

Dec 19, 2022 - 04:17 am GMT

PDB ID 7BHP : EMDB ID : EMD-12189 Title : Cryo-EM structure of the human Ebp1 - 80S ribosome Authors Desogus, J.; Bhaskar, V.; Chao, J.A. : Deposited on 2021-01-11 : 3.30 Å(reported) Resolution : Based on initial models 2Q8K, 2V6C, 6Y0G :

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.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 3.30 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM\ structures}\ (\#{ m Entries})$
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 chain	
1	L5	5070	50% 22% ·	28%
2	L7	120	82%	18%
3	L8	156	77%	22% •
4	LA	257	94%	
5	LB	403	97%	
6	LC	427	84%	16%
7	LD	297	98%	·
8	LE	288	76% .	23%



Mol	Chain	Length	Quality of chain	
9	LF	248	90%	• 9%
10	LG	266	82%	17%
11	LH	192	99%	
12	LI	214	94%	• 5%
13	LJ	178	90%	• 10%
14	LL	211	94%	6%
15	LM	215	59% • 40%	
16	LN	204	100%	
17	LO	203	98%	
18	LP	184	83%	17%
19	LQ	188	97%	
20	LB	196	76%	23%
20	LS	176		2370
21		160	96%	
<u>22</u>		100	98%	•
20		120	79%	21%
24		157	27% 73%	
25		156	75%	25%
26	LY	145	91%	9%
27	LZ	136	95%	••
28	La	148	99%	••
29	Lb	159	43% 57%	
30	Lc	115	82%	18%
31	Ld	125	86%	14%
32	Le	135	93%	7%
33	Lf	110	98%	•

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Mol	Chain	Length	Quality of chain	
34	Lg	117	87%	• 12%
35	Lh	123	95%	•••
36	Li	105	91%	• 8%
37	Lj	97	87%	• 11%
38	Lk	70	99%	
39	Ll	51	96%	•••
40	Lm	128	4 0% • 59%	
41	Lo	106	97%	•••
42	Lp	92	78%	22%
43	Lr	137	88%	• 11%
44	А	394	81%	18%
45	В	36	53% 47%	

Continued from previous page...



2 Entry composition (i)

There are 48 unique types of molecules in this entry. The entry contains 136812 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 28S ribosomal RNA.

Mol	Chain	Residues			AltConf	Trace			
1	L5	3644	Total 78119	C 34786	N 14297	O 25393	Р 3643	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	С	G	conflict	GB 86475748

• Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues		A	AltConf	Trace			
2	L7	120	Total 2558	C 1141	N 456	0 842	Р 119	0	0

• Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues		А	AltConf	Trace			
3	L8	156	Total 3314	C 1480	N 585	O 1094	Р 155	0	0

• Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	247	Total 1887	C 1183	N 388	0 310	S 6	0	0

• Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	395	Total 3183	C 2028	N 600	0 541	S 14	0	0

• Molecule 6 is a protein called 60S ribosomal protein L4.



Mol	Chain	Residues		At	AltConf	Trace			
6	LC	359	Total 2855	C 1797	N 571	O 472	S 15	0	0

• Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues		At		AltConf	Trace		
7	LD	290	Total 2354	C 1492	N 428	O 420	S 14	0	0

• Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	221	Total 1777	C 1142	N 337	0 294	$\frac{S}{4}$	0	0

• Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
9	LF	225	Total 1870	C 1202	N 358	O 301	S 9	0	0

• Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues		At	AltConf	Trace			
10	LG	220	Total 1780	C 1135	N 343	0 298	$\frac{S}{4}$	0	0

• Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues		At	oms	AltConf	Trace		
11	LH	190	Total 1518	C 956	N 284	0 272	S 6	0	0

• Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues		At	AltConf	Trace			
12	LI	204	Total 1643	C 1042	N 316	0 272	S 13	0	0

• Molecule 13 is a protein called 60S ribosomal protein L11.



Mol	Chain	Residues		At	oms	AltConf	Trace		
13	LJ	161	Total 1294	C 815	N 244	O 229	S 6	0	0

• Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues		At	AltConf	Trace			
14	LL	199	Total 1612	C 1011	N 337	O 260	${f S}$ 4	0	0

• Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues		At	oms	AltConf	Trace		
15	LM	129	Total 1067	C 684	N 205	0 171	${f S}{7}$	0	0

• Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues		At	oms			AltConf	Trace
16	LN	203	Total 1701	C 1072	N 359	O 266	$\frac{S}{4}$	0	0

• Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues		At	AltConf	Trace			
17	LO	198	Total 1625	C 1048	N 317	0 255	$\frac{S}{5}$	0	0

• Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues		At	oms			AltConf	Trace
18	LP	153	Total 1242	С 776	N 241	O 216	${ m S} 9$	0	0

• Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues		At	oms			AltConf	Trace
19	LQ	187	Total 1513	C 944	N 314	O 250	${ m S}{ m 5}$	0	0

• Molecule 20 is a protein called 60S ribosomal protein L19.



Mol	Chain	Residues		At	oms			AltConf	Trace
20	LR	151	Total 1264	C 787	N 273	O 195	S 9	0	0

• Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues		\mathbf{A}	toms	AltConf	Trace		
21	LS	175	Total 1453	C 925	N 283	O 235	S 10	0	0

• Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues		At	oms		AltConf	Trace	
22	LT	157	Total 1284	C 815	N 250	0 214	${ m S}{ m 5}$	0	0

• Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues		At	oms			AltConf	Trace
23	LU	101	Total 821	C 526	N 143	O 150	${ m S} { m 2}$	0	0

• Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
24	LW	42	Total 350	C 223	N 69	O 56	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 25 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues		At	oms			AltConf	Trace
25	LX	117	Total 946	C 604	N 178	O 163	S 1	0	0

• Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues		At	oms			AltConf	Trace
26	LY	132	Total 1102	C 692	N 223	0 184	${ m S} { m 3}$	0	0

• Molecule 27 is a protein called 60S ribosomal protein L27.



Mol	Chain	Residues		At	oms			AltConf	Trace
27	LZ	130	Total 1074	C 697	N 203	0 171	${ m S} { m 3}$	0	0

• Molecule 28 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues		At	oms		Atoms					
28	La	147	Total 1162	C 736	N 237	0 186	${ m S} { m 3}$	0	0			

• Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues		Ate	\mathbf{oms}		AltConf	Trace	
29	Lb	68	Total 559	C 344	N 122	O 90	${ m S} { m 3}$	0	0

• Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues		At	oms			AltConf	Trace
30	Lc	94	Total 737	C 468	N 130	0 133	S 6	0	0

• Molecule 31 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues		At	oms	AltConf	Trace		
31	Ld	107	Total 888	C 560	N 171	O 155	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues		At	oms	AltConf	Trace		
32	Le	126	Total 1043	C 661	N 214	O 163	${ m S}{ m 5}$	0	0

• Molecule 33 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
33	Lf	108	Total 870	C 552	N 173	0 142	${ m S} { m 3}$	0	0

• Molecule 34 is a protein called 60S ribosomal protein L34.



Mol	Chain	Residues		At	oms	AltConf	Trace		
34	Lg	103	Total 821	C 513	N 170	0 132	S 6	0	0

• Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues		At	oms	AltConf	Trace		
35	Lh	119	Total 995	C 629	N 201	0 164	S 1	0	0

• Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues		At	oms	AltConf	Trace		
36	Li	97	Total 803	C 503	N 171	0 124	${ m S}{ m 5}$	0	0

• Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues		At	oms			AltConf	Trace
37	Lj	86	Total 705	C 434	N 155	0 111	${ m S}{ m 5}$	0	0

• Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
38	Lk	69	Total 569	C 366	N 103	O 99	S 1	0	0

• Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf	Trace
30	TI	50	Total	С	N	0	S	0	0
- 39		50	444	281	98	64	1	0	0

• Molecule 40 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
40	Lm	52	Total 429	C 266	N 90	O 67	S 6	0	0

• Molecule 41 is a protein called 60S ribosomal protein L36a.



Mol	Chain	Residues		At	oms	AltConf	Trace		
41	Lo	105	Total 862	C 542	N 175	O 139	S 6	0	0

• Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
42	Lp	72	Total 558	C 353	N 107	0 91	S 7	0	0

• Molecule 43 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues		At	AltConf	Trace			
43	Lr	122	Total 980	C 607	N 204	0 165	$\begin{array}{c} \mathrm{S} \\ \mathrm{4} \end{array}$	0	0

• Molecule 44 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues		At	AltConf	Trace			
44	А	322	Total 2352	C 1514	N 413	0 412	S 13	0	0

• Molecule 45 is a RNA chain called Poly GC double helix strand modeled for ES27L density next to EBP1 density.

Mol	Chain	Residues		A	AltConf	Trace			
45	В	36	Total 774	C 342	N 144	O 252	Р 36	0	0

• Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
46	L5	33	Total Mg 33 33	0
46	L7	3	Total Mg 3 3	0
46	L8	4	Total Mg 4 4	0
46	Ll	1	Total Mg 1 1	0

• Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).



Mol	Chain	Residues	Atoms	AltConf
47	Lj	1	Total Zn 1 1	0
47	Lm	1	Total Zn 1 1	0
47	Lo	1	Total Zn 1 1	0
47	Lp	1	Total Zn 1 1	0

• Molecule 48 is water.

Mol	Chain	Residues	Atoms	AltConf
48	L5	5	Total O 5 5	0
48	L7	4	Total O 4 4	0
48	LI	1	Total O 1 1	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.

- Chain L5: 50% 22% 28%
- \bullet Molecule 1: 28S ribosomal RNA



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G1174	G1178	01179 C1180	C1181 C1182	C1183 A1184		C1192	C1193 G1194	G1195 G1196	C1197	G1198 G1199	G1200	C1202	G1203 C1204	G1205	C1210	G1211 G1212	G1213	C1214 C1215	C1216 G1217	G1218 C1218	G1220 G1220	61221 A1222	5 5	U U	C D	C	0 U U	5 CJ	G1234	C1241	G1244 C1245	C1249 C1250	C1251
C1252 C1253	A .	G	A1257 G1258	G1259 G1260	G1261	70719	G1266 C1267	G1268 G1269	A1270	G1271 C1272	01075	C1276	G1277	<mark>C1280</mark>	G1284	U1285 C1286	G1287	G1288 C1289	G1290	A1294	G1296	<mark>C1301</mark>	C1314	<mark>C1315</mark> G1316	U1317 C1318	<mark>U1319</mark> 111320	61321 41322	A1323	A1324 C1325	A1326 C1327	G1328	61338	C1344
A1345	G1353	A1354	G1358 G1359	111 364	C1365	01367 C1367	G1377	C1378 C1379	G1380	U1381	G1385	A1387	A1388	G1394	A1397	A1398 G1399	G1400	C1401 C1402	G1403	G1406	G1408	C1409 U1410	C1411	C1414 G1415	G1416 C1417	C1418 C1419	A1420	17510	G1425	U1438 C1439	01440 C1441 C1413	C1772 A1443 G1444	
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24		0 00	61 (76 77			86 (1 0		97 98 08	1 66	5 <mark>-1-</mark>	0 0 0 03 0 03 0	04	<mark>م 9</mark>	07 1		-	-	14		11	19 1	31 0	34	41 40		010 010	- - -		67		63
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G1919 C1920	C1921	61922 A1923	C1924 G1925	C1926	C1931	TORTH	C1935 C1936	C1937 C1938	A1939	G1940 A1941	A1942	G1945	61948	U1949	U1954	U1959	A1960	61961 A1962	G1965	C1966 A1967	G1968	G1969 A1970	C1971	U1974 G1975	G1976 C1977	ບ 🖣	: D C	5 C	A1983 A1984	G1985 U1986	5 9 5	e a	: р
С С1994	G1995	C1996 U1997	A1998 A1999	G2000 G2001	A2002	0	G2005 U2006	G2007 112008	A2009	A2010 C2011	A2012 A2013	C2014	U2015 C2016	A2017	07018	G2021 C2022	C2023	62024 A2025	A2026 112027	c2028	G2034	U2044	G2045 G2046	A2047 U2048	G2052	CODE5	G2056	A2069	C2084	G2085	62089	G2094 G2094 A2095	G2096
U2097 G2098	G2099	A2100 C2101	G2102 G2103	G2104 A2105	G2106	G2108	62109 C	5 5	, U	G G2115	C2116 C2117	G2118	C2119 G2120	C2121	C2123	5 5	. ლ ი	ე ლ	C2127 G2128	C2129 C2130	C2131	n C	D C	ი ი	D D	ם ט	, U C	n n	0 ೮	5 A (9 9 9	, U C	5 25
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6006		A23(G23(G23(A23(A20	G23.	G23:	6231	G231		G234	C23	G23	N23	C23		673	A23	A23:	A236	6238 C238	U23	A23	4 A230 G235	C24(A24(1.7V	U24 C24:	G241	024 024	624C	C24:
A2423 G2424	U2425	C2437	C2441	112447		00470	A2453	A2460	G2463	C2464 C2465	C:0470		G2474 G2475		6.5 4 / A	G2483 A2484		G248/ C2488	C2489 112490	C2491	G2493	0.24.94	U2500 C2501	G2502 G2503	C2504	G2506	A2513	A2517	G2518 U2519	A2537	G2542	A2543 G2544	02546 G2546











 \bullet Molecule 5: 60S ribosomal protein L3

Chain LB:	97%	
MET 82 831 831 831 838 838 838 838 838		
• Molecule 6:	60S ribosomal protein L4	
Chain LC:	84%	16%
M1 M188 R188 N286 A359 ALA LEU GLN	ALA ALA SER ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	THR LYS LYS PRO ALA ALA PRO GLU LYS LYS
PRO ALA GLU CYS LYS PRO PRO GLU GLU	LYS PRO ALA ALA	
• Molecule 7:	60S ribosomal protein L5	
Chain LD:	98%	·
MET G2 G2 GLU GLU ALA ALA ALA CLU SER SER		
• Molecule 8:	60S ribosomal protein L6	
Chain LE:	76% · 239	6
MET ALA ALA GLU CLU CLU VAL CLU CLU PRO ASP	THR THR LVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLV CLVS CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	LYS LYS LYS CLU LYS VAL LEU LEU A90
K130 R158 K221 LEU LEU LYS PRO ARG	HIS CLN CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 9:	60S ribosomal protein L7	
Chain LF:	90%	• 9%
MET GLU GLV GLV GLU GLU CLYS LYS LYS GLU GLU	VAL PRO ALA VAL PRO GLU GLU CVS CLVS ARG ARG M132 N248 N248	
• Molecule 10): 60S ribosomal protein L7a	
Chain LG:	82% •	17%



MET PRO PRO GLY CLYS CLYS CLYS CLYS CLYS CLYS CLYS CL	VAL VAL LYS CLN GLN GLN GLN CLS E119 CYS CLYS CLYS CLYS CLYS CLYS CLYS CLYS	THR K131 N240 LVS LVS LVS LVS LVS LLV LLV LLV LLV LLV
• Molecule 11: 60S ribe	osomal protein L9	
Chain LH:	99%	
A190		
• Molecule 12: 60S ribe	osomal protein L10-like	
Chain LI:	94%	• 5%
MET G2 G2 R82 C103 SER C103 A103 A103 A104 A104 A104 A104 A104 A104 A113 A113	F176 K208 S214	
• Molecule 13: 60S ribo	osomal protein L11	
Chain LJ:	90%	• 10%
MET ALA GLN GLN ASP GLN GLY GLY K8 F113 L13 L13 L13 L12 L12 L12 L12 L12 L12 L12 L12	TYR D120 LEU LEU GLY LYS	
• Molecule 14: 60S ribe	osomal protein L13	
Chain LL:	94%	6%
MET A2 A2 A2 A2 A2 A2 A2 A2 A2 A2 A2 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1		
• Molecule 15: 60S ribe	osomal protein L14	
Chain LM:	59% ·	40%
MET V2 V2 D32 L130 L130 L130 L130 L130 L130 L15U L15U L15U L15U L15U L15U L15U L15U	PRO LYS LYS LYS ALA GLY GLY GLY GLY GLY ALA ALA ALA ALA ALA ALA ALA ALA ALA A	ALA LYSS LYSS LYSS LYSS ALA ALA PRO ALA PRO ALA ALA PRO CYSS VAL
ALA THR GLV GLV GLV GLV CLYS ALA PRO PRO PRO PRO CLYS GLV CLYS GLV CLYS CLV	ALA PRO ALA GLIN GLIN LYS PRO PRO PRO FILA SER CLYS LYS LYS LYS ALA	
• Molecule 16: 60S ribe	osomal protein L15	
Chain LN:	100%	
MET C2 N204		
• Molecule 17: 60S ribo	osomal protein L13a	

W O R L D W I D E PROTEIN DATA BANK

Chain LO:	98%	•
MET ALA GLU GLN VAL VAL VO V203		
• Molecule 18	: 60S ribosomal protein L17	
Chain LP:	83%	17%
MET V2 GLN GLN ILE VAL PRO PRO PRO	GLU GLU VAL ALA ALA GLU GLU CYS CLYS CLYS GLU MET ALA ALA ALA ALA GLU GLU	
• Molecule 19	: 60S ribosomal protein L18	
Chain LQ:	97%	· ·
MET C2 L28 R108 P159 R160 S161		
• Molecule 20	: 60S ribosomal protein L19	
Chain LR:	76%	• 23%
MET 82 82 896 M96 K167 LVS LEU	LEU ALA ASP ALA ALA ALA ALA ALA ALA ALA ARG ALU CLY GLU GLU GLU GLU GLU GLU TLE TLY CLY GLU CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	SER LVS GLU GLU GLU GLU CLV LVS LVS
• Molecule 21	: 60S ribosomal protein L18a	
Chain LS:	98%	••
MET K21 K21 R1 20 R1 60 F1 76		
• Molecule 22	: 60S ribosomal protein L21	
Chain LT:	98%	
MET T2 F158 MET ALA		
• Molecule 23	: 60S ribosomal protein L22	
Chain LU:	79%	21%
MET ALA PRO VAL LYS LYS LVS LEU VAL VAL VAL		
• Molecule 24	: 60S ribosomal protein L24	



Chain LW	: 2	7%			7	73%						
MET LYS VAL GLU CG CG	ARG ARG ARG ARG ALA ARG ARG THR	ASP GLY LYS VAL PHE GLN PHE	LEU N33 G62 GLN SER	GLU GLU GLU GLU GLU	LYS ARG ARG ARG	ALA VAL LYS PHE	GLN ARG ALA ILE	THR GLY ALA	SER LEU ALA	ASP ILE	ALA T VS	ARG ASN GLN
LYS PRO GLU VAL ARG ALA ALA CLN	ARG GLU GLN ALA ARG ALA	ALA LYS GLU ALA LYS LYS ALA	LYS GLN ALA SER LYS LYS	THR ALA MET ALA ALA	ALA LYS ALA PRO THR	LYS ALA ALA PRO	LYS GLN ILF	VAL LYS PRO	VAL LYS VAL	SER	ARG	GLY GLY LYS
ARG												
• Molecule	25:60S	ribosomal	protein	L23a								
Chain LX:			75%						25%	-	_	
MET ALA PRO LYS ALA LYS LYS CIU	ALA PRO PRO PRO LYS ALA	GLU ALA LYS ALA LYS ALA LEU LEU	LYS ALA LYS LYS ALA VAL	LEU LYS GLY VAL HIS	SER LYS LYS LYS	LYS 140 1156						
• Molecule	e 26: 60S	ribosomal	protein	L26								
Chain LY:				91%					_	9%	0	
M1 K132 GLY LYS LYS LYS LYS CUI	GLU GLU GLU MET GLN GLN	GLU										
• Molecule	27:60S	ribosomal	protein	L27								
Chain LZ:				95%						·	·	
MET G2 ASP GLY THR SFR	ASP R36 R102 F136											
• Molecule	e 28: 60S i	ribosomal	protein	L27a								
Chain La:				99%								
MET P2 K116 A148												
• Molecule	29:60S	ribosomal	protein	L29								
Chain Lb:		43%		_		5	7%			-	_	
MET A2 A69 GLU ALA I VE	ALA LEU LEU LYS PRO GLU	VAL LYS PRO LYS PRO LYS	GLY VAL SER ARG LYS LEU	ASP ARG LEU ALA TYR	ALA ALA PRO LYS	LEU GLY LYS ARG	ALA ARG ALA ARG	ILE ALA LYS	GLY LEU ARG	LEU CYS	PRO 1 VS	ALA ALA ALA ALA
LYS ALA LYS ALA ALA LYS ASP GLN THR	LYS ALA GLN ALA ALA ALA PRO	ALA SER VAL PRO ALA ALA	PRO LYS ARG THR GLN ALA	PRO THR LYS ALA SER	GLU GLU							

• Molecule 30: 60S ribosomal protein L30



Chain Lc:	82%	18%
•		
NET VALLA ALA ALA ALA ALA ALA ALA CS CS SER SER SER SER SER SER SER SER SER SE	KB7 KB7 KB10 SER MC17 PR00 CLN CLN CLN CLN CLN CLN CLN CLN CLN CLN	
• Molecule 31: 60S ri	bosomal protein L31	
Chain Ld:	86%	14%
MET ALA PRO ALA CLYS CLYS GLY CLYS CLYS CLYS CLYS CLYS SER ARG SER	ILE N18 E124 ASN	
• Molecule 32: 60S ri	bosomal protein L32	
Chain Le:	93%	7%
MET ALA ALA L4 L4 L129 CLU GLU GLU GLU GLU GLU GLU		
• Molecule 33: 60S ri	bosomal protein L35a	
Chain Lf:	98%	·
MET SER G3 I110		
• Molecule 34: 60S ri	bosomal protein L34	
Chain Lg:	87%	• 12%
MET V2 V2 V2 V2 V2 V2 LYS LYS LYS LLEU LYS LLEU LYS CLM GLM SER GLM GLM	LYS ALA LYS	
• Molecule 35: 60S ri	bosomal protein L35	
Chain Lh:	95%	
MET ALA K25 K25 K74 V121 LYS ALA		
• Molecule 36: 60S ri	bosomal protein L36	
Chain Li:	91%	• 8%
MET L3 K35 AL4 AL4 AL4 AL4 AL4 ASP ASP		

 \bullet Molecule 37: 60S ribosomal protein L37



Chain Lj:	87%	• 11%
MET T2 Y39 K87 ALA ALA ALA	VAL ALA ALA SER SER SER SER	
• Molecule 38:	60S ribosomal protein L38	
Chain Lk:	99%	
MET P2 K70		
• Molecule 39:	60S ribosomal protein L39	
Chain Ll:	96%	• •
MET S2 R11 L51		
• Molecule 40:	Ubiquitin-60S ribosomal protein L40	
Chain Lm:	40% • 59%	
MET GLN GLN CLLE CVAL VAL VAL VAL VAL THR THR THR CLY GLY	THRE TREAT TO THE TREAT THE TREAT TR	ALLE ALLE GLYS GLYS GLV GLV GLV GLY GLY CLU CLU CLU ASP ASP ASP ASP
ILLE MET CLAN CLAN CLAN CLAN CLAN CLAN CLAN CLAN CLAN CLAN CLAN CLAN CLAN	ARG LEU ARG GLY CIT CIT CIT CIT CIT CIT CIT CIT CIT CIT	PHER PHER CITY CITY CITY CITY CITY CITY CITY CITY
Molecule 41:	E E	PHER PHER CITY CITY CITY CITY CITY CITY CITY CITY
 Molecule 41: Chain Lo: 	E E	PHER PHER CIV CIV CIV CIV CIV CIV CIV CIV CIV CIV
 Molecule 41: Chain Lo: 	Image: Second	PHER PHER CIV CIV CIV CIV CIV CIV CIV CIV CIV CIV
• Molecule 41: • Molecule 41: • Molecule 41:	Image: Second protein L36a 60S ribosomal protein L37a	PHER PHER CITY CITY CITY CITY CITY CITY CITY CITY
Image: Second system Image: Second system	Image: Second protein L36a 60S ribosomal protein L37a 78%	222%
Image: Second system Image: Second system	Image: Second secon	1994 1997 1997 1997 1997 1997 1997 1997
Image: Second system Image: Second system	Image: Second protein L36a 60S ribosomal protein L37a 78% 60S ribosomal protein L28	222%





• Molecule 44: Proliferation-associated protein 2G4



Chain B:		53	3%	47%
<mark>ម ម ម ទ</mark> ទ ទ	C13 C14 C18	G 303 G304 G307 G307 G309 G309	G313 G314 G314 G315 G315 G315 G317 G317	



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44556	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	D 1
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.029	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	516.0, 516.0, 516.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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: MG, ZN

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	Chain	Bo	ond lengths	Bond angles	
WIOI	Ullaill	RMSZ	# Z > 5	RMSZ	# Z > 5
1	L5	0.74	1/87379~(0.0%)	0.92	93/136294~(0.1%)
2	L7	0.72	0/2858	0.87	0/4455
3	L8	0.77	1/3701~(0.0%)	0.92	7/5766~(0.1%)
4	LA	0.42	0/1925	0.60	1/2581~(0.0%)
5	LB	0.40	0/3251	0.55	1/4351~(0.0%)
6	LC	0.39	0/2909	0.52	0/3907
7	LD	0.38	0/2400	0.50	0/3215
8	LE	0.36	0/1811	0.51	0/2428
9	LF	0.43	0/1905	0.54	1/2539~(0.0%)
10	LG	0.37	0/1811	0.50	0/2441
11	LH	0.38	0/1537	0.53	0/2066
12	LI	0.41	0/1682	0.52	0/2247
13	LJ	0.34	0/1314	0.53	0/1754
14	LL	0.38	0/1643	0.53	0/2199
15	LM	0.42	0/1089	0.58	2/1457~(0.1%)
16	LN	0.45	0/1746	0.49	0/2338
17	LO	0.41	0/1657	0.52	0/2216
18	LP	0.43	0/1268	0.54	0/1701
19	LQ	0.41	0/1537	0.55	1/2052~(0.0%)
20	LR	0.35	0/1280	0.51	1/1694~(0.1%)
21	LS	0.41	0/1493	0.53	0/2003
22	LT	0.40	0/1312	0.49	0/1753
23	LU	0.34	0/835	0.52	0/1122
24	LW	0.38	0/359	0.49	0/477
25	LX	0.39	0/963	0.55	0/1299
26	LY	0.38	0/1119	0.51	0/1488
27	LZ	0.40	0/1096	0.54	$0/1\overline{459}$
28	La	0.41	$0/1\overline{191}$	0.52	$0/1\overline{591}$
29	Lb	0.39	0/569	0.53	0/750
30	Lc	0.38	0/746	0.53	0/1000
31	Ld	0.39	0/903	0.51	0/1216
32	Le	0.41	0/1061	0.52	0/1415



Mal	Chain	Bo	ond lengths	Bond angles		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
33	Lf	0.43	0/889	0.54	0/1190	
34	Lg	0.41	0/831	0.58	1/1108~(0.1%)	
35	Lh	0.35	0/1003	0.55	1/1326~(0.1%)	
36	Li	0.36	0/814	0.51	0/1076	
37	Lj	0.45	0/720	0.59	0/952	
38	Lk	0.36	0/575	0.57	0/761	
39	Ll	0.37	0/454	0.60	1/599~(0.2%)	
40	Lm	0.34	0/435	0.51	0/575	
41	Lo	0.40	0/876	0.58	1/1156~(0.1%)	
42	Lp	0.44	0/568	0.53	0/754	
43	Lr	0.39	0/995	0.51	0/1334	
44	А	0.32	0/2387	0.49	0/3218	
45	В	0.45	0/861	1.16	4/1338~(0.3%)	
All	All	0.63	2/147758~(0.0%)	0.81	115/218661~(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
5	LB	0	1
8	LE	0	1
9	LF	0	1
12	LI	0	1
19	LQ	0	1
37	Lj	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms		Observed(Å)	Ideal(Å)
3	L8	62	A	N9-C4	-6.35	1.34	1.37
1	L5	1296	G	N9-C4	-5.16	1.33	1.38

All (115) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	L5	1296	G	N3-C4-N9	-9.46	120.32	126.00
1	L5	1296	G	C4-N9-C1'	-8.94	114.87	126.50
1	L5	1996	С	N1-C2-O2	8.34	123.91	118.90
1	L5	468	U	C5-C6-N1	8.30	126.85	122.70



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Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
1	L5	468	U	C2-N1-C1'	8.27	127.62	117.70
1	L5	1296	G	N3-C4-C5	8.22	132.71	128.60
1	L5	1296	G	C8-N9-C1'	7.89	137.26	127.00
1	L5	4886	С	N1-C2-O2	7.80	123.58	118.90
1	L5	2409	U	C2-N1-C1'	7.50	126.70	117.70
9	LF	132	MET	CA-CB-CG	7.36	125.81	113.30
1	L5	1996	С	C2-N1-C1'	7.24	126.77	118.80
35	Lh	25	LYS	CA-CB-CG	7.15	129.12	113.40
1	L5	450	G	N7-C8-N9	7.13	116.67	113.10
3	L8	123	U	N1-C2-O2	7.00	127.70	122.80
1	L5	2563	С	N1-C2-O2	6.97	123.08	118.90
1	L5	657	С	C2-N1-C1'	6.91	126.40	118.80
1	L5	1969	G	N1-C6-O6	-6.85	115.79	119.90
1	L5	1971	С	C2-N1-C1'	6.78	126.25	118.80
1	L5	4886	С	C2-N1-C1'	6.65	126.11	118.80
1	L5	2904	U	C2-N1-C1'	6.59	125.61	117.70
1	L5	138	G	N3-C4-N9	-6.58	122.05	126.00
3	L8	123	U	C2-N1-C1'	6.51	125.51	117.70
1	L5	1296	G	C6-C5-N7	6.50	134.30	130.40
1	L5	1996	С	N3-C2-O2	-6.43	117.40	121.90
1	L5	456	С	O4'-C1'-N1	6.39	113.32	108.20
1	L5	450	G	C8-N9-C4	-6.31	103.88	106.40
1	L5	4990	С	N1-C2-O2	6.30	122.68	118.90
1	L5	2563	С	C2-N1-C1'	6.29	125.72	118.80
39	Ll	11	ARG	CA-CB-CG	6.26	127.16	113.40
1	L5	125	С	C2-N1-C1'	6.23	125.65	118.80
1	L5	260	С	N3-C2-O2	-6.21	117.55	121.90
1	L5	4091	G	C5-C6-O6	-6.19	124.89	128.60
1	L5	914	U	C5-C4-O4	-6.17	122.20	125.90
1	L5	4921	С	N1-C2-O2	6.16	122.60	118.90
1	L5	1082	С	N3-C2-O2	-6.09	117.64	121.90
1	L5	5031	G	N3-C4-N9	-6.08	122.35	126.00
1	L5	1631	А	N1-C2-N3	6.07	132.34	129.30
1	L5	209	U	C2-N1-C1'	6.05	124.97	117.70
1	L5	468	U	C2-N3-C4	6.02	130.61	127.00
45	В	309	G	N1-C6-O6	-5.97	116.32	119.90
1	L5	4091	G	C6-C5-N7	-5.93	126.84	130.40
3	L8	128	С	C2-N1-C1'	5.92	125.31	118.80
1	L5	5031	G	N3-C2-N2	-5.90	115.77	119.90
1	L5	468	U	N1-C2-O2	5.89	126.93	122.80
5	LB	31	SER	C-N-CA	-5.88	107.00	121.70
1	L5	655	С	N3-C2-O2	-5.86	117.80	121.90



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	L5	125	С	N1-C2-O2	5.81	122.38	118.90
1	L5	4091	G	N3-C4-N9	5.80	129.48	126.00
1	L5	4091	G	C8-N9-C1'	-5.78	119.48	127.00
1	L5	693	С	N3-C2-O2	-5.76	117.86	121.90
1	L5	657	С	C6-N1-C1'	-5.75	113.90	120.80
1	L5	1252	С	C2-N1-C1'	5.71	125.08	118.80
3	L8	51	U	N3-C2-O2	-5.71	118.20	122.20
1	L5	468	U	C6-N1-C1'	-5.70	113.22	121.20
1	L5	657	С	C5-C4-N4	-5.70	116.21	120.20
1	L5	914	U	N3-C4-O4	5.69	123.38	119.40
1	L5	450	G	C6-C5-N7	-5.68	126.99	130.40
15	LM	32	ASP	CB-CG-OD2	5.67	123.41	118.30
1	L5	4734	А	O4'-C1'-N9	5.65	112.72	108.20
1	L5	4886	С	N3-C2-O2	-5.65	117.95	121.90
3	L8	123	U	N3-C2-O2	-5.64	118.25	122.20
1	L5	3598	С	N1-C2-O2	5.62	122.27	118.90
1	L5	2904	U	N1-C2-O2	5.61	126.73	122.80
1	L5	488	G	C4-N9-C1'	5.60	133.78	126.50
1	L5	1996	С	C6-N1-C1'	-5.60	114.08	120.80
1	L5	4091	G	C4-C5-N7	5.58	113.03	110.80
1	L5	4393	G	C2-N3-C4	-5.58	109.11	111.90
1	L5	4973	U	C2-N1-C1'	5.58	124.39	117.70
1	L5	2904	U	N3-C2-O2	-5.58	118.30	122.20
1	L5	4921	С	C2-N1-C1'	5.57	124.92	118.80
15	LM	118	MET	CG-SD-CE	-5.56	91.31	100.20
1	L5	4091	G	N9-C4-C5	-5.54	103.19	105.40
1	L5	2563	С	N3-C2-O2	-5.53	118.03	121.90
1	L5	3816	А	OP2-P-O3'	5.51	117.33	105.20
1	L5	5018	С	C2-N3-C4	-5.49	117.15	119.90
1	L5	1816	С	C6-N1-C2	-5.44	118.12	120.30
4	LA	96	LEU	CA-CB-CG	5.41	127.74	115.30
1	L5	138	G	N9-C4-C5	5.41	107.56	105.40
1	L5	4773	С	C2-N1-C1'	5.41	124.75	118.80
1	L5	496	G	C5-C6-O6	-5.39	125.36	128.60
1	L5	4091	G	C4-N9-C1'	5.38	133.49	126.50
20	LR	96	MET	CA-CB-CG	5.36	122.42	113.30
45	В	9	C	N1-C2-O2	5.34	122.11	118.90
1	L5	4345	С	C2-N1-C1'	5.34	124.67	118.80
1	L5	1438	U	C2-N1-C1'	5.33	124.10	117.70
34	Lg	65	MET	CB-CG-SD	-5.33	96.41	112.40
1	L5	138	G	C5-C6-O6	5.31	131.78	128.60
1	L5	488	G	C6-C5-N7	-5.30	127.22	130.40



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	L5	4862	G	N9-C4-C5	-5.30	103.28	105.40
45	В	10	С	C6-N1-C2	-5.30	118.18	120.30
3	L8	51	U	N1-C2-O2	5.26	126.48	122.80
1	L5	1703	С	C2-N1-C1'	5.25	124.58	118.80
41	Lo	39	ARG	CG-CD-NE	-5.25	100.78	111.80
1	L5	294	G	C2-N3-C4	5.22	114.51	111.90
1	L5	2409	U	N1-C2-O2	5.20	126.44	122.80
19	LQ	28	LEU	CA-CB-CG	5.18	127.22	115.30
1	L5	4886	С	C6-N1-C1'	-5.17	114.59	120.80
1	L5	131	С	C6-N1-C2	-5.17	118.23	120.30
1	L5	2501	С	N1-C2-O2	5.17	122.00	118.90
1	L5	688	U	N3-C2-O2	-5.16	118.59	122.20
1	L5	2409	U	C6-N1-C1'	-5.15	113.99	121.20
45	В	9	С	N3-C2-O2	-5.15	118.29	121.90
1	L5	1971	С	C6-N1-C1'	-5.14	114.63	120.80
1	L5	2738	С	C2-N1-C1'	-5.14	113.15	118.80
1	L5	4862	G	C4-C5-N7	5.12	112.85	110.80
1	L5	4193	С	N1-C2-O2	5.12	121.97	118.90
1	L5	5031	G	N9-C4-C5	5.11	107.44	105.40
1	L5	2096	G	C4-N9-C1'	5.10	133.12	126.50
1	L5	4932	U	C2-N1-C1'	5.08	123.79	117.70
1	L5	249	С	C2-N1-C1'	5.08	124.38	118.80
3	L8	128	С	N1-C2-O2	5.07	121.94	118.90
1	L5	491	G	N3-C4-N9	-5.06	122.97	126.00
1	L5	4932	U	N1-C2-O2	5.02	126.32	122.80
1	L5	1521	С	O5'-P-OP2	-5.01	101.19	105.70
1	L5	2487	G	N3-C4-N9	-5.01	123.00	126.00

Continued from previous page...

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	LB	390	GLY	Peptide
8	LE	130	LYS	Peptide
9	LF	162	ILE	Peptide
12	LI	176	PHE	Peptide
19	LQ	161	SER	Peptide
37	Lj	39	TYR	Peptide



5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
4	LA	245/257~(95%)	205 (84%)	39~(16%)	1 (0%)	34	66
5	LB	393/403~(98%)	339 (86%)	54 (14%)	0	100	100
6	LC	357/427~(84%)	316 (88%)	41 (12%)	0	100	100
7	LD	288/297~(97%)	262 (91%)	26~(9%)	0	100	100
8	LE	215/288~(75%)	183 (85%)	32~(15%)	0	100	100
9	LF	223/248~(90%)	210 (94%)	13 (6%)	0	100	100
10	LG	216/266~(81%)	191 (88%)	25 (12%)	0	100	100
11	LH	188/192~(98%)	168 (89%)	20 (11%)	0	100	100
12	LI	200/214~(94%)	165 (82%)	35 (18%)	0	100	100
13	LJ	157/178 (88%)	138 (88%)	19 (12%)	0	100	100
14	LL	197/211~(93%)	178 (90%)	19 (10%)	0	100	100
15	LM	127/215~(59%)	115 (91%)	12 (9%)	0	100	100
16	LN	201/204~(98%)	190 (94%)	11 (6%)	0	100	100
17	LO	196/203~(97%)	180 (92%)	16 (8%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	172 (93%)	11 (6%)	2 (1%)	14	45
20	LR	149/196~(76%)	140 (94%)	9 (6%)	0	100	100
21	LS	173/176~(98%)	147 (85%)	26 (15%)	0	100	100
22	LT	155/160~(97%)	137 (88%)	18 (12%)	0	100	100
23	LU	99/128~(77%)	89 (90%)	10 (10%)	0	100	100
24	LW	38/157~(24%)	33 (87%)	5 (13%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
25	LX	115/156~(74%)	99~(86%)	16 (14%)	0	100	100
26	LY	130/145~(90%)	117 (90%)	13 (10%)	0	100	100
27	LZ	126/136~(93%)	114 (90%)	12 (10%)	0	100	100
28	La	145/148 (98%)	129 (89%)	16 (11%)	0	100	100
29	Lb	66/159~(42%)	56 (85%)	10 (15%)	0	100	100
30	Lc	90/115 (78%)	83 (92%)	7 (8%)	0	100	100
31	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
32	Le	124/135~(92%)	114 (92%)	10 (8%)	0	100	100
33	Lf	106/110 (96%)	93 (88%)	13 (12%)	0	100	100
34	Lg	101/117~(86%)	87 (86%)	14 (14%)	0	100	100
35	Lh	117/123~(95%)	108 (92%)	9 (8%)	0	100	100
36	Li	95/105~(90%)	90 (95%)	5 (5%)	0	100	100
37	Lj	84/97~(87%)	71 (84%)	13 (16%)	0	100	100
38	Lk	67/70~(96%)	60 (90%)	7 (10%)	0	100	100
39	Ll	48/51~(94%)	42 (88%)	6 (12%)	0	100	100
40	Lm	50/128~(39%)	46 (92%)	4 (8%)	0	100	100
41	Lo	103/106~(97%)	87 (84%)	15 (15%)	1 (1%)	15	46
42	Lp	70/92~(76%)	61 (87%)	9 (13%)	0	100	100
43	Lr	120/137~(88%)	104 (87%)	16 (13%)	0	100	100
44	А	300/394~(76%)	265 (88%)	35 (12%)	0	100	100
All	All	6315/7441 (85%)	5623 (89%)	688 (11%)	4 (0%)	54	81

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All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LA	247	ARG
19	LQ	160	HIS
41	Lo	103	VAL
19	LQ	159	PRO

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.



Mol	Chain	Analysed	Rotameric	Outliers	ers Percentil	
4	LA	188/199~(94%)	185~(98%)	3(2%)	62	79
5	LB	342/349~(98%)	339~(99%)	3 (1%)	78	87
6	LC	298/348~(86%)	296 (99%)	2 (1%)	84	90
7	LD	243/250~(97%)	243 (100%)	0	100	100
8	LE	195/252~(77%)	193 (99%)	2 (1%)	76	86
9	LF	194/215~(90%)	194 (100%)	0	100	100
10	LG	190/223~(85%)	188 (99%)	2 (1%)	73	85
11	LH	169/171~(99%)	169 (100%)	0	100	100
12	LI	172/181~(95%)	171 (99%)	1 (1%)	86	91
13	LJ	136/149~(91%)	135 (99%)	1 (1%)	84	90
14	LL	167/177~(94%)	166 (99%)	1 (1%)	86	91
15	LM	111/161 (69%)	111 (100%)	0	100	100
16	LN	171/172~(99%)	171 (100%)	0	100	100
17	LO	170/174 (98%)	170 (100%)	0	100	100
18	LP	134/163~(82%)	134 (100%)	0	100	100
19	LQ	164/165~(99%)	163 (99%)	1 (1%)	86	91
20	LR	135/175~(77%)	134 (99%)	1 (1%)	84	90
21	LS	156/157~(99%)	154 (99%)	2 (1%)	69	82
22	LT	138/140~(99%)	138 (100%)	0	100	100
23	LU	90/115~(78%)	90 (100%)	0	100	100
24	LW	37/126~(29%)	37 (100%)	0	100	100
25	LX	102/133~(77%)	102 (100%)	0	100	100
26	LY	123/135~(91%)	123 (100%)	0	100	100
27	LZ	113/118 (96%)	112 (99%)	1 (1%)	78	87
28	La	120/121 (99%)	119 (99%)	1 (1%)	81	89
29	Lb	58/126~(46%)	58 (100%)	0	100	100
30	Lc	80/97~(82%)	80 (100%)	0	100	100
31	Ld	98/110~(89%)	98 (100%)	0	100	100
32	Le	$114/121 \ (94\%)$	114 (100%)	0	100	100
33	Lf	87/89~(98%)	87 (100%)	0	100	100

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
34	Lg	89/100~(89%)	89 (100%)	0	100	100
35	Lh	108/110~(98%)	107 (99%)	1 (1%)	78	87
36	Li	85/89~(96%)	84 (99%)	1 (1%)	71	83
37	Lj	73/80~(91%)	72 (99%)	1 (1%)	67	82
38	Lk	64/65~(98%)	64 (100%)	0	100	100
39	Ll	47/48~(98%)	47 (100%)	0	100	100
40	Lm	48/116 (41%)	47 (98%)	1 (2%)	53	75
41	Lo	93/94~(99%)	93 (100%)	0	100	100
42	Lp	57/75~(76%)	57 (100%)	0	100	100
43	Lr	106/121~(88%)	105 (99%)	1 (1%)	78	87
44	А	223/336~(66%)	222 (100%)	1 (0%)	91	95
All	All	5488/6346~(86%)	5461 (100%)	27 (0%)	89	93

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All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	163	ARG
4	LA	193	ARG
4	LA	242	ARG
5	LB	238	LYS
5	LB	261	ARG
5	LB	358	ARG
6	LC	188	ARG
6	LC	286	ASN
8	LE	56	ARG
8	LE	158	ARG
10	LG	85	GLN
10	LG	240	ASN
12	LI	208	LYS
13	LJ	58	ARG
14	LL	103	ARG
19	LQ	108	ARG
20	LR	107	ARG
21	LS	120	ARG
21	LS	160	ARG
27	LZ	102	ARG
28	La	116	LYS
35	Lh	74	LYS



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Mol	Chain	Res	Type
36	Li	35	LYS
37	Lj	75	ARG
40	Lm	106	ARG
43	Lr	107	ARG
44	А	243	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
6	LC	61	GLN
7	LD	39	GLN
7	LD	202	GLN
7	LD	203	ASN
7	LD	225	GLN
9	LF	110	GLN
9	LF	131	ASN
9	LF	226	HIS
10	LG	85	GLN
10	LG	108	GLN
10	LG	112	GLN
10	LG	159	HIS
11	LH	8	GLN
12	LI	133	GLN
12	LI	144	ASN
13	LJ	97	ASN
14	LL	111	GLN
14	LL	115	GLN
16	LN	91	GLN
17	LO	63	ASN
17	LO	173	GLN
18	LP	80	GLN
22	LT	54	HIS
25	LX	108	GLN
28	La	120	GLN
30	Lc	40	GLN
30	Lc	72	HIS
36	Li	26	HIS

5.3.3 RNA (i)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3627/5070~(71%)	1096~(30%)	32~(0%)
2	L7	119/120~(99%)	22 (18%)	0
3	L8	155/156~(99%)	33 (21%)	2(1%)
45	В	33/36~(91%)	14 (42%)	0
All	All	3934/5382~(73%)	1165 (29%)	34~(0%)

All (1165) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	5	А
1	L5	13	U
1	L5	18	С
1	L5	21	G
1	L5	23	С
1	L5	25	А
1	L5	39	А
1	L5	42	А
1	L5	45	U
1	L5	48	G
1	L5	58	G
1	L5	59	А
1	L5	64	А
1	L5	65	А
1	L5	69	А
1	L5	72	С
1	L5	73	А
1	L5	91	G
1	L5	105	А
1	L5	109	G
1	L5	110	С
1	L5	116	G
1	L5	119	G
1	L5	120	А
1	L5	121	А
1	L5	125	С
1	L5	133	С
1	L5	134	G
1	L5	135	G
1	L5	136	С
1	L5	137	G
1	L5	139	G
1	L5	144	G



Mol	Chain	Res	Type
1	L5	145	G
1	L5	146	G
1	L5	151	G
1	L5	155	С
1	L5	156	G
1	L5	159	С
1	L5	160	G
1	L5	161	G
1	L5	165	А
1	L5	170	С
1	L5	171	U
1	L5	172	С
1	L5	173	С
1	L5	175	С
1	L5	176	G
1	L5	177	G
1	L5	179	G
1	L5	180	С
1	L5	181	С
1	L5	183	С
1	L5	185	С
1	L5	186	G
1	L5	188	G
1	L5	199	G
1	L5	200	U
1	L5	209	U
1	L5	218	A
1	L5	220	С
1	L5	226	G
1	L5	233	U
1	L5	234	G
1	L5	246	G
1	L5	249	С
1	L5	250	С
1	L5	253	G
1	L5	255	C
1	L5	256	G
1	L5	261	G
1	L5	263	G
1	L5	264	C
1	L5	267	G
1	L5	276	С

Continued from previous page...


Mol	Chain	Res	Type
1	L5	278	G
1	L5	280	G
1	L5	295	А
1	L5	297	U
1	L5	306	А
1	L5	309	С
1	L5	315	G
1	L5	316	U
1	L5	319	А
1	L5	340	С
1	L5	354	U
1	L5	358	С
1	L5	361	C
1	L5	373	G
1	L5	387	G
1	L5	389	A
1	L5	393	U
1	L5	394	G
1	L5	399	G
1	L5	401	G
1	L5	408	А
1	L5	409	G
1	L5	410	А
1	L5	411	G
1	L5	413	G
1	L5	414	С
1	L5	415	G
1	L5	440	U
1	L5	449	С
1	L5	450	G
1	L5	452	A
1	L5	453	G
1	L5	456	C
1	L5	457	G
1	L5	467	U
1	L5	468	U
1	L5	469	C
1	L5	470	A
1	L5	472	C
1	L5	473	C
1	L5	478	G
1	L5	483	G



Mol	Chain	Res	Type
1	L5	485	С
1	L5	486	С
1	L5	487	G
1	L5	489	С
1	L5	490	С
1	L5	495	С
1	L5	496	G
1	L5	497	G
1	L5	498	С
1	L5	499	G
1	L5	500	G
1	L5	501	С
1	L5	502	С
1	L5	503	С
1	L5	504	G
1	L5	505	G
1	L5	509	А
1	L5	510	U
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	515	С
1	L5	516	С
1	L5	519	С
1	L5	643	С
1	L5	648	G
1	L5	654	С
1	L5	657	С
1	L5	660	А
1	L5	665	С
1	L5	666	G
1	L5	667	A
1	L5	668	С
1	L5	677	G
1	L5	683	С
1	L5	685	С
1	L5	686	A
1	L5	687	U
1	L5	688	U
1	L5	694	C
1	L5	695	G
1	L5	697	G



Mol	Chain	Res	Type
1	L5	700	G
1	L5	701	G
1	L5	703	G
1	L5	704	С
1	L5	708	G
1	L5	719	С
1	L5	721	G
1	L5	730	G
1	L5	731	G
1	L5	738	С
1	L5	739	G
1	L5	740	G
1	L5	742	G
1	L5	746	A
1	L5	747	А
1	L5	748	G
1	L5	750	U
1	L5	753	С
1	L5	756	G
1	L5	757	G
1	L5	758	G
1	L5	904	С
1	L5	905	С
1	L5	911	U
1	L5	913	U
1	L5	914	U
1	L5	915	А
1	L5	917	А
1	L5	918	G
1	L5	923	С
1	L5	924	С
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	935	А
1	L5	936	C
1	L5	941	С
1	L5	944	A
1	L5	945	U
1	L5	946	C
1	L5	959	G
1	L5	960	A



Mol	Chain	Res	Type
1	L5	961	G
1	L5	962	С
1	L5	963	G
1	L5	965	G
1	L5	966	А
1	L5	968	С
1	L5	969	С
1	L5	971	U
1	L5	972	С
1	L5	977	С
1	L5	978	G
1	L5	982	U
1	L5	984	С
1	L5	987	С
1	L5	988	С
1	L5	991	С
1	L5	992	С
1	L5	993	G
1	L5	995	С
1	L5	996	G
1	L5	1066	G
1	L5	1070	G
1	L5	1071	С
1	L5	1072	С
1	L5	1074	G
1	L5	1075	G
1	L5	1080	С
1	L5	1082	С
1	L5	1083	U
1	L5	1084	С
1	L5	1100	U
1	L5	1168	G
1	L5	1169	G
1	L5	1172	C
1	L5	1173	G
1	L5	1174	G
1	L5	1178	G
1	L5	1179	U
1	L5	1180	С
1	L5	1181	С
1	L5	1183	С
1	L5	1184	А



Mol	Chain	Res	Type
1	L5	1191	С
1	L5	1193	С
1	L5	1194	G
1	L5	1196	G
1	L5	1198	G
1	L5	1200	G
1	L5	1202	С
1	L5	1203	G
1	L5	1204	С
1	L5	1205	G
1	L5	1210	С
1	L5	1211	G
1	L5	1212	G
1	L5	1214	С
1	L5	1215	С
1	L5	1216	С
1	L5	1217	G
1	L5	1218	G
1	L5	1219	G
1	L5	1220	G
1	L5	1222	А
1	L5	1241	С
1	L5	1244	G
1	L5	1245	С
1	L5	1249	С
1	L5	1251	С
1	L5	1253	G
1	L5	1258	G
1	L5	1260	G
1	L5	1261	G
1	L5	1262	G
1	L5	1266	G
1	L5	$1\overline{267}$	C
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	С
1	L5	1275	G
1	L5	1277	G
1	L5	1280	С
1	L5	1284	G
1	L5	1285	U



Mol	Chain	Res	Type
1	L5	1287	G
1	L5	1289	С
1	L5	1290	G
1	L5	1294	А
1	L5	1301	С
1	L5	1314	С
1	L5	1316	G
1	L5	1318	С
1	L5	1320	U
1	L5	1323	А
1	L5	1324	А
1	L5	1326	А
1	L5	1328	G
1	L5	1337	A
1	L5	1338	G
1	L5	1344	С
1	L5	1345	А
1	L5	1353	G
1	L5	1354	А
1	L5	1358	G
1	L5	1359	G
1	L5	1364	U
1	L5	1365	С
1	L5	1366	G
1	L5	1367	С
1	L5	1377	G
1	L5	1378	С
1	L5	1379	С
1	L5	1381	U
1	L5	1385	G
1	L5	1387	A
1	L5	1388	А
1	L5	1394	G
1	L5	1397	A
1	L5	1399	G
1	L5	1401	С
1	L5	1402	C
1	L5	1403	G
1	L5	1406	G
1	L5	1408	G
1	L5	1409	С
1	L5	1410	U



Mol	Chain	Res	Type
1	L5	1411	С
1	L5	1414	С
1	L5	1415	G
1	L5	1417	С
1	L5	1418	С
1	L5	1419	G
1	L5	1420	А
1	L5	1421	G
1	L5	1425	G
1	L5	1439	С
1	L5	1441	С
1	L5	1442	С
1	L5	1443	А
1	L5	1444	G
1	L5	1447	С
1	L5	1457	G
1	L5	1472	С
1	L5	1473	U
1	L5	1480	С
1	L5	1481	С
1	L5	1482	G
1	L5	1483	С
1	L5	1497	А
1	L5	1498	G
1	L5	1502	G
1	L5	1516	G
1	L5	1518	А
1	L5	1520	С
1	L5	1521	С
1	L5	1523	А
1	L5	1525	А
1	L5	1534	А
1	L5	1547	А
1	L5	1560	А
1	L5	1564	А
1	L5	1566	С
1	L5	1571	G
1	L5	1578	U
1	L5	1581	G
1	L5	1585	С
1	L5	1591	U
1	L5	1596	U



Mol	Chain	Res	Type
1	L5	1597	G
1	L5	1613	А
1	L5	1624	G
1	L5	1625	G
1	L5	1631	А
1	L5	1632	А
1	L5	1633	G
1	L5	1634	А
1	L5	1654	G
1	L5	1659	U
1	L5	1661	С
1	L5	1676	С
1	L5	1677	U
1	L5	1679	А
1	L5	1680	G
1	L5	1686	С
1	L5	1691	G
1	L5	1697	G
1	L5	1698	С
1	L5	1699	А
1	L5	1701	А
1	L5	1702	С
1	L5	1705	G
1	L5	1706	А
1	L5	1707	C
1	L5	1715	С
1	L5	1716	G
1	L5	1718	C
1	L5	1719	А
1	L5	1731	С
1	L5	1734	G
1	L5	1741	G
1	L5	1742	А
1	L5	1750	G
1	L5	1751	A
1	L5	1752	G
1	L5	1755	С
1	L5	1757	U
1	L5	1758	G
1	L5	1760	G
1	L5	1763	С
1	L5	1765	А



Mol	Chain	Res	Type
1	L5	1766	А
1	L5	1785	С
1	L5	1786	А
1	L5	1787	А
1	L5	1797	G
1	L5	1804	А
1	L5	1805	А
1	L5	1806	G
1	L5	1810	G
1	L5	1812	С
1	L5	1820	С
1	L5	1821	G
1	L5	1822	U
1	L5	1823	G
1	L5	1829	G
1	L5	1830	G
1	L5	1832	С
1	L5	1833	G
1	L5	1835	G
1	L5	1836	G
1	L5	1837	А
1	L5	1842	G
1	L5	1851	G
1	L5	1855	G
1	L5	1856	С
1	L5	1869	G
1	L5	1881	С
1	L5	1891	А
1	L5	1893	С
1	L5	1899	G
1	L5	1901	С
1	L5	1910	G
1	L5	1918	U
1	L5	1919	G
1	L5	1920	С
1	L5	1921	С
1	L5	1922	G
1	L5	1924	С
1	L5	1926	С
1	L5	1931	С
1	L5	1932	А
1	L5	1935	С



1 L5 1936 C 1 L5 1940 G 1 L5 1940 G 1 L5 1942 A 1 L5 1942 A 1 L5 1945 G 1 L5 1944 G 1 L5 1949 U 1 L5 1960 A 1 L5 1962 A 1 L5 1967 A 1 L5 1969 G 1 L5 1970 A 1 L5 1977 C 1 L5 1984 A 1 L5 1986 U 1	Mol	Chain	Res	Type
1L51938C1L51940G1L51942A1L51945G1L51948G1L51949U1L51954U1L51959U1L51960A1L51960A1L51961G1L51962A1L51965G1L51967A1L51967A1L51970A1L51977C1L51976G1L51976G1L51977C1L51984A1L51985G1L51996C1L51997U1L51996C1L51997U1L51998A1L52002A1L52003G1L52004U1L52007G1L52010A1L52010A1L52010A1L52010A1L52011C1L52012A1L52013A1L5 <td>1</td> <td>L5</td> <td>1936</td> <td>С</td>	1	L5	1936	С
1 L5 1940 G 1 L5 1942 A 1 L5 1945 G 1 L5 1948 G 1 L5 1949 U 1 L5 1954 U 1 L5 1959 U 1 L5 1959 U 1 L5 1960 A 1 L5 1960 A 1 L5 1960 A 1 L5 1962 A 1 L5 1962 A 1 L5 1962 A 1 L5 1967 A 1 L5 1967 A 1 L5 1970 A 1 L5 1974 U 1 L5 1977 C 1 L5 1984 A 1 L5 1985 G 1 L5 1998 A 1	1	L5	1938	С
1 L5 1942 A 1 L5 1945 G 1 L5 1948 G 1 L5 1949 U 1 L5 1954 U 1 L5 1959 U 1 L5 1960 A 1 L5 1960 A 1 L5 1960 A 1 L5 1962 A 1 L5 1962 A 1 L5 1967 A 1 L5 1967 A 1 L5 1970 A 1 L5 1971 C 1 L5 1974 U 1 L5 1974 U 1 L5 1977 C 1 L5 1984 A 1 L5 1985 G 1 L5 1997 U 1 L5 1998 A 1	1	L5	1940	G
1L51945G1L51948G1L51949U1L51954U1L51959U1L51960A1L51960A1L51961G1L51962A1L51965G1L51967A1L51967A1L51970A1L51971C1L51974U1L51975G1L51976G1L51984A1L51985G1L51985G1L51995G1L51996C1L51997U1L51998A1L51999A1L52001G1L52003G1L52004U1L52007G1L52007G1L52010A1L52010A1L52010A1L52011C1L52012A1L52013A1L52014C1L52014C	1	L5	1942	А
1 L5 1948 G 1 L5 1949 U 1 L5 1954 U 1 L5 1959 U 1 L5 1960 A 1 L5 1960 A 1 L5 1961 G 1 L5 1962 A 1 L5 1962 A 1 L5 1967 A 1 L5 1967 A 1 L5 1967 A 1 L5 1970 A 1 L5 1974 U 1 L5 1974 U 1 L5 1975 G 1 L5 1977 C 1 L5 1984 A 1 L5 1985 G 1 L5 1995 G 1 L5 1997 U 1 L5 1997 U 1	1	L5	1945	G
1 L5 1949 U 1 L5 1954 U 1 L5 1959 U 1 L5 1960 A 1 L5 1960 A 1 L5 1961 G 1 L5 1962 A 1 L5 1962 A 1 L5 1967 A 1 L5 1969 G 1 L5 1970 A 1 L5 1970 A 1 L5 1977 C 1 L5 1977 C 1 L5 1976 G 1 L5 1984 A 1 L5 1985 G 1 L5 1985 G 1 L5 1995 G 1 L5 1997 U 1 L5 1997 U 1 L5 2001 G 1	1	L5	1948	G
1L51954U1L51959U1L51960A1L51961G1L51962A1L51965G1L51967A1L51967A1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51986U1L51995G1L51996C1L51997U1L51997U1L51998A1L52001G1L52002A1L52003G1L52004U1L52007G1L52007G1L52010A1L52010A1L52010A1L52014C1L52014C1L52015U	1	L5	1949	U
1L51959U1L51960A1L51961G1L51962A1L51965G1L51967A1L51969G1L51970A1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51985G1L51995G1L51996C1L51997U1L51997U1L51998A1L52001G1L52002A1L52003G1L52006U1L52007G1L52008U1L52010A1L52010A1L52011C1L52012A1L52014C1L52014C1L52015U	1	L5	1954	U
1L51960A1L51961G1L51962A1L51965G1L51967A1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51986U1L51996C1L51997U1L51998A1L51997U1L51997U1L51997U1L52001G1L52002A1L52003G1L52006U1L52007G1L52008U1L52010A1L52010A1L52011C1L52012A1L52013A1L52014C1L52015U	1	L5	1959	U
1L51961G1L51962A1L51965G1L51967A1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51985G1L51986U1L51996C1L51997U1L51997U1L51997U1L51998A1L52001G1L52002A1L52003G1L52006U1L52007G1L52008U1L52010A1L52010A1L52011C1L52012A1L52013A1L52014C1L52015U	1	L5	1960	A
1L51962A1L51965G1L51967A1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51986U1L51995G1L51996C1L51997U1L51998A1L51999A1L52001G1L52002A1L52003G1L52006U1L52007G1L52008U1L52010A1L52010A1L52011C1L52012A1L52013A1L52013A1L52014C1L52015U	1	L5	1961	G
1L51965G1L51967A1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51985G1L51995G1L51996C1L51997U1L51998A1L51999A1L52001G1L52002A1L52003G1L52007G1L52007G1L52007G1L52010A1L52010A1L52010A1L52011C1L52012A1L52013A1L52013A1L52014C1L52015U	1	L5	1962	A
1L51967A1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51986U1L51995G1L51996C1L51997U1L51998A1L51999A1L52001G1L52002A1L52003G1L52006U1L52007G1L52008U1L52010A1L52010A1L52011C1L52012A1L52013A1L52013A1L52014C1L52015U	1	L5	1965	G
1L51969G1L51970A1L51971C1L51974U1L51975G1L51976G1L51977C1L51984A1L51985G1L51985G1L51986U1L51995G1L51996C1L51997U1L51998A1L51999A1L52001G1L52002A1L52003G1L52006U1L52007G1L52008U1L52010A1L52010A1L52011C1L52012A1L52013A1L52013A1L52014C1L52015U	1	L5	1967	A
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1969	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1970	A
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1971	С
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1974	U
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1975	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1976	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1977	С
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1984	А
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1985	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1986	U
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1995	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1996	С
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	L5	1997	U
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	1998	А
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	L5	1999	А
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	L5	2001	G
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	L5	2002	A
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	L5	2003	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	2006	U
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	L5	2007	G
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	2008	U
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	2009	A
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	2010	A
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	2011	С
1 L5 2013 A 1 L5 2014 C 1 L5 2015 U	1	L5	2012	A
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	L5	2013	A
1 L5 2015 U	1	L5	2014	С
	1	L5	2015	U



Mol	Chain	Res	Type
1	L5	2016	С
1	L5	2017	А
1	L5	2018	С
1	L5	2021	G
1	L5	2022	С
1	L5	2023	С
1	L5	2025	А
1	L5	2026	А
1	L5	2028	С
1	L5	2034	G
1	L5	2044	U
1	L5	2046	G
1	L5	2048	U
1	L5	2052	G
1	L5	2055	G
1	L5	2056	G
1	L5	2069	А
1	L5	2084	С
1	L5	2085	G
1	L5	2089	G
1	L5	2093	А
1	L5	2094	G
1	L5	2095	А
1	L5	2096	G
1	L5	2097	U
1	L5	2098	G
1	L5	2099	G
1	L5	2100	А
1	L5	2101	С
1	L5	2102	G
1	L5	2103	G
1	L5	2105	А
1	L5	2106	G
1	L5	2107	С
1	L5	2108	G
1	L5	2109	G
1	L5	2116	С
1	L5	2117	G
1	L5	2118	G
1	L5	2119	С
1	L5	2120	G
1	L5	2121	С



Mol	Chain	Res	Type
1	L5	2123	С
1	L5	2128	G
1	L5	2130	G
1	L5	2131	С
1	L5	2251	G
1	L5	2252	G
1	L5	2253	А
1	L5	2254	G
1	L5	2255	С
1	L5	2256	С
1	L5	2257	С
1	L5	2258	С
1	L5	2259	G
1	L5	2261	G
1	L5	2263	А
1	L5	2264	С
1	L5	2266	С
1	L5	2269	С
1	L5	2282	А
1	L5	2284	G
1	L5	2288	G
1	L5	2289	С
1	L5	2294	G
1	L5	2300	А
1	L5	2301	G
1	L5	2306	G
1	L5	2307	А
1	L5	2308	А
1	L5	2313	A
1	L5	2316	G
1	L5	2322	G
1	L5	2328	G
1	L5	$2\overline{333}$	G
1	L5	2344	U
1	L5	2346	С
1	L5	2347	A
1	L5	$2\overline{348}$	G
1	L5	2349	A
1	L5	2350	U
1	L5	2351	С
1	L5	2352	U
1	L5	2357	G



Mol	Chain	Res	Type
1	L5	2360	А
1	L5	2379	А
1	L5	2381	А
1	L5	2383	С
1	L5	2384	U
1	L5	2389	А
1	L5	2396	А
1	L5	2397	G
1	L5	2402	G
1	L5	2404	А
1	L5	2410	С
1	L5	2414	G
1	L5	2417	А
1	L5	2421	G
1	L5	2422	С
1	L5	2424	G
1	L5	2425	U
1	L5	2437	С
1	L5	2441	С
1	L5	2447	U
1	L5	2450	G
1	L5	2453	А
1	L5	2460	А
1	L5	2463	G
1	L5	2464	С
1	L5	2465	С
1	L5	2470	С
1	L5	2474	G
1	L5	2475	G
1	L5	2479	G
1	L5	2483	G
1	L5	2484	A
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2491	C
1	L5	2493	G
1	L5	2494	U
1	L5	2500	U
1	L5	2502	G
1	L5	2503	G
1	L5	2504	С



Mol	Chain	Res	Type
1	L5	2505	С
1	L5	2506	G
1	L5	2513	А
1	L5	2517	А
1	L5	2519	U
1	L5	2537	А
1	L5	2542	G
1	L5	2543	А
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U
1	L5	2555	G
1	L5	2556	G
1	L5	2559	G
1	L5	2563	С
1	L5	2564	G
1	L5	2570	U
1	L5	2573	А
1	L5	2574	G
1	L5	2583	С
1	L5	2586	G
1	L5	2587	А
1	L5	2588	С
1	L5	2589	С
1	L5	2601	А
1	L5	2602	G
1	L5	2611	А
1	L5	2618	G
1	L5	2627	С
1	L5	2638	G
1	L5	2643	G
1	L5	2647	A
1	L5	2653	С
1	L5	2658	G
1	L5	$2\overline{659}$	A
1	L5	2661	U
1	L5	2662	G
1	L5	2675	G
1	L5	$2\overline{676}$	A
1	L5	$2\overline{681}$	G
1	L5	2687	U



Mol	Chain	Res	Type
1	L5	2694	G
1	L5	2695	А
1	L5	2696	А
1	L5	2708	U
1	L5	2709	С
1	L5	2710	С
1	L5	2711	G
1	L5	2712	G
1	L5	2719	С
1	L5	2721	G
1	L5	2724	G
1	L5	2725	А
1	L5	2726	G
1	L5	2727	С
1	L5	2735	G
1	L5	2739	С
1	L5	2742	G
1	L5	2743	А
1	L5	2754	G
1	L5	2758	G
1	L5	2760	G
1	L5	2761	U
1	L5	2763	U
1	L5	2764	А
1	L5	2769	U
1	L5	2770	С
1	L5	2788	U
1	L5	2790	U
1	L5	2794	С
1	L5	2796	G
1	L5	2806	A
1	L5	2814	С
1	L5	2815	А
1	L5	2825	А
1	L5	2826	U
1	L5	2827	G
1	L5	2835	А
1	L5	2842	G
1	L5	2847	G
1	L5	2855	G
1	L5	2856	С
1	L5	2874	U



Mol	Chain	Res	Type
1	L5	2877	G
1	L5	2895	А
1	L5	2896	G
1	L5	2897	G
1	L5	2900	U
1	L5	2901	G
1	L5	2902	G
1	L5	2903	G
1	L5	2905	С
1	L5	2907	G
1	L5	2908	U
1	L5	3585	G
1	L5	3587	С
1	L5	3588	С
1	L5	3589	G
1	L5	3590	G
1	L5	3591	С
1	L5	3592	G
1	L5	3594	С
1	L5	3595	U
1	L5	3596	А
1	L5	3597	G
1	L5	3600	G
1	L5	3604	А
1	L5	3605	С
1	L5	3611	А
1	L5	3615	G
1	L5	3618	С
1	L5	3621	А
1	L5	3625	G
1	L5	3626	G
1	L5	3630	A
1	L5	3635	A
1	L5	3643	А
1	L5	3644	U
1	L5	3646	А
1	L5	3648	А
1	L5	3653	A
1	L5	3656	А
1	L5	3662	А
1	L5	3673	С
1	L5	3674	G



Mol	Chain	Res	Type
1	L5	3678	G
1	L5	3680	U
1	L5	3684	G
1	L5	3685	С
1	L5	3690	U
1	L5	3692	А
1	L5	3696	С
1	L5	3697	U
1	L5	3698	G
1	L5	3699	С
1	L5	3706	С
1	L5	3710	G
1	L5	3711	A
1	L5	3713	U
1	L5	3726	А
1	L5	3727	А
1	L5	3736	А
1	L5	3744	G
1	L5	3746	А
1	L5	3748	А
1	L5	3750	G
1	L5	3752	С
1	L5	3753	G
1	L5	3758	U
1	L5	3759	А
1	L5	3760	А
1	L5	3764	U
1	L5	3765	G
1	L5	3770	U
1	L5	3771	С
1	L5	3775	A
1	L5	3776	G
1	L5	$3\overline{777}$	G
1	L5	3778	U
1	L5	3779	А
1	L5	3784	A
1	L5	3786	U
1	L5	3787	G
1	L5	3802	U
1	L5	3810	С
1	L5	3811	G
1	L5	3813	A



Mol	Chain	Res	Type
1	L5	3814	U
1	L5	3815	G
1	L5	3816	A
1	L5	3817	А
1	L5	3818	U
1	L5	3819	G
1	L5	3823	G
1	L5	3824	А
1	L5	3838	U
1	L5	3839	G
1	L5	3841	С
1	L5	3843	С
1	L5	3851	U
1	L5	3867	А
1	L5	3877	А
1	L5	3878	С
1	L5	3879	G
1	L5	3890	А
1	L5	3892	U
1	L5	3897	G
1	L5	3901	А
1	L5	3905	А
1	L5	3906	А
1	L5	3907	G
1	L5	3908	А
1	L5	3915	U
1	L5	3930	U
1	L5	3938	G
1	L5	3941	G
1	L5	3943	А
1	L5	3944	G
1	L5	3947	A
1	L5	3948	С
1	L5	3949	А
1	L5	4066	U
1	L5	4068	U
1	L5	4070	U
1	L5	4076	G
1	L5	4084	G
1	L5	4085	A
1	L5	4086	G
1	L5	4090	G



Mol	Chain	Res	Type
1	L5	4091	G
1	L5	4092	G
1	L5	4094	G
1	L5	4097	G
1	L5	4099	G
1	L5	4100	С
1	L5	4101	С
1	L5	4102	С
1	L5	4104	G
1	L5	4105	А
1	L5	4107	G
1	L5	4108	G
1	L5	4113	U
1	L5	4114	С
1	L5	4115	G
1	L5	4116	С
1	L5	4117	U
1	L5	4119	С
1	L5	4120	U
1	L5	4121	G
1	L5	4122	G
1	L5	4127	А
1	L5	4128	А
1	L5	4134	С
1	L5	4135	G
1	L5	4140	С
1	L5	4141	G
1	L5	4143	G
1	L5	4146	G
1	L5	4158	С
1	L5	4159	С
1	L5	4160	С
1	L5	4162	С
1	L5	4163	U
1	L5	4164	С
1	L5	4170	A
1	L5	4177	C
1	L5	4183	G
1	L5	4184	G
1	L5	4188	U
1	L5	4191	G
1	L5	4196	G



Mol	Chain	Res	Type
1	L5	4203	А
1	L5	4206	С
1	L5	4212	А
1	L5	4222	G
1	L5	4225	G
1	L5	4229	U
1	L5	4233	А
1	L5	4234	A
1	L5	4249	G
1	L5	4251	А
1	L5	4253	А
1	L5	4254	G
1	L5	4256	А
1	L5	4257	A
1	L5	4258	С
1	L5	4265	U
1	L5	4273	А
1	L5	4280	А
1	L5	4281	А
1	L5	4289	U
1	L5	4296	U
1	L5	4297	G
1	L5	4304	А
1	L5	4305	G
1	L5	4306	U
1	L5	4314	С
1	L5	4317	А
1	L5	4319	С
1	L5	4321	U
1	L5	4330	G
1	L5	4339	A
1	L5	4345	С
1	L5	4349	С
1	L5	4350	C
1	L5	4353	U
1	L5	4354	U
1	L5	4364	G
1	L5	4373	G
1	L5	4377	G
1	L5	4378	А
1	L5	4379	A
1	L5	4380	А



Mol	Chain	Res	Type
1	L5	4387	С
1	L5	4390	А
1	L5	4391	G
1	L5	4393	G
1	L5	4394	А
1	L5	4396	А
1	L5	4410	G
1	L5	4415	A
1	L5	4419	U
1	L5	4421	С
1	L5	4422	А
1	L5	4426	С
1	L5	4430	G
1	L5	4440	G
1	L5	4444	C
1	L5	4448	G
1	L5	4449	А
1	L5	4450	U
1	L5	4452	U
1	L5	4453	C
1	L5	4464	А
1	L5	4466	С
1	L5	4471	U
1	L5	4476	С
1	L5	4500	U
1	L5	4510	А
1	L5	4512	U
1	L5	4513	A
1	L5	4515	G
1	L5	4518	A
1	L5	4519	С
1	L5	4524	G
1	L5	4543	G
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4554	G
1	L5	4556	U
1	L5	4560	С
1	L5	4567	G
1	L5	4570	G
1	L5	4572	U



Mol	Chain	Res	Type
1	L5	4573	G
1	L5	4575	G
1	L5	4576	U
1	L5	4584	А
1	L5	4590	А
1	L5	4599	А
1	L5	4600	G
1	L5	4601	U
1	L5	4606	G
1	L5	4608	G
1	L5	4617	G
1	L5	4635	А
1	L5	4636	U
1	L5	4637	G
1	L5	4639	G
1	L5	4647	G
1	L5	4652	G
1	L5	4656	A
1	L5	4658	G
1	L5	4669	А
1	L5	4670	С
1	L5	4672	А
1	L5	4677	U
1	L5	4687	А
1	L5	4691	А
1	L5	4694	G
1	L5	4695	С
1	L5	4700	А
1	L5	4707	А
1	L5	4708	А
1	L5	4709	U
1	L5	4719	G
1	L5	4728	U
1	L5	4730	C
1	L5	4731	G
1	L5	4732	G
1	L5	4733	С
1	L5	4734	A
1	L5	4735	G
1	L5	4740	G
1	L5	4741	C
1	L5	4742	G



Mol	Chain	Res	Type
1	L5	4743	G
1	L5	4744	А
1	L5	4745	G
1	L5	4747	С
1	L5	4750	G
1	L5	4754	G
1	L5	4757	С
1	L5	4759	С
1	L5	4760	G
1	L5	4761	G
1	L5	4764	А
1	L5	4765	G
1	L5	4771	С
1	L5	4772	С
1	L5	4774	С
1	L5	4775	С
1	L5	4859	С
1	L5	4861	G
1	L5	4862	G
1	L5	4864	U
1	L5	4867	G
1	L5	4870	G
1	L5	4871	С
1	L5	4875	G
1	L5	4876	U
1	L5	4877	G
1	L5	4880	С
1	L5	4882	U
1	L5	4883	С
1	L5	4886	С
1	L5	4887	С
1	L5	4888	U
1	L5	4889	G
1	L5	4891	G
1	L5	4892	A
1	L5	4893	А
1	L5	4894	А
1	L5	4895	С
1	L5	4896	G
1	L5	4897	G
1	L5	4899	G
1	L5	4900	С



Mol	Chain	Res	Type
1	L5	4901	G
1	L5	4902	С
1	L5	4908	G
1	L5	4910	G
1	L5	4912	G
1	L5	4913	G
1	L5	4914	С
1	L5	4918	С
1	L5	4919	G
1	L5	4923	С
1	L5	4925	U
1	L5	4928	С
1	L5	4929	С
1	L5	4931	G
1	L5	4932	U
1	L5	4938	А
1	L5	4939	С
1	L5	4941	G
1	L5	4943	А
1	L5	4949	G
1	L5	4955	А
1	L5	4960	G
1	L5	4961	G
1	L5	4962	С
1	L5	4964	С
1	L5	4973	U
1	L5	4975	G
1	L5	4976	U
1	L5	4985	U
1	L5	4988	U
1	L5	4989	U
1	L5	4991	U
1	L5	4992	G
1	L5	5014	A
1	L5	5017	G
1	L5	5020	G
1	L5	5021	C
1	L5	5022	U
1	L5	5024	С
1	L5	5025	С
1	L5	5026	U
1	L5	5028	G



Mol	Chain	Res	Type	
1	L5	5029	С	
1	L5	5034	А	
1	L5	5040	U	
1	L5	5041	G	
1	L5	5045	G	
1	L5	5047	С	
1	L5	5050	С	
1	L5	5054	С	
1	L5	5055	G	
1	L5	5060	А	
1	L5	5061	А	
1	L5	5069	U	
2	L7	2	U	
2	L7	7	G	
2	L7	20	U	
2	L7	22	A	
2	L7	23	A	
2	L7	24	С	
2	L7	25	G	
2	L7	36	С	
2	L7	39	С	
2	L7	41	G	
2	L7	49	A	
2	L7	53	U	
2	L7	54	А	
2	L7	63	C	
2	L7	64	G	
2	L7	86	G	
2	L7	90	А	
2	L7	97	G	
2	L7	100	A	
2	L7	102	U	
2	L7	110	G	
2	L7	120	U	
3	L8	2	G	
3	L8	23	C	
3	L8	34	U	
3	L8	35	C	
3	L8	39	G	
3	L8	48	A	
3	L8	59	A	
3	L8	63	U	



Mol Chain H		Res	Type	
3	L8	77	А	
3	L8	79	G	
3	L8	80	А	
3	L8	82	А	
3	L8	83	С	
3	L8	84	А	
3	L8	85	U	
3	L8	86	U	
3	L8	87	G	
3	L8	88	А	
3	L8	103	А	
3	L8	105	С	
3	L8	110	U	
3	L8	111	U	
3	L8	112	G	
3	L8	114	G	
3	L8	122	G	
3	L8	123	U	
3	L8	124	U	
3	L8	125	С	
3	L8	126	С	
3	L8	127	U	
3	L8	143	G	
3	L8	147	G	
3	L8	155	С	
45	В	2	С	
45	В	3	С	
45	В	4	С	
45	В	13	С	
45	В	14	С	
45	В	18	С	
45	В	303	G	
45	В	304	G	
45	В	307	G	
45	В	308	G	
45	В	313	G	
45	В	315	G	
45	В	316	G	
45	В	317	G	

All (34) RNA pucker outliers are listed below:



Mol	Chain	Res	Type	
1	L5	12	А	
1	L5	44	А	
1	L5	143	С	
1	L5	504	G	
1	L5	914	U	
1	L5	1322	А	
1	L5	1410	U	
1	L5	1522	G	
1	L5	1633	G	
1	L5	1706	А	
1	L5	1959	U	
1	L5	2084	С	
1	L5	2108	G	
1	L5	2281	U	
1	L5	2351	С	
1	L5	2416	G	
1	L5	2474	G	
1	L5	2675	G	
1	L5	2708	U	
1	L5	2760	G	
1	L5	2763	U	
1	L5	3588	С	
1	L5	3604	А	
1	L5	3620	G	
1	L5	3673	С	
1	L5	3816	А	
1	L5	4065	G	
1	L5	4600	G	
1	L5	4699	U	
1	L5	4731	G	
1	L5	4869	U	
1	L5	4913	G	
3	L8	86	U	
3	L8	87	G	

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)

Of 45 ligands modelled in this entry, 45 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	В	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	В	18:C	O3'	300:G	Р	15.70
1	В	313:G	O3'	314:G	Р	4.54



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-12189. 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.

Orthogonal projections (i) 6.1

6.1.1Primary map



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

6.2Central slices (i)

6.2.1Primary map



X Index: 300

Y Index: 300



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: 303

Y Index: 267

Z Index: 241

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



6.5 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 2181 $\rm nm^3;$ this corresponds to an approximate mass of 1970 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 0.303 \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-12189 and PDB model 7BHP. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.004 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 (0.004).



9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.004) and Q-score for the entire model and for each chain.

\mathbf{Chain}	Atom inclusion	Q-score
All	0.9783	0.4390
А	0.9526	0.3530
В	0.9264	0.2410
L5	0.9925	0.4370
L7	0.9992	0.4440
L8	0.9931	0.4510
LA	0.9337	0.4700
LB	0.9491	0.4600
LC	0.9576	0.4730
LD	0.9759	0.4060
LE	0.9572	0.4200
LF	0.9507	0.4530
LG	0.9467	0.4110
LH	0.9642	0.4410
LI	0.9649	0.4400
LJ	0.9665	0.3810
LL	0.9586	0.4390
LM	0.9672	0.4410
LN	0.9599	0.4870
LO	0.9529	0.4540
LP	0.9569	0.4650
LQ	0.9475	0.4740
LR	0.9677	0.4520
LS	0.9586	0.4650
LT	0.9592	0.4600
LU	0.9714	0.3950
LW	0.9320	0.4300
LX	0.9554	0.4550
LY	0.9850	0.4530
LZ	0.9615	0.4250
La	0.9584	0.4760
Lb	0.9595	0.4330
Lc	0.9292	0.4070
Ld	0.9627	0.4640
Le	0.9543	0.4920

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Chain	Atom inclusion	Q-score
Lf	0.9713	0.4890
Lg	0.9605	0.4730
Lh	0.9417	0.4360
Li	0.9597	0.4340
Lj	0.9866	0.4900
Lk	0.9048	0.3940
Ll	0.9670	0.4550
Lm	0.9591	0.4470
Lo	0.9618	0.4360
Lp	0.9503	0.4780
Lr	0.9681	0.4680

