are no outlier residues recorded for this chain.

- Molecule 30: RNA Expansion segment ES7 part I

Chain BD:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: RNA Expansion segment ES7 part II

Chain BE:  100%

There are no outlier residues recorded for this chain.

- Molecule 32: RNA Expansion segment ES7 part III

Chain BF:  100%

There are no outlier residues recorded for this chain.

- Molecule 33: RNA Expansion segment ES9

Chain BG:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: RNA Expansion segment ES12

Chain BH:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: RNA Expansion segment ES15 part I

Chain BI:  100%

There are no outlier residues recorded for this chain.

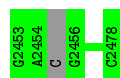
- Molecule 36: RNA Expansion segment ES15 part II

Chain BJ:  100%

There are no outlier residues recorded for this chain.

- Molecule 37: RNA Expansion segment ES19

Chain BK:  96%



- Molecule 38: RNA Expansion segment ES20

Chain BL:  100%

There are no outlier residues recorded for this chain.

- Molecule 39: RNA Expansion segment ES24

Chain BM:  100%

There are no outlier residues recorded for this chain.

- Molecule 40: RNA Expansion segment ES27

Chain BN:  100%

There are no outlier residues recorded for this chain.

- Molecule 41: RNA Expansion segment ES30

Chain BO:  100%

There are no outlier residues recorded for this chain.

- Molecule 42: RNA Expansion segment ES31 part I

Chain BP:  100%

There are no outlier residues recorded for this chain.

- Molecule 43: RNA Expansion segment ES31 part II

Chain BQ:  100%

There are no outlier residues recorded for this chain.

- Molecule 44: RNA Expansion segment ES39 part I

Chain BR:  100%

There are no outlier residues recorded for this chain.

- Molecule 45: RNA Expansion segment ES39 part II

Chain BS:  100%

There are no outlier residues recorded for this chain.

- Molecule 46: RNA Expansion segment ES39 part III

Chain BT:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: RNA Expansion segment ES41

Chain BU:  100%

There are no outlier residues recorded for this chain.

- Molecule 48: RNA Expansion segment ES9 part2

Chain BV:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: RNA Expansion segment ES10

Chain BW:  100%

There are no outlier residues recorded for this chain.

- Molecule 50: RNA helices

Chain BX:  100%

There are no outlier residues recorded for this chain.

- Molecule 51: 5S Ribosomal RNA

Chain BY:  100%

There are no outlier residues recorded for this chain.

- Molecule 52: E site t-RNA

Chain BZ:  99%



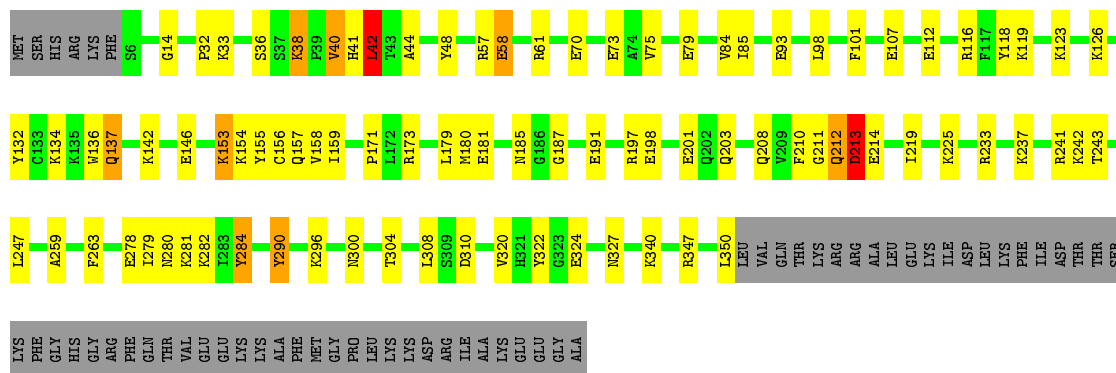
- Molecule 53: 60S Ribosomal protein L8

Chain Ba: 88% 6% • 5%



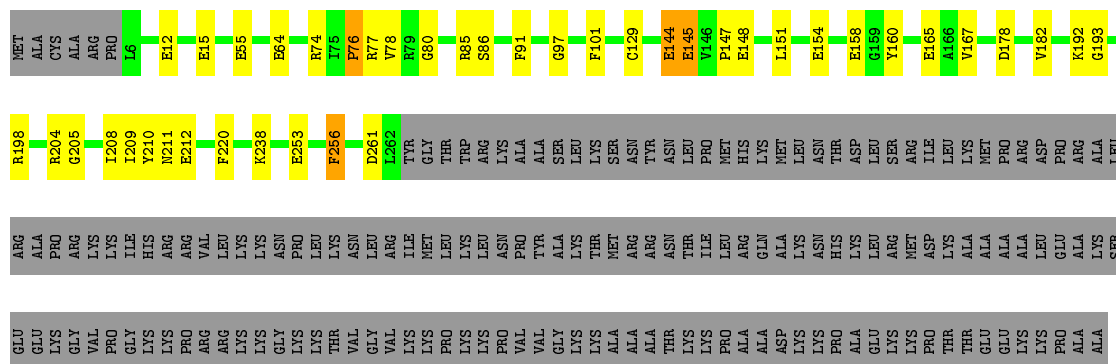
- Molecule 54: 60S Ribosomal protein L3

Chain Bb:  64% 20% • 14%

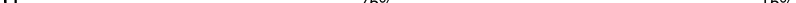


- Molecule 55: 60S Ribosomal protein L4

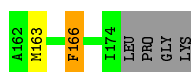
Chain Bc:  51% 9% 39%



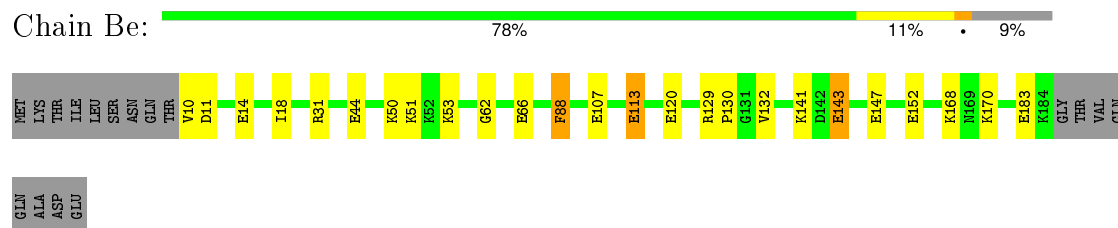
- Molecule 56: 60S Ribosomal protein L11

Chain Bd: 

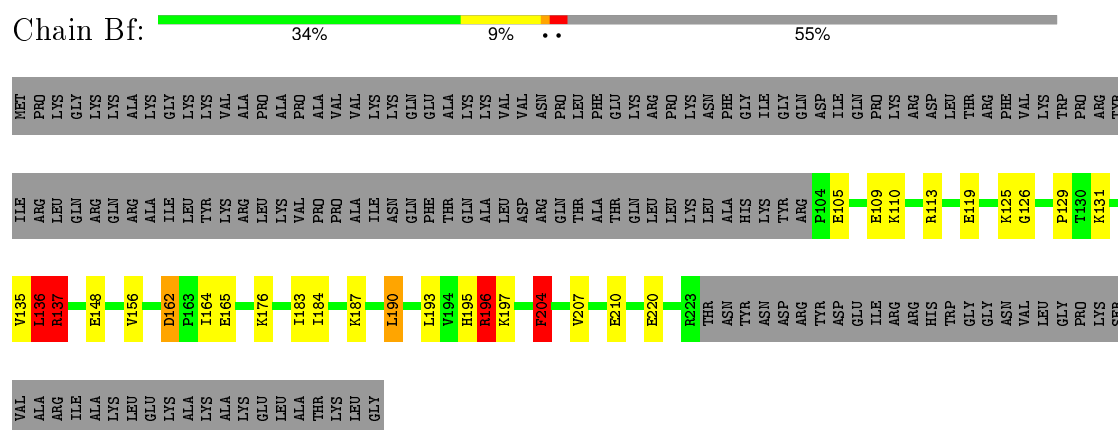




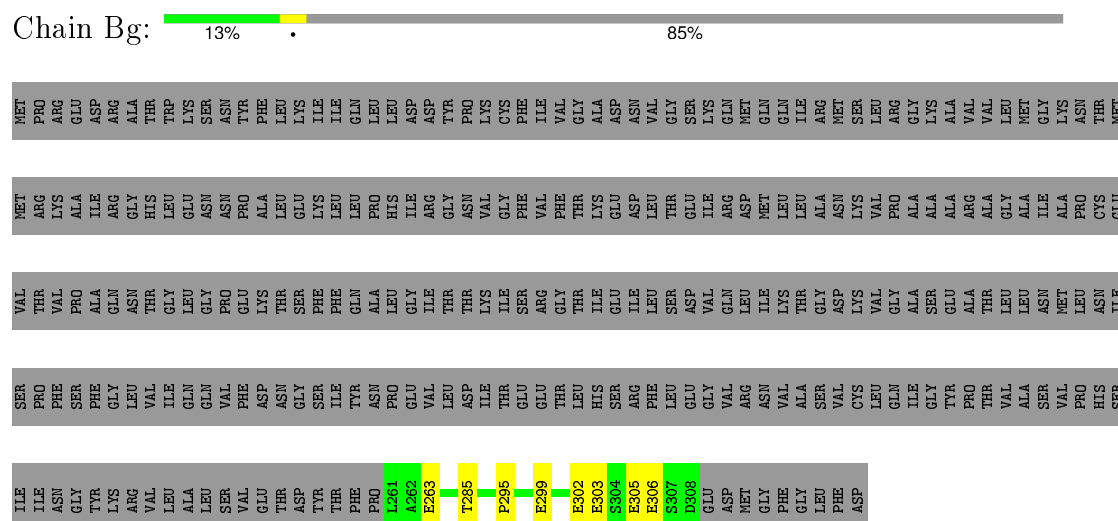
- Molecule 57: 60S Ribosomal protein L9



- Molecule 58: 60S Ribosomal protein L7a

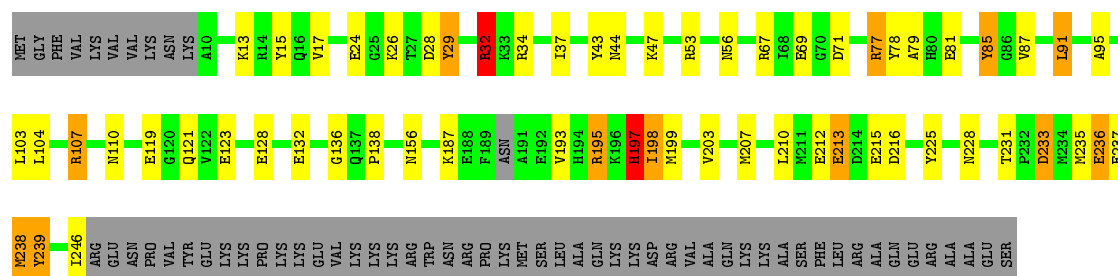


- Molecule 59: 60S acidic ribosomal protein P0

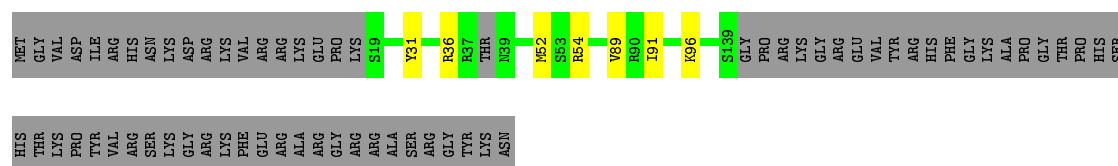


- Molecule 60: 60S Ribosomal protein L10

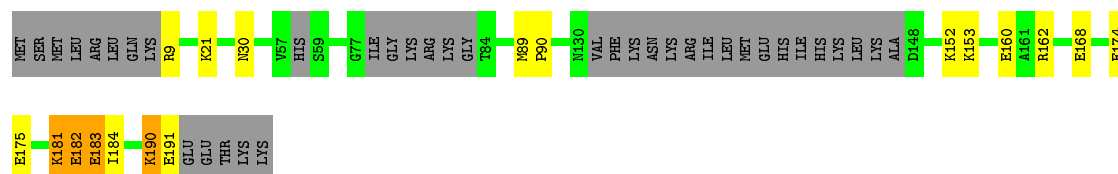




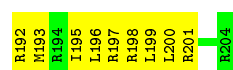
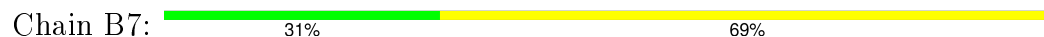
- Molecule 67: 60S Ribosomal protein L18



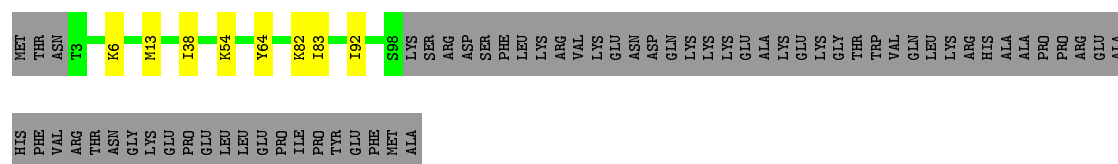
- Molecule 68: 60S Ribosomal protein L19



- Molecule 69: 60S Ribosomal protein L19

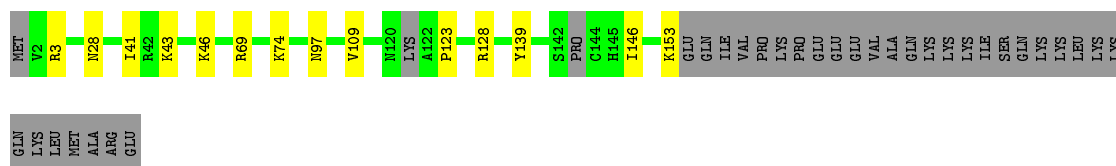


- Molecule 70: 60S Ribosomal protein L21

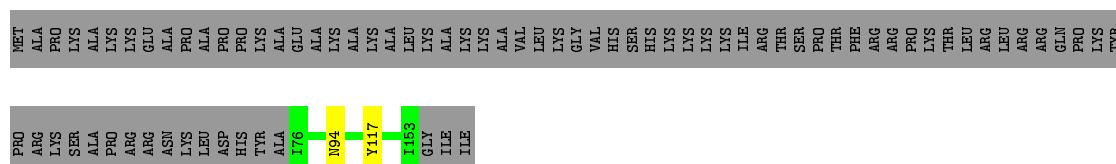


- Molecule 71: 60S Ribosomal protein L17

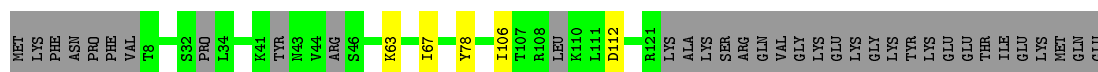




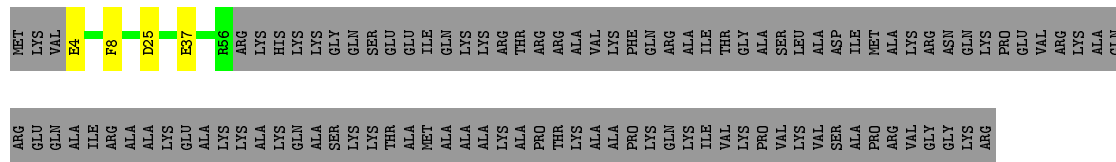
- Molecule 72: 60S Ribosomal protein L23a



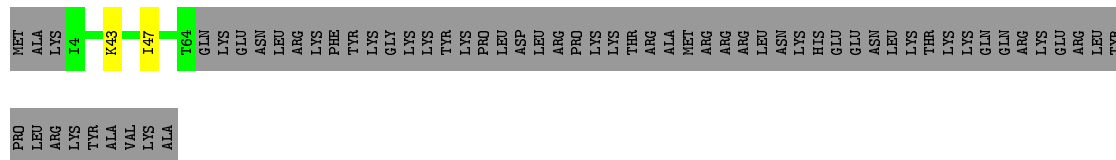
- Molecule 73: 60S Ribosomal protein L26



- Molecule 74: 60S Ribosomal protein L24



- Molecule 75: 60S Ribosomal protein L35



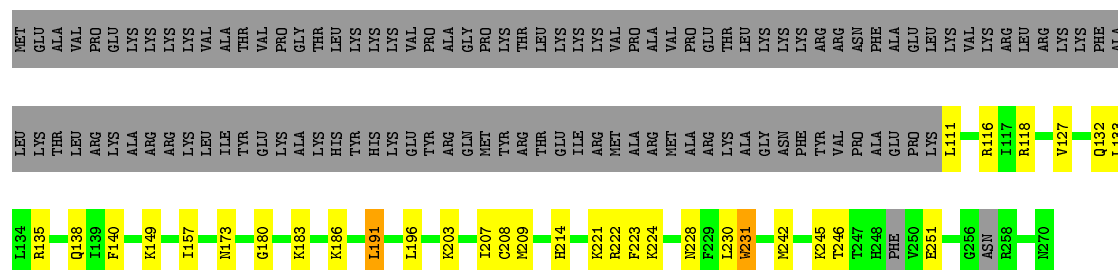
- Molecule 76: 60S Ribosomal protein L35



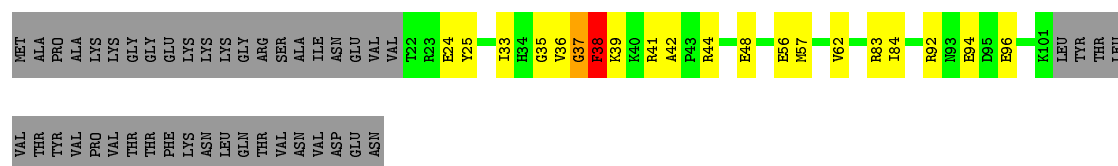
There are no outlier residues recorded for this chain.

- Molecule 77: 60S Ribosomal protein L7

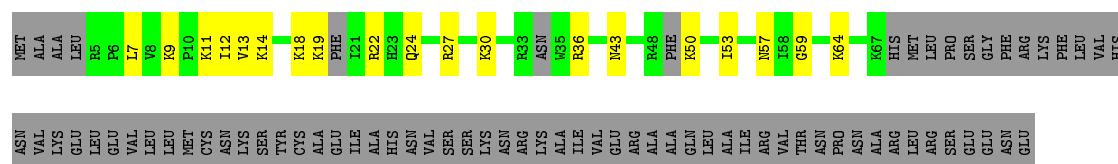
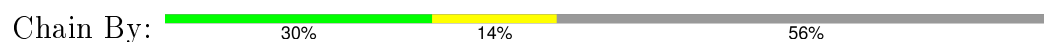




• Molecule 78: 60S Ribosomal protein L31



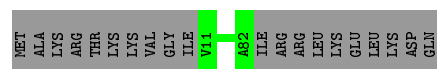
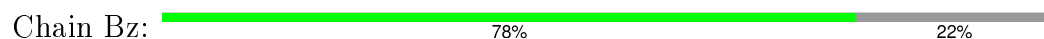
• Molecule 79: 60S Ribosomal protein L32



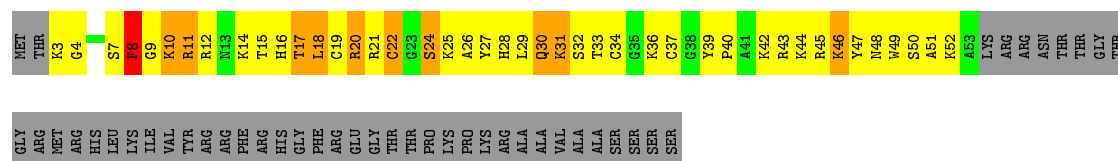
• Molecule 80: 60S Ribosomal protein L32



• Molecule 81: 60S Ribosomal protein L37a



• Molecule 82: 60S Ribosomal protein L37e



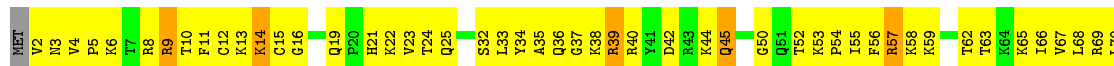
- Molecule 83: 60S Ribosomal protein L39e

Chain B3:  27% 63% 6%



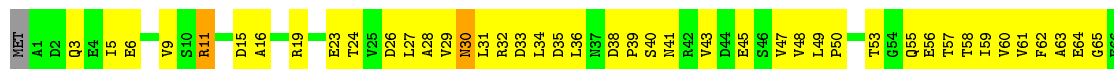
- Molecule 84: 60S Ribosomal protein L44e

Chain B4:  26% 56% 5% 13%



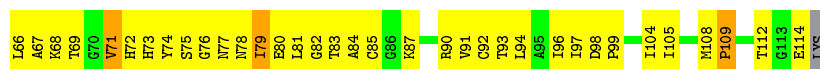
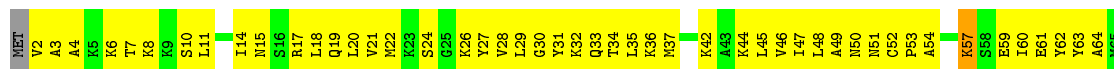
- Molecule 85: 60S Ribosomal protein L10a

Chain B5:  36% 62%



- Molecule 86: 60S Ribosomal protein L30e

Chain B6:  26% 69%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction using phase flipping and setsf in EMAN to correct the amplitudes	Depositor
Microscope	TF20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1500	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	4400	Depositor
Magnification	50000	Depositor
Image detector	Not provided	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	$\# Z > 2$
10	Ab	0.98	0/1556	1.11	2/2115 (0.1%)
11	Ac	1.13	14/1518 (0.9%)	1.08	3/2038 (0.1%)
12	Ad	1.09	0/856	1.01	1/1144 (0.1%)
13	Ae	1.00	0/1115	1.17	1/1505 (0.1%)
14	Ag	1.04	1/1288 (0.1%)	1.22	8/1725 (0.5%)
15	Ah	0.96	0/1033	1.10	1/1382 (0.1%)
16	Ai	1.08	1/1118 (0.1%)	1.20	3/1493 (0.2%)
17	Aj	1.04	0/781	1.17	0/1048
18	Ak	1.14	6/947 (0.6%)	1.24	3/1271 (0.2%)
19	Al	0.98	0/884	1.16	1/1184 (0.1%)
20	Am	1.10	0/1165	1.16	0/1555
21	An	1.14	0/420	1.22	1/557 (0.2%)
22	Ao	1.30	8/721 (1.1%)	1.25	3/962 (0.3%)
23	Aq	1.09	0/637	1.23	0/849
24	As	1.06	0/735	1.20	2/980 (0.2%)
53	Ba	1.05	0/1904	1.15	2/2552 (0.1%)
54	Bb	1.13	15/2824 (0.5%)	1.26	13/3786 (0.3%)
55	Bc	1.04	12/2076 (0.6%)	1.13	5/2790 (0.2%)
56	Bd	1.22	14/1347 (1.0%)	1.37	16/1801 (0.9%)
57	Be	1.05	10/1426 (0.7%)	1.13	4/1916 (0.2%)
58	Bf	1.11	7/932 (0.8%)	1.48	12/1256 (1.0%)
59	Bg	1.42	6/332 (1.8%)	1.10	1/454 (0.2%)
60	Bh	1.00	7/1358 (0.5%)	1.21	9/1811 (0.5%)
61	Bi	1.00	0/578	1.05	0/775
62	Bj	1.10	0/1118	1.13	0/1502
63	Bk	0.92	4/940 (0.4%)	1.07	4/1264 (0.3%)
64	Bl	1.04	0/972	1.22	2/1299 (0.2%)
65	Bm	1.10	0/1491	1.13	4/1999 (0.2%)
66	Bn	1.19	14/1949 (0.7%)	1.55	33/2615 (1.3%)
67	Bo	1.11	1/965 (0.1%)	1.17	1/1292 (0.1%)
68	Bp	1.22	6/1338 (0.4%)	1.19	4/1766 (0.2%)
69	B7	1.44	0/129	1.14	0/167
70	Bq	1.05	0/788	1.14	1/1049 (0.1%)
71	Br	1.03	0/1240	1.17	3/1660 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
72	Bs	0.88	0/630	1.09	1/850 (0.1%)
73	Bt	1.06	0/924	1.16	1/1223 (0.1%)
74	Bu	1.01	2/455 (0.4%)	1.03	1/610 (0.2%)
75	Bv	1.01	0/476	1.02	0/632
76	B8	1.09	0/77	1.08	0/103
77	Bw	1.07	0/1301	1.31	2/1737 (0.1%)
78	Bx	1.22	5/681 (0.7%)	1.50	10/908 (1.1%)
79	By	1.19	0/519	1.21	1/680 (0.1%)
80	B9	0.98	0/467	1.05	0/626
81	Bz	0.96	0/558	1.17	0/745
82	B2	1.13	0/415	1.36	3/547 (0.5%)
83	B3	1.11	0/439	1.03	0/580
84	B4	1.06	0/773	1.13	0/1022
85	B5	0.98	0/1638	1.13	0/2222
86	B6	0.97	0/885	1.11	0/1186
9	Aa	1.00	8/2434 (0.3%)	1.29	19/3309 (0.6%)
All	All	1.08	141/51153 (0.3%)	1.20	181/68542 (0.3%)

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
11	Ac	0	1
18	Ak	1	5
22	Ao	0	4
23	Aq	0	1
54	Bb	1	19
55	Bc	0	9
56	Bd	0	6
57	Be	0	1
58	Bf	1	6
60	Bh	0	5
63	Bk	1	1
66	Bn	0	9
68	Bp	1	2
74	Bu	0	1
78	Bx	1	6
9	Aa	0	17
All	All	6	93

The worst 5 of 141 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	Bn	81	GLU	CD-OE2	10.45	1.37	1.25
55	Bc	55	GLU	CD-OE2	9.63	1.36	1.25
14	Ag	122	ARG	C-N	9.62	1.56	1.34
68	Bp	183	GLU	CD-OE2	9.38	1.35	1.25
9	Aa	282	GLU	CD-OE2	9.37	1.35	1.25

The worst 5 of 181 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Bf	196	ARG	CA-CB-CG	16.48	149.66	113.40
56	Bd	115	LEU	CB-CG-CD1	15.28	136.98	111.00
54	Bb	211	GLY	C-N-CA	13.91	156.47	121.70
78	Bx	38	PHE	CB-CA-C	13.85	138.10	110.40
18	Ak	99	ALA	N-CA-CB	13.56	129.09	110.10

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
18	Ak	99	ALA	CA
54	Bb	137	GLN	CA
58	Bf	197	LYS	CA
63	Bk	21	PRO	CA
68	Bp	191	GLU	CA

5 of 93 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	Aa	14	HIS	Sidechain
9	Aa	34	ALA	Peptide
9	Aa	64	HIS	Sidechain
9	Aa	65	PHE	Sidechain
9	Aa	77	PHE	Sidechain

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	1391	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AB	32	0	0	0	0
3	AC	29	0	0	0	0
4	AD	42	0	0	0	0
5	AE	32	0	0	0	0
6	AF	31	0	0	0	0
7	AG	14	0	0	0	0
8	AH	41	0	0	0	0
9	Aa	2380	0	2337	0	0
10	Ab	1521	0	1531	0	0
11	Ac	1498	0	1575	0	0
12	Ad	845	0	879	0	0
13	Ae	1096	0	1160	0	0
14	Ag	1277	0	1325	0	0
15	Ah	1016	0	1057	0	0
16	Ai	1102	0	1160	0	0
17	Aj	772	0	839	0	0
18	Ak	935	0	951	0	0
19	Al	871	0	927	0	0
20	Am	1150	0	1202	0	0
21	An	410	0	408	0	0
22	Ao	710	0	743	0	0
23	Aq	629	0	674	0	0
24	As	721	0	759	0	0
25	B1	97	0	0	12	0
26	B0	2407	0	0	102	0
27	BA	21	0	0	0	0
28	BB	27	0	0	0	0
29	BC	17	0	0	0	0
30	BD	16	0	0	0	0
31	BE	54	0	0	0	0
32	BF	120	0	0	0	0
33	BG	48	0	0	0	0
34	BH	25	0	0	0	0
35	BI	72	0	0	0	0
36	BJ	30	0	0	0	0
37	BK	25	0	0	0	0
38	BL	20	0	0	0	0
39	BM	19	0	0	0	0
40	BN	78	0	0	0	0
41	BO	20	0	0	0	0
42	BP	15	0	0	0	0
43	BQ	30	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BR	30	0	0	0	0
45	BS	38	0	0	0	0
46	BT	30	0	0	0	0
47	BU	16	0	0	0	0
48	BV	22	0	0	0	0
49	BW	16	0	0	0	0
50	BX	113	0	0	0	0
51	BY	115	0	0	0	0
52	BZ	72	0	0	4	0
53	Ba	1867	0	1961	0	0
54	Bb	2765	0	2877	0	0
55	Bc	2035	0	2119	0	0
56	Bd	1325	0	1358	0	0
57	Be	1407	0	1481	0	0
58	Bf	920	0	1003	0	0
59	Bg	327	0	323	0	0
60	Bh	1331	0	1384	0	0
61	Bi	573	0	608	0	0
62	Bj	1095	0	1188	0	0
63	Bk	927	0	986	0	0
64	Bl	951	0	985	0	0
65	Bm	1454	0	1498	0	0
66	Bn	1912	0	1887	0	0
67	Bo	956	0	1057	0	0
68	Bp	1329	0	1449	0	0
69	B7	129	0	152	9	0
70	Bq	773	0	829	0	0
71	Br	1217	0	1241	0	0
72	Bs	622	0	661	0	0
73	Bt	916	0	977	0	0
74	Bu	443	0	435	0	0
75	Bv	477	0	546	0	0
76	B8	78	0	84	0	0
77	Bw	1281	0	1362	0	0
78	Bx	670	0	710	0	0
79	By	514	0	578	0	0
80	B9	460	0	481	80	0
81	Bz	548	0	567	0	0
82	B2	407	0	423	148	0
83	B3	429	0	466	84	0
84	B4	760	0	820	143	0
85	B5	1621	0	1559	330	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	B6	874	0	920	191	0
All	All	55531	0	52502	984	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 80.

The worst 5 of 984 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)
26:B0:4255:U:P	84:B4:13:LYS:HE2	1.35	1.64
25:B1:54:A:P	83:B3:21:ARG:HG2	1.40	1.61
26:B0:4192:U:P	84:B4:2:VAL:HG21	1.53	1.48
52:BZ:75:C:P	84:B4:54:PRO:HG2	1.51	1.47
26:B0:2757:C:P	83:B3:7:PHE:CD1	2.08	1.47

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	
9	Aa	300/317 (95%)	256 (85%)	31 (10%)	13 (4%)	3	34
10	Ab	188/295 (64%)	180 (96%)	5 (3%)	3 (2%)	12	56
11	Ac	190/243 (78%)	171 (90%)	12 (6%)	7 (4%)	4	38
12	Ad	101/209 (48%)	100 (99%)	1 (1%)	0	100	100
13	Ae	144/179 (80%)	136 (94%)	6 (4%)	2 (1%)	14	58
14	Ag	153/204 (75%)	147 (96%)	4 (3%)	2 (1%)	15	60
15	Ah	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
16	Ai	134/146 (92%)	120 (90%)	11 (8%)	3 (2%)	8	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Aj	95/119 (80%)	87 (92%)	3 (3%)	5 (5%)	2	29
18	Ak	123/151 (82%)	86 (70%)	31 (25%)	6 (5%)	3	31
19	Al	113/143 (79%)	88 (78%)	17 (15%)	8 (7%)	1	22
20	Am	138/152 (91%)	125 (91%)	9 (6%)	4 (3%)	6	43
21	An	47/56 (84%)	42 (89%)	4 (8%)	1 (2%)	9	50
22	Ao	83/89 (93%)	67 (81%)	15 (18%)	1 (1%)	16	61
23	Aq	70/158 (44%)	65 (93%)	4 (6%)	1 (1%)	14	58
24	As	86/145 (59%)	75 (87%)	7 (8%)	4 (5%)	3	32
53	Ba	240/257 (93%)	219 (91%)	14 (6%)	7 (3%)	6	43
54	Bb	343/403 (85%)	255 (74%)	58 (17%)	30 (9%)	1	17
55	Bc	255/421 (61%)	211 (83%)	33 (13%)	11 (4%)	3	34
56	Bd	163/178 (92%)	140 (86%)	19 (12%)	4 (2%)	7	46
57	Be	173/192 (90%)	155 (90%)	14 (8%)	4 (2%)	8	48
58	Bf	118/266 (44%)	103 (87%)	8 (7%)	7 (6%)	2	27
59	Bg	46/317 (14%)	37 (80%)	8 (17%)	1 (2%)	8	49
60	Bh	164/214 (77%)	154 (94%)	8 (5%)	2 (1%)	16	61
61	Bi	72/165 (44%)	67 (93%)	4 (6%)	1 (1%)	14	58
62	Bj	134/203 (66%)	129 (96%)	4 (3%)	1 (1%)	26	71
63	Bk	122/140 (87%)	114 (93%)	6 (5%)	2 (2%)	12	56
64	Bl	116/148 (78%)	110 (95%)	4 (3%)	2 (2%)	11	55
65	Bm	173/204 (85%)	164 (95%)	8 (5%)	1 (1%)	30	74
66	Bn	232/297 (78%)	186 (80%)	30 (13%)	16 (7%)	1	23
67	Bo	116/188 (62%)	109 (94%)	5 (4%)	2 (2%)	11	55
68	Bp	151/196 (77%)	141 (93%)	6 (4%)	4 (3%)	7	45
69	B7	11/13 (85%)	11 (100%)	0	0	100	100
70	Bq	94/160 (59%)	86 (92%)	7 (7%)	1 (1%)	17	63
71	Br	144/184 (78%)	137 (95%)	6 (4%)	1 (1%)	26	71
72	Bs	76/156 (49%)	74 (97%)	2 (3%)	0	100	100
73	Bt	100/145 (69%)	95 (95%)	3 (3%)	2 (2%)	9	51
74	Bu	51/157 (32%)	49 (96%)	2 (4%)	0	100	100
75	Bv	59/123 (48%)	59 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	B8	8/10 (80%)	8 (100%)	0	0	100	100
77	Bw	152/270 (56%)	119 (78%)	22 (14%)	11 (7%)	1	22
78	Bx	78/125 (62%)	66 (85%)	7 (9%)	5 (6%)	2	25
79	By	52/135 (38%)	39 (75%)	7 (14%)	6 (12%)	0	9
80	B9	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
81	Bz	70/92 (76%)	65 (93%)	5 (7%)	0	100	100
82	B2	49/97 (50%)	33 (67%)	10 (20%)	6 (12%)	0	8
83	B3	46/51 (90%)	46 (100%)	0	0	100	100
84	B4	90/106 (85%)	87 (97%)	2 (2%)	1 (1%)	17	63
85	B5	208/212 (98%)	199 (96%)	7 (3%)	2 (1%)	19	65
86	B6	111/115 (96%)	104 (94%)	5 (4%)	2 (2%)	11	53
All	All	6163/8734 (71%)	5492 (89%)	479 (8%)	192 (3%)	9	42

5 of 192 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	Aa	65	PHE
9	Aa	162	ASN
9	Aa	270	LEU
11	Ac	48	ILE
11	Ac	131	ALA

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	
9	Aa	265/275 (96%)	262 (99%)	3 (1%)	80	91
10	Ab	160/244 (66%)	152 (95%)	8 (5%)	30	66
11	Ac	157/202 (78%)	145 (92%)	12 (8%)	16	53
12	Ad	89/181 (49%)	88 (99%)	1 (1%)	80	91
13	Ae	117/146 (80%)	111 (95%)	6 (5%)	29	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	Ag	138/170 (81%)	131 (95%)	7 (5%)	29	66
15	Ah	110/113 (97%)	108 (98%)	2 (2%)	66	87
16	Ai	114/121 (94%)	110 (96%)	4 (4%)	43	74
17	Aj	90/107 (84%)	84 (93%)	6 (7%)	20	57
18	Ak	98/119 (82%)	90 (92%)	8 (8%)	14	49
19	Al	90/115 (78%)	89 (99%)	1 (1%)	80	91
20	Am	120/132 (91%)	114 (95%)	6 (5%)	30	66
21	An	43/49 (88%)	42 (98%)	1 (2%)	58	83
22	Ao	77/80 (96%)	71 (92%)	6 (8%)	16	51
23	Aq	72/142 (51%)	67 (93%)	5 (7%)	19	56
24	As	79/130 (61%)	71 (90%)	8 (10%)	9	38
53	Ba	187/199 (94%)	177 (95%)	10 (5%)	28	64
54	Bb	298/348 (86%)	271 (91%)	27 (9%)	12	43
55	Bc	214/351 (61%)	204 (95%)	10 (5%)	32	68
56	Bd	139/149 (93%)	134 (96%)	5 (4%)	42	74
57	Be	156/171 (91%)	147 (94%)	9 (6%)	25	61
58	Bf	100/223 (45%)	86 (86%)	14 (14%)	4	26
59	Bg	29/258 (11%)	29 (100%)	0	100	100
60	Bh	141/181 (78%)	136 (96%)	5 (4%)	43	74
61	Bi	64/137 (47%)	62 (97%)	2 (3%)	47	77
62	Bj	114/174 (66%)	110 (96%)	4 (4%)	43	74
63	Bk	97/107 (91%)	91 (94%)	6 (6%)	23	60
64	Bl	99/122 (81%)	97 (98%)	2 (2%)	63	85
65	Bm	148/172 (86%)	143 (97%)	5 (3%)	44	75
66	Bn	197/251 (78%)	177 (90%)	20 (10%)	9	37
67	Bo	108/165 (66%)	105 (97%)	3 (3%)	51	78
68	Bp	141/175 (81%)	134 (95%)	7 (5%)	30	66
69	B7	13/13 (100%)	13 (100%)	0	100	100
70	Bq	82/139 (59%)	76 (93%)	6 (7%)	17	54
71	Br	131/163 (80%)	120 (92%)	11 (8%)	14	48
72	Bs	69/133 (52%)	68 (99%)	1 (1%)	74	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Bt	103/135 (76%)	101 (98%)	2 (2%)	65	86
74	Bu	46/126 (36%)	46 (100%)	0	100	100
75	Bv	53/110 (48%)	51 (96%)	2 (4%)	40	73
76	B8	9/9 (100%)	9 (100%)	0	100	100
77	Bw	137/234 (58%)	115 (84%)	22 (16%)	3	20
78	Bx	71/110 (64%)	66 (93%)	5 (7%)	19	56
79	By	56/121 (46%)	44 (79%)	12 (21%)	1	9
80	B9	51/51 (100%)	48 (94%)	3 (6%)	24	61
81	Bz	57/75 (76%)	57 (100%)	0	100	100
82	B2	42/80 (52%)	38 (90%)	4 (10%)	11	41
83	B3	45/48 (94%)	43 (96%)	2 (4%)	35	69
84	B4	83/94 (88%)	78 (94%)	5 (6%)	24	60
85	B5	177/178 (99%)	173 (98%)	4 (2%)	58	83
86	B6	95/97 (98%)	92 (97%)	3 (3%)	46	76
All	All	5371/7425 (72%)	5076 (94%)	295 (6%)	31	63

5 of 295 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	Bd	107	PHE
61	Bi	103	ASN
79	By	50	LYS
57	Be	18	ILE
58	Bf	137	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
68	Bp	30	ASN
77	Bw	228	ASN
85	B5	185	HIS
70	Bq	69	HIS
77	Bw	248	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	0/1563	-	-
2	AB	0/35	-	-
25	B1	0/123	-	-
26	B0	0/2903	-	-
27	BA	0/21	-	-
28	BB	0/27	-	-
29	BC	0/17	-	-
3	AC	0/32	-	-
30	BD	0/16	-	-
31	BE	0/54	-	-
32	BF	0/120	-	-
33	BG	0/48	-	-
34	BH	0/25	-	-
35	BI	0/72	-	-
36	BJ	0/30	-	-
37	BK	0/26	-	-
38	BL	0/20	-	-
39	BM	0/19	-	-
4	AD	0/42	-	-
40	BN	0/78	-	-
41	BO	0/20	-	-
42	BP	0/15	-	-
43	BQ	0/30	-	-
44	BR	0/30	-	-
45	BS	0/38	-	-
46	BT	0/30	-	-
47	BU	0/16	-	-
48	BV	0/22	-	-
49	BW	0/16	-	-
5	AE	0/32	-	-
50	BX	0/113	-	-
51	BY	0/115	-	-
52	BZ	0/72	-	-
6	AF	0/31	-	-
7	AG	0/14	-	-
8	AH	0/41	-	-
All	All	0/5906	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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](#)

There are no chain breaks in this entry.