

Full wwPDB EM Validation Report (i)

Apr 16, 2024 – 05:24 am BST

PDB ID : 8CGU

EMDB ID : EMD-16651

Title: Gentamicin bound to the 30S body

Authors : Paternoga, H.; Crowe-McAuliffe, C.; Novacek, J.; Wilson, D.N.

Deposited on : 2023-02-06

Resolution : 1.89 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*A user guide is available at

https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev92

Mogul : 1.8.4, CSD as541be (2020)

 $\begin{array}{lll} \text{MolProbity} & : & 4.02\text{b-}467 \\ \text{buster-report} & : & 1.1.7 \ (2018) \end{array}$

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

MapQ : 1.9.13

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

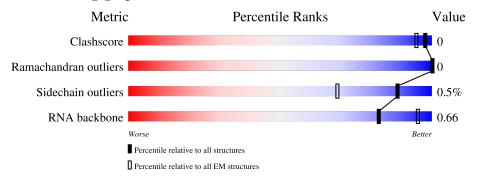
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 1.89 Å.

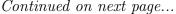
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive $(\# \mathrm{Entries})$	${ m EM\ structures} \ (\#{ m Entries})$
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion <40%). The numeric value is given above the bar.

Mol	Chain	Length	Quali	ty of chain
1	A	1540	58%	10% • 32%
2	D	206	15%	5%
3	Е	167	8%92'	% - 7%
4	F	131	31%	22%
5	Н	130	<u>-</u>	98%
6	K	129	29%	• 14%
7	L	124	94	4%





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Mol	Chain	Length	Quality of chain	
0	0	90	13%	
8	О	89	99%	•
9	Р	82	98%	
		02	15%	
10	Q	84	90% . 8	%
11	R	75	20% 84% • 12°	%
12	Т	87	9%	•••
13	U	71	62% • 34%	
14	a	2904	99%	_



2 Entry composition (i)

There are 18 unique types of molecules in this entry. The entry contains 35196 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		A	toms			AltConf	Trace
1	A	1047	Total 22517	C 10045	N 4159	O 7266	P 1047	0	0

• Molecule 2 is a protein called Small ribosomal subunit protein uS4.

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

• Molecule 3 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues		At	oms			AltConf	Trace
3	Е	156	Total 1152	C 717	N 217	O 212	S 6	0	0

• Molecule 4 is a protein called Small ribosomal subunit protein bS6, non-modified isoform.

Mol	Chain	Residues		At	oms			AltConf	Trace
4	F	102	Total 831	C 525	N 150	O 150	S 6	0	0

• Molecule 5 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues		At	oms			AltConf	Trace
5	Н	129	Total 979	C 616	N 173	O 184	S 6	0	0

• Molecule 6 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues		At	oms			AltConf	Trace
6	K	111	Total 827	C 511	N 162	O 151	S 3	0	0



There is a discrepancy between the modelled and reference sequences:

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

• Molecule 7 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues		At	oms			AltConf	Trace
7	Т	110	Total	С	N	О	S	0	0
'	Ъ	119	925	571	188	161	5	0	U

• Molecule 8 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	0	88	Total	С	N	О	S	0	0
		00	714	439	144	130	1		

• Molecule 9 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues		At	oms			AltConf	Trace
9	Р	81	Total	С	N	О	S	0	0
	1	01	643	403	127	112	1		

• Molecule 10 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	Q	77	Total 624	C 394	N 117	O 110	S 3	0	0

• Molecule 11 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues		Ato	oms			AltConf	Trace
11	R	66	Total 544	C 345	N 102	O 96	S 1	0	0

• Molecule 12 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues		At	oms			AltConf	Trace
12	Т	86	Total 670	C 414	N 138	O 115	S 3	0	0

• Molecule 13 is a protein called Small ribosomal subunit protein bS21.



Mol	Chain	Residues		Ato	ms			AltConf	Trace
13	IJ	47	Total	С	N	О	S	0	0
	O	11	386	241	82	62	1		O

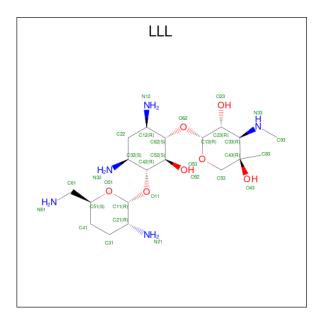
• Molecule 14 is a RNA chain called 23S rRNA.

Mol	Chain	Residues		A	toms			AltConf	Trace
14	a	31	Total 664	C 297	N 121	O 215	P 31	0	0

• Molecule 15 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
15	A	22	Total K 22 22	0
15	D	1	Total K 1 1	0
15	F	1	Total K 1 1	0

• Molecule 16 is (2R,3R,4R,5R)-2-((1S,2S,3R,4S,6R)-4,6-DIAMINO-3-((2R,3R,6S)-3-AMI NO-6-(AMINOMETHYL)-TETRAHYDRO-2H-PYRAN-2-YLOXY)-2-HYDR OXYCYC LOHEXYLOXY)-5-METHYL-4-(METHYLAMINO)-TETRAHYDRO-2H-PYRAN-3,5-DIOL (three-letter code: LLL) (formula: $C_{19}H_{39}N_5O_7$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	A	Aton	ns		AltConf
16	Λ	1	Total	С			0
10	Λ	1	31	19	5	7	U
16	Δ	1	Total				0
10	Λ	1	31	19	5	7	U
16	Δ	1	Total	С	N	O	0
10	Λ	1	31	19	5	7	U
16	Δ	1	Total	С	N	О	0
10	Λ	1	31	19	5	7	0

• Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mo	Chair	Residues	Ato	ms	AltConf
17	A	58	Total 58	Mg 58	0

• Molecule 18 is water.

Mol	Chain	Residues	Atoms	AltConf
18	A	1631	Total O 1631 1631	0
18	D	37	Total O 37 37	0
18	E	31	Total O 31 31	0
18	F	1	Total O 1 1	0
18	Н	30	Total O 30 30	0
18	K	12	Total O 12 12	0
18	L	32	Total O 32 32	0
18	О	18	Total O 18 18	0
18	Р	27	Total O 27 27	0
18	Q	11	Total O 11 11	0
18	R	11	Total O 11 11	0
18	Т	25	Total O 25 25	0
18	U	4	Total O 4 4	0



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Mol	Chain	Residues	Atoms	AltConf
18	a	1	Total O 1 1	0



• Molecule 1: 16S rRNA

3 Residue-property plots (i)

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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

Chain A: 58% 10% - 32%

| 10% - 32% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10% | 10%



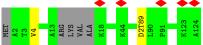






• Molecule 7: Small ribosomal subunit protein uS12

Chain L: 94% . .



 \bullet Molecule 8: Small ribosomal subunit protein uS15

Chain O: 99%



• Molecule 9: 30S ribosomal protein S16

Chain P: 98% ...



• Molecule 10: Small ribosomal subunit protein uS17

Chain Q: 90% • 8%



 \bullet Molecule 11: Small ribosomal subunit protein bS18

Chain R: 84% . 12%



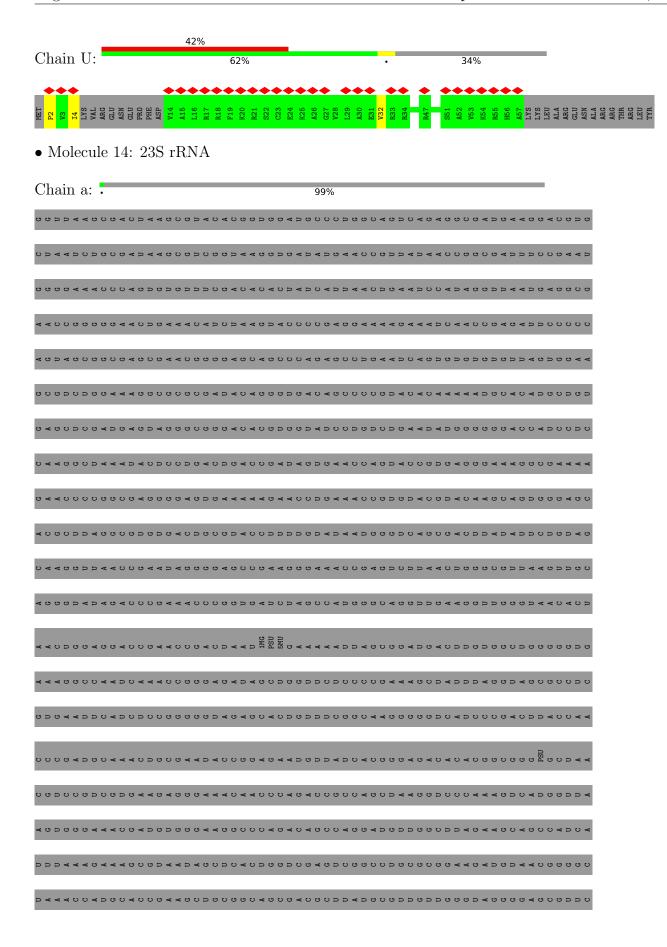
 \bullet Molecule 12: 30S ribosomal protein S20

Chain T: 97%

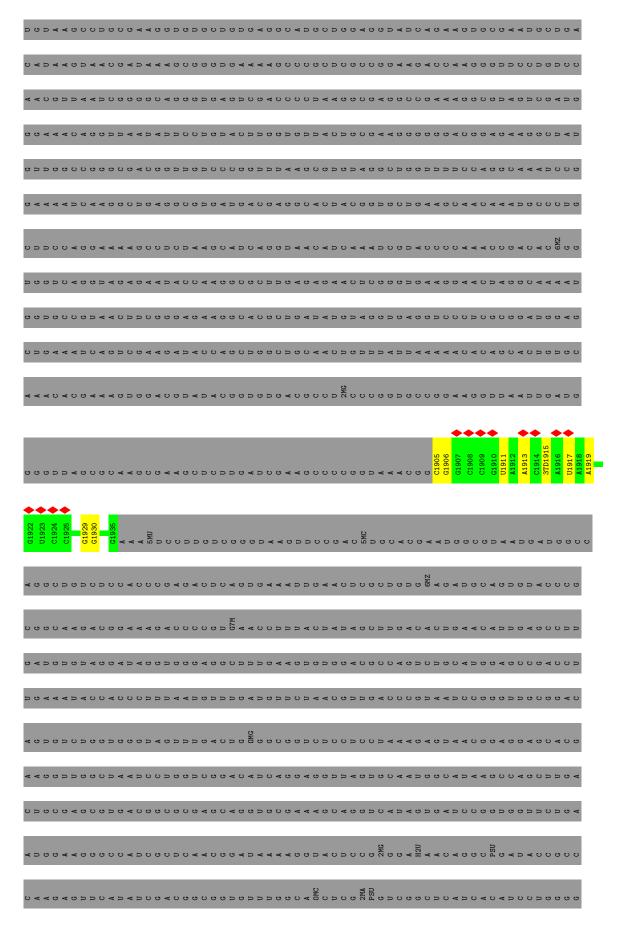


• Molecule 13: Small ribosomal subunit protein bS21











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4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1301160	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	45	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.162	Depositor
Minimum map value	-0.052	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	363.36002, 363.36002, 363.36002	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.757, 0.757, 0.757	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, 2MG, IAS, 3TD, K, MG, PSU, LLL, 5MC, 4OC, MA6, D2T, UR3

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	
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.50	0/25016	1.17	$45/39020 \ (0.1\%)$
2	D	0.30	0/1665	0.62	0/2227
3	Е	0.31	0/1165	0.66	0/1568
4	F	0.29	0/850	0.65	0/1150
5	Н	0.30	0/989	0.63	0/1326
6	K	0.32	0/834	0.68	0/1125
7	L	0.31	0/927	0.75	0/1241
8	О	0.29	0/722	0.58	0/964
9	Р	0.31	0/653	0.68	0/877
10	Q	0.28	0/633	0.63	0/849
11	R	0.30	0/553	0.67	0/742
12	Т	0.28	0/676	0.57	0/895
13	U	0.31	0/390	0.70	0/515
14	a	0.56	0/674	1.19	1/1047 (0.1%)
All	All	0.46	0/35747	1.06	46/53546 (0.1%)

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
1	A	0	1
2	D	0	4
3	E	0	1
4	F	0	1
5	Н	0	1
9	Р	0	1
11	R	0	1
12	Т	0	2
All	All	0	12



There are no bond length outliers.

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	321	A	O5'-P-OP2	-16.18	91.14	105.70
1	A	22	G	O5'-P-OP2	-9.06	97.55	105.70
1	A	1529	G	O3'-P-O5'	-8.90	87.08	104.00
1	A	378	G	O5'-P-OP2	-8.32	98.21	105.70
14	a	1905	С	O3'-P-O5'	-7.72	89.32	104.00
1	A	802	A	O5'-P-OP2	-7.45	98.99	105.70
1	A	746	A	O3'-P-O5'	-6.99	90.72	104.00
1	A	587	G	O4'-C1'-N9	6.93	113.75	108.20
1	A	1530	G	O4'-C1'-N9	6.92	113.74	108.20
1	A	390	U	O5'-P-OP2	-6.91	99.48	105.70
1	A	44	A	O5'-P-OP2	-6.89	99.50	105.70
1	A	176	С	O3'-P-O5'	-6.80	91.08	104.00
1	A	587	G	N9-C1'-C2'	-6.55	104.79	112.00
1	A	655	A	O3'-P-O5'	-6.33	91.97	104.00
1	A	652	U	O3'-P-O5'	-6.21	92.21	104.00
1	A	376	G	O5'-P-OP1	6.17	118.10	110.70
1	A	401	С	O5'-P-OP2	-6.00	100.31	105.70
1	A	13	U	C1'-O4'-C4'	-5.90	105.18	109.90
1	A	126	G	O3'-P-O5'	-5.90	92.79	104.00
1	A	376	G	O5'-P-OP2	-5.89	100.40	105.70
1	A	561	U	O3'-P-O5'	-5.89	92.81	104.00
1	A	921	U	O3'-P-O5'	-5.87	92.86	104.00
1	A	411	A	P-O3'-C3'	5.82	126.69	119.70
1	A	36	С	O5'-P-OP2	-5.78	100.50	105.70
1	A	643	С	O5'-P-OP2	-5.57	100.69	105.70
1	A	505	G	O5'-P-OP2	5.54	117.35	110.70
1	A	884	U	OP1-P-O3'	5.53	117.37	105.20
1	A	572	A	O4'-C1'-N9	-5.45	103.84	108.20
1	A	835	U	O3'-P-O5'	-5.40	93.73	104.00
1	A	455	G	O3'-P-O5'	-5.39	93.76	104.00
1	A	225	С	O3'-P-O5'	-5.37	93.79	104.00
1	A	240	G	O5'-P-OP2	-5.36	100.87	105.70
1	A	1446	A	O5'-P-OP1	5.31	117.07	110.70
1	A	356	A	O5'-P-OP2	-5.30	100.93	105.70
1	A	803	G	O5'-P-OP2	-5.28	100.94	105.70
1	A	1530	G	O5'-P-OP2	5.27	117.02	110.70
1	A	402	G	O5'-P-OP2	-5.26	100.97	105.70
1	A	522	С	O5'-P-OP2	-5.26	100.97	105.70
1	A	143	A	O3'-P-O5'	-5.24	94.05	104.00
1	A	1517	G	O5'-P-OP2	-5.20	101.02	105.70



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	23	С	OP2-P-O3'	5.20	116.63	105.20
1	A	307	С	O5'-P-OP2	-5.18	101.04	105.70
1	A	415	A	N1-C6-N6	5.18	121.71	118.60
1	A	544	G	O3'-P-O5'	-5.16	94.19	104.00
1	A	355	С	OP2-P-O3'	5.08	116.37	105.20
1	A	450	G	O5'-P-OP2	-5.07	101.14	105.70

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	587	G	Sidechain
2	D	184	ARG	Sidechain
2	D	188	ARG	Sidechain
2	D	3	ARG	Sidechain
2	D	62	ARG	Sidechain
3	Е	54	ARG	Sidechain
4	F	24	ARG	Sidechain
5	Н	117	ARG	Sidechain
9	Р	35	ARG	Sidechain
11	R	12	ARG	Sidechain
12	Т	24	ARG	Sidechain
12	Т	74	ARG	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	A	22517	0	11332	11	0
2	D	1643	0	1706	4	0
3	Е	1152	0	1196	1	0
4	F	831	0	821	0	0
5	Н	979	0	1031	1	0
6	K	827	0	832	2	0
7	L	925	0	976	1	0
8	О	714	0	734	0	0
9	Р	643	0	661	0	0



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Mol	Chain	Non-H	- 0	H(added)	Clashes	Symm-Clashes
10	Q	624	0	658	1	0
11	R	544	0	565	1	0
12	Т	670	0	719	0	0
13	U	386	0	417	1	0
14	a	664	0	338	0	0
15	A	22	0	0	0	0
15	D	1	0	0	0	0
15	F	1	0	0	0	0
16	A	124	0	156	0	0
17	A	58	0	0	0	0
18	A	1631	0	0	0	0
18	D	37	0	0	0	0
18	Е	31	0	0	0	0
18	F	1	0	0	0	0
18	Н	30	0	0	0	0
18	K	12	0	0	0	0
18	L	32	0	0	0	0
18	Ο	18	0	0	0	0
18	Р	27	0	0	0	0
18	Q	11	0	0	0	0
18	R	11	0	0	0	0
18	Т	25	0	0	0	0
18	U	4	0	0	0	0
18	a	1	0	0	0	0
All	All	35196	0	22142	19	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 0.

All (19) 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)
1:A:823:C:HO2'	5:H:2:SER:N	1.89	0.70
1:A:664:G:H22	1:A:741:G:H1	1.43	0.67
2:D:9:LEU:HD23	2:D:32:CYS:HB3	1.87	0.54
1:A:677:U:H3	1:A:713:G:H22	1.56	0.53
7:L:4:VAL:HG23	10:Q:34:TYR:HB3	1.89	0.53
1:A:415:A:H61	1:A:427:U:H3	1.56	0.52
1:A:769:G:H4'	1:A:1513:A:H4'	1.93	0.50
1:A:404:G:N7	2:D:2:ALA:HB3	2.27	0.50
2:D:123:ILE:HD13	2:D:145:ILE:HD12	1.96	0.48



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Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ (\rm \AA) \end{array}$	Clash overlap (Å)
1:A:371:A:H2'	1:A:372:C:O4'	2.15	0.47
2:D:145:ILE:CG2	2:D:150:LYS:HG2	2.48	0.44
11:R:32:TYR:HB3	11:R:55:LEU:HD21	2.00	0.44
1:A:1391:U:H2'	1:A:1392:G:C8	2.51	0.44
1:A:502:A:H2'	1:A:503:C:O4'	2.18	0.44
3:E:88:VAL:HG22	3:E:93:ARG:HG2	1.99	0.44
6:K:114:THR:HG21	13:U:32:VAL:HG21	2.00	0.44
6:K:67:ALA:HB2	6:K:96:THR:HG23	2.00	0.43
1:A:232:G:H1'	1:A:262:A:N1	2.35	0.41
1:A:767:A:H2'	1:A:768:A:O4'	2.19	0.41

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	Percer	ntiles
2	D	203/206~(98%)	200 (98%)	3 (2%)	0	100	100
3	E	154/167~(92%)	150 (97%)	4 (3%)	0	100	100
4	F	100/131 (76%)	98 (98%)	2 (2%)	0	100	100
5	Н	127/130~(98%)	123 (97%)	4 (3%)	0	100	100
6	K	107/129~(83%)	102 (95%)	5 (5%)	0	100	100
7	L	114/124~(92%)	112 (98%)	2 (2%)	0	100	100
8	О	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
9	Р	79/82~(96%)	75 (95%)	4 (5%)	0	100	100
10	Q	75/84~(89%)	74 (99%)	1 (1%)	0	100	100
11	R	64/75~(85%)	62 (97%)	2 (3%)	0	100	100
12	Т	84/87 (97%)	84 (100%)	0	0	100	100
13	U	43/71~(61%)	43 (100%)	0	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1236/1375 (90%)	1207 (98%)	29 (2%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	Perce	ntiles
2	D	172/173~(99%)	171 (99%)	1 (1%)	86	87
3	E	119/126 (94%)	119 (100%)	0	100	100
4	F	89/112 (80%)	87 (98%)	2 (2%)	52	47
5	Н	104/105 (99%)	104 (100%)	0	100	100
6	K	83/98 (85%)	83 (100%)	0	100	100
7	L	99/103 (96%)	99 (100%)	0	100	100
8	О	76/77 (99%)	76 (100%)	0	100	100
9	Р	65/65 (100%)	65 (100%)	0	100	100
10	Q	71/78 (91%)	71 (100%)	0	100	100
11	R	57/65 (88%)	57 (100%)	0	100	100
12	Τ	65/66~(98%)	65 (100%)	0	100	100
13	U	39/61 (64%)	37 (95%)	2 (5%)	24	14
All	All	1039/1129 (92%)	1034 (100%)	5 (0%)	89	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	145	ILE
4	F	24	ARG
4	F	102	MET
13	U	2	PRO
13	U	4	ILE



Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such side chains are listed below:

Mol	Chain	Res	Type
2	D	136	GLN
5	Н	18	GLN
6	K	81	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1039/1540 (67%)	98 (9%)	15 (1%)
14	a	29/2904 (0%)	5 (17%)	0
All	All	1068/4444 (24%)	103 (9%)	15 (1%)

All (103) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	7	A
1	A	22	G
1	A	32	A
1	A	39 47	G
1	A	47	С
1 1	A	48	С
1	A	51	A
1	A	69	G
1	A	71	A
1	A	94	G
1	A	95	С
1	A	119	A
1	A	120	A
1	A	121 131 144	U
1	A	131	A
1	A	144	G
1	A	159	G
1	A A A A A A A A A A A A A A A A A A A	164	U A G A G C C A G A G A G C A G A G C A G C A A G C A A G G C A A G G G G
1	A	197	A
1	A	204	G
1	A	240	G
1	A	245	U
1	A	247	G
1		250	A
1	A	251	G



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Mol	Chain	Res	Type					
1	A	266	G					
1	A	267	С					
1	A	280	С					
1	A	289	G					
1	A	321	A					
1	A	328	С					
1	A	348	G					
1	A	352	С					
1	A	354	G					
1	A	367	U					
1	A	372	С					
1	A	384	G					
1	A	406	G					
1	A A A A A A A A A A A A A A A A A A A	411	G C C G A C G C G U C G G U C G G G U C G G U U C G G U U U G G G U U U G G G U U G G G U U G G G G G U U G G G G G U U D G G G G					
1	A	412	A					
1	A	413	G					
1	A	420	U					
1	A	421	U					
1	A	423	G					
1	A	424	G					
1	A	429	U					
1	A	446	G					
1	A	451 453	G A G G A U					
1	A	453	G					
1	A	457	G					
1	A	460	A					
1	A	463	U					
1		468	A					
1	A	484	G					
1	A	511	G C C A A A A U					
1	A	518	\overline{C}					
1	A	532	A					
1	A	533	A					
1	A	547	A					
1	A	559	A					
1	A	562	U					
1	A A A A A A A A A A A A A	572	A A C G					
1	A	573	A					
1	A	576	С					
1	A	577	G					
1	A A	579	A G					
1	A	633	G					



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Mol	Chain	Res	Type
1	A	653	U
1	A	654	G
1	A	665	A
1	A	703	G
1	A	723	A G U
1	A	724	G
1	A	748	G
1	A	755	G G G A U
1	A	777	A
1	A	793	U
1	A	794	A
1	A	815	A A C G G A G U
1	A	817	С
1	A	874	G
1	A	890	G
1	A	914	A
1	A	926	G
1	A	1419	G
1	A	1451	U
1	A	1452	С
1	A	1492	C A G A U
1	A	1497	G
1	A	1503	A
1	A	1505	G
1	A	1506	U
1	A A A A A A A A A A A A A A A A A A A	1517	G G
1	A	1529	G
1		1530	G
1	A	1531	A
1	A	1534	A
14	a	1906	G
14	a	1913	A
14	a	1919	A
14	a	1929	G
14	a	1930	G

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	13	U
1	A	70	U
1	A	94	G



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Mol	Chain	Res	Type
1	A	119	A
1	A	250	A
1	A	251	G
1	A	411	A
1	A	412	A
1	A	421	U
1	A	532	A
1	A	575	G
1	A	653	U
1	A	793	U
1	A	847	G
1	A	1447	A

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

13 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).

N / - 1	Т	Clasica	Das	T :1-	Во	Bond lengths			Bond angles		
Mol	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
1	PSU	A	516	1,17	18,21,22	1.02	1 (5%)	22,30,33	0.60	0	
1	2MG	A	1516	1	18,26,27	1.01	2 (11%)	16,38,41	0.88	0	
1	4OC	A	1402	1	20,23,24	0.41	0	26,32,35	0.68	0	
14	3TD	a	1915	14	19,22,23	0.98	1 (5%)	21,32,35	0.74	0	
14	PSU	a	1917	14	18,21,22	0.99	1 (5%)	22,30,33	0.67	0	
7	D2T	L	89	7	7,9,10	0.88	0	6,11,13	1.70	2 (33%)	
14	PSU	a	1911	14	18,21,22	0.99	1 (5%)	22,30,33	0.71	0	
1	5MC	A	1407	1	18,22,23	0.38	0	26,32,35	0.86	0	
1	MA6	A	1518	1	18,26,27	0.82	1 (5%)	19,38,41	0.62	0	
1	UR3	A	1498	1	19,22,23	0.27	0	26,32,35	0.75	1 (3%)	
1	MA6	A	1519	1	18,26,27	0.82	2 (11%)	19,38,41	0.78	1 (5%)	
6	IAS	K	119	6	6,7,8	0.90	0	6,8,10	0.96	0	
1	G7M	A	527	1	20,26,27	1.07	2 (10%)	17,39,42	0.60	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
1	PSU	A	516	1,17	-	0/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/5/27/28	0/3/3/3
1	4OC	A	1402	1	-	0/9/29/30	0/2/2/2
14	3TD	a	1915	14	-	0/7/25/26	0/2/2/2
14	PSU	a	1917	14	-	0/7/25/26	0/2/2/2
7	D2T	L	89	7	-	2/7/12/14	-
14	PSU	a	1911	14	-	2/7/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	MA6	A	1519	1	-	3/7/29/30	0/3/3/3
6	IAS	K	119	6	-	0/7/7/8	-
1	G7M	A	527	1	-	0/3/25/26	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(Å)
1	A	516	PSU	C6-C5	4.00	1.40	1.35
14	a	1917	PSU	C6-C5	3.95	1.39	1.35
14	a	1911	PSU	C6-C5	3.95	1.39	1.35
14	a	1915	3TD	C6-C5	3.77	1.39	1.35
1	A	527	G7M	C8-N9	3.38	1.39	1.33
1	A	1516	2MG	C5-C6	-2.60	1.42	1.47
1	A	527	G7M	C8-N7	2.22	1.37	1.33
1	A	1519	MA6	C6-N1	2.15	1.36	1.33
1	A	1518	MA6	C6-N1	2.14	1.36	1.33
1	A	1519	MA6	C8-N7	-2.03	1.31	1.34
1	A	1516	2MG	C5-C4	-2.00	1.38	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
7	L	89	D2T	O-C-CA	-2.67	117.77	124.78
1	A	1498	UR3	C6-N1-C2	-2.23	119.79	121.79
1	A	1519	MA6	C2'-C3'-C4'	-2.04	98.68	102.64
7	L	89	D2T	OD2-CG-CB	2.01	117.49	113.15

There are no chirality outliers.



All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	L	89	D2T	SB-CB-CG-OD2
14	a	1911	PSU	O4'-C1'-C5-C4
14	a	1911	PSU	O4'-C1'-C5-C6
1	A	1519	MA6	O4'-C4'-C5'-O5'
1	A	1519	MA6	C3'-C4'-C5'-O5'
7	L	89	D2T	CG-CB-SB-CB1
1	A	1519	MA6	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 86 ligands modelled in this entry, 82 are monoatomic - leaving 4 for Mogul analysis.

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	Trino	vpe Chain Res Link			Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	LLL	A	1604	-	29,33,33	0.36	0	34,49,49	1.03	3 (8%)
16	LLL	A	1606	-	29,33,33	0.34	0	34,49,49	1.02	1 (2%)
16	LLL	A	1605	-	29,33,33	0.37	0	34,49,49	1.31	5 (14%)
16	LLL	A	1603	-	29,33,33	0.34	0	34,49,49	1.01	1 (2%)

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
16	LLL	A	1604	-	-	4/11/65/65	0/3/3/3
16	LLL	A	1606	-	-	5/11/65/65	0/3/3/3
16	LLL	A	1605	-	-	4/11/65/65	0/3/3/3
16	LLL	A	1603	-	-	2/11/65/65	0/3/3/3

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
16	A	1605	LLL	C11-O51-C51	4.18	117.76	113.13
16	A	1603	LLL	C11-O51-C51	4.03	117.59	113.13
16	A	1605	LLL	C13-O62-C62	3.71	127.14	117.96
16	A	1606	LLL	C11-O51-C51	2.96	116.41	113.13
16	A	1605	LLL	C53-O53-C13	2.65	115.79	111.53
16	A	1604	LLL	C62-C52-C42	2.49	114.13	108.96
16	A	1604	LLL	C11-O51-C51	2.43	115.82	113.13
16	A	1605	LLL	O53-C13-C23	2.11	113.29	110.04
16	A	1605	LLL	O62-C62-C12	2.05	114.06	109.18
16	A	1604	LLL	O11-C42-C32	-2.03	104.35	109.18

There are no chirality outliers.

All (15) torsion outliers are listed below:

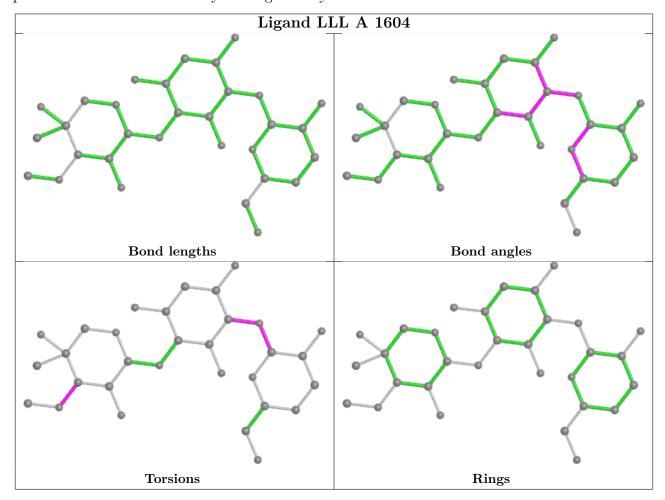
Mol	Chain	Res	Type	Atoms
16	A	1603	LLL	C23-C33-N33-C93
16	A	1604	LLL	C23-C33-N33-C93
16	A	1605	LLL	C12-C62-O62-C13
16	A	1606	LLL	O51-C51-C61-N61
16	A	1606	LLL	O51-C11-O11-C42
16	A	1604	LLL	O51-C11-O11-C42
16	A	1604	LLL	C52-C42-O11-C11
16	A	1605	LLL	C52-C62-O62-C13
16	A	1606	LLL	C52-C42-O11-C11
16	A	1604	LLL	C32-C42-O11-C11
16	A	1606	LLL	C32-C42-O11-C11
16	A	1605	LLL	C23-C13-O62-C62
16	A	1605	LLL	O53-C13-O62-C62
16	A	1603	LLL	C52-C42-O11-C11
16	A	1606	LLL	C23-C33-N33-C93

There are no ring outliers.

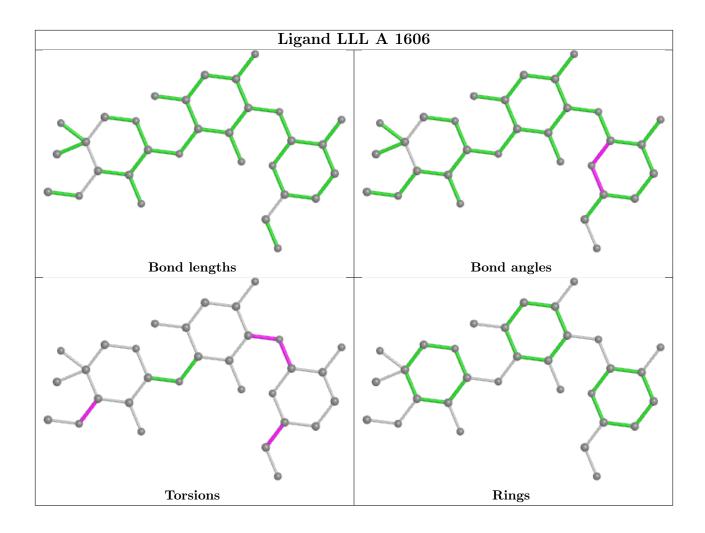


No monomer is involved in short contacts.

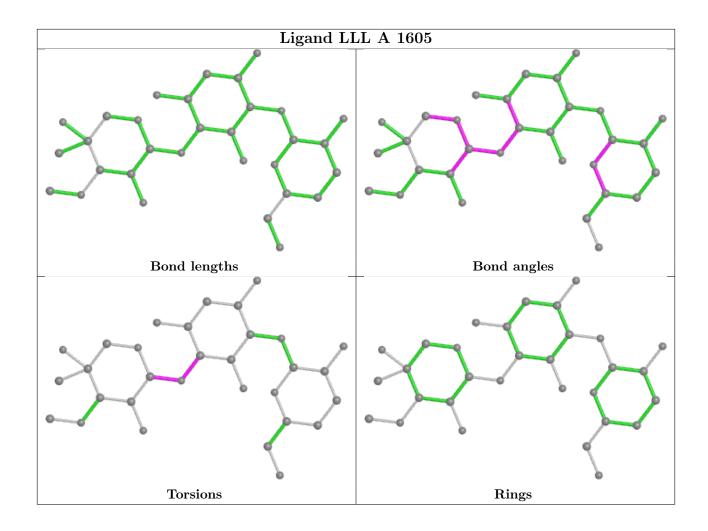
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



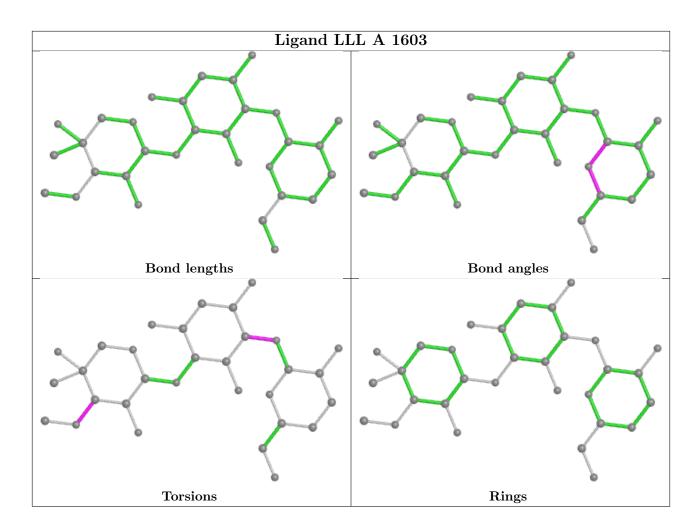












5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



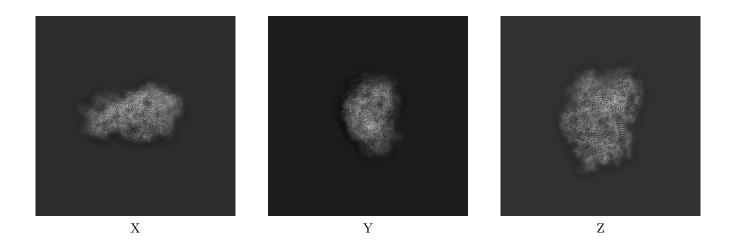
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-16651. These allow visual inspection of the internal detail of the map and identification of artifacts.

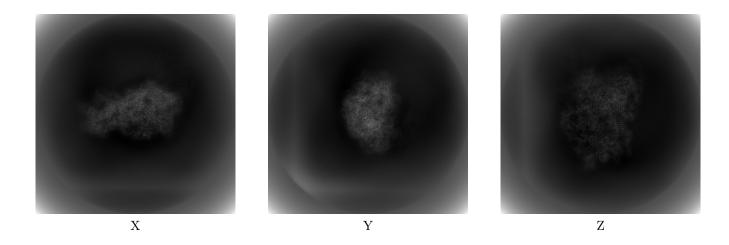
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map

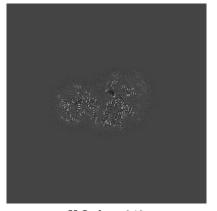


The images above show the map projected in three orthogonal directions.



6.2 Central slices (i)

6.2.1 Primary map





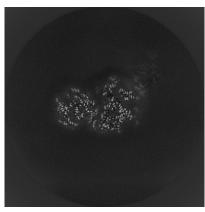


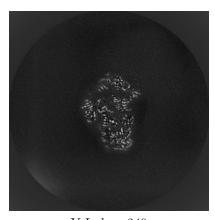
X Index: 240

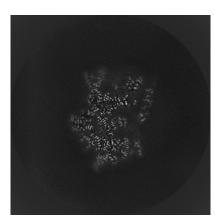
Y Index: 240

Z Index: 240

6.2.2 Raw map







X Index: 240

Y Index: 240

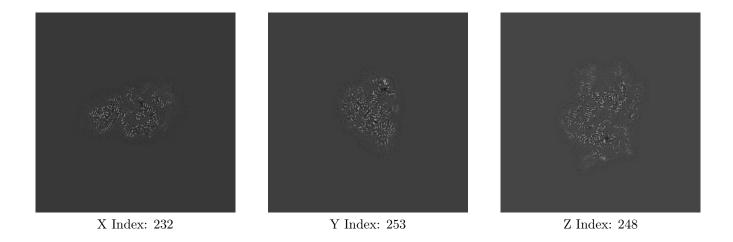
Z Index: 240

The images above show central slices of the map in three orthogonal directions.

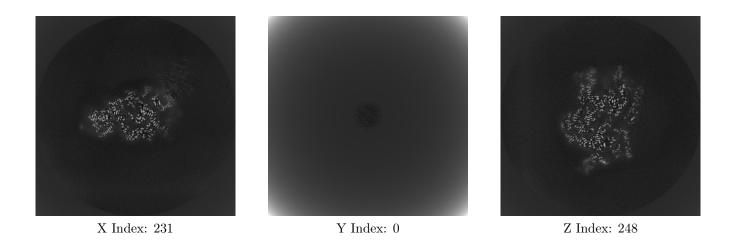


6.3 Largest variance slices (i)

6.3.1 Primary map



6.3.2 Raw map

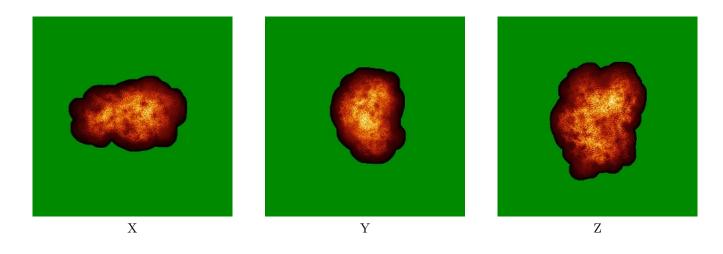


The images above show the largest variance slices of the map in three orthogonal directions.

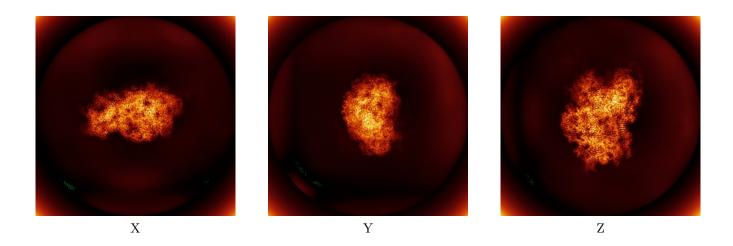


6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation (i)

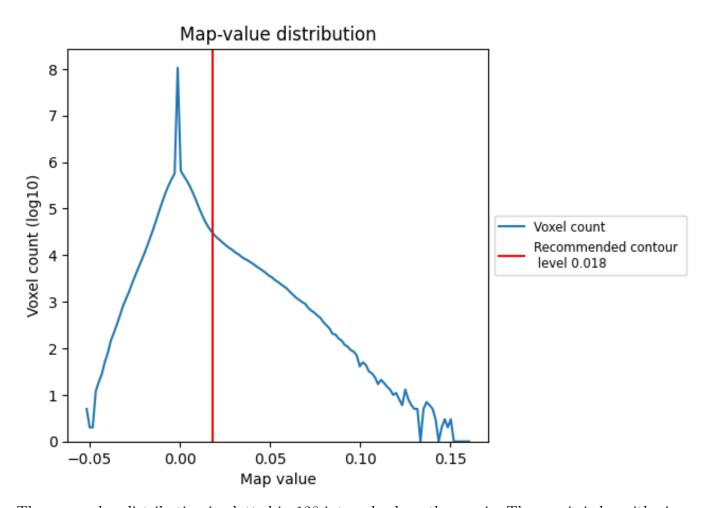
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

This section contains the results of statistical analysis of the map.

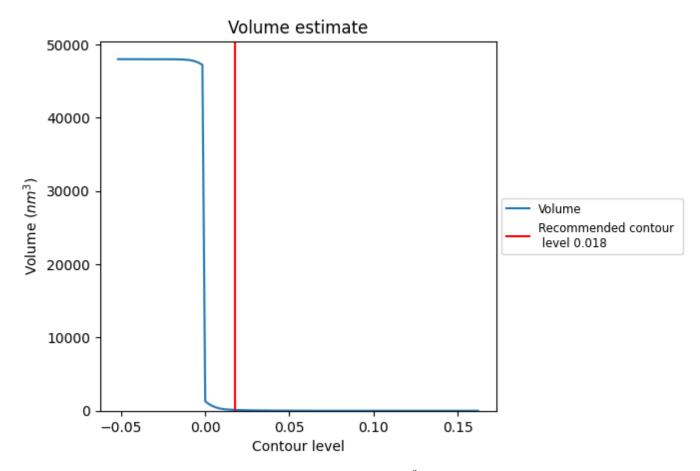
7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)

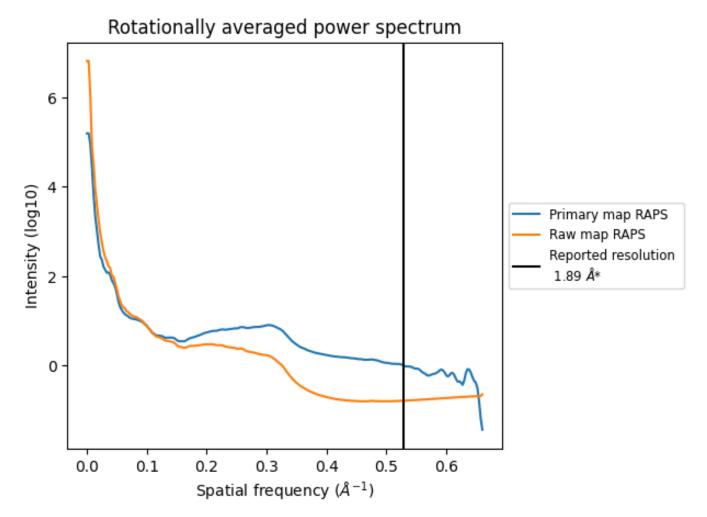


The volume at the recommended contour level is $115~\mathrm{nm}^3$; this corresponds to an approximate mass of $104~\mathrm{kDa}$.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



7.3 Rotationally averaged power spectrum (i)



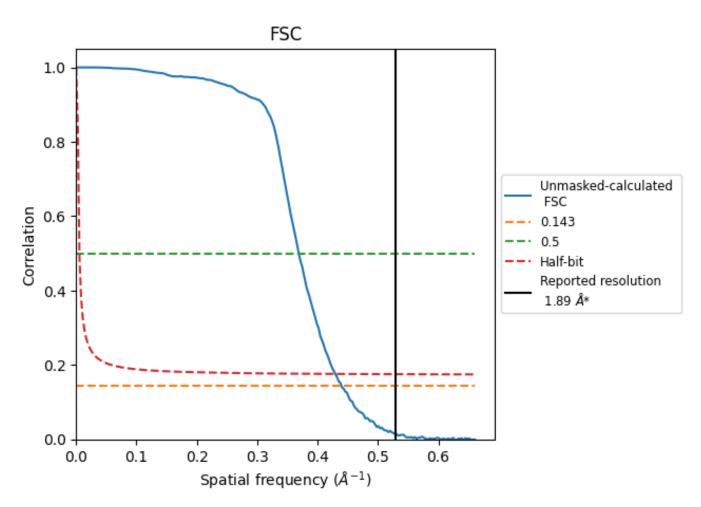
*Reported resolution corresponds to spatial frequency of 0.529 $\rm \AA^{-1}$



8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.529 $\rm \mathring{A}^{-1}$



8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
resolution estimate (A)	0.143	0.5	Half-bit	
Reported by author	1.89	-	-	
Author-provided FSC curve	-	-	-	
Unmasked-calculated*	2.28	2.71	2.33	

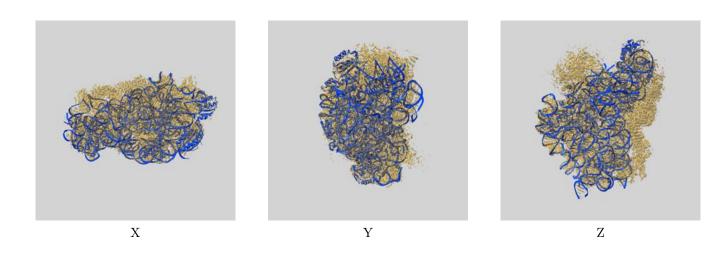
^{*}Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.28 differs from the reported value 1.89 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-16651 and PDB model 8CGU. Per-residue inclusion information can be found in section 3 on page 9.

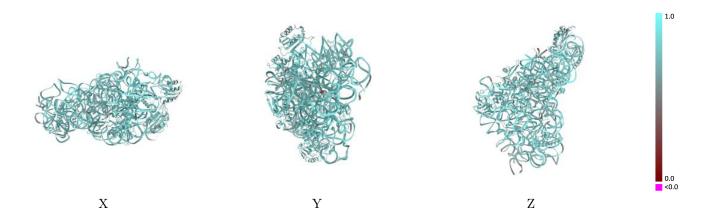
9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

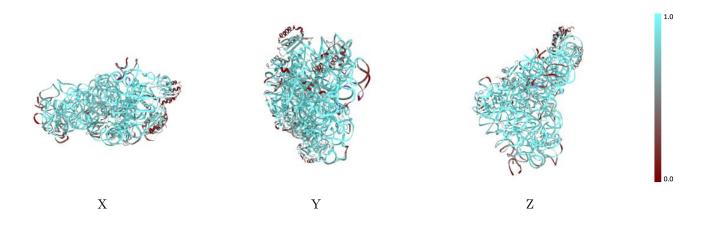


9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

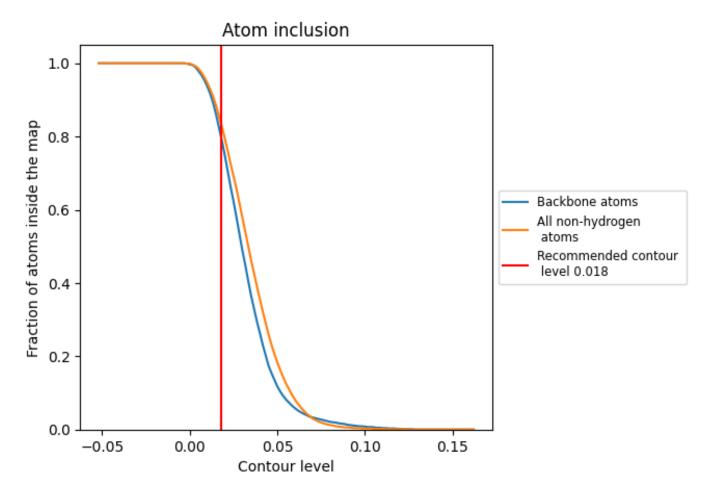
9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.018).



9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8350	0.7600
A	0.8900	0.7700
D	0.7590	0.7510
E	0.8000	0.7570
F	0.5090	0.6680
Н	0.8430	0.7780
K	0.5730	0.6990
L	0.8560	0.7850
О	0.7680	0.7560
Р	0.8390	0.7800
Q	0.7070	0.7180
R	0.6650	0.6980
Т	0.8340	0.7710
U	0.4300	0.6720
a	0.5210	0.6990



