

wwPDB EM Validation Summary Report (i)

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PDB ID	:	4CSU
EMDB ID	:	EMD-2605
Title	:	Cryo-EM structures of the 50S ribosome subunit bound with ObgE
Authors	:	Feng, B.; Mandava, C.S.; Guo, Q.; Wang, J.; Cao, W.; Li, N.; Zhang, Y.;
		Zhang, Y.; Wang, Z.; Wu, J.; Sanyal, S.; Lei, J.; Gao, N.
Deposited on	:	2014-03-10
Resolution	:	5.50 Å(reported)
Based on initial model	:	3OFC

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 (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. dev 92
MolProbity	:	4.02b-467
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)	:	2.36.2

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 5.50 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM\ structures}\ (\#{f Entries})$		
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 $\geq=3, 2, 1$ 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 $\leq=5\%$ 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	Quality of chai	n		
1	0	77	• 56%	32%		9% •
2	1	63	71%		24%	5%
3	2	58	72%		24%	•
4	3	56	57%	34%		7% •
5	4	54	17%		19%	• 6%
6	5	234	91%		21%	, •
7	6	46	54%	30%	•	11%

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Continued from previous page... Chain Length Quality of chain Mol 8 764 58% 28% 11% • 9 8 3871% 24% 5% 22% 10 9 390 45% 25% 10% 6% 14% 11 А 11828% 57% 13% ė 12В 2903 31% 45% 25% С 1327264% 29% 7% D 209145% • 67% 26% ÷ Ε 152016% 63% 30% F 1617868% 24% 7% • ė \mathbf{G} 1717669% 25% 6% 64% 18Η 14960% 30% 10% 6% Ι 1914135% 11% 51% . 20J 1428% • 61% 30% Κ 2112359% 29% 10% •• 22 \mathbf{L} 14369% 25% • • 23М 1367% • 65% 27% Ν 1272454% 31% 8% • 5% Ο 2511666% 27% 7% Р 26114 7% • 66% 25% Q 2711760% 32% 7% • 28R 1038% • 66% 25% \mathbf{S} 2911060% 26% 10% • 30 Т 10055% 30% 8% • 6% i U 3110371% 9% •• 18% 32W 9477% 18% 5%

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Mol	Chain	Length	Quality of cha	ain		
33	Y	84	6 0%	27%	7%	6%



2 Entry composition (i)

There are 33 unique types of molecules in this entry. The entry contains 94625 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 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues		At	oms	AltConf	Trace		
1	0	77	Total 625	C 388	N 129	0 106	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	63	Total	С	N	0	S	0	0
			509	313	99	95	2	-	-

• Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
3	2	58	Total 449	C 281	N 87	O 79	${ m S} { m 2}$	0	0

• Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
4	3	56	Total 444	C 269	N 94	O 80	S 1	0	0

• Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues		Aton	ıs	AltConf	Trace	
5	4	51	Total 410	C 263	N 76	O 71	0	1

• Molecule 6 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues		Ate	AltConf	Trace			
6	5	234	Total 1733	C 1081	N 315	O 330	S 7	0	0



• Molecule 7 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	46	Total 377	C 228	N 90	O 57	${ m S} { m 2}$	0	0

• Molecule 8 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
8	7	64	Total 504	C 323	N 105	0 74	${ m S} { m 2}$	0	0

• Molecule 9 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues		Ato	ms			AltConf	Trace
9	8	38	Total 302	C 185	N 65	0 48	$\begin{array}{c} \mathrm{S} \\ \mathrm{4} \end{array}$	0	0

• Molecule 10 is a protein called GTPASE OBGE/CGTA.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	9	334	Total 2541	C 1596	N 448	0 485	S 12	0	1

• Molecule 11 is a RNA chain called 5S RRNA.

Mol	Chain	Residues		At	toms			AltConf	Trace
11	А	115	Total 2455	C 1097	N 451	O 795	Р 112	0	0

• Molecule 12 is a RNA chain called 23S RRNA.

Mol	Chain	Residues		-	Atoms			AltConf	Trace
12	В	2903	Total 62317	C 27801	N 11467	O 20147	Р 2902	0	0

• Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues		At	oms			AltConf	Trace
13	С	272	Total 2083	C 1288	N 424	0 364	${ m S} 7$	0	1

• Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L3.



Mol	Chain	Residues		At	oms			AltConf	Trace
14	D	209	Total 1565	C 979	N 288	O 294	$\frac{S}{4}$	0	0

• Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues		At	oms		AltConf	Trace	
15	Е	201	Total 1552	C 974	N 283	O 290	${ m S}{ m 5}$	0	0

• Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues		At	oms			AltConf	Trace
16	F	178	Total 1420	C 905	N 251	O 258	S 6	0	0

• Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues		At	oms			AltConf	Trace
17	G	176	Total 1317	C 827	N 243	0 245	${ m S} { m 2}$	0	1

• Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues		At	oms			AltConf	Trace
18	Н	149	Total 1111	C 699	N 197	0 214	S 1	0	0

• Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues		Atc	\mathbf{ms}			AltConf	Trace
10	Т	60	Total	С	Ν	Ο	\mathbf{S}	0	0
19	1	09	495	303	90	99	3	0	0

• Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues		At	oms		AltConf	Trace	
20	J	142	Total 1129	С 714	N 212	O 199	${S \atop 4}$	0	0

 $\bullet\,$ Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L14.



Mol	Chain	Residues		At	oms		AltConf	Trace	
21	К	122	Total 932	C 582	N 180	O 164	S 6	0	1

• Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues		At	oms	AltConf	Trace		
22	L	143	Total 1045	C 649	N 206	0 189	S 1	0	0

• Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues		At	oms		AltConf	Trace	
23	М	136	Total 1074	C 686	N 205	0 177	S 6	0	0

• Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues		At	\mathbf{oms}	AltConf	Trace		
24	Ν	121	Total 961	C 593	N 197	0 166	${ m S}{ m 5}$	0	1

• Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace	
25	О	116	Total 892	$\begin{array}{c} \mathrm{C} \\ 552 \end{array}$	N 178	O 162	0	0

• Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues		At	oms			AltConf	Trace
26	Р	114	Total 917	C 574	N 179	0 163	S 1	0	0

• Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
27	Q	117	Total 947	C 604	N 192	O 151	0	0

 $\bullet\,$ Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L21.



Mol	Chain	Residues		At	oms	AltConf	Trace		
28	R	103	Total 816	C 516	N 153	0 145	${ m S} { m 2}$	0	0

• Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues		At	oms	AltConf	Trace		
29	S	110	Total 857	C 532	N 166	0 156	${ m S} { m 3}$	0	0

• Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues		At	oms		AltConf	Trace	
30	Т	94	Total 739	C 466	N 140	0 131	${S \atop 2}$	0	1

• Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace	
31	II	102	Total	С	Ν	0	0	3
01	U	102	758	479	143	136	0	5

• Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues		At	oms			AltConf	Trace
32	W	94	Total 753	C 479	N 137	0 134	${ m S} { m 3}$	0	0

• Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues		At	oms			AltConf	Trace
33	Y	79	Total 596	C 367	N 120	0 108	S 1	0	0



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.

• Molecule 1: 50S RIBOSOMAL PROTEIN L28













A541	C542 C542	C544	U545	0540 A547	G548	G549	G551	U552	G553	0555 C555	A556	C557	U558	GERD CERD	G561	U562	A563	C564	U566	U567	U568	0203 G570	U571	A572	U573 A574	A575	U576	G578	G579	U580	4582	G583	C584 G585	A586	C587 11588	U589	A590	U591 A592	U593	U594 GFOF	0596 U596	G597	U598 A599	G600	
C601	A602 A603	G604	G605		A608	A609 C610	C611 C611	G612	A613	A614 TE15	4616	G617	G618	G619 G620	A621	G622	C623	C624	A626	A627	G628	G630	A631	A632	A633 C634	C635	G636	A637 G638	U639	C640	0041 0642	A643	A644 C645	U646	6647 6648	G649	C650	0651 0652	U653	A654	A000 G656	U657	0658 C659	C660	
A661	G662 C663	G664	U665 A666	A000 U667	A668	G669 A670	C671	C672	C673	G6/4 A675	A676	A677	C678	C6/9	G681	G682	U683	G684 A685	U686	C687	U688 1680	4009 6690	C691	C692	A693 11694	G695	0696 0000	1697 C698	A699	G701	U702	U703	G704 A705	A706	G707 G708	0709	U710	G711 G712	G713	U714	A716 A716	C717	A718 C719	0220	
A721	A722 C723	U724	G725 C726	4727 A727	G728	G729 A730	C731	C732	G733	A/34 A735	C736	C737	G738	A / 39 C740	U741	A742	A743	0744 6745	U746	U747	G748 A740	A750	A751	A752	A753 11754	0755	A756	G758	G759	G760	N 01 U762	<mark>G763</mark>	A764 C765	<mark>0766</mark>	0767 6768	0769	G770	G771 C772	U773	G774	G776	G777	G778 11779	G780	
A781	A782	G784	G785 C786	C787	A788	A789 11790	01.90 C791	A792	A793	A/94 C705	C796	G797	G7 98	67.99 AROO	G801	A802	U803	A804 CB05	C806	U807	6808 6800	11810	U811	C812	0813 C814	C815	C816	C81/ G818	A819	4820 4821	R021 G822	C823	0824 A825	U826	U827 11828	A829	G830	G831 U832	A833	G834	0836 0836	C837	C838 118,30	C840	
G841	U842	A844	A845	0640 U847	C848	4849 11850	C851	U852	C853	C854 C855	G856	G857	G858 2010	11860	A861	<mark>G862</mark>	A863	C865	A866	C867	U868	02 8U	U871	U872	C873 G874	G875	C876	A877 A878	<mark>G879</mark>	G880	G882	G883	U884 C885	A886	0887 C888	C889	C890	G891 A892	C893	U894	A896	C897	C898 A899	A900	
C901	C902	G904	A905 11906	0,900 0,907	C908	A909	A911	C912	U913	6914 7015	G916 G916	A917	A918	00190 0020	C921	C922	G923	6924 A975	G926	A927	A928	6930 6930	U931	U932	A933 11934	C935	A936	6938	G939	G940	6942	A943	C944 A945	C946	A947 C948	G949	G950	C951 G952	G953	G954	0200 G956	C957	U958 A959	A960	
C961	6962	C964	C965 C966	0967	C968	G969 11970	G971	A972	A973	0974 1075	G976	C977	G978	A9/9	A981	C982	A983	A984 C085	C986	C987	A988	4990	C991	C992	G993 C994	C995	A996	C998	0999	A1000	G1002	G1003	01004 C1005	C1006	C1007 41008	A1009	A1010	G1011 U1012	C1013	A1014	61016	G1017	U1018	A1020	
A1021	G1022	G1024	G1025	01020 A1027	A1028	A1029	G1031	A1032	U1033	G1034 111035	G1036	G1037	G1038	A1039	G1041	G1042	C1043	C1044	A1046	G1047	A1048	A1050	G1051	C1052	C1053 A1054	G1055	G1056	A 105 / U 105 8	G1059	U1060	G1062	G1063	01064 01065	U1066	A1067 C1068	A1069	A1070	G1071 C1072	A1073	G1074	C1076	A1077	U1078	A1080	
U1081	U1082	A1084	A1085	G1087	A1088	A1089	G1091	C1092	G1093	01094 A1095	A1096	U1097	A1098	G1099	U1101	C1102	A1103	C1104	G1106	G1107	U1108	G1110 G1110	A1111	G1112	01113 C1114	G1115	G1116		U1119	G1120	G1122	C1123	G1124 G1125	A1126	A1127 C1128	A1129	U1130	G1131 U1132	A1133	A1134	C1135 G1136	G1137	G1138 C1139	C1140	
U1141	A1142 A1143	A1144	C1145	01140 A1147	U1148	G1149 C1150	A1151	C1152	C1153	G1 154 A1 155	A1156	G1157	C1158	01159 61160	C1161	G1162	G1163	C1164 A1165	G1166	C1167	G1168	C1170	G1171	C1172	U1173 U1174	A1175	U1176	G1178 C1178	G1179	U1180	G1182	U1183	01184 G1185	G1186	G1187 11188	A1189	G1190	G1191 G1192	G1193	A1194	G1196	G1197	U1 198 111 199	C1200	
U1201	G1202	A1204	A1205 C1206	G1200 C1207	C1208	U1209 G1210	G1211	G1212	A1213	A1214 C1215	G1216 G1216	U1217	G1218	61210	C1221	U1222	G1223	01224 61225	A1226	G1227	G1228	A1230	U1231	G1232	C1233 111234	G1235	G1236	A1 237 G1 238	<mark>G1239</mark>	U1240	A1241 U1242	C1243	A1244 G1245	A1246	A1247 C1248	U1249	G1250	C1251 G1252	A1253	A1254	01255	C1257	01258 61259	A1260	
C1261	A1262	A1264	A1265	01267 U1267	A1268	A1269 C1270	G1271	A1272	U1273	A12/4 A1975	A1276	G1277	C1278	G1279 C1280	G1281	U1282	G1283	A1284 A1285	A1286	A1287	G1288	C1209 C1290	C1291	G1292	C1293 111294	C1295	G1296	C129/ C1298	G1299	G1300 A1201	A1301 A1302	G1303	A1304 C1305	C1306	A1307 A1308	G1309	G1310	G1311 U1312	U1313	C1314	01316 U1316	G1317	U1318 C1219	C1320	
A1321	A1322	G1324	U1325 111326	01320 A1327	A1328	01329	G1331	G1332	G1333	G1334 C1335	A1336	G1337	G1338	61339 111340	G1341	A1342	G1343	U1344 C1345	G1346	A1347	C1348	C1350	C1351	U1352	A1353 A1354	G1355	G1356	C1357 G1358	A1359	G1360	C1362	C1363	G1364 A1365	A1366	A1367 C1368	G1369	C1370	G1371 U1372	A1373	G1374	01375 C1376	G1377	A1378	G1380	
G1381	G1382 A1202	A1384	A1385 C1386	01300 A1387	G1388	G1389 111 300	01391	A1392	A1393	01394 A1395	U1396	U1397	C1398	C1399 111400	G1401	U1402	A1403	C1404 111405	U1406	G1407	G1408	01409 G1410	U1411	U1412	A1413 C1414	U1415	G1416	C1417 G1418	A1419	A1420	G1422	G1423	G1424 G1425	G1426	A1427 C1428	G1429	G1430	A1431 G1432	A1433	A1434	61435 61436	C1437	U1438 A1439	U1440	
G1441	U1442	G1444	G1445	C1440 C1447	G1448	G1449 C1450	C1451	G1452	A1453	C1 454 C1 455	G1456	U1457	U1458	G1459 111460	C1461	C1462	C1463	G1464 C1465	U1466	U1467	U1468	A1470	G1471	C1472	G1473 111474	G1475	U1476	A1477 G1478	G1479	C1480	01401 G1482	G1483	01484 01485	U1486	U1487	C1 488	C1489	A1490	G1491 C1492	C1 493	41494	A1495	A1496	C1498	
G1501	A1502	A1503	A1504 A1505	U1506	C1507 41508	A1509	G1510	G1511 C1512	01513	G1514	A1515	G1516 C1517	C1518	G1519	U1520	G1521	A1522 111523	G1524	A1525	C1526 C1527	A1528	G1529	G1530	C1531 A1532	C1533	U1534	A1535	C1536	G1537 C1538	U1539	G1540 C1541	01542	G1543	A1544 A1545	G1546	C1547	A1549	C1550	A1551 A1552	A1553	U1554	G1555 C1556	C1557	C1558 U1559	G1560



C1561	U1562 U1563	C1564	A1566	G1568 G1568	A1569 A1570	A1571 A1572	G1573	C1574 C1575	U1576 C1577	U1578	A1579 A1580	G1581	C1582 A1583	U1584	C1585 A1586	G1587	G1588 11589	A1590	A1591 C1592	A1593	01594 C1595	A1596 A1597	A1598 111500	C1600	G1601 U1602	A1603	C1605	C1606 C1607	A1608	A1609 A1610	C1611	G1613	A1614 C1615	A1616	C1617 A1618	G1619	G1620						
U1621	G1622 G1623	U1624	A1626	G1627 G1628	U1629 A1630	G1631 A1632	G1633	A1634 A1635	U1636 A1637	C1638	C1639 A1640	A1641	G1642 G1643	C1644	G1645 C1646	U1647	U1648 G1649	A1650	G1651 A1652	G1653	A1034 A1655	C1656 U1657	C1658 C1650	G1660	G1661 U1662	G1663	A1004 A1665	G1666 G1667	A1668	A1669 C1670	U1671	G1673	G1674 C1675	A1676	A1677 A1678	A1679	U1680						
G1681	G1682 U1683	G1684 C1685	C1686	01687 01688	A1689 A1690	C1691 II1692	U1693	C1694 G1695	G1696 C1697	A1698	G1699 A1700	A1701	G1702 G1703	C1704	A1705 C1706	G1707 G1707	C1708 II1709	G1710	A1711 U1712	A1713	01/14 G1715	U1716 A1717	G1718 C1719	U1720	G1721 A1722	G1723	01725	C1726 C1727	C1728	01729 C1730	G1731 C1730	G1733	G1734 A1735	U1736	G1737 G1738	A1739	G1740						
C1741	01742 G1743	A1744	A1746	01/4/ C1748	A1749 G1750	U1751 C1752	G1753	A1754 A1755	G1756 A1757	U1758	A1759 C1760	C1761	A1762 C1763	C1764	01765 01766	G1767	C1768 111769	G1770	C1771 A1772	A1773	U1775	G1776 U1777	U1778 111770	A1780	U1781 U1782	A1783	A1785	A1786 A1787	C1788	A1789 C1790	A1791	C1793	A1794 C1795	U1796	G1797 U1798	G1799	C1800						
A1801	A1802 A1803	C1804	C1806	41807 A1808	A1809 A1810	G1811 11812	G1813	G1814 A1815	C1816	U1818	A1819 U1820	A1821	C1822 C1823	G1824	U1825 C1826	U1827	G1828 41829	C1830	G1831 C1832	C1833	01034 G1835	C1836 C1837	C1838 C1830	G1840	U1841 G1842	C1843	G1845	G1846 A1847	A1848	G1849 G1850	U1851	01032 A1853	A1854 U1855	U1856	G1857 A1858	U1859	G1860						
G1861	G1862 G1863	U1864	A1866	G1867 C1868	G1869 C1870	A1871 A1872	G1873	C1874 G1875	A1876 A1877	G1878	C1879 U1880	C1881	U1882 II1883	G1884	A1885 11886	C1887	G1888 A1889	A1890	G1891 C1892	C1893	C1895	G1896 G1897	U1898 A1800	A1900	A1901 C1902	G1903	C1905	G1906 G1907	C1908	C1909 G1910	U1911 01917	A1912 A1913	C1914 U1915	A1916	01917 A1918	A1919	C1920						
G1921	G1922 U1923	C1924	U1926	A192/ A1928	G1929 G1930	U1931 A1932	G1933	C1934 G1935	A1936 A1937	A1938	U1939 U1940	C1941	C1942	U1944	G1945 111946	01940 C1947	G1948 G1949	G1950	01951 A1952	A1953	U1955	U1956 C1957	C1958 C1958	A1960	C1961 C1962	U1963	C1965	A1966 C1967	G1968	A1969 A1970	U1971	G1973	C1974 G1975	U1976	A1977 A1978	U1979	G1980						
A1981	01982 G1983	G1984	C1986	61988 G1988	G1989 C1990	U1991 (1992	U1993	C1994 U1995	C1996	A1998	C1999 C2000	C2001	G2002 42003	G2004	A2005	U2007	C2008 A2009	G2010	02011 G2012	A2013	A2014 A2015	U2016 U2017	G2018 A2019	A2010	C2021 U2022	C2023	C2025	U2026 G2027	U2028	G2029 A2030	A2031	42032 A2033	U2034 G2035	C2036	62038 G2038	U2039	G2040						
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U204	A2043	C204	G204	G204	G204 C205	A205 A205	G205	C205t	G2056	A2058	A2059 A2060	G2061	A2062 C2063	C2064	C2065	G2067	U2068 G2069	A2070	A2071 C2072	C2073	U2075	U2076 A2077	C2078	A2080	U2081 A2082	G2083	U208	U208 G208	A208	C208 A209	C209	G2090	A209. A2091	C209	N2098	U209	G210(
A2101 U204	G2102 A2043 C2103 C2040	C2104 C2104	U2105 4 G204 U2106	G2107 6204 6204	U2109 C205	G2110 A205	U2111 G205 G205		A2114 • G2056	G2115 A A2058	A2117 A2059 A2117 A2060	U2118 G2061	A2119 A2062	G2121 C2064		G2123 G2067	G2124 G2125 G2125	A2126 A2070	G2128 C2073	C2129 C2073	U2130 U2130 U2075	U2132 V2132 V2076	(22133 (22078) (22078)	A2135	G2136 A2082	U2137 4 G2083	G2138 U208	02139 G2140 G2140	G2141 A A208	A2142 A2142 A209	C2143 C209	C2145 C2145 C209	C2146 A209	A2147 C209	G2148 V A209 112149 U2098	C2150 U2099	U2151 G2100	G2153	A2154	U2155 • • • • • • • • • • • • • • • • • •	G2157	A2158	G2160
C2161 A2101 U204	G2162 G2102 A204. A2163 C2103 C204.	C2164 C2104 C2104 C204			$\begin{array}{cccccccccccccccccccccccccccccccccccc$	A2170 42110 4205	A2171 U2111 A2172 G205 G205 G205	A2173 A2173 A2056	$\begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \end{array}\\ \end{array}\\ \end{array} \end{array} \\ \end{array} \end{array} \\ \end{array} \end{array} \\ \end{array} \end{array} \\ \begin{array}{c} \begin{array}{c} \end{array} \end{array} \\ $			C2178 U2118 G2061	C2179 A2119 A2062	02180 62120 C2064		A2183 G2123 G2067	A2184 G2124 U2068 U2185 G2125 G2069	G2186 A2126 A2070	U2188 G2128 C2073	U2189 (2190 (2190	A2191 U2130 U207E	02192 02131 02076 02193 02132 02077	U2194 G2133 C C2078 C2078 U2195 C2078	C2196 A2134 A2136 A2080	0219/ 02081 A2198 G2136 A2082	A2199 U2137 Q G2083 G2200	G2201 G2138 U208	U2202 U2202 U2203 G2140 0 (2208	G2204 G2141 A A208	C208 A2142 A2142 A2142 A2100	C2207 C2143 C2209 C2208	G2209 C2144 0 C209	02210 A2211 C2146 ← A209	A2212 A2147 C209	C2214 C2214 N209	C2215 C2150 U2099	G2216 U2151 G210 G2217 C2152	G2218 42152 U2219 C2153	U2220 A2154		G2157	A2158	C2160
G2221 C2161 A2101 U204	C2222 G2162 G2102 A204. G2223 A2163 C2103 C204.	G2224 C2164 C204 ♦ C204	C2226 U2166 V U2105 V C27 C2226 U2166 V U2106 C200	G2228 U2167 G204 G204 G204 G204 G204 G204 G204 G204	U2229 G2168 A A2100 G204 G2230 A2169 V U2109 C205	U2231 A2170 G2110 A205	U2233 A2171 U2111 G205 U2233 U2172 C2119	G2234 A2173 A2056 G2235 A2173 U2113 C2055	$\begin{array}{cccc} U2236 & \underbrace{C2174}_{C2056} & \underbrace{A2114}_{C2056} & \underbrace{A2114}_{C2056} & \underbrace{A2114}_{C2056} & \underbrace{A2114}_{C2067} & \underbrace{A2114}_{C2077} & \underbrace{A2114}_{C20777} & \underbrace{A2114}_{C207777} & \underbrace{A2114}_{C207777} & \underbrace{A2114}_{C207777} & \underbrace{A2114}_{C2077777} & \underbrace{A2114}_{C20777777} & \underbrace{A2114}_{C20777777777777777777777777777777777777$	G2238 A2176 A C2115 A A2058	G2239 C2177 A2059 A2117 A2050	A2241 C2178 U2118 G2061	G2242 C2179 A2119 A2062 112243 110160 A2062 C2068	02140 02180 02180 02180 02160 02064 0210181 0 02064	U2245 02101 02182 02182 02182 02182 02065	A2247 A2183 G2123 G2067	C2248 A2184 G2124 U2068 U2185 G2125 G2069	G2250 G2186 A2126 A2070 10167 C0107	G2251 02187 62128 62128 C2072 C2072	G2253 U2189 C2129 C2773	G2255 A2191 U2130 U2075	G2256 U2192 U2131 U2076 U2257 G2193 U2132 A A2077	C2258 U2194 C2133 C C278	C2260 C2196 A2134 A2080	C2261 U219/ U2081 U2262 A2198 G2136 A2082	C2263 A2199 U2137 Q G2083	U2265 G2201 G2138 U2081 U2081	A2266 UZ202 UZ139 U2108 A2267 U2203 G2140 (2008	A2268 G2204 G2141 A A208	G2269 A2200 A2270 C2206 A2142 A209	G2271 C2207 C2143 C209	A2273 G2209 G2144 G2093 G2093	A2274 0 2210 C2146 A209 C2275 A2211 C2146 A209	G2276 A2212 A2147 C209	G22// G2214 G2148 A 209 A2078 G2214 II2149 U2096	G2279 C2215 C2150 U2099	G2280 G2216 U2151 G2100 G2217 C2152	G2218 G2152 112219 C2153	U2220 A2154	02155 G2156	G2157	A2158	G2160 C2160
A2281 G2221 C2161 A2101 U204	G2282 C2222 G2162 G2162 A204. C2283 G2223 A2163 C204.	A2284 G2224 C2164 C2104 ♦ C204	C2286 C2226 U2166 U2105 C2226 U2166 C200	A2287 A2227 U2167 G2107 C204 A2288 G2228 U2167 G204	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	U2291 U2231 A2170 G2110 A205 A205	C2293 U2233 U2172 U2172 C2111 C206	62294 G2234 A2173 A205 C2296 G2235 C2173 U2113 C2066	U2296 U2236 C2174 A2114 C2056	A2298 G2238 A2176 A2298 G2238 A2176 A2098	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	C2301 A2241 C2178 U2118 C2061	U2302 G2242 C2179 A2119 A2062 C2303 U2343 U12243 C2068	C2304 U2244 II2181 C2064 C2064	U2305 U2245 C101 C1306 C2045 U2182 U2122 C2065	G2307 A2247 A2183 G2123 G2067	G2308 C2248 A2184 G2124 U2068 A2309 II7249 U2185 G2125 G2069	C2310 G2250 G2186 A2126 A2070	A2311 G2251 02161 4217 A2071 02312 G2252 02188 G2128 C2072	C2313 G2253 U2189 C2129 C2073	C2215 C2204 C2204 U2130 U2130 C2205 C2205 C2205	G2316 G2256 U2192 U2151 U2076 A2317 U2257 G2193 U2132 A2077	G2318 C2258 U2194 G2133 C2078 C0340 110250 U2195 0.000 0.000	U2320 C2260 C2196 A21.44 A2080 U2320 C2260 W10107 A21.35 A A2080	U2321 C2261 U219/ U2081 A2322 U2262 A2198 G2136 A2082	62323 C2263 Å2199 U2137 Q2080 T02024 C2263 G2200	C2325 U2265 C2201 C2138 U2209 U208	C2326 A2266 U2202 U2139 U208 A2397 A2967 U2203 G2140 C308	A2328 A2268 G2204 G2141 A A208	U2329 G2269 A2209 C2208 C208 C208 C208 C208 C208 C208 C20	G2331 G2271 C2207 C2143 C209 C1333 11072 C2208 00111 0000	42333 42273 G2209 C2144 ↓ 0209	U2334 A2274 0.2210 A209 A2335 C2275 A2211 C2146 A209	A2336 G2276 A2212 A2147 C209	4233/ 422/7 422/7 4209 4209 C2338 A2278 C2214 II/2149 U209	C2339 G2279 C2215 C2150 U2099	A2340 G2280 G2215 G210 G2217 C2151 G2100	G2218 G2215 112219 G2153	U2220 A2154		G2157	A2158	C2160
G2341 A2281 G2221 C2161 A2101 U204	C2342 G2382 C2222 G2162 G2102 A204 U2343 C2283 G2223 A2163 C2103 C204	U2344 A2284 G224 C2164 C204 C204 C001E C001E C001E C001E C001E C001E	42346 02286 02226 02166 012105 0200 42346 02286 02226 02166 012105 0200	U234 A228 A2221 U2167 C204 U2348 A2288 G2228 U2167 G204 C204	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	C2351 U2291 U2231 A2170 C2110 A205 A205 C2282 A2170 A205 A205	C2353 C2293 U2233 U2233 U2172 C2113 C205	C2354 G2294 G2234 A2173 C2295 G2295 G2255 C3173 C2065	U2356 U2296 U2236 U2265	A2358 A2358 A2298 G2238 A2176 A2356 A2068	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	C2361 C2301 A2241 C2178 U2118 G2061	C2362 U2302 G2242 C2179 A2119 A2062 (2363 C2303 112243 1114.00 A2165 C2065	C2364 C2364 U2244 ID181 C2064 C2064	G2365 U2305 U2245 U211 U2122 U2122 U2122 U2122 U2152 U2066	G2367 G2307 A2247 A2183 G2067 G23067 G2067	C2368 G2308 C2248 A2184 G2124 U2068 A2369 A2309 U2185 G2125 G2069	G2370 C2310 G2250 G2186 A2126 A2070	G2371 A2311 G2251 U210 U2372 U2312 G2252 U2188 G2128 C2072	C2313 C2253 U2189 C2129 C2313 C2253 U2189 C2072	C2375 G2315 G2255 A2191 U2130 U2075 U2075	A2376 G2316 G2256 U2192 U2131 U2076 A2377 A2317 U2257 G2193 U2132 A2077	A2378 G2318 C2268 U2194 G2133 C2078	C2380 U2320 C2260 C2196 A2134 A2080	A2381 U2321 C2261 U219/ U2081 Q2382 A2322 U2262 A2198 Q2196 A2082	(2383 (2323 (2263 Å2199 U2137 (22083 Å2199 Å2190 Å2190 Å2190 Å2190 Å219 Å2190 Å2100 Å21000Å2000Å20000Å20000Å20000Å200000Å2	C2385 C2325 U2265 C2201 U208 U208	A2386 C2326 A2266 U2202 U2299 U208 U2387 A2327 A2267 U2203 G2140 G208	A2388 A2328 A2268 G2204 G2141 A A208	G2389 02329 G2269 7220 02390 G2330 A2270 C2206 A2142 A209	G2391 G2371 G2271 G2207 C2143 C209 A 7300 C7332 T10770 C2208 C444 C209	A2352 02312 02412 0209 U2893 A2333 A2273 G2209 C2145 0 G209	C2394 U2334 A2274 0.2210 A209 C2395 A235 C2275 A2211 C2146 A209	G2396 A2336 G2276 A2212 A2147 C209	G239/ G235/ G221/ G2148 ♦ A209 U2398 C2338 A2278 C2214 II7149 U209	G2399 C2339 G2279 C2215 C2150 U2099	G2400 A2340 G2280 G2215 U2151 G210 G2217 C215 C215	G2218 G2153 C2153	U2220 A2154	02155 0 22156 0	G2157	A2168	0.21.60
U2401 G2341 A2281 G2221 C2161 A2101 U204	U2402 C2342 G2282 C2222 G2162 G2102 A204. C2408 U2343 C2283 G2223 A2163 C2103 C204.	U2404 U2344 A2284 G2224 C2164 C204 CAME CAME CAME CAME C204	4240 4246 4228 4229 4209 4209 4209 02105 ♦ 0209 4240 42346 62286 52226 02166 ♦ 02105 6 5200	7204 12408 12348 12228 12167 2204 12408 12348 12288 22228 12167 2204	(22409 (2234) (2229) (2168 7.100 (2204) </th <th>A241 G2351 U2291 U2231 A2170 G2110 A205</th> <th>G2413 G2363 G2293 U2233 U2172 U2111 G205</th> <th>$\begin{array}{cccccccccccccccccccccccccccccccccccc$</th> <th>C2416 U2356 U2296 U2236 C217 C3417 C3457 A3967 C337 C2175 A2114 C3057</th> <th>42418 42358 42298 62238 42176 72115 42058</th> <th>U2419 C2869 U2299 G2239 C2177 A 2217 A2059 C2450 G2860 C2300 U240 A2060</th> <th>G2421 G2361 C2301 A2241 C2178 U2118 C2061</th> <th>C2422 C2362 U2302 G2242 C2179 A2119 A2062 112423 C2363 112243 mileo A2065</th> <th>C2424 C2364 C2304 U2244 II2181 C2064 C2064</th> <th>A2425 G2365 U2305 U2245 02147 02122 02065 02046 02182 02182 02065</th> <th>C2427 C2367 C2307 A2247 A2183 C2128 C2067</th> <th>G2428 C2368 G2308 C2248 A2184 G2124 U2068 G2429 A2369 A3309 117549 U2185 G2125 G5069</th> <th>A2430 G2370 C2310 G2250 G2186 A2126 A2070</th> <th>02431 02371 A2311 02251 0210 02121 A2071 A2432 02372 02312 02252 02188 02128 02075</th> <th>A2433 C2373 C2313 C2253 U2189 C2129 C2073</th> <th>A2435 G2375 G2315 G2255 A2191 02130 02075 02075</th> <th>C2436 A2376 C2316 C2256 U2192 U2131 U2076 C2437 A2317 U2257 C2193 U2132 A2077</th> <th>U2438 A2378 G2318 C2268 U2194 G2133 C2078 A0430 C3270 C10560 U2195 C2078</th> <th>C2440 C2380 U2320 C2260 C2196 A134 A2080</th> <th>U2441 A2381 U2321 C2261 U219/ U2081 C2442 G2882 A2322 U2262 A2198 G2136 A2082</th> <th>C2443 G2383 G2323 G2263 A2199 U2137 Q2083</th> <th>Q2445 C2385 Q2455 G2201 G2138 U208</th> <th>G2446 A2386 C2326 A2266 U2202 U2139 U208 G2447 H13387 A3337 A3357 A3367 U2208 G2140 G208</th> <th>A2448 A2388 A238 A2268 G2204 G2141 A208</th> <th>U2449 G2389 U2329 G2269 A2200 C208 A2450 U2390 G2330 A2270 C206 A2142 A209</th> <th>A2451 G2391 G2331 G2271 G2207 C2143 C209 CMED A360 C333 H10770 C2208 C444 H1000</th> <th>42453 U2993 A2333 A2273 G2209 C2145 C209</th> <th>G2454 C2394 U2334 A2274 0.2210 A209 G2455 C2395 A2335 C2275 A2211 C2146 A209</th> <th>C2456 G2396 A2336 G2276 A2212 A2147 C209</th> <th>0245/ 0239/ 0233/ 0221/ 02214 0210 02458 02338 A2078 02214 102149 0209</th> <th>A2459 G2399 G2279 G2215 C2150 U209</th> <th>U2460 G2400 A2340 G2280 G2217 U2151 G210 G2217 C2150</th> <th>G2218 U.2152 17219 C2153</th> <th>U2220 A2154</th> <th></th> <th>G2157</th> <th>A2158</th> <th>02160 C2160</th>	A241 G2351 U2291 U2231 A2170 G2110 A205	G2413 G2363 G2293 U2233 U2172 U2111 G205	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	C2416 U2356 U2296 U2236 C217 C3417 C3457 A3967 C337 C2175 A2114 C3057	42418 42358 42298 62238 42176 72115 42058	U2419 C2869 U2299 G2239 C2177 A 2217 A2059 C2450 G2860 C2300 U240 A2060	G2421 G2361 C2301 A2241 C2178 U2118 C2061	C2422 C2362 U2302 G2242 C2179 A2119 A2062 112423 C2363 112243 mileo A2065	C2424 C2364 C2304 U2244 II2181 C2064 C2064	A2425 G2365 U2305 U2245 02147 02122 02065 02046 02182 02182 02065	C2427 C2367 C2307 A2247 A2183 C2128 C2067	G2428 C2368 G2308 C2248 A2184 G2124 U2068 G2429 A2369 A3309 117549 U2185 G2125 G5069	A2430 G2370 C2310 G2250 G2186 A2126 A2070	02431 02371 A2311 02251 0210 02121 A2071 A2432 02372 02312 02252 02188 02128 02075	A2433 C2373 C2313 C2253 U2189 C2129 C2073	A2435 G2375 G2315 G2255 A2191 02130 02075 02075	C2436 A2376 C2316 C2256 U2192 U2131 U2076 C2437 A2317 U2257 C2193 U2132 A2077	U2438 A2378 G2318 C2268 U2194 G2133 C2078 A0430 C3270 C10560 U2195 C2078	C2440 C2380 U2320 C2260 C2196 A134 A2080	U2441 A2381 U2321 C2261 U219/ U2081 C2442 G2882 A2322 U2262 A2198 G2136 A2082	C2443 G2383 G2323 G2263 A2199 U2137 Q2083	Q2445 C2385 Q2455 G2201 G2138 U208	G2446 A2386 C2326 A2266 U2202 U2139 U208 G2447 H13387 A3337 A3357 A3367 U2208 G2140 G208	A2448 A2388 A238 A2268 G2204 G2141 A208	U2449 G2389 U2329 G2269 A2200 C208 A2450 U2390 G2330 A2270 C206 A2142 A209	A2451 G2391 G2331 G2271 G2207 C2143 C209 CMED A360 C333 H10770 C2208 C444 H1000	42453 U2993 A2333 A2273 G2209 C2145 C209	G2454 C2394 U2334 A2274 0.2210 A209 G2455 C2395 A2335 C2275 A2211 C2146 A209	C2456 G2396 A2336 G2276 A2212 A2147 C209	0245/ 0239/ 0233/ 0221/ 02214 0210 02458 02338 A2078 02214 102149 0209	A2459 G2399 G2279 G2215 C2150 U209	U2460 G2400 A2340 G2280 G2217 U2151 G210 G2217 C2150	G2218 U.2152 17219 C2153	U2220 A2154		G2157	A2158	02160 C2160







Chain I:

35%

11%

51%

• Molecule 16: 50S RIBOSOMAL PROTEIN L5







• Molecule 25: 50S RIBOSOMAL PROTEIN L18







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	102814	Depositor
Resolution determination method	Not provided	
CTF correction method	INDIVIDUAL PARTICLES	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE $(4k \times 4k)$	Depositor
Maximum map value	0.191	Depositor
Minimum map value	-0.046	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.045	Depositor
Map size (Å)	384.0, 384.0, 384.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.5, 1.5, 1.5	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

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).

Mal	Clasin		Bond lengths		Bond angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	0	1.91	12/635~(1.9%)	2.26	26/848~(3.1%)
2	1	1.71	3/510~(0.6%)	1.90	8/677~(1.2%)
3	2	1.85	8/453~(1.8%)	1.91	10/605~(1.7%)
4	3	1.79	6/450~(1.3%)	2.16	16/599~(2.7%)
5	4	1.66	1/417~(0.2%)	1.93	5/556~(0.9%)
6	5	1.69	15/1748~(0.9%)	1.91	38/2355~(1.6%)
7	6	1.86	6/380~(1.6%)	2.24	15/498~(3.0%)
8	7	1.76	6/513~(1.2%)	1.99	14/676~(2.1%)
9	8	1.77	4/303~(1.3%)	1.84	3/397~(0.8%)
10	9	1.75	31/2584~(1.2%)	2.10	81/3487~(2.3%)
11	А	3.31	347/2744~(12.6%)	3.75	664/4276~(15.5%)
12	В	3.41	9451/69796~(13.5%)	3.79	16403/108888~(15.1%)
13	С	1.82	28/2122~(1.3%)	2.15	58/2854~(2.0%)
14	D	1.74	16/1586~(1.0%)	1.95	36/2134~(1.7%)
15	Е	1.77	16/1571~(1.0%)	2.04	50/2113~(2.4%)
16	F	1.79	13/1444~(0.9%)	2.00	35/1937~(1.8%)
17	G	1.72	7/1336~(0.5%)	1.90	26/1805~(1.4%)
18	Н	1.80	17/1122~(1.5%)	2.05	42/1515~(2.8%)
19	Ι	1.61	4/497~(0.8%)	1.98	9/662~(1.4%)
20	J	1.74	7/1152~(0.6%)	2.02	42/1551~(2.7%)
21	Κ	1.77	10/941~(1.1%)	2.00	29/1260~(2.3%)
22	L	1.81	17/1054~(1.6%)	2.02	32/1403~(2.3%)
23	М	1.84	20/1093~(1.8%)	1.97	26/1460~(1.8%)
24	Ν	1.80	11/974~(1.1%)	2.02	28/1303~(2.1%)
25	0	1.79	9/902~(1.0%)	2.02	28/1209~(2.3%)
26	Р	1.77	9/929~(1.0%)	2.06	24/1242~(1.9%)
27	Q	1.81	11/960~(1.1%)	2.20	45/1278~(3.5%)
28	R	1.78	9/829~(1.1%)	2.04	24/1107~(2.2%)
29	S	1.83	13/864~(1.5%)	2.05	31/1156~(2.7%)
30	Т	1.69	4/745~(0.5%)	2.01	22/996~(2.2%)
31	U	1.71	5/764~(0.7%)	1.86	11/1019~(1.1%)
32	W	1.76	8/766~(1.0%)	1.92	13/1025~(1.3%)
33	Y	1.76	5/603~(0.8%)	2.03	15/797~(1.9%)
All	All	3.02	10129/102787~(9.9%)	3.41	17909/153688~(11.7%)



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	0	0	2
2	1	0	2
3	2	0	1
4	3	0	2
5	4	0	2
6	5	0	3
7	6	0	6
8	7	0	3
9	8	0	1
10	9	0	27
11	А	0	55
12	В	0	1482
13	С	0	9
14	D	0	4
15	Е	0	5
16	F	0	6
17	G	0	4
18	Н	0	2
20	J	0	6
21	Κ	0	7
22	L	0	2
23	М	0	7
24	N	0	7
25	0	0	5
26	Р	0	3
27	Q	0	4
28	R	0	5
29	S	0	3
30	Т	0	2
31	U	0	2
32	W	0	3
33	Y	0	3
All	All	0	1675

The worst 5 of 10129 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	В	2225	A	N7-C5	-20.53	1.26	1.39
12	В	2105	U	C2-N3	19.07	1.51	1.37

Continued on next page...



	v	-	10				
Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
12	В	1853	А	N7-C5	-18.25	1.28	1.39
12	В	548	G	N7-C5	-17.75	1.28	1.39
12	В	1501	G	C6-N1	17.64	1.51	1.39

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The worst 5 of 17909 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
12	В	751	А	N1-C6-N6	26.85	134.71	118.60
12	В	370	G	N1-C6-O6	26.32	135.69	119.90
12	В	928	А	N1-C6-N6	24.76	133.45	118.60
12	В	2360	G	N1-C6-O6	24.64	134.69	119.90
12	В	668	А	N1-C6-N6	24.57	133.34	118.60

There are no chirality outliers.

5 of 1675 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	37	PHE	Sidechain
1	0	56	ARG	Sidechain
2	1	23	ARG	Sidechain
2	1	7	ARG	Sidechain
3	2	44	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	0	625	0	655	4	0
2	1	509	0	543	1	0
3	2	449	0	491	0	0
4	3	444	0	461	3	0
5	4	410	0	440	2	0
6	5	1733	0	1824	6	0
7	6	377	0	418	3	0
8	7	504	0	574	8	0
9	8	302	0	343	1	0
10	9	2541	0	2555	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	А	2455	0	1253	15	0
12	В	62317	0	31306	522	0
13	С	2083	0	2157	14	0
14	D	1565	0	1616	9	0
15	Е	1552	0	1619	6	0
16	F	1420	0	1460	8	0
17	G	1317	0	1364	7	0
18	Н	1111	0	1148	2	0
19	Ι	495	0	525	4	0
20	J	1129	0	1162	7	0
21	Κ	932	0	1003	9	0
22	L	1045	0	1117	8	0
23	М	1074	0	1157	7	0
24	Ν	961	0	1000	8	0
25	0	892	0	923	3	0
26	Р	917	0	965	13	0
27	Q	947	0	1022	4	0
28	R	816	0	839	5	0
29	S	857	0	922	9	0
30	Т	739	0	807	7	0
31	U	758	0	807	8	0
32	W	753	0	780	1	0
33	Y	596	0	610	5	0
All	All	94625	0	63866	702	0

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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 4.

The worst 5 of 702 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)
12:B:1481:U:H3	12:B:1511:G:H21	1.23	0.85
12:B:2267:A:H61	12:B:2271:G:H1	1.25	0.79
30:T:20:ALA:H	30:T:23:ALA:HB3	1.50	0.75
10:9:279:TRP:CG	10:9:328:VAL:HG13	2.21	0.75
12:B:2507:C:H41	12:B:2576:G:H22	1.35	0.74

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	Perce	entiles
1	0	75/77~(97%)	61 (81%)	10 (13%)	4(5%)	2	19
2	1	61/63~(97%)	50 (82%)	8 (13%)	3~(5%)	2	20
3	2	56/58~(97%)	50 (89%)	5 (9%)	1 (2%)	8	40
4	3	54/56~(96%)	43 (80%)	4(7%)	7~(13%)	0	5
5	4	49/54~(91%)	43 (88%)	4 (8%)	2(4%)	3	22
6	5	232/234~(99%)	197 (85%)	25~(11%)	10 (4%)	2	22
7	6	44/46~(96%)	33~(75%)	8 (18%)	3~(7%)	1	15
8	7	62/64~(97%)	47 (76%)	10~(16%)	5 (8%)	1	12
9	8	36/38~(95%)	27 (75%)	7~(19%)	2(6%)	2	18
10	9	332/390~(85%)	261 (79%)	43 (13%)	28 (8%)	1	11
13	С	270/272~(99%)	216 (80%)	31 (12%)	23 (8%)	1	11
14	D	207/209~(99%)	160 (77%)	34 (16%)	13 (6%)	1	16
15	Е	199/201~(99%)	163 (82%)	16 (8%)	20 (10%)	0	9
16	F	176/178~(99%)	135 (77%)	22~(12%)	19 (11%)	0	8
17	G	172/176~(98%)	126 (73%)	31~(18%)	15~(9%)	1	11
18	Н	147/149~(99%)	112 (76%)	21 (14%)	14 (10%)	0	10
19	Ι	67/141~(48%)	65~(97%)	0	2(3%)	4	28
20	J	140/142~(99%)	108 (77%)	20 (14%)	12 (9%)	1	11
21	K	120/123~(98%)	98 (82%)	16~(13%)	6 (5%)	2	20
22	L	141/143~(99%)	115 (82%)	17~(12%)	9 (6%)	1	16
23	М	134/136~(98%)	112 (84%)	16 (12%)	6 (4%)	2	22
24	Ν	119/127~(94%)	94 (79%)	17 (14%)	8 (7%)	1	15
25	Ο	114/116~(98%)	88 (77%)	20 (18%)	6 (5%)	2	19
26	Р	112/114~(98%)	84 (75%)	19 (17%)	9 (8%)	1	12
27	Q	115/117 (98%)	95 (83%)	12 (10%)	8 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
28	R	101/103~(98%)	83 (82%)	14 (14%)	4 (4%)	3 23
29	S	108/110~(98%)	87 (81%)	11 (10%)	10 (9%)	0 10
30	Т	92/100~(92%)	68 (74%)	16 (17%)	8 (9%)	1 11
31	U	96/103~(93%)	73~(76%)	15~(16%)	8 (8%)	1 12
32	W	92/94~(98%)	78~(85%)	11 (12%)	3 (3%)	4 26
33	Y	77/84~(92%)	54 (70%)	15 (20%)	8 (10%)	0 8
All	All	3800/4018~(95%)	3026 (80%)	498 (13%)	276 (7%)	2 13

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5 of 276 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	73	ARG
3	2	9	THR
4	3	3	GLN
6	5	40	GLU
10	9	54	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	0	67/67~(100%)	60~(90%)	7 (10%)	7 26
2	1	55/55~(100%)	51 (93%)	4 (7%)	14 40
3	2	48/48~(100%)	46 (96%)	2(4%)	30 54
4	3	47/47~(100%)	44 (94%)	3~(6%)	17 44
5	4	45/48~(94%)	43~(96%)	2(4%)	28 53
6	5	$181/181 \ (100\%)$	179~(99%)	2(1%)	73 84
7	6	38/38~(100%)	35~(92%)	3~(8%)	12 38
8	7	51/51~(100%)	45 (88%)	6 (12%)	5 21
9	8	34/34~(100%)	31 (91%)	3(9%)	10 33
10	9	268/321 (84%)	231 (86%)	37 (14%)	3 18

Continued on next page...



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
13	С	216/217~(100%)	208 (96%)	8 (4%)	34	58
14	D	164/164~(100%)	146 (89%)	18 (11%)	6	24
15	Е	165/165~(100%)	156 (94%)	9 (6%)	21	48
16	F	149/149~(100%)	143 (96%)	6 (4%)	31	56
17	G	136/137~(99%)	128 (94%)	8 (6%)	19	46
18	Н	114/114 (100%)	105 (92%)	9 (8%)	12	38
19	Ι	51/109~(47%)	46 (90%)	5 (10%)	8	28
20	J	116/116~(100%)	108 (93%)	8 (7%)	15	42
21	К	102/104 (98%)	95~(93%)	7 (7%)	15	42
22	L	102/102~(100%)	95~(93%)	7 (7%)	15	42
23	М	109/109~(100%)	98 (90%)	11 (10%)	7	27
24	Ν	100/103~(97%)	93~(93%)	7 (7%)	15	41
25	Ο	86/86~(100%)	82 (95%)	4 (5%)	26	52
26	Р	99/99~(100%)	94 (95%)	5 (5%)	24	50
27	Q	89/89~(100%)	84 (94%)	5 (6%)	21	47
28	R	84/84 (100%)	79~(94%)	5 (6%)	19	46
29	S	93/93~(100%)	89 (96%)	4 (4%)	29	54
30	Т	80/84~(95%)	72 (90%)	8 (10%)	7	27
31	U	81/84~(96%)	76 (94%)	5 (6%)	18	45
32	W	78/78~(100%)	74 (95%)	4 (5%)	24	50
33	Y	59/62~(95%)	54 (92%)	5 (8%)	10	35
All	All	3107/3238~(96%)	2890 (93%)	217 (7%)	19	41

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5 of 217 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	G	88	LEU
21	Κ	61	VAL
30	Т	48	GLN
18	Н	19	VAL
19	Ι	105	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:



Mol	Chain	Res	Type
21	Κ	29	HIS
25	0	34	HIS
22	L	38	GLN
24	Ν	3	HIS
27	Q	58	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	А	112/118~(94%)	21 (18%)	3~(2%)
12	В	2902/2903~(99%)	540 (18%)	96~(3%)
All	All	3014/3021~(99%)	561 (18%)	99~(3%)

5 of 561 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	А	9	G
11	А	13	G
11	А	14	U
11	А	16	G
11	А	26	С

5 of 99 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	В	1786	А
12	В	2133	G
12	В	1847	А
12	В	2051	А
12	В	2158	А

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 monosaccharides in this entry.



5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-2605. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map



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

6.2 Central slices (i)

6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128



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

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 129

Y Index: 126

Z Index: 143

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



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 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

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 1748 nm^3 ; this corresponds to an approximate mass of 1579 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 0.182 ${\rm \AA}^{-1}$



8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-2605 and PDB model 4CSU. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.045 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 (0.045).



9.4 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.045) and Q-score for the entire model and for each chain.

\mathbf{Chain}	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.9330	0.1580
0	0.9020	0.1240
1	0.9860	0.1510
2	0.9150	0.1450
3	0.8510	0.0740
4	0.7790	0.0940
5	0.0840	0.0310
6	0.9350	0.1170
7	0.9330	0.1150
8	0.9730	0.0750
9	0.6850	0.1020
А	0.9980	0.1940
В	0.9730	0.1770
С	0.9440	0.1260
D	0.9600	0.1280
Е	0.9070	0.1380
F	0.9530	0.1170
G	0.9250	0.1390
Н	0.3160	0.0780
Ι	0.8100	0.0820
J	0.9560	0.1520
Κ	0.9610	0.1330
L	0.9490	0.1220
М	0.9600	0.1390
Ν	0.9320	0.1200
О	0.9820	0.1260
Р	0.9460	0.1390
\mathbf{Q}	0.9390	0.1150
R	0.9440	0.1360
S	0.9220	0.1300
Т	0.9540	0.1280
U	0.9560	0.1220
W	0.9250	0.1430
Y	0.9240	0.0970

