



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Dec 10, 2019 – 11:58 PM EST

PDB ID : 6NQB  
EMDB ID: : EMD-0482  
Title : Role of Era in Assembly and Homeostasis of the Ribosomal Small Subunit  
Authors : Ortega, J.  
Deposited on : 2019-01-20  
Resolution : 3.80 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

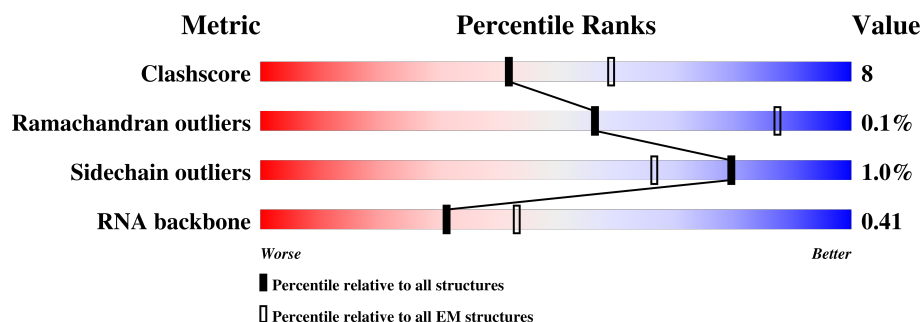
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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  $\geq 3$ , 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	C	206	77% 23%
2	J	98	74% 24% .
3	N	99	76% 19% . .
4	S	74	70% 30%
5	A	1542	38% 38% 10% 13%
6	D	205	79% 20% .
7	E	149	82% 18%
8	F	93	71% 12% 17%

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Mol	Chain	Length	Quality of chain
9	H	129	 79%21%
10	L	123	 84%15%.
11	O	86	 83%15%.
12	P	79	 81%15%.
13	Q	79	 85%15%
14	R	52	 67%27%6%
15	T	85	 78%22%
16	B	217	 83%17%

## 2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 42570 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 protein called 30S ribosomal protein S3.

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

- Molecule 2 is a protein called 30S ribosomal protein S10.

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

- Molecule 3 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	?	-	GLU	deletion	UNP A0A090BZT4

- Molecule 4 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	74	Total	C	N	O	S	0	0
			594	381	110	101	2		

- Molecule 5 is a RNA chain called 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	1341	Total	C	N	O	P	0	0
			28767	12830	5276	9320	1341		

- Molecule 6 is a protein called 30S ribosomal protein S4.

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

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	149	Total	C	N	O	S	0	0
			1089	675	209	199	6		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	77	Total	C	N	O	S	0	0
			630	401	109	114	6		

- Molecule 9 is a protein called 30S ribosomal protein S8.

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

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 11 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	86	Total	C	N	O	S	0	0
			698	431	141	125	1		

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	79	Total	C	N	O	S	0	0
			629	394	124	110	1		

- Molecule 13 is a protein called 30S ribosomal protein S17.

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

- Molecule 14 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	R	49	Total	C	N	O	0	0
			405	258	76	71		

- Molecule 15 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	85	Total	C	N	O	S	0	0
			659	408	134	114	3		

- Molecule 16 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	217	Total	C	N	O	S	0	0
			1696	1076	304	310	6		

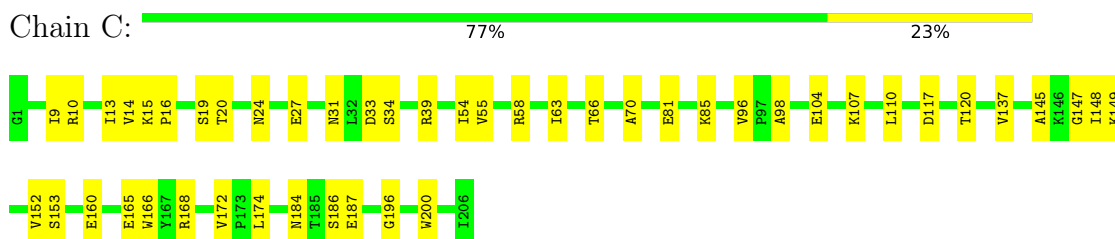
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
17	A	1	Total	Mg	0
			1	1	

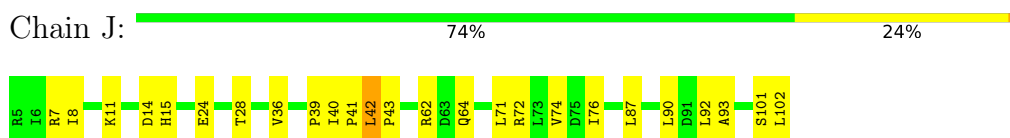
### 3 Residue-property plots

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

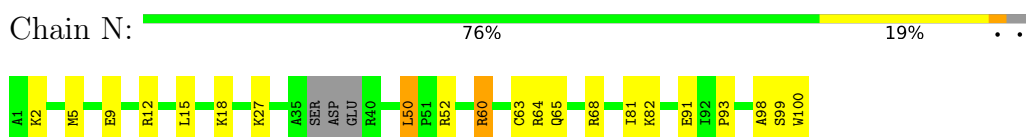
- Molecule 1: 30S ribosomal protein S3



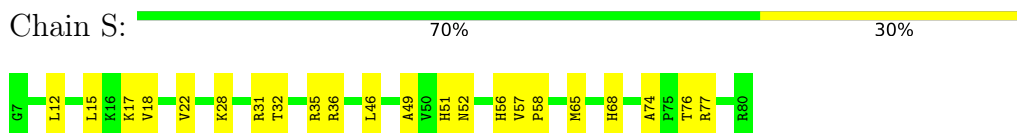
- Molecule 2: 30S ribosomal protein S10



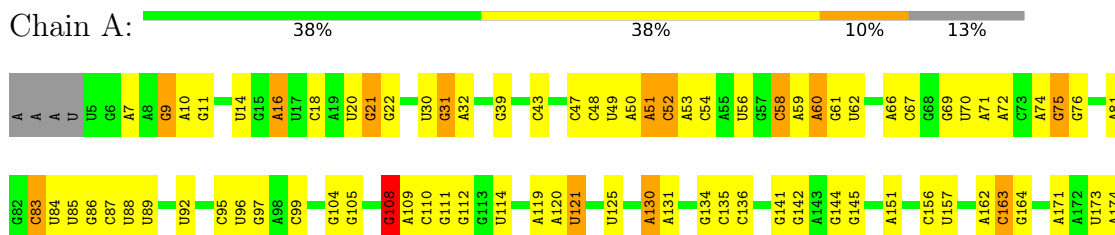
- Molecule 3: 30S ribosomal protein S14



- Molecule 4: 30S ribosomal protein S19

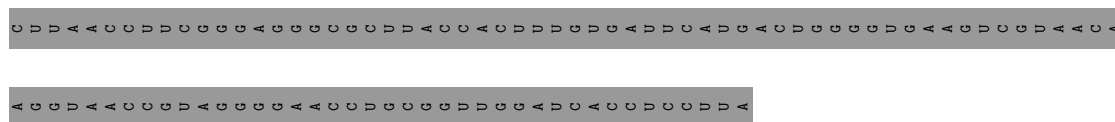


- Molecule 5: 16S RIBOSOMAL RNA

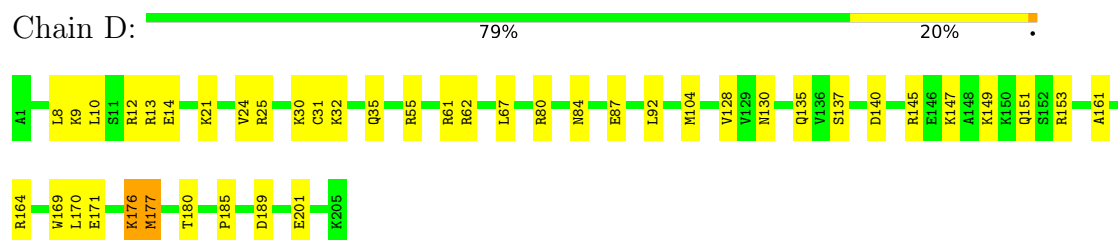


A1377	G1309	U1168	G1094	A1016	G942	G869	G	C735	G669	C580	A502	C352	C175
G1378	G1244	A1169	U1095	G1020	G945	U870	U801	C736	G669	G581	U421	A353	C176
G1379	C1245	G1310	C1096	G1097	G945	U871	A802	C737	G670	C582	C422	G354	G177
U1380	A1178	G1179	C1097	A1021	C948	A872	G803	C738	G671	A583	G423	C355	C178
U1381	U1247	G1178	U1098	G1024	C948	A873	U804	C739	U672	C584	G424	A356	A179
U1313	A1248	A1180	G1099	G1024	C948	A873	C805	U740	A673	G584	U508	C357	U180
C1314	C1249	G1181	U1100	U1025	U952	C876	C306	G741	A674	G587	U427	G	A181
U1315	G1182	U1101	A1101	G1026	G954	A878	G877	G742	A675	G588	A509	G360	A182
U1316	U1183	G1183	A1102	G1026	G954	A878	A675	G742	A675	G588	A510	G361	C183
C1317	G1184	G1185	G1104	U1030	U955	C881	C811	G745	A676	G592	A428	G362	G184
A1318	G1185	G1186	A1105	C1031	C958	C882	G812	A746	U678	G	A430	A363	U185
A1319	G1186	G1187	A1105	G1032	A958	C883	U813	A747	C679	U598	A435	A363	U185
C1320	A1256	G1190	U1108	G1033	A959	C883	A914	G748	C680	C599	G	A364	C186
U1321	A1257	G1191	U1109	G1034	U960	U884	A815	U751	A	U585	C517	A366	C194
C1322	G1258	A1191	C1109	A1035	U961	C885	A816	G752	G	A602	U438	A367	A195
A	G1323	C1259	G1110	A1036	C962	C890	C817	G752	U	U603	U439	U368	A196
C	A1324	G1193	A1111	C1037	G963	G890	G818	A753	U	G604	A448	G369	C290
C	G1325	U1194	C1112	C1038	C963	U891	A819	C754	G	U605	C522	C370	A197
U1326	C1262	C1195	C1113	U1039	G966	A892	U820	G755	U	G606	A451	A371	G200
C	C1263	A1196	C1114	U1040	C967	C893	G821	C758	A	A607	G455	C372	G201
C	U1264	A1197	A1104	G1041	A968	G894	U822	G760	C	C373	G456	A374	G202
A	A1329	G1198	U1118	A1043	A969	C895	C823	G760	G	U610	G457	A298	G203
C	U1330	U1199	C1119	G1043	C970	C896	G824	U762	U	G	U459	U375	G204
U	G1266	C1200	C1120	A1044	G971	C897	A825	G761	U	C613	U458	A300	A205
C	C1267	A1201	U1121	A1045	C972	C897	C826	U762	G	C614	A532	C379	G206
A	G1268	U1202	G1124	A1046	G973	A900	U827	G763	G	G615	A533	G380	G207
C	A1333	C1269	U1125	U1049	A974	A901	U828	C764	G	G616	A461	C381	U208
A	G1334	G1270	U1205	C1053	A975	G902	G829	G765	A	G617	G462	A382	U209
C	C1335	A1271	G1206	U1056	G976	G976	G830	A766	A	C383	C305	A306	C210
C	C1336	G1272	U1126	U1057	A977	U905	A831	A767	U	U619	U463	C384	G211
C	G1337	C1273	G1207	U1058	A977	U905	G832	A768	U	C620	G465	C385	G212
A	A1340	U1274	C1208	U1059	A978	U905	G833	C769	C	C623	A466	G388	G213
U	G1343	C1278	C1209	C1054	C979	A908	G833	C770	G	C624	U467	A315	C214
C	G1347	A1280	U1210	A1055	U981	A909	U834	C771	U	C624	C469	A389	U219
C	U1348	A1213	U1212	U1056	U982	A913	G836	U773	A	G	C470	C390	G220
A	G1349	A1213	C1136	C1063	A983	A914	U837	G773	G	G633	A547	C391	C221
G	U1348	C1214	C1137	G1064	C984	A915	G838	A777	A	G639	C549	C392	C222
U	A1349	G1215	U1616	U1065	C985	U916	U1065	G778	G	A640	G474	A320	A223
A	C1350	G1139	G1139	C1066	U986	G917	C941	C779	U	U641	U551	G393	A223
C	A1285	G	A1067	A1067	G987	A918	U842	C779	U	C642	C477	C401	G226
C	U1286	C1218	G988	G988	G988	A919	U843	A780	C	A642	A477	A397	G227
C	A1287	A1219	G143	U1070	U990	U920	U843	A	U	C328	U479	C328	G227
U	A1288	G1220	G144	U1071	U991	U921	G844	A	U	U398	U479	A329	A228
U	G1355	G1221	A145	C1071	U991	U921	G844	A	G	G646	U480	C399	U229
U	C1290	G1222	A146	G1072	U992	G922	G846	C	G	C647	G481	C400	G230
C	U1291	U1073	C1223	U1073	G993	G922	G846	A	U	C647	A559	C401	G230
A	A1362	G1292	C1223	G1074	A994	G926	G849	G	A712	C651	U562	G404	C235
A	C1363	A1225	U1075	U1075	C995	G926	U850	G	G714	U652	A563	G484	A236
U	U1364	C1226	U1076	U1076	A996	G927	G851	A	A715	U653	C564	U485	G237
A	G1365	U1295	A1155	G1077	U997	G928	G852	U	A716	G654	U486	A405	G238
A	C1366	A1229	U1156	U1078	C998	G929	C953	U	U	A655	G567	U407	U239
G	C1367	G1297	G1156	G1078	C999	C930	U854	U	A717	A655	A487	A408	G240
A	A1368	G1231	C1158	A1080	A1000	C931	U855	U	A718	A655	A487	A408	U240
C	C1369	U1298	U1159	A1081	A1000	C931	C856	G	A	U659	G491	U409	G240
U	G1370	A1236	G1160	A1081	A1004	C934	C857	A	G721	C660	U570	U409	A243
U	C1371	C1237	C1161	U1085	A1005	C937	C858	U	G722	G661	A572	G410	U244
A	U1372	A1162	C1162	U1085	A1005	A937	G858	A	C	U662	A573	A493	U245
C	G1373	A1163	A1163	U1010	U1010	A938	A865	C	G730	A663	G494	A493	A246
U	A1374	U1240	U1090	U1090	U1010	C939	A866	C	C732	G664	G497	A414	G247
A	C1375	G1241	U1091	U1091	A1014	C940	G867	U	G733	G665	C577	A415	A247
U	U1376	A1205	A1157	C1015	C1015	C941	C869	C	G734	G666	C578	G416	A250
													C251

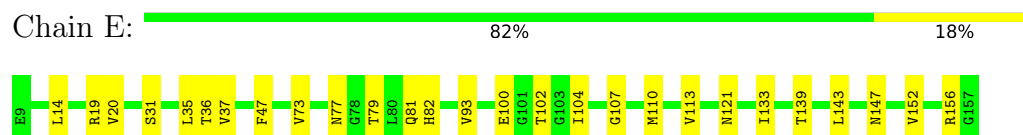




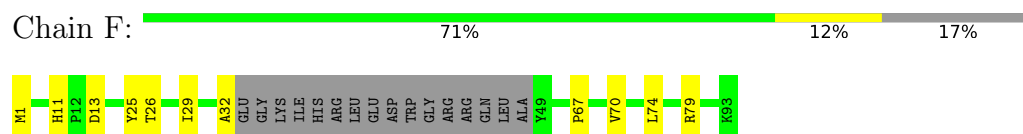
- Molecule 6: 30S ribosomal protein S4



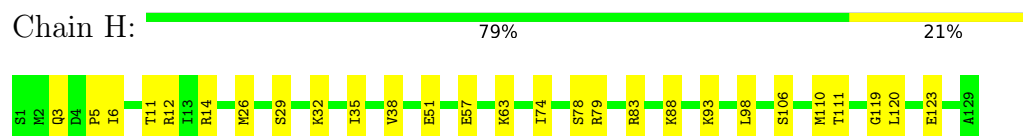
- Molecule 7: 30S ribosomal protein S5



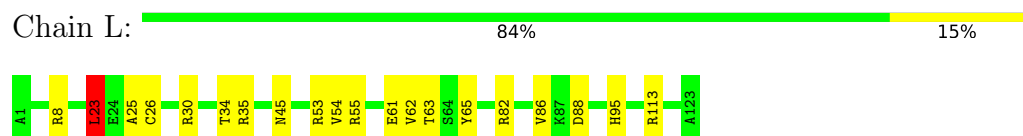
- Molecule 8: 30S ribosomal protein S6



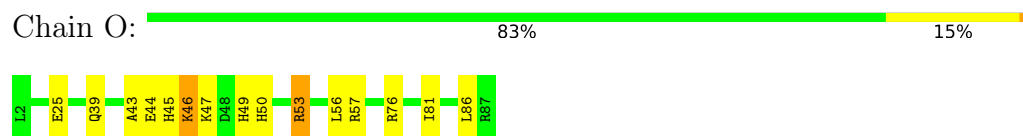
- Molecule 9: 30S ribosomal protein S8




- Molecule 10: 30S ribosomal protein S12



- Molecule 11: 30S ribosomal protein S15




- Molecule 12: 30S RIBOSOMAL PROTEIN bS16

Chain P:  81% 15% .



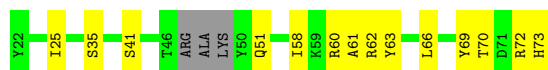
- Molecule 13: 30S ribosomal protein S17

Chain Q:  85% 15%




- Molecule 14: 30S ribosomal protein S18

Chain R:  67% 27% 6%




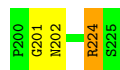
- Molecule 15: 30S ribosomal protein S20

Chain T:  78% 22%



- Molecule 16: 30S ribosomal protein S2

Chain B:  83% 17%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	423567	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	35	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	C	0.30	0/1651	0.58	0/2225
10	L	0.39	0/969	0.72	1/1300 (0.1%)
11	O	0.29	0/706	0.59	0/944
12	P	0.41	0/639	0.71	2/859 (0.2%)
13	Q	0.40	0/650	0.62	0/871
14	R	0.31	0/411	0.58	0/552
15	T	0.31	0/665	0.53	0/881
16	B	0.31	0/1727	0.62	0/2328
2	J	0.29	0/796	0.64	1/1077 (0.1%)
3	N	0.28	0/785	0.62	1/1043 (0.1%)
4	S	0.28	0/609	0.56	0/822
5	A	0.62	0/32207	1.11	130/50237 (0.3%)
6	D	0.37	0/1665	0.63	0/2227
7	E	0.36	0/1101	0.62	0/1482
8	F	0.29	0/643	0.59	0/868
9	H	0.42	1/989 (0.1%)	0.70	2/1326 (0.2%)
All	All	0.55	1/46213 (0.0%)	1.00	137/69042 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2
10	L	0	1
16	B	0	1
2	J	0	2
6	D	0	1
9	H	0	2
All	All	0	9

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	H	78	SER	C-N	-5.83	1.20	1.34

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1158	C	N1-C2-O2	14.70	127.72	118.90
5	A	1158	C	C2-N1-C1'	12.75	132.83	118.80
5	A	1158	C	N3-C2-O2	-12.14	113.40	121.90
5	A	365	U	C2-N1-C1'	11.88	131.95	117.70
5	A	866	C	C6-N1-C2	-9.31	116.58	120.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	166	TRP	Peptide
1	C	24	ASN	Peptide
6	D	176	LYS	Peptide
2	J	14	ASP	Peptide
2	J	41	PRO	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1624	0	1699	28	0
2	J	786	0	828	15	0
3	N	774	0	827	17	0
4	S	594	0	610	16	0
5	A	28767	0	14485	267	0
6	D	1643	0	1710	28	0
7	E	1089	0	1128	19	0
8	F	630	0	626	7	0
9	H	979	0	1033	18	0
10	L	955	0	1019	15	0
11	O	698	0	721	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	P	629	0	643	10	0
13	Q	641	0	682	7	0
14	R	405	0	425	10	0
15	T	659	0	703	15	0
16	B	1696	0	1723	22	0
17	A	1	0	0	0	0
All	All	42570	0	28862	431	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 431 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)
5:A:1349:A:H62	5:A:1373:G:H21	1.36	0.71
5:A:674:G:H1	5:A:715:A:H61	1.38	0.71
5:A:993:G:H2'	5:A:995:C:H41	1.58	0.67
5:A:659:U:H3	5:A:746:A:H61	1.44	0.66
5:A:928:G:H1	5:A:1389:C:H42	1.42	0.66

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	
1	C	204/206 (99%)	178 (87%)	26 (13%)	0	100	100
2	J	96/98 (98%)	76 (79%)	20 (21%)	0	100	100
3	N	92/99 (93%)	79 (86%)	13 (14%)	0	100	100
4	S	72/74 (97%)	67 (93%)	5 (7%)	0	100	100
6	D	203/205 (99%)	179 (88%)	24 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	E	147/149 (99%)	126 (86%)	21 (14%)	0	100	100
8	F	73/93 (78%)	68 (93%)	5 (7%)	0	100	100
9	H	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
10	L	121/123 (98%)	88 (73%)	33 (27%)	0	100	100
11	O	84/86 (98%)	75 (89%)	8 (10%)	1 (1%)	14	56
12	P	77/79 (98%)	61 (79%)	16 (21%)	0	100	100
13	Q	77/79 (98%)	68 (88%)	9 (12%)	0	100	100
14	R	45/52 (86%)	45 (100%)	0	0	100	100
15	T	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
16	B	215/217 (99%)	181 (84%)	34 (16%)	0	100	100
All	All	1716/1774 (97%)	1481 (86%)	234 (14%)	1 (0%)	56	87

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	O	46	LYS

### 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	
1	C	170/170 (100%)	169 (99%)	1 (1%)	87	94
2	J	86/86 (100%)	86 (100%)	0	100	100
3	N	79/82 (96%)	77 (98%)	2 (2%)	50	77
4	S	65/65 (100%)	64 (98%)	1 (2%)	67	85
6	D	172/172 (100%)	169 (98%)	3 (2%)	63	84
7	E	111/112 (99%)	111 (100%)	0	100	100
8	F	69/82 (84%)	69 (100%)	0	100	100
9	H	104/104 (100%)	103 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	L	103/103 (100%)	103 (100%)	0	100	100
11	O	74/74 (100%)	73 (99%)	1 (1%)	69	86
12	P	64/64 (100%)	61 (95%)	3 (5%)	29	64
13	Q	73/73 (100%)	71 (97%)	2 (3%)	48	75
14	R	43/45 (96%)	43 (100%)	0	100	100
15	T	64/65 (98%)	64 (100%)	0	100	100
16	B	179/179 (100%)	178 (99%)	1 (1%)	87	94
All	All	1456/1476 (99%)	1441 (99%)	15 (1%)	80	89

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	D	177	MET
9	H	93	LYS
13	Q	76	ARG
6	D	176	LYS
12	P	51	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	24	ASN
15	T	74	HIS
16	B	119	GLN
16	B	121	GLN
16	B	202	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	A	1338/1542 (86%)	471 (35%)	15 (1%)

5 of 471 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	7	A
5	A	9	G

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Mol	Chain	Res	Type
5	A	14	U
5	A	16	A
5	A	21	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	484	G
5	A	913	A
5	A	1201	A
5	A	428	G
5	A	1101	A

## 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](#)

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

There are no chain breaks in this entry.