

wwPDB EM Validation Summary Report (i)

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PDB ID	:	8I9R
EMDB ID	:	EMD-35281
Title	:	Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit - State 5S BNP
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Deposited on	:	2023-02-07
Resolution	:	3.10 Å(reported)

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 (i)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev50
Mogul	:	1.8.5 (274361), CSD as541be (2020)
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)	:	2.34

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 3.10 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 >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length			Qua	ality of ch	ain		
1	C1	3341	8%	45%		15%	•	39%	
2	C2	256	-		63%			25%	• 11%
3	CA	316	•		78%			•	18%
4	CB	391			62%		5%	3	4%
5	CC	801	9%	32%	•		66%		
6	CE	598	•		75%			•	23%
7	СН	661	9% 15%			84%			
8	CI	414		34%	·		65%		



Mol	Chain	Length	Quality of cha	ain
9	CJ	679	54%	44%
10	СМ	249	68%	7% 25%
10	LF	249	94%	
	CDI	2.4.0	59%	
11	CN	246	97%	•
12	CQ	225	48% •	50%
13	CR	237	67%	• 30%
14	CU	451	25% •	73%
15	Ch	354	19% • 80	%
16	LB	392	<u>6%</u> 80%	7% 13%
17	LC	365	97%	
18	LE	200	82%	• 15%
19	LG	262	• 66%	•• 30%
20	LL	213	54%	45%
21	LM	142	5%	
22	LN	203	87%	10%
- <u></u>	LO	200	0770	• 10/0
20	LO	204		•
24	LP	187	81%	• 18%
25	LQ	213	60%	39%
26	LS	174	97%	•
27	LT	160	74%	5% 21%
28	LV	139	93%	· ·
29	LY	138	93%	· ·
30	Le	131	• 97%	
31	Lf	109	95%	•••
32	Lh	935	13% 87%	

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Mol	Chain	Length	Quality of chain		
	т:	110			
- 33	Ll	110	75%	5%	20%
34	Lj	95	77%	•	22%
35	Cc	282	80%	•	16%
36	Cd	436	76%	•	20%
37	Ce	336	56% •	42%	
38	Cf	570	25% 74%		
39	Су	350	70%	3	30%
40	Cg	478	46% •	51%	
41	CP	751	35% 43% 57'	%	
42	CG	184	43%		·
43	Lq	217	95% 94%		• 5%
44	Cx	202	45% 50%	50%	
45	LJ	173	94%		·
46	LD	304	90%		10%
47	C4	119	83%		18% •
48	CX	203	9% 31% 69%		

Continued from previous page...



2 Entry composition (i)

There are 49 unique types of molecules in this entry. The entry contains 117417 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 RNA (3341-MER).

Mol	Chain	Residues		1		AltConf	Trace		
1	C1	2048	Total 43814	C 19561	N 7931	O 14274	Р 2048	0	0

• Molecule 2 is a RNA chain called RNA (256-MER).

Mol	Chain	Residues		Α		AltConf	Trace		
2	C2	228	Total 4846	C 2162	N 864	O 1592	Р 228	0	0

• Molecule 3 is a protein called Brix domain-containing protein.

Mol	Chain	Residues		Ate		AltConf	Trace		
3	CA	260	Total 2144	C 1371	N 393	O 373	${f S}{7}$	0	0

• Molecule 4 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues		Ate		AltConf	Trace		
4	СВ	260	Total 2063	C 1322	N 367	0 371	${ m S} { m 3}$	0	0

• Molecule 5 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues		Ate	AltConf	Trace			
5	CC	272	Total 2258	C 1438	N 379	0 434	S 7	0	0

• Molecule 6 is a protein called RNA helicase.

Mol	Chain	Residues		At	AltConf	Trace			
6	CE	463	Total 3673	C 2352	N 643	O 667	S 11	0	0



Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP GORYU9
CE	544	SER	_	insertion	UNP G0RYU9
CE	545	PHE	_	insertion	UNP GORYU9
CE	546	GLY	-	insertion	UNP GORYU9
CE	547	PHE	-	insertion	UNP GORYU9
CE	548	SER	_	insertion	UNP GORYU9
CE	549	THR	_	insertion	UNP GORYU9
CE	550	PRO	_	insertion	UNP GORYU9
CE	551	PRO	_	insertion	UNP GORYU9
CE	552	ARG	_	insertion	UNP GORYU9
CE	553	VAL	-	insertion	UNP GORYU9
CE	554	ASP	-	insertion	UNP GORYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP GORYU9
CE	557	LEU	-	insertion	UNP GORYU9
CE	558	SER	-	insertion	UNP GORYU9
CE	559	ALA	-	insertion	UNP GORYU9
CE	560	SER	-	insertion	UNP GORYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP GORYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP GORYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP GORYU9
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP GORYU9
CE	578	ARG	-	insertion	UNP G0RYU9
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

There are 42 discrepancies between the modelled and reference sequences:



• Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues		At	oms			AltConf	Trace
7	СН	108	Total 891	C 561	N 146	0 183	S 1	0	0

• Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues		At	oms	AltConf	Trace		
8	CI	146	Total 1196	C 763	N 224	O 204	${f S}{5}$	0	0

• Molecule 9 is a protein called Pescadillo homolog.

Mol	Chain	Residues		At	AltConf	Trace			
9	CJ	380	Total 3109	C 2003	N 547	O 549	S 10	0	0

• Molecule 10 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues		At	oms		AltConf	Trace	
10	CM	187	Total 1525	C 987	N 278	O 257	S 3	0	0
10	LF	240	Total 1967	C 1264	N 368	0 332	${ m S} { m 3}$	0	0

• Molecule 11 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues		At	AltConf	Trace			
11	CN	246	Total 1856	C 1158	N 322	O 369	${f S}{7}$	0	0

• Molecule 12 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues		A	toms			AltConf	Trace
12	CQ	112	Total 960	C 607	N 195	0 148	S 10	0	0

• Molecule 13 is a protein called Nucleolar protein 16.

Mol	Chain	Residues		At	oms	AltConf	Trace		
13	CR	167	Total 1354	C 827	N 278	0 247	${ m S} { m 2}$	0	0



• Molecule 14 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues		At	oms	AltConf	Trace		
14	CU	121	Total 969	C 604	N 179	0 183	${ m S} { m 3}$	0	0

• Molecule 15 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues		At	oms	AltConf	Trace		
15	Ch	71	Total 562	$\begin{array}{c} \mathrm{C} \\ 350 \end{array}$	N 109	O 102	S 1	0	0

• Molecule 16 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues		At	AltConf	Trace			
16	LB	341	Total 2708	C 1721	N 493	O 482	S 12	0	0

• Molecule 17 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
17	LC	362	Total 2752	C 1738	N 526	0 479	S 9	0	0

• Molecule 18 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues		At	oms			AltConf	Trace
18	LE	170	Total 1338	C 861	N 241	0 233	${ m S} { m 3}$	0	0

• Molecule 19 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LG	183	Total 1470	C 951	N 263	O 252	${S \atop 4}$	0	0

• Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues		At	oms		AltConf	Trace	
20	LL	117	Total 964	C 608	N 206	0 148	${ m S} { m 2}$	0	0

• Molecule 21 is a protein called 60S ribosomal protein L14-like protein.



Mol	Chain	Residues		At	oms			AltConf	Trace
21	LM	137	Total 1101	C 699	N 211	O 190	S 1	0	0

• Molecule 22 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	183	Total 1563	C 974	N 332	O 253	$\frac{S}{4}$	0	0

• Molecule 23 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	204	Total 1618	C 1039	N 306	0 267	S 6	0	0

• Molecule 24 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues		At	oms		AltConf	Trace	
24	LP	154	Total 1212	C 758	N 233	O 218	${ m S} { m 3}$	0	0

• Molecule 25 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues		At	oms		AltConf	Trace	
25	LQ	129	Total 1021	C 646	N 200	0 173	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 26 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues		At	oms		AltConf	Trace	
26	LS	174	Total 1433	C 922	N 267	O 239	${ m S}{ m 5}$	0	0

• Molecule 27 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues		At	oms			AltConf	Trace
27	LT	126	Total	C 642	N 106	0_{172}	S 2	0	0
			1014	045	190	179	Z		

• Molecule 28 is a protein called 60S ribosomal protein l23-like protein.



Mol	Chain	Residues		At	oms			AltConf	Trace
28	LV	135	Total 995	C 633	N 185	0 170	${ m S} 7$	0	0

• Molecule 29 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues		At	oms	AltConf	Trace		
29	LY	134	Total 1065	C 664	N 215	0 184	${S \over 2}$	0	0

• Molecule 30 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues		At	oms		AltConf	Trace	
30	Le	131	Total 1055	C 663	N 213	0 172	S 7	0	0

• Molecule 31 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues		At	oms		AltConf	Trace	
31	Lf	108	Total 862	C 546	N 171	0 144	S 1	0	0

• Molecule 32 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
32	Lh	121	Total 995	C 633	N 196	O 166	0	0

• Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues		At	oms		AltConf	Trace	
33	Li	88	Total 731	C 449	N 162	0 119	S 1	0	0

• Molecule 34 is a protein called Ribosomal protein L37.

Mol	Chain	Residues		Ate	oms		AltConf	Trace	
34	Lj	74	Total 595	C 365	N 132	O 93	${S \atop 5}$	0	0

• Molecule 35 is a protein called Ribosomal RNA-processing protein 1.



Mol	Chain	Residues		At	AltConf	Trace			
35	Cc	236	Total 1898	C 1208	N 337	O 343	S 10	0	0

• Molecule 36 is a protein called Brix domain-containing protein.

Mol	Chain	Residues		At	AltConf	Trace			
36	Cd	347	Total 2800	C 1764	N 538	0 494	$\frac{S}{4}$	0	0

• Molecule 37 is a protein called Protein MAK16.

Mol	Chain	Residues		Ate		AltConf	Trace		
37	Ce	194	Total 1609	C 1020	N 304	0 276	S 9	0	0

• Molecule 38 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues		At	oms	AltConf	Trace		
38	Cf	147	Total 1225	C 755	N 245	0 224	S 1	0	0

• Molecule 39 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
39	Су	244	Total 1210	С 722	N 244	0 244	0	0

• Molecule 40 is a protein called Brix domain-containing protein.

Mol	Chain	Residues		At	AltConf	Trace			
40	Cg	233	Total 1850	C 1168	N 348	0 324	S 10	0	0

• Molecule 41 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
41	СР	324	Total 1596	C 948	N 324	O 324	0	0

• Molecule 42 is a protein called 60S ribosome subunit biogenesis protein NIP7.



Mol	Chain	Residues	Atoms			AltConf	Trace	
42	CG	177	Total 873	C 519	N 177	0 177	0	0

• Molecule 43 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms			AltConf	Trace	
43	Lq	207	Total 1021	C 607	N 207	O 207	0	0

• Molecule 44 is a protein called Ribosome biogenesis regulatory protein.

Mol	Chain	Residues	Atoms			AltConf	Trace	
44	Cx	102	Total 565	C 340	N 114	0 111	0	0

• Molecule 45 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms			AltConf	Trace	
45	LJ	169	Total 831	C 492	N 169	O 170	0	0

• Molecule 46 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms			AltConf	Trace	
46	LD	273	Total 1346	C 801	N 273	O 272	0	0

• Molecule 47 is a RNA chain called RNA (119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	C4	119	Total 2536	C 1131	N 453	O 833	Р 119	0	0

• Molecule 48 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms			AltConf	Trace	
48	CX	63	Total 375	C 233	N 68	О 74	0	0

• Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).



Mol	Chain	Residues	Atoms	AltConf
49	C1	1	Total Zn 1 1	0
49	Lj	1	Total Zn 1 1	0
49	Ce	1	Total Zn 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.

• Molecule 1: RNA (3341-MER)











ALA

• Molecule 10: 60S ribosomal protein l7-like protein

• Molecule 10: 60S ribosomal protein l7-like protein

Chain LF: 94% $\cdot \cdot$

G229 P230 C231 A232 1233 1233 N234 N234 N234 S236 S236 S236 N239 N239 S244 V242 C243 C243 S244 S2245 S244 S2245

• Molecule 12: Ribosome biogenesis protein RLP24

Chain	CQ:	11%	48%			50%		I
M1 R2 E7	816 M22	D25 G26 K27 A28	K 43 K 43 R 44	K48 Y55 V64 V65 D66	T68 L69 Q70 A72 A73 A73	R75 K88 E94	S97	M112 ALA ALA CLY LYS ARG ARG GLU VAL ALA
ALA ALA ARG LYS	VAL ALA GLU ASN	HIS LEU PRO ARG LEU	GLY SER GLU LYS ARG ARG LEU	ALA GLU LEU ALA ALA GLU GLU GLY	VAL ASP VAL GLU GLU GLU ARG CT U	GLU LEU LEU LEU ALA SER	LYS LYS LYS SER LYS ALA ALA PHE GLY	GLU CLU VAL ARG
ARG VAL ARG VAL	THR ASP GLY GLY VAT	GLU GLU THR GLU SER SER	GLY GLY GLY ASN VAL ASP GLU	GLU MET ASP ASP ASP HIS ASP	ASP SER ASP ASP ASP ASP ASP ASP ASP	ASP THR ASP		
• Mol	ecule 1	3: Nucleol	lar protein	16				
Chain	CR:		6	7%		•	30%	
MET GLY R3	R24 K24	K60 K70 L73 LYS	LEU ASP PRO LEU ALA ILE	LYS SER GLY ASP GLN GLN LEU ILE	LYS ERR SER GLU VAL LYS VAL CLU GLU	ASP GLU GLV GLY ARG ILE ILE	ARG VAL VAL ARG ASP ASN PRO	LEU ASP PRO
LEU ASN ASP LEU	ASF SER ASP S126	E138 GLN PRO VAL LEU	N144 E154 ASN VAL ALA ALA	ASP VAL ASP GLU GLU K230 K230	L235 SER ALA			
• Mol	ecule 1	4: rRNA-]	processing	protein EB	SP2			
Chain	CU:	25%	·		73%			
MET ALA LYS LYS	ALA THR GLN SER	LYS ALA GLY SER LYS PRO	SER GLN THR GLY ASP ALA GLN	SER LYS ASN GLN LYS ALA ASP ARG	ARG LYS SER ASN GLU PRO VAL VAL	LYS VAL ALA GLU GLU GLU GLU	GLN ARG GLU GLU GLU GLU	SEK GLU ASP
GLU SER GLU ASP	GLN GLN GLN	ALA ALA ASN ASN GLU GLU	ASP SER GLU ASP SER ASP	GLU ASN SER GLU ASP GLU GLU	SER ASP ASP ASP SER GLY GLY GLU HIS	PRO THR HIS ILE ASP PHE	GLU ALA ASP ASP SER SER SER	SER GLU LEU
ASP SER ASP GLU	ASP ASP LYS LYS	ASP ASP ASN ASN ALA GLN	GLY MET SER GLU ASP LYS MET	ASP VAL ASP LYS ASP GLY GLU ASP	LYS SER GLY GLU GLU GLU GLU GLU	GLU GLU ASP ASP GLU GLU GLU	LEU GLU GLU GLU GLU GLU ASP	GLU GLU GLU
ALA ALA GLY THR	THR ARG GLN THR	F216 E249 L253	L255 L258 L289	K310 PHE GLY GLY ALA VAL GLN	VAL GLN LYS GLN LEU GLU ARG ALA	LYS LYS ARG GLU ALA LEU ASP	LYS ILE ASN GLN LEU LYS ARG LYS	ARG ALA GLU GLY
GLY SER ALA ALA	GLY GLY THR GLU	ASP ASP PRO PHE ASP VAL	VAL VAL ASP ASP GLU CLU LEU SER ARG	ASP SER LYS PRO LYS LYS ARG ARG	ALA ASP GLY ASP HIS PRO PRO PRO	PRO LYS ARG GLN LYS LYS ASN	ALA LYS CLY GLY GLY GLY GLY	LTS ARG GLY SER
LYS SER GLY ASP	ILE SER SER GLY ASD	LEU SER GLY PHE SER VAL T VS	ARG MET LYS LYS GLY GLY GLY	ALA GLY GLY GLY CLYS LYS LYS ALA	ASN ARG PRO GLY LYS ALA ARG ARG ARG	ALA ALA ALA ALA ALA LYS ARG		
• Mol	ecule 1	5: Riboso	mal RNA-	processing 1	protein 15			
Chain	Ch:	19%			80%			
MET ALA GLY SER	VAL LYS LYS ARG SER	SER ASP GLY LEU LYS GLY	VAL ALA PRO PRO LYS LYS	GLN LYS LYS MET GLU TYR ARG SER	SER SER GLU SER SER SER SER SER SER	ASP ASP GLY CLY VAL PRO LEU	PRO PRO ASN LEU LEU ASP SER	ASP GLU ASP PHE
ASP ASN ILE GLU	ASP ASP GLY ALA TUP	THR ALA SER SER ASP ASP	ASP SER ASP SER SER PHE	SER GLU SER GLU PRO LYS PRO LYS	LYS SER LYS SER SER LYS GLN ATA	PRO LYS PRO LYS LYS ASP	ASP LYS ASN PHE VAL ALA LYS ASP	ALA SER SER SER

GGLU SERRASP PHE GGLU GGLU GGLU GGLU GGLU ASSER HHE MALLA MA SLY SLY SLY SLY LYS LYS LYS LEU LLU • Molecule 16: 60S ribosomal protein L3-like protein 6% Chain LB: 80% 7% 13% MET SER SER ARG CYS CYS CYS SLU SLU ALA ALA ALA ARG • Molecule 17: 60S ribosomal protein L4-like protein Chain LC: 97% ALASER • Molecule 18: 60S ribosomal protein L6 Chain LE: 82% 15% MET SER ALA ALA ALA ALA PRO FIR CLYS CLY CLYS CLY VAL THR THR ARG CLY VAL ARG ALA ALA ALA • Molecule 19: 60S ribosomal protein L8 Chain LG: 66% 30% MET PRIO PRIO CLUYS CLYS CLYS CLYS CLYS PRIO PRIO PRIO CLIVS CLUYS CLUSS CLUS

 \bullet Molecule 20: 60S ribosomal protein L13

Chain LL:	54%	45%	
MET ALA LLYS LLYS LLYS HLS ASN GLN CLN GLN ASN ASN ASN	R87 K129 SER ASW LYS LYS LYS LYS ASP THR THR THR THR CLV CSP CLN	THR THR GLA GLA CLA CLA CLA CLA CLA CLA CLA CLA CLA C	ILE SER LYS SER GLU
ILE PRO CLY CLU CLU CLU CLU CLU CLU CLU ALA ALA ALA ALA ALA	ARG LYS ALA ARG ARG ARG ARG ARG CLEU VAL CLEU CLEU CLE ARG ALA ARG ALA ARG ALA ARG ALA	GLU LYS ALA ALA GLU GLU GLU CLYS LYS LYS LYS	
• Molecule 21: 60	S ribosomal protein L14-	like protein	
Chain LM:	929	% ·	.
MET A2 E3 E3 I4 N5 E7 A8 R12 R12	K49 K71 K702 0103 1104 1104 L104 L105 A10 A1A ALA ALA		
• Molecule 22: R	ibosomal protein L15		
Chain LN:	87%	• 10%	-
MET 62 62 746 87 1 78 1 78 7 8 7 8 7 8 7 8 7 8 7 8 8 8 8	LYN LYN GLY ALA TYR CLY CLY CLY TYR ASN CLN CLN CLN CLN CLN CLN CLN CLN CLN CL	Y94 S97 S97 R99 R140 R140 R203	
• Molecule 23: 60	S ribosomal protein L16-	like protein	
Chain LO:	g	8%	•
M1 L53 L53 R69 Y170 K173 K173			
• Molecule 24: 60	S ribosomal protein 117-l	ike protein	
Chain LP:	81%	• 18%	-
MET V2 K55 K55 S66 G68 R69 R69	Arta Arta G73 G73 G75 G77 G77 G77 Arta Arta Arta Arta Arta Arta Arta	HIS: GLY ARG ARG ARG ARA ASN ASN ASN ASS ASD ASS ASS ASS ASS ASS ASS ASS ASS	ILE ARG ARG ALA LEU THR
• Molecule 25: R	ibosomal protein L18-like	protein	
Chain LQ:	60%	39%	-
MET ASP LEU LEU VAL VAL ALA ALA ALA GLY PHE PRO PHE ALA	PRO ALA ALA ARG ARG ARG ARG CLU CLEU CLEU CLU CLU CLU CLU CLU SER SER SER SER SER SER SER SER	ASP ASP LEU ARG TRP TRP TRP TSS ARG SER ARG ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	HIS PHE BHI CLY
PRO HIS LYS HIS HIS LYS PRO PRO PRO SER LYS SER LYS GLY	ARG LYS PHE GLU GLU ARG ARG GLY ARG ARG ARG CLY SER ARG CLY VAL		
• Molecule 26: 60	S ribosomal protein L20		

Chain LS:	97%	.
M1 K50 K50 K50 K50 K50 K50 K50 K50 K50 K50	S 174	
• Molecule 27: 60S rib	osomal protein l21-like protein	
^{8%} Chain LT:	74% 5%	21%
MET GLY GLY ALA ALA ALA ALA ALA CLY CLY CLY THR THR ARG SER ARG ARG ARG ARG	RIC PHE PHE PHE PHE PHE PHE PHE PHE	K81 H83 R92 R97 K97 K12 K118 Q127 N146
Ei57		
• Molecule 28: 60S rib	osomal protein l23-like protein	
Chain LV:	93%	· ·
MET ALLA ALLA ALLA ALLA GLN GLN G1 C10 C10 C10 C10 C11 C11 K12 K13	M15 T16 C18 C18 C18 C22 C22 A23 A23 A23 A23 A24 C32 A24 A24 C43 C43 C43 C43 C43 C43 C43 C43 C43 C4	RE0 L51 P52 P52 P52 A62 K65 K65 K65 K65 K65 K65 K65 K73 K73 K73 K73 K73 K73 K73 K73 K73 K73
V79 180 K85 F94 F94 E58 D99 N100 A101 G102	V103 1104 P107 V108 V114 V112 V117 V117 V113 V135 V138	ectw
• Molecule 29: 60S rib	osomal protein L26-like protein	
Chain LY:	93%	• •
M1 88 88 88 88 88 88 88 86 88 86 88 87 84 84 84 84 84 84 84 84 84 84 84 84 84	ALA	
• Molecule 30: 60S rib	osomal protein L32-like protein	
Chain Le:	97%	•
MI K6 K6 K12 V131		
• Molecule 31: 60S rib	osomal protein 133-like protein	
Chain Lf:	95%	
MET P2 R56 R62 P92 A93 109		

• Molecule	32: dolichyl-dipho	sphooligosaccharide	eprotein glycotra	nsferase
Chain Lh:	13%	879	%	
MET SER ASN GS R35	K38 ♦ S41 S41 S41 S42	TYR SER GLU GLU PRO ALA ILA ILA TYR HIS SER SER SER SER	ARG ALA ALA ALA ALA ALA ALA SER SER SER CYS CYS CYS THR PHE	GLU PRO GLU GLU GLU ARG GLU SER LEU LEU LEU LEU PRO
VAL ALA ALA ALA SER SER LEU LYS GLY PRO	ASN THR THR ARG ARG GLU HIS ARG GLN ARG ASN PRO SER GLU	ALA THR MET SER SER ALA ALA ALA ALA CLU CLU LEU LEU LEU SER SER	ALA ALA GLY CTYS CTYS CTYS SER ARG SER VAL LEU VAL	ALA TLEU LEU VAL LEU TLEU TLE ALA ALA ALA VAL
ALA SER ARG LEU PHE SER VAL ILE	ARG ARG GLU SER ILE ILE HIS CLU ASP PHE PHC PHR ASN	PHE ARG ALA ALA THR LYS LYS LYS ALA ALA ASN ASN ASN ASN TYS TYS	PHE TRP ASP PHE ASP ASP ASP ASC ASP ASC ASP ASC ASC ASP ASC ASP ASC ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	GLY ARG VAL THR GLY GLY THR TYR PRO GLY
LEU MET VAL THR SER GLY VAL ILLE	TYR LEU LEU LEU ARG ARG THR THR VAL VAL VAL ARG ARG	ASN TILE CYS CYS CAS LEU LEU ALA ALA PLEU SER CIY CLU THEU	ALA ALA ALA ALA ALA LEU LEU LEU LEU CLU GLU MET THR THR	SER PRO SER ALA GLY LEU LEU ALA ALA ALA PHE
MET GLY ILE ALA PRO GLY TYR ILE	SER SER SER VAL ALA GLY ASP ASN ASN ALA ALA	ILE PHE LEU LEU LEU VAL PHE PHE PHE PHE LEU TRP LEU TRP ALA	LEU LYS GLN GLN GLN SER MET LEU TRP GLY GLY CVS ALA	LEU PHE TYR GLY TYR MET VAL ALA SER TRP GLY
GLY TYR ALA PHE ILE THR CYS CYS	LEU PRO LEU HIS PHE PHE VAL LEU TLE CYS GLY ARG TYR	SER THR ARG LEU VAL TYR THR THR THR TRP TRP TRP	GLY THR LEU ALA SER MET GLN GLN TLE PRO PRO PRO PRO PRO	LEU PRO VAL LYS THR SER GLU HIS MET PRO
LEU GLY PHE PHE CLY GLY GLN GLN	LEU LEU ALA PHE LEU ASP TYR VAL ARG SER THR THR TLE SER SER	ARG GLM GLM CHHE GLM CHHE LEU THR LEU THR CHY GLY GLY GLY	PHE GLY GLY GLY GLY GLY CLEU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	ALA GLY LEU LEU ILE ALA PRO FRO SER GLY ARG PHE
TYR SER LEU TRP ASP THR GLY TYR	ALA LYS LYS TLE HTS PRO TLE TLE TLE TLE TLE SER SER SER SER SER SER	GLN PRO THR ALA PRO PRO PHE PHE CASP CLEU ASP MET MET	LEU VAL TRP LEU PHE PRO VAL VAL TYR LEU CYS	GLN GLN GLN LEU GLV ASP GLU HIS PHE ILLE ILLE
VAL TYR ALA LEU PHE GLY SER TYR	PHE ALA ALA CALY CAL ALA MET ARG ARG LEU LEU LEU THR THR THR PRO	VAL VAL CYS CYS CYS ALA ALA ALA ALA ALA ALA ALA ALA SER SER SER SER SER	ASP THR TYR TYR LEU ASN FRO ASN PRO ASN PRO GLN GLN	ALA GLM ALA ALA THR GLU ALP GLU CLY LYS LYS LYS
SER GLY LEU LYS ALA ALA SER LYS	PRO ALA ALA ALA CLY CLY ALA ALA LEU TRP CLY S CLY TRP MET MET	TLE SER SER GLY CLY CLY CLU THR THR TEU LEU CLEU CLEU VAL CLEU VAL	CYS THR TRP VAL THR VAL THR SER ASN ASN ASN SER SER SER SER SER	VAL VAL LEU LEU ALA SER ARG FLU ASP GLY SER
GLN HIS ILE ILE ASP ASP ASP ASP	GLU ALA TRP GLN GLN GLN LEU ARG GLN ARG GLU ALA ALA	LYS LIVS TILE MET SER SER TRP TRP ASP ASP ASP ASP ASP ASP ASP ASP ASP AS	MET ALA ALA ASP ASP PRO PRO THR VAL CEU VAL ASN ASN TRP TRP	ASN ASN THR HIS IIE ALA CVAL GLY LYS ALA
MET ALA SER ARG GLU GLU VAL SER	TYR PRO ILE MET ARG GLN HIS GLN HIS GLU ASP TYR VAL LEU VAL	VAL PHE GLY GLY GLY CLY CLY CLY CLY CLY CLY CLY ASP ASP ASP ASP ASN	LYS LYS PHE TRP TRP MET VAL ARG ALA GLU GLU TRP TRP	PRO ASP GLU VAL SER GLU ARG GLU ARG ALA PHE PHE PHE THR
PRO ARG GLY GLU TYR ARG VAL ASP	ALA GLU ASP THR ASP MET ASN ASN SER LEU MET TTR TYS	MET CYS TYR TYR ASN ASN ASN ASN ASN CFEU PHE PHC PRO CLY GLY	ALA VAL ASP ASP ARG ARG GLY VAL ARG CLY PRO GLU VAL	GLY PRO THR LEU ASN THR LEU GLU GLU ALA PHE
THR SER GLU ASN ASN TRP ILE ILE	TLE TYR LYS VAL LYS LYS LY LSV ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	ALA SER ALA ALA ALA ALA ALA CLU GLU GLU CLY CLYS LLYS LLYS	ALA THR LYS LYS ARG GLY PRO PRO ARG VAL LEU ARG VAL CLU	
• Molecule	33: 60S ribosomal	protein L36		
Chain Li:		75%	5%	20%
MET SER SER GLU ASP ALA THR PRO LYS	ALA PRO VAL ANG ANG ANG CLEU LEU ANG ANG CLEU LEU LEU LEU LEU LYS	0233 H24 K25 S36 R37 R37 K41 K94 K94		
• Molecule	34: Ribosomal pro	tein L37		

Chain Lj:

77%

22%

•

• Molecule 48: 60S ribosomal subunit-like protein

31%

Chain CX:

69%

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4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41599	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT $(4k \ge 4k)$	Depositor
Maximum map value	0.491	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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: OMU, 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).

Mol Chain		Bond lengths		Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	C1	0.55	1/48945~(0.0%)	1.02	181/76270~(0.2%)	
2	C2	0.57	0/5415	0.96	11/8436~(0.1%)	
3	CA	0.34	0/2190	0.68	0/2940	
4	CB	0.34	0/2109	0.65	2/2866~(0.1%)	
5	CC	0.33	0/2325	0.67	4/3164~(0.1%)	
6	CE	0.35	0/3743	0.61	1/5045~(0.0%)	
7	CH	0.31	0/909	0.68	0/1229	
8	CI	0.34	0/1225	0.64	0/1645	
9	CJ	0.28	0/3189	0.58	2/4309~(0.0%)	
10	CM	0.31	0/1555	0.65	1/2091~(0.0%)	
10	LF	0.37	0/2004	0.60	1/2686~(0.0%)	
11	CN	0.30	0/1881	0.66	1/2560~(0.0%)	
12	CQ	0.34	0/981	0.70	0/1301	
13	CR	0.33	0/1369	0.62	0/1828	
14	CU	0.28	0/980	0.64	1/1314~(0.1%)	
15	Ch	0.26	0/563	0.68	1/746~(0.1%)	
16	LB	0.35	0/2760	0.72	5/3701~(0.1%)	
17	LC	0.36	0/2809	0.58	0/3787	
18	LE	0.34	0/1363	0.57	0/1833	
19	LG	0.36	0/1492	0.59	1/2003~(0.0%)	
20	LL	0.36	0/983	0.66	0/1318	
21	LM	0.34	0/1120	0.64	1/1507~(0.1%)	
22	LN	0.37	0/1595	0.63	1/2132~(0.0%)	
23	LO	0.36	0/1652	0.64	1/2215~(0.0%)	
24	LP	0.29	0/1231	0.56	0/1658	
25	LQ	0.35	0/1033	0.61	0/1391	
26	LS	0.35	0/1468	0.63	0/1975	
27	LT	0.31	$0/1\overline{033}$	0.62	$0/1\overline{389}$	
28	LV	0.32	0/1013	0.66	2/1361~(0.1%)	
29	LY	0.34	0/1079	0.59	$0/1\overline{443}$	
30	Le	0.34	0/1073	0.57	0/1431	
31	Lf	0.38	0/883	0.62	0/1187	

Mal	Chain	Bo	ond lengths	I	Bond angles
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
32	Lh	0.30	0/1006	0.56	0/1338
33	Li	0.32	0/738	0.63	0/971
34	Lj	0.37	0/606	0.64	0/803
35	Cc	0.33	0/1934	0.58	1/2614~(0.0%)
36	Cd	0.33	0/2857	0.59	0/3843
37	Ce	0.38	0/1638	0.63	1/2196~(0.0%)
38	Cf	0.31	0/1238	0.67	2/1631~(0.1%)
39	Су	0.24	0/1208	0.43	0/1682
40	Cg	0.51	2/1887~(0.1%)	0.85	4/2544~(0.2%)
41	CP	0.24	0/1595	0.46	0/2217
42	CG	0.26	0/872	0.50	0/1212
43	Lq	0.26	0/1020	0.49	0/1418
44	Cx	0.25	0/567	0.49	0/783
45	LJ	0.24	0/830	0.44	0/1150
46	LD	0.23	0/1344	0.41	0/1868
47	C4	0.30	0/2833	1.08	19/4414~(0.4%)
48	CX	0.58	0/377	0.66	0/518
All	All	0.44	3/124520~(0.0%)	0.84	244/179963~(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
4	CB	0	1
15	Ch	0	1
16	LB	0	1
19	LG	0	1
25	LQ	0	1
40	Cg	0	1
43	Lq	0	1
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
40	Cg	204	PRO	CG-CD	-15.22	1.00	1.50
40	Cg	204	PRO	N-CD	6.92	1.57	1.47
1	C1	3215	U	C1'-N1	6.65	1.58	1.48

The worst 5 of 244 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
40	Cg	204	PRO	N-CD-CG	-16.54	78.39	103.20
1	C1	1050	С	N3-C2-O2	-12.57	113.10	121.90
1	C1	1050	С	N1-C2-O2	10.13	124.98	118.90
37	Ce	186	CYS	C-N-CA	10.04	146.80	121.70
1	C1	625	С	C6-N1-C2	-10.02	116.29	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	CB	42	ARG	Peptide
15	Ch	282	LEU	Peptide
16	LB	58	ARG	Sidechain
19	LG	161	ASP	Peptide
25	LQ	147	ARG	Sidechain

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
3	CA	254/316~(80%)	236~(93%)	18 (7%)	0	100	100
4	CB	256/391~(66%)	235~(92%)	20 (8%)	1 (0%)	34	69
5	CC	264/801~(33%)	250~(95%)	14 (5%)	0	100	100
6	CE	459/598~(77%)	440 (96%)	19 (4%)	0	100	100
7	CH	106/661~(16%)	101 (95%)	4 (4%)	1 (1%)	17	52
8	CI	144/414~(35%)	133 (92%)	10 (7%)	1 (1%)	22	57
9	CJ	374/679~(55%)	357 (96%)	16 (4%)	1 (0%)	41	73

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	9	1	1 0

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
10	CM	183/249~(74%)	171 (93%)	12 (7%)	0	100	100
10	LF	238/249~(96%)	230~(97%)	7 (3%)	1 (0%)	34	69
11	CN	244/246~(99%)	228~(93%)	16 (7%)	0	100	100
12	CQ	110/225~(49%)	107 (97%)	3 (3%)	0	100	100
13	CR	159/237~(67%)	153 (96%)	6 (4%)	0	100	100
14	CU	119/451~(26%)	113 (95%)	6 (5%)	0	100	100
15	Ch	69/354~(20%)	66 (96%)	3 (4%)	0	100	100
16	LB	337/392~(86%)	319 (95%)	18 (5%)	0	100	100
17	LC	360/365~(99%)	349 (97%)	11 (3%)	0	100	100
18	LE	166/200~(83%)	161 (97%)	5 (3%)	0	100	100
19	LG	179/262~(68%)	174 (97%)	5 (3%)	0	100	100
20	LL	115/213~(54%)	111 (96%)	4 (4%)	0	100	100
21	LM	135/142~(95%)	131 (97%)	4 (3%)	0	100	100
22	LN	179/203~(88%)	175~(98%)	4 (2%)	0	100	100
23	LO	202/204~(99%)	194 (96%)	8 (4%)	0	100	100
24	LP	150/187~(80%)	148 (99%)	2 (1%)	0	100	100
25	LQ	127/213~(60%)	123 (97%)	4 (3%)	0	100	100
26	LS	172/174~(99%)	164 (95%)	8 (5%)	0	100	100
27	LT	124/160~(78%)	115~(93%)	8 (6%)	1 (1%)	19	54
28	LV	133/139~(96%)	127~(96%)	6 (4%)	0	100	100
29	LY	132/138~(96%)	128~(97%)	4 (3%)	0	100	100
30	Le	129/131~(98%)	127~(98%)	2 (2%)	0	100	100
31	Lf	106/109~(97%)	102 (96%)	2 (2%)	2 (2%)	8	33
32	Lh	119/935~(13%)	117 (98%)	2 (2%)	0	100	100
33	Li	86/110~(78%)	84 (98%)	2 (2%)	0	100	100
34	Lj	72/95~(76%)	71 (99%)	1 (1%)	0	100	100
35	Cc	$\overline{232/282}~(82\%)$	222 (96%)	10 (4%)	0	100	100
36	Cd	$\overline{343/436}$ (79%)	321 (94%)	22 (6%)	0	100	100
37	Ce	192/336~(57%)	188 (98%)	4 (2%)	0	100	100
38	Cf	$\overline{145/570}\ (25\%)$	136 (94%)	9 (6%)	0	100	100
39	Су	240/350~(69%)	238 (99%)	2 (1%)	0	100	100

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
40	Cg	229/478~(48%)	215~(94%)	12~(5%)	2(1%)	17	52
41	CP	322/751~(43%)	314 (98%)	8 (2%)	0	100	100
42	CG	175/184~(95%)	171~(98%)	4 (2%)	0	100	100
43	Lq	205/217~(94%)	183~(89%)	21 (10%)	1 (0%)	29	64
44	Cx	98/202~(48%)	98 (100%)	0	0	100	100
45	LJ	167/173~(96%)	167 (100%)	0	0	100	100
46	LD	269/304~(88%)	266 (99%)	3~(1%)	0	100	100
48	CX	59/203~(29%)	56~(95%)	$\overline{3(5\%)}$	0	100	100
All	All	8678/14729~(59%)	8315 (96%)	352 (4%)	11 (0%)	54	83

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5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CB	117	PRO
8	CI	268	VAL
40	Cg	154	ASP
31	Lf	93	ALA
7	CH	403	LEU

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	Perce	entiles
3	CA	231/276~(84%)	218~(94%)	13~(6%)	21	52
4	CB	222/329~(68%)	206~(93%)	16 (7%)	14	44
5	CC	252/710~(36%)	236~(94%)	16 (6%)	18	48
6	CE	398/517~(77%)	383~(96%)	15~(4%)	33	66
7	CH	95/575~(16%)	88~(93%)	7~(7%)	13	42
8	CI	121/336~(36%)	117~(97%)	4(3%)	38	69
9	CJ	332/579~(57%)	$321 \ (97\%)$	11 (3%)	38	69
10	CM	161/215~(75%)	145 (90%)	16 (10%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
10	LF	206/215~(96%)	202~(98%)	4 (2%)	57	81
11	CN	206/206~(100%)	199~(97%)	7 (3%)	37	69
12	CQ	100/192~(52%)	96~(96%)	4 (4%)	31	65
13	CR	144/206~(70%)	136~(94%)	8 (6%)	21	52
14	CU	104/376~(28%)	98~(94%)	6~(6%)	20	51
15	Ch	58/291~(20%)	56~(97%)	2(3%)	37	69
16	LB	290/331~(88%)	267~(92%)	23~(8%)	12	40
17	LC	283/285~(99%)	274 (97%)	9~(3%)	39	69
18	LE	143/166~(86%)	137~(96%)	6~(4%)	30	62
19	LG	157/222~(71%)	146~(93%)	11 (7%)	15	45
20	LL	99/176~(56%)	98~(99%)	1 (1%)	76	90
21	LM	115/117~(98%)	110 (96%)	5 (4%)	29	62
22	LN	164/180~(91%)	158 (96%)	6 (4%)	34	66
23	LO	163/163~(100%)	160 (98%)	3~(2%)	59	82
24	LP	125/152~(82%)	122 (98%)	3(2%)	49	76
25	LQ	110/178~(62%)	110 (100%)	0	100	100
26	LS	154/154~(100%)	148~(96%)	6 (4%)	32	65
27	LT	109/135~(81%)	102 (94%)	7~(6%)	17	48
28	LV	99/102~(97%)	95~(96%)	4 (4%)	31	65
29	LY	117/119~(98%)	112~(96%)	5~(4%)	29	62
30	Le	114/114~(100%)	110~(96%)	4 (4%)	36	68
31	Lf	89/90~(99%)	87~(98%)	2(2%)	52	78
32	Lh	108/781~(14%)	104 (96%)	4 (4%)	34	66
33	Li	75/93~(81%)	69~(92%)	6 (8%)	12	40
34	Lj	61/78~(78%)	60~(98%)	1 (2%)	62	84
35	$\overline{\mathrm{Cc}}$	204/244~(84%)	194 (95%)	10 (5%)	25	57
36	Cd	$\overline{295/367}~(80\%)$	279~(95%)	16 (5%)	22	53
37	Ce	173/297~(58%)	167 (96%)	6 (4%)	36	68
38	Cf	127/482~(26%)	121 (95%)	6 (5%)	26	59
40	Cg	$\overline{210/417}$ (50%)	202 (96%)	8 (4%)	33	66
44	Cx	14/176~(8%)	14 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
48	CX	22/172~(13%)	21~(96%)	1 (4%)	27	60	
All	All	6250/10814~(58%)	5968~(96%)	282~(4%)	31	60	

5 of 282 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
33	Li	68	GLU
35	Cc	61	CYS
36	Cd	436	LEU
10	CM	202	LYS
10	CM	144	TYR

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such side chains are listed below:

Mol	Chain	Res	Type
40	Cg	100	ASN
32	Lh	47	ASN
12	CQ	45	ASN
10	CM	242	ASN
15	Ch	321	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2026/3341~(60%)	482 (23%)	17~(0%)
2	C2	225/256~(87%)	61 (27%)	1 (0%)
47	C4	118/119~(99%)	23 (19%)	0
All	All	2369/3716~(63%)	566 (23%)	18 (0%)

5 of 566 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	26	А
1	C1	40	А
1	C1	43	А
1	C1	49	А

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3257	U
2	C2	123	G
1	C1	3297	U
1	C1	2569	U
1	C1	3255	G

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

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

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

Mal	Turne	Chain Deg Link		Tiple	Bo	ond leng	$_{\rm ths}$	Bond angles		
INIOI	туре	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
1	OMU	C1	2689	1	19,22,23	2.98	8 (42%)	26,31,34	1.68	4 (15%)
1	OMU	C1	2687	1	19,22,23	2.96	8 (42%)	26,31,34	1.67	4 (15%)
1	OMU	C1	2682	1	19,22,23	2.97	8 (42%)	26,31,34	1.64	4 (15%)

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

Mol	Type	Chain	\mathbf{Res}	Link	Chirals	Torsions	Rings
1	OMU	C1	2689	1	-	2/9/27/28	0/2/2/2
1	OMU	C1	2687	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2682	1	-	1/9/27/28	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
1	C1	2682	OMU	C2-N1	7.20	1.50	1.38
1	C1	2689	OMU	C2-N1	7.20	1.50	1.38
1	C1	2687	OMU	C2-N1	7.15	1.49	1.38
1	C1	2689	OMU	C2-N3	6.72	1.49	1.38
1	C1	2682	OMU	C2-N3	6.71	1.49	1.38

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	C1	2689	OMU	C4-N3-C2	-5.14	119.80	126.58
1	C1	2687	OMU	C4-N3-C2	-5.12	119.83	126.58
1	C1	2682	OMU	C4-N3-C2	-4.98	120.01	126.58
1	C1	2689	OMU	N3-C2-N1	3.71	119.82	114.89
1	C1	2687	OMU	N3-C2-N1	3.67	119.77	114.89

The worst 5 of 12 bond angle outliers are listed below:

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	2682	OMU	C1'-C2'-O2'-CM2
1	C1	2689	OMU	C3'-C4'-C5'-O5'
1	C1	2689	OMU	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-35281. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections (i)

6.1.1 Primary map

6.1.2 Raw map

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

6.2 Central slices (i)

6.2.1 Primary map

X Index: 210

Y Index: 210

Z Index: 210

6.2.2 Raw map

X Index: 210

Y Index: 210

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: 243

Y Index: 229

Z Index: 216

6.3.2 Raw map

X Index: 241

Y Index: 233

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

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

6.4.1 Primary map

6.4.2 Raw map

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

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

6.6 Mask visualisation (i)

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

7 Map analysis (i)

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

7.1 Map-value distribution (i)

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

7.2 Volume estimate (i)

The volume at the recommended contour level is 1087 nm^3 ; this corresponds to an approximate mass of 982 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 0.323 ${\rm \AA^{-1}}$

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)

*Reported resolution corresponds to spatial frequency of 0.323 $\mathrm{\AA^{-1}}$

8.2 Resolution estimates (i)

$\mathbf{Bosolution} \text{ ostimato } (\mathbf{\hat{\lambda}})$	Estimation criterion (FSC cut-off)		
Resolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	3.73	3.16
Unmasked-calculated*	3.78	6.45	3.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.78 differs from the reported value 3.1 by more than 10 %

9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-35281 and PDB model 8I9R. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay (i)

The images above show the 3D surface view of the map at the recommended contour level 0.02 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 (0.02).

9.4 Atom inclusion (i)

At the recommended contour level, 77% of all backbone atoms, 76% 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 (0.02) and Q-score for the entire model and for each chain.

\mathbf{Chain}	Atom inclusion	Q-score
All	0.7610	0.4050
C1	0.8260	0.4090
C2	0.9150	0.4740
C4	0.1690	0.1000
CA	0.8840	0.4900
CB	0.8480	0.4450
$\mathbf{C}\mathbf{C}$	0.6290	0.3320
CE	0.9000	0.5130
CG	0.5290	0.1640
CH	0.3820	0.2080
CI	0.8720	0.4490
CJ	0.4900	0.1550
CM	0.6900	0.3100
CN	0.3660	0.1790
CP	0.1970	0.1380
CQ	0.6160	0.2450
CR	0.9140	0.5420
CU	0.8040	0.4050
CX	0.6150	0.3430
Cc	0.8530	0.5030
Cd	0.9130	0.5400
Ce	0.9410	0.5680
Cf	0.7690	0.4040
Cg	0.7650	0.3980
Ch	0.7200	0.3060
Cx	0.1520	0.1030
Cy	0.0000	0.0720
LB	0.7710	0.3770
LC	0.9510	0.5860
	0.0010	0.0380
LE	0.9140	0.5320
LF	0.9320	0.5550
LG	0.9050	0.5470
LJ	0.0380	0.0310
LL	0.9420	0.5770

Continued	from	previous	page

Chain	Atom inclusion	Q-score
LM	0.8660	0.4960
LN	0.9470	0.5970
LO	0.9350	0.5440
LP	0.8320	0.4810
LQ	0.9480	0.5760
LS	0.9110	0.5070
LT	0.7370	0.3560
LV	0.3700	0.1870
LY	0.9300	0.5690
Le	0.9430	0.5900
Lf	0.9470	0.5880
Lh	0.8670	0.4900
Li	0.8930	0.5270
Lj	0.9590	0.6060
Lq	0.0080	0.0760

