



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2025 – 05:13 pm GMT

PDB ID : 8PVA
EMDB ID : EMD-17959
Title : Structure of bacterial ribosome determined by cryoEM at 100 keV
Authors : McMullan, G.; Naydenova, K.; Mihaylov, D.; Peet, M.J.; Wilson, H.; Yamashita, K.; Dickerson, J.L.; Chen, S.; Cannone, G.; Lee, Y.; Hutchings, K.A.; Gittins, O.; Sobhy, M.; Wells, T.; El-Gomati, M.M.; Dalby, J.; Meffert, M.; Schulze-Briese, C.; Henderson, R.; Russo, C.J.
Deposited on : 2023-07-17
Resolution : 4.50 Å(reported)
Based on initial model : 7k00

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : **FAILED**
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41

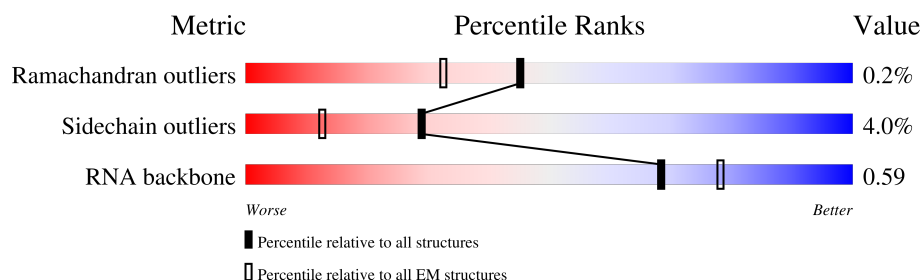
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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





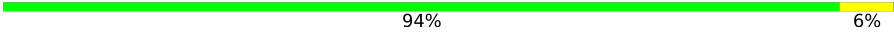

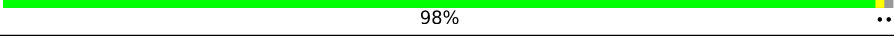
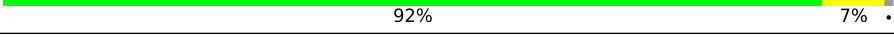
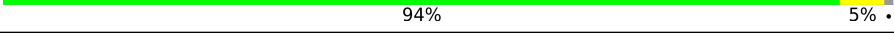

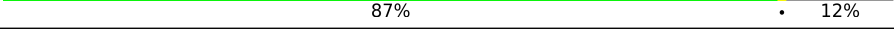

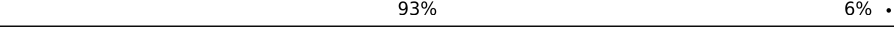
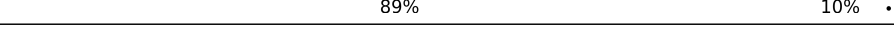

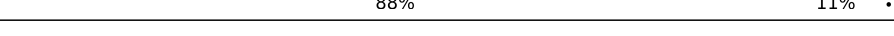
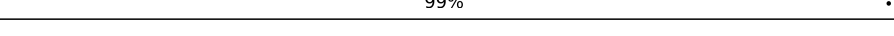
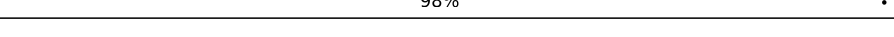
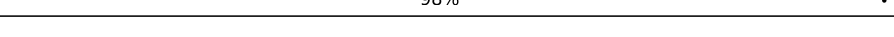
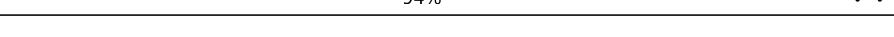
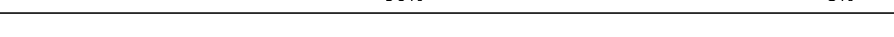






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	1542	
2	B	241	
3	C	233	
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	
9	I	130	


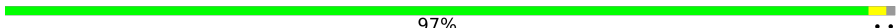
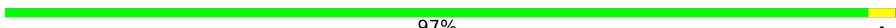
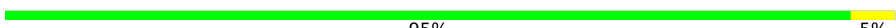
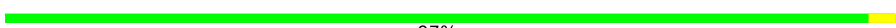








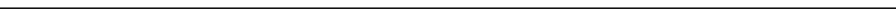

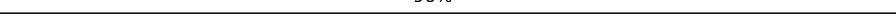
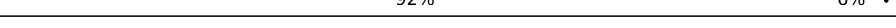
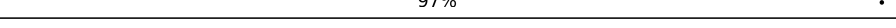




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Mol	Chain	Length	Quality of chain
10	J	103	 89% 5% • 5%
11	K	129	 86% 5% 9%
12	L	124	 94% 6% •
13	M	118	 90% 8% •
14	N	101	 98% ••
15	O	89	 92% 7% •
16	P	82	 94% 5% •
17	Q	84	 89% 5% 6%
18	R	75	 87% • 12%
19	S	92	 90% • 9%
20	T	87	 93% 6% •
21	U	71	 89% 10% •
22	a	2904	 82% 13% 5%
23	b	120	 88% 11% •
24	c	273	 99% ••
25	d	209	 98% •
26	e	201	 98% •
27	f	179	 94% ••
28	g	177	 90% 8% ••
29	h	149	 26% • 72%
30	i	142	 99% •
31	j	123	 98% •
32	k	144	 99% •
33	l	136	 99% •
34	m	127	 93% 7%

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Mol	Chain	Length	Quality of chain
35	n	117	94% 
36	o	115	97% 
37	p	118	97% 
38	q	103	95% 
39	r	110	97% 
40	s	100	92% 
41	t	104	91% 
42	u	94	99% 
43	v	85	92% 
44	w	78	94% 
45	x	63	92% 
46	y	59	93% 
47	z	57	96% 
48	0	55	87% 
49	1	46	96% 
50	2	65	92% 
51	3	38	97% 
52	4	70	83% 
53	X	28	36% 
54	Y	76	55% 
55	Z	76	62% 
56	5	2	50% 

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 141565 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1519	Total	C	N	O	P	0	0
			32612	14552	5986	10555	1519		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 28 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 29 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 30 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 33 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	conflict	UNP P0ADY7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	116	Total	C	N	O		0	0
			892	552	178	162			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	p	117	Total	C	N	O		0	0
			947	604	192	151			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	q	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	r	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	s	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	102	Total	C	N	O	S	0	0
			779	492	146	141			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	u	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	78	Total	C	N	O	S	0	0
			586	362	116	107	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	w	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	y	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	z	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	51	Total	C	N	O		0	0
			417	269	76	72			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	X	12	Total	C	N	O	P	0	0
			260	117	51	80	12		

- Molecule 54 is a RNA chain called A-site tRNA-val.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Y	74	Total	C	N	O	P	0	0
			1579	705	287	514	73		

- Molecule 55 is a RNA chain called P-site tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Z	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

- Molecule 56 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

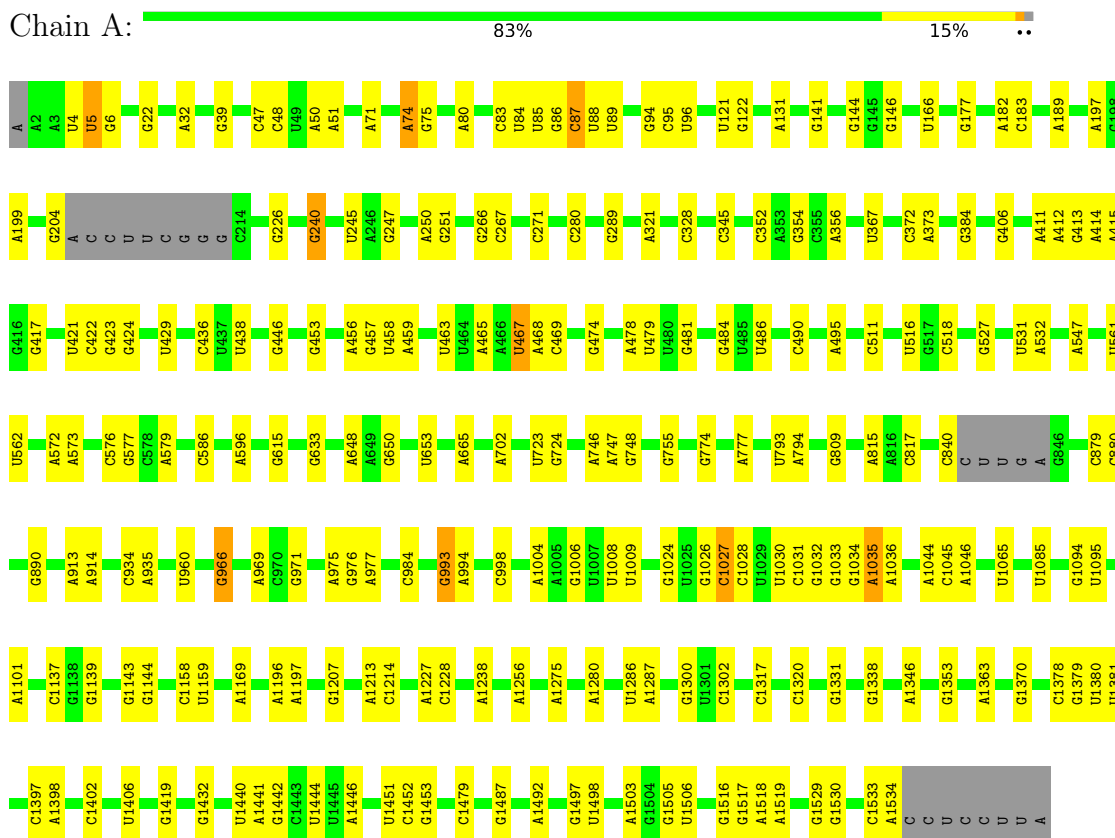
- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	3	1	Total	Zn	0
			1	1	
57	4	1	Total	Zn	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S rRNA



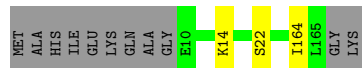
- Molecule 4: Small ribosomal subunit protein uS4

Chain D:  93% 6%



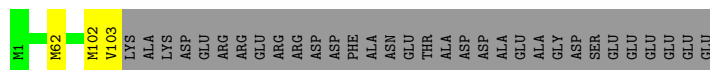
- Molecule 5: Small ribosomal subunit protein uS5

Chain E:  92% 7%



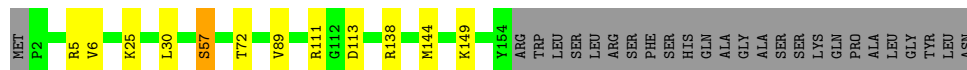
- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform

Chain F:  74% 24%



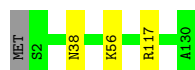
- Molecule 7: Small ribosomal subunit protein uS7

Chain G:  79% 6% 15%



- Molecule 8: Small ribosomal subunit protein uS8

Chain H:  97% ..




- Molecule 9: Small ribosomal subunit protein uS9

Chain I:  94% ..




- Molecule 10: Small ribosomal subunit protein uS10

Chain J:  89% 5% 5%



- Molecule 11: Small ribosomal subunit protein uS11

Chain K:  86% 5% 9%



- Molecule 12: Small ribosomal subunit protein uS12

Chain L:  94% 6% .



- Molecule 13: Small ribosomal subunit protein uS13

Chain M:  90% 8% .



- Molecule 14: Small ribosomal subunit protein uS14

Chain N:  98% ..



- Molecule 15: Small ribosomal subunit protein uS15

Chain O:  92% 7% .




- Molecule 16: Small ribosomal subunit protein bS16

Chain P:  94% 5% .



- Molecule 17: Small ribosomal subunit protein uS17

Chain Q:  89% 5% 6%



- Molecule 18: Small ribosomal subunit protein bS18

MET
ALA
ARG
TYR
PHE
ARG
ARG
ARG
K9
E35
H74
GLN

- Chain S: 90% 9%

MET
P2
N43
A85
ASP
LYS
LYS
ALA
LYS
LYS
LYS

- Chain T:  93% 6%

- Chain U: 89% 10%

Diagram illustrating the 100-residue protein sequence with residues MET, P2, N9, R18, R21, E44, R47, L60, E63, and Y71 highlighted in yellow.

- Chain a: 82% 13% 5%

U	U1012	A789	G543	A272	G1
A	C1013	G805	C544	G273	A10
U	G1017		U545	C274	
A		C812	U546	G277	G15
G	G1022		A547	A278	
C	U1033	C815	G548	A279	U34
U		U827	G549		
C	G1041	U828	A563	A282	A42
C					
C	C1045	U846	U573	G285	G45
G	A1046	U847	A574	U286	
	G1047		A575	G289	G58
U1108	A1048	G856			A71
	C1049		A603	U293	
A1111	A1050	G859	A614	U294	A74
G1112	G1051		U615	A294	G75
	C1052	G869		A311	G80
G1115		A877	A627		
G1116		A878	G329	A84	
G1120		G879	A637	A330	A84
G1121					
G1122			C645	A345	A101
		G883	U646		U102
U1132		U884	G647	C357	G110
A1133		G885			
A1134		A886	U853	G361	A118
C1135		U887	A854	A362	A119
			A655		U120
A1142		G890		G386	G121
		C891			G122
G1171		U895	A685	U397	
G1172		A896	U686		U139
U		C897		A404	C140
U		C898	G704	U405	G141
A		A899	U714		A142
U		C		G411	
G1177		A905	C717	A412	C163
					C164
G1227		A910	A721	U451	A165
A1253		G914	A730	G481	A181
G1256		C915			
		C	G745	G491	A196
G1271		A	U746		
A1272		U	U747	A504	G215
		U		A505	A216
A1275		C961	A764	C509	
		A	C765		A221
U1294					A222
		G974	G775	G512	
			G776		A231
G1300		A983		A528	
A1301		A984	A782	A529	C248
		C985	G830	G530	
C1314			A784	C531	C264
		G	G785	A532	A265
A1351		C		C532	

Chain e:  98% .




- Molecule 27: Large ribosomal subunit protein uL5

Chain f:  94% ..



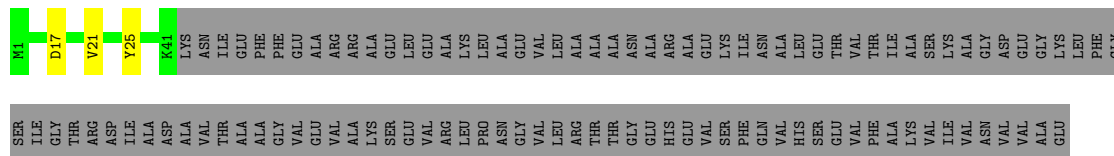
- Molecule 28: Large ribosomal subunit protein uL6

Chain g:  90% 8% ..



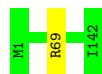
- Molecule 29: Large ribosomal subunit protein bL9

Chain h:  26% . 72%



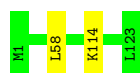
- Molecule 30: Large ribosomal subunit protein uL13

Chain i:  99% .



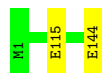
- Molecule 31: 50S ribosomal protein L14

Chain j:  98% .



- Molecule 32: 50S ribosomal protein L15

Chain k:  99% .



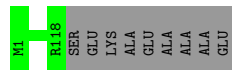
- Molecule 33: Large ribosomal subunit protein uL16

Chain l:  99%



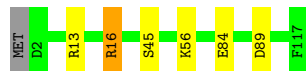
- Molecule 34: 50S ribosomal protein L17

Chain m:  93%



- Molecule 35: 50S ribosomal protein L18

Chain n:  94%



- Molecule 36: 50S ribosomal protein L19

Chain o:  97%



- Molecule 37: 50S ribosomal protein L20

Chain p:  97%



- Molecule 38: 50S ribosomal protein L21

Chain q:  95%



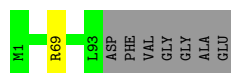
- Molecule 39: 50S ribosomal protein L22

Chain r:  97%



- Molecule 40: 50S ribosomal protein L23

Chain s:  92% 7%



- Molecule 41: 50S ribosomal protein L24

Chain t:  91% 7%



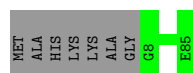
- Molecule 42: 50S ribosomal protein L25

Chain u:  99%



- Molecule 43: 50S ribosomal protein L27

Chain v:  92% 8%



- Molecule 44: 50S ribosomal protein L28

Chain w:  94% 5%



- Molecule 45: 50S ribosomal protein L29

Chain x:  92% 6%



- Molecule 46: 50S ribosomal protein L30

Chain y:  93%




- Molecule 47: 50S ribosomal protein L32

Chain z:  96% ..



- Molecule 48: 50S ribosomal protein L33

Chain 0:  87% 5% 7%



- Molecule 49: 50S ribosomal protein L34

Chain 1:  96% .



- Molecule 50: 50S ribosomal protein L35

Chain 2:  92% 6% .




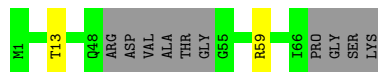
- Molecule 51: 50S ribosomal protein L36

Chain 3:  97% .




- Molecule 52: Large ribosomal subunit protein bL31A

Chain 4:  83% . 14%



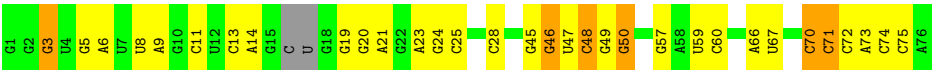
- Molecule 53: mRNA

Chain X:  36% 7% 57%



- Molecule 54: A-site tRNA-val

Chain Y:  55% 34% 8% .



• Molecule 55: P-site tRNA-fMet



• Molecule 56: E-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11872	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 1400/HR + YPS FEG	Depositor
Voltage (kV)	100	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	DECTRIS SINGLE (1k x 1k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, H2U, 1MG, 2MA, OMC, PSU, ZN, 2MG, UR3, G7M, 3TD, MS6, 4OC, OMU, 5MC, 5MU, D2T, 4D4, MA6, IAS, MEQ, 6MZ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.66	0/36236	1.17	24/56520 (0.0%)
2	B	0.45	0/1784	0.85	0/2403
3	C	0.43	0/1651	0.84	2/2225 (0.1%)
4	D	0.44	0/1665	0.88	1/2227 (0.0%)
5	E	0.44	0/1165	0.84	0/1568
6	F	0.45	0/858	0.85	0/1160
7	G	0.44	0/1219	0.95	1/1635 (0.1%)
8	H	0.43	0/989	0.83	1/1326 (0.1%)
9	I	0.44	0/1034	0.90	2/1375 (0.1%)
10	J	0.42	0/796	0.97	3/1077 (0.3%)
11	K	0.43	0/884	0.84	0/1191
12	L	0.43	0/960	0.89	1/1286 (0.1%)
13	M	0.46	0/900	0.99	5/1204 (0.4%)
14	N	0.42	0/817	0.81	0/1088
15	O	0.42	0/722	0.78	0/964
16	P	0.42	0/653	0.87	0/877
17	Q	0.42	0/650	0.86	0/871
18	R	0.43	0/553	0.89	0/742
19	S	0.45	0/685	0.83	0/922
20	T	0.41	0/676	0.83	0/895
21	U	0.43	0/597	1.01	2/792 (0.3%)
22	a	0.64	0/65651	1.18	31/102413 (0.0%)
23	b	0.68	0/2850	1.20	0/4444
24	c	0.43	0/2121	0.86	1/2852 (0.0%)
25	d	0.41	0/1576	0.80	1/2119 (0.0%)
26	e	0.41	0/1571	0.80	0/2113
27	f	0.45	0/1434	0.83	1/1926 (0.1%)
28	g	0.45	0/1343	0.91	1/1816 (0.1%)
29	h	0.48	0/306	0.96	0/413
30	i	0.42	0/1152	0.81	1/1551 (0.1%)
31	j	0.42	0/955	0.87	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	k	0.45	0/1062	0.83	0/1413
33	l	0.41	0/1073	0.85	0/1433
34	m	0.41	0/958	0.86	0/1281
35	n	0.43	0/902	0.88	1/1209 (0.1%)
36	o	0.41	0/929	0.87	1/1242 (0.1%)
37	p	0.40	0/960	0.80	0/1278
38	q	0.43	0/829	0.87	0/1107
39	r	0.40	0/864	0.84	0/1156
40	s	0.41	0/744	0.87	1/994 (0.1%)
41	t	0.43	0/787	0.88	0/1051
42	u	0.42	0/766	0.86	0/1025
43	v	0.43	0/593	0.84	0/785
44	w	0.43	0/635	0.88	1/848 (0.1%)
45	x	0.44	0/502	0.83	0/667
46	y	0.41	0/453	0.86	0/605
47	z	0.42	0/450	0.84	0/599
48	0	0.44	0/424	0.90	0/565
49	1	0.40	0/380	0.88	0/498
50	2	0.41	0/513	0.91	1/676 (0.1%)
51	3	0.41	0/303	0.91	0/397
52	4	0.45	0/488	0.82	0/649
53	X	0.71	0/292	1.10	0/453
54	Y	0.75	0/1764	1.43	10/2747 (0.4%)
55	Z	0.74	0/1813	1.31	2/2825 (0.1%)
56	5	0.99	0/46	1.12	0/69
All	All	0.60	0/152983	1.11	95/228846 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
12	L	0	1
28	g	0	2
46	y	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	71	ARG	NE-CZ-NH1	10.38	125.49	120.30
22	a	512	G	O4'-C1'-N9	9.34	115.67	108.20
54	Y	46	G	O4'-C1'-N9	8.20	114.76	108.20
22	a	122	G	O5'-P-OP2	-8.18	98.33	105.70
54	Y	70	C	C6-N1-C2	-7.59	117.26	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	130	THR	Peptide
12	L	101	ALA	Peptide
28	g	43	VAL	Peptide
28	g	47	ASP	Peptide
46	y	3	LYS	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/241 (92%)	208 (94%)	14 (6%)	0	100	100
3	C	204/233 (88%)	196 (96%)	8 (4%)	0	100	100
4	D	203/206 (98%)	195 (96%)	8 (4%)	0	100	100
5	E	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
6	F	101/135 (75%)	96 (95%)	5 (5%)	0	100	100
7	G	151/179 (84%)	138 (91%)	10 (7%)	3 (2%)	6	32
8	H	127/130 (98%)	121 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
10	J	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	13	49
11	K	113/129 (88%)	108 (96%)	5 (4%)	0	100	100
12	L	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
13	M	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
14	N	98/101 (97%)	95 (97%)	2 (2%)	1 (1%)	13	49
15	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
16	P	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
17	Q	77/84 (92%)	74 (96%)	3 (4%)	0	100	100
18	R	64/75 (85%)	59 (92%)	5 (8%)	0	100	100
19	S	82/92 (89%)	80 (98%)	2 (2%)	0	100	100
20	T	84/87 (97%)	84 (100%)	0	0	100	100
21	U	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
24	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
25	d	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
26	e	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
27	f	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
28	g	174/177 (98%)	152 (87%)	19 (11%)	3 (2%)	7	36
29	h	39/149 (26%)	35 (90%)	4 (10%)	0	100	100
30	i	140/142 (99%)	140 (100%)	0	0	100	100
31	j	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
32	k	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
33	l	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
34	m	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
35	n	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
36	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
37	p	115/118 (98%)	115 (100%)	0	0	100	100
38	q	101/103 (98%)	99 (98%)	1 (1%)	1 (1%)	13	49
39	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
40	s	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
41	t	100/104 (96%)	90 (90%)	9 (9%)	1 (1%)	13	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	u	92/94 (98%)	92 (100%)	0	0	100	100
43	v	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
44	w	75/78 (96%)	75 (100%)	0	0	100	100
45	x	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
46	y	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
47	z	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
48	0	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
51	3	36/38 (95%)	36 (100%)	0	0	100	100
52	4	56/70 (80%)	53 (95%)	3 (5%)	0	100	100
All	All	5481/5913 (93%)	5273 (96%)	198 (4%)	10 (0%)	45	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	g	47	ASP
28	g	92	VAL
7	G	57	SER
10	J	57	VAL
14	N	33	ASP

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	B	186/199 (94%)	173 (93%)	13 (7%)	12	33
3	C	170/190 (90%)	163 (96%)	7 (4%)	26	48
4	D	172/173 (99%)	158 (92%)	14 (8%)	9	29
5	E	119/126 (94%)	116 (98%)	3 (2%)	42	62
6	F	90/116 (78%)	87 (97%)	3 (3%)	33	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	126/147 (86%)	117 (93%)	9 (7%)	12	32
8	H	104/105 (99%)	102 (98%)	2 (2%)	52	69
9	I	105/107 (98%)	102 (97%)	3 (3%)	37	58
10	J	86/90 (96%)	83 (96%)	3 (4%)	31	52
11	K	89/98 (91%)	83 (93%)	6 (7%)	13	34
12	L	102/103 (99%)	98 (96%)	4 (4%)	27	49
13	M	93/96 (97%)	88 (95%)	5 (5%)	18	40
14	N	83/84 (99%)	83 (100%)	0	100	100
15	O	76/77 (99%)	70 (92%)	6 (8%)	10	29
16	P	65/65 (100%)	61 (94%)	4 (6%)	15	37
17	Q	73/78 (94%)	69 (94%)	4 (6%)	18	40
18	R	57/65 (88%)	56 (98%)	1 (2%)	54	71
19	S	72/79 (91%)	71 (99%)	1 (1%)	62	75
20	T	65/66 (98%)	60 (92%)	5 (8%)	10	30
21	U	60/61 (98%)	55 (92%)	5 (8%)	9	28
24	c	216/218 (99%)	215 (100%)	1 (0%)	86	89
25	d	163/163 (100%)	160 (98%)	3 (2%)	54	71
26	e	165/165 (100%)	160 (97%)	5 (3%)	36	56
27	f	148/150 (99%)	141 (95%)	7 (5%)	22	44
28	g	137/138 (99%)	124 (90%)	13 (10%)	7	23
29	h	32/114 (28%)	29 (91%)	3 (9%)	7	23
30	i	116/116 (100%)	116 (100%)	0	100	100
31	j	104/104 (100%)	102 (98%)	2 (2%)	52	69
32	k	103/103 (100%)	101 (98%)	2 (2%)	52	69
33	l	107/107 (100%)	106 (99%)	1 (1%)	75	83
34	m	98/103 (95%)	98 (100%)	0	100	100
35	n	86/87 (99%)	80 (93%)	6 (7%)	12	33
36	o	99/100 (99%)	98 (99%)	1 (1%)	73	81
37	p	89/90 (99%)	86 (97%)	3 (3%)	32	53
38	q	84/84 (100%)	80 (95%)	4 (5%)	21	43
39	r	93/93 (100%)	90 (97%)	3 (3%)	34	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	s	80/84 (95%)	80 (100%)	0	100	100
41	t	83/85 (98%)	77 (93%)	6 (7%)	12	32
42	u	78/78 (100%)	77 (99%)	1 (1%)	65	77
43	v	58/63 (92%)	58 (100%)	0	100	100
44	w	67/68 (98%)	64 (96%)	3 (4%)	23	46
45	x	54/55 (98%)	50 (93%)	4 (7%)	11	31
46	y	48/49 (98%)	45 (94%)	3 (6%)	15	36
47	z	47/48 (98%)	46 (98%)	1 (2%)	48	67
48	0	46/49 (94%)	43 (94%)	3 (6%)	14	35
49	1	38/38 (100%)	36 (95%)	2 (5%)	19	41
50	2	51/52 (98%)	48 (94%)	3 (6%)	16	38
51	3	34/34 (100%)	33 (97%)	1 (3%)	37	58
52	4	55/62 (89%)	53 (96%)	2 (4%)	30	52
All	All	4572/4825 (95%)	4391 (96%)	181 (4%)	29	48

5 of 181 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	g	18	LYS
37	p	51	ARG
28	g	75	MET
31	j	58	LEU
39	r	66	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
24	c	115	GLN
29	h	20	ASN
45	x	15	ASN
24	c	117	GLN
28	g	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1513/1542 (98%)	207 (13%)	6 (0%)
22	a	2745/2904 (94%)	344 (12%)	0
23	b	118/120 (98%)	13 (11%)	0
53	X	11/28 (39%)	2 (18%)	0
54	Y	72/76 (94%)	29 (40%)	6 (8%)
55	Z	75/76 (98%)	27 (36%)	1 (1%)
56	5	1/2 (50%)	1 (100%)	0
All	All	4535/4748 (95%)	623 (13%)	13 (0%)

5 of 623 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	22	G
1	A	32	A

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	Y	19	G
54	Y	45	G
55	Z	58	A
54	Y	48	C
54	Y	60	C

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

39 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
11	IAS	K	119	11	6,7,8	0.94	0	6,8,10	1.02	0
22	H2U	a	2449	22	18,21,22	0.86	1 (5%)	21,30,33	0.78	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	4D4	l	81	33	9,11,12	0.50	0	8,13,15	0.70	0
22	OMG	a	2251	22,55	18,26,27	1.02	2 (11%)	19,38,41	0.74	0
22	2MA	a	2503	22	19,25,26	1.15	2 (10%)	21,37,40	2.00	5 (23%)
22	PSU	a	955	22	18,21,22	0.99	1 (5%)	22,30,33	0.75	0
22	PSU	a	2504	22	18,21,22	0.98	1 (5%)	22,30,33	0.74	0
22	PSU	a	2604	22	18,21,22	1.03	1 (5%)	22,30,33	0.90	0
1	2MG	A	1516	1	18,26,27	1.03	1 (5%)	16,38,41	0.80	0
1	MA6	A	1519	1	18,26,27	0.85	1 (5%)	19,38,41	0.79	0
1	UR3	A	1498	1	19,22,23	0.41	0	26,32,35	0.83	2 (7%)
1	G7M	A	527	1	20,26,27	1.12	2 (10%)	17,39,42	0.72	0
22	PSU	a	746	22	18,21,22	1.16	1 (5%)	22,30,33	0.84	0
22	PSU	a	1917	22	18,21,22	1.01	1 (5%)	22,30,33	0.77	1 (4%)
22	PSU	a	2457	22	18,21,22	1.00	1 (5%)	22,30,33	0.75	0
22	G7M	a	2069	22	20,26,27	1.07	2 (10%)	17,39,42	0.75	0
1	MA6	A	1518	1	18,26,27	0.85	1 (5%)	19,38,41	0.47	0
22	5MU	a	1939	22	19,22,23	0.42	0	28,32,35	0.50	0
22	6MZ	a	1618	22	18,25,26	0.74	0	16,36,39	0.84	1 (6%)
1	4OC	A	1402	1	20,23,24	0.49	0	26,32,35	0.82	1 (3%)
1	5MC	A	1407	1	18,22,23	0.45	0	26,32,35	0.86	0
1	2MG	A	966	1	18,26,27	1.07	2 (11%)	16,38,41	0.67	0
25	MEQ	d	150	25	8,9,10	0.45	0	5,10,12	1.71	2 (40%)
1	2MG	A	1207	1	18,26,27	1.02	1 (5%)	16,38,41	0.79	0
1	5MC	A	967	1	18,22,23	0.44	0	26,32,35	0.77	0
22	2MG	a	2445	22	18,26,27	1.04	2 (11%)	16,38,41	0.78	0
12	D2T	L	89	12	7,9,10	1.04	0	6,11,13	1.64	3 (50%)
22	5MC	a	1962	22	18,22,23	0.44	0	26,32,35	0.84	1 (3%)
22	PSU	a	1911	22	18,21,22	1.02	1 (5%)	22,30,33	0.74	0
1	PSU	A	516	1	18,21,22	1.02	1 (5%)	22,30,33	0.73	0
22	3TD	a	1915	22	19,22,23	1.03	1 (5%)	21,32,35	1.00	2 (9%)
22	1MG	a	745	22	18,26,27	1.07	2 (11%)	19,39,42	0.49	0
22	6MZ	a	2030	22	18,25,26	0.70	0	16,36,39	0.87	1 (6%)
22	OMU	a	2552	22	19,22,23	0.36	0	26,31,34	0.50	0
22	OMC	a	2498	22	19,22,23	0.42	0	26,31,34	0.74	0
22	5MU	a	747	22	19,22,23	0.44	0	28,32,35	0.51	0
22	PSU	a	2605	22	18,21,22	1.03	1 (5%)	22,30,33	0.89	0
22	PSU	a	2580	22	18,21,22	1.00	1 (5%)	22,30,33	0.83	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	2MG	a	1835	22	18,26,27	1.02	2 (11%)	16,38,41	0.67	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	IAS	K	119	11	-	0/7/7/8	-
22	H2U	a	2449	22	-	0/7/38/39	0/2/2/2
33	4D4	l	81	33	-	1/11/12/14	-
22	OMG	a	2251	22,55	-	0/5/27/28	0/3/3/3
22	2MA	a	2503	22	-	2/3/25/26	0/3/3/3
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2504	22	-	2/7/25/26	0/2/2/2
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/5/27/28	0/3/3/3
1	MA6	A	1519	1	-	2/7/29/30	0/3/3/3
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	1/3/25/26	0/3/3/3
22	PSU	a	746	22	-	1/7/25/26	0/2/2/2
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
22	G7M	a	2069	22	-	2/3/25/26	0/3/3/3
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
22	6MZ	a	1618	22	-	0/5/27/28	0/3/3/3
1	4OC	A	1402	1	-	0/9/29/30	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	2MG	A	966	1	-	0/5/27/28	0/3/3/3
25	MEQ	d	150	25	-	2/8/9/11	-
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	1/5/27/28	0/3/3/3
12	D2T	L	89	12	-	2/7/12/14	-
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2
22	3TD	a	1915	22	-	0/7/25/26	0/2/2/2
22	1MG	a	745	22	-	0/3/25/26	0/3/3/3
22	6MZ	a	2030	22	-	2/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	OMU	a	2552	22	-	1/9/27/28	0/2/2/2
22	OMC	a	2498	22	-	0/9/27/28	0/2/2/2
22	5MU	a	747	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
22	2MG	a	1835	22	-	0/5/27/28	0/3/3/3

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	746	PSU	C6-C5	4.46	1.40	1.35
22	a	2605	PSU	C6-C5	4.07	1.40	1.35
1	A	516	PSU	C6-C5	4.06	1.40	1.35
22	a	1911	PSU	C6-C5	4.04	1.40	1.35
22	a	2580	PSU	C6-C5	4.02	1.40	1.35

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2503	2MA	C5-C6-N1	-6.76	116.57	121.01
22	a	2503	2MA	C5-C6-N6	3.64	125.89	120.35
22	a	2503	2MA	CM2-C2-N1	3.24	122.22	117.15
22	a	2030	6MZ	C2-N1-C6	2.49	118.72	116.59
22	a	2503	2MA	C2-N1-C6	2.36	121.76	118.08

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	L	89	D2T	CG-CB-SB-CB1
22	a	2030	6MZ	O4'-C4'-C5'-O5'
25	d	150	MEQ	NE2-CD-CG-CB
25	d	150	MEQ	OE1-CD-CG-CB
22	a	2030	6MZ	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.