

# wwPDB EM Validation Summary Report (i)

#### Feb 22, 2024 – 02:06 PM EST

PDB ID	:	4V6V
EMDB ID	:	EMD-5562
Title	:	Tetracycline resistance protein $Tet(O)$ bound to the ribosome
Authors	:	Li, W.; Atkinson, G.C.; Thakor, N.S.; Allas, U.; Lu, C.; Chan, K.Y.; Tenson,
		T.; Schulten, K.; Wilson, K.S.; Hauryliuk, V.; Frank, J.
Deposited on	:	2013-02-25
Resolution	:	9.80 Å(reported)
Based on initial models	:	2I2U, 2I2V

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

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/EMValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev70
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	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 9.80 Å.

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



Metric	Whole archive	EM structures		
	(#Entries)	(#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	AJ	103	89%	10% •
2	AK	128	91%	8% •
3	AL	123	89%	9% •
4	AM	117	87%	13%
5	AN	100	89%	11%
6	AO	88	91%	7% ••
7	AP	82	88%	11% •
8	AQ	83	93%	6% •



Conti	nued from	n previous	page		
Mol	Chain	Length		Quality of chain	
9	AR	74	7%	82%	16% •
10	AS	91	•	87%	13%
11	AB	240	<u> </u>	95%	5%
12	AT	86	6%	93%	7%
13	AU	70		77%	20% •
14	AC	232	<b>—</b>	91%	9%
15	AD	205		90%	9% •
16	AE	166	170/	92%	8% •
17	AF	135	1770	90%	9% •
18	AG	178	•	90%	9% •
19	AH	129	<u> </u>	93%	6% ·
20	AI	129		87%	12% •
21	A1	639	<u> </u>	94%	6%
22	AA	1542	15%	58%	24% •
23	A2	47	23%	51%	26%
24	A3	77	12%	61%	27%
05	DC	09.4	10%		
25	BC	234	7%	95%	5%
26	BJ	164	·	93%	5% •
27	BK	141		95%	5%
28	BN	142		87%	12% •
29	BO	123	-	84%	13% ••
30	BP	144	<b></b>	88%	10% •
31	BQ	136		87%	13%
32	BR	127	<u>-</u>	84%	15% •
33	BS	117		91%	9%



Mol	Chain	Length	Quality of chain	
34	BT	114	<b>•</b> 89%	11% •
35	BD	272	88%	11% •
36	BU	117	85%	13% •
37	BV	103	88%	12%
38	BW	110	90%	8% •
39	BX	100	94%	5% •
40	BY	103	94%	5% •
41	BZ	94	94%	6%
42	B0	84	85%	12% •
43	B1	77	<b>•</b> 87%	10% •
44	B2	63	92%	6% ·
45	BE	209	<b>•</b> 92%	7%
46	B3	58	90%	10%
47	B4	70	93%	6% ·
48	B5	56	82%	18%
49	B6	54	94%	6%
50	B7	46	80%	20%
51	B8	64	89%	9% •
52	B9	38	87%	13%
53	BF	201	92%	7% •
54	BG	178	88%	11% •
55	BH	176	92%	
56	BL	149	18% 95%	5%
57	ВА	2904	15% 58%	24%
58	Ba	120	18% 64%	17% •

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# 2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 154956 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues		At	oms	AltConf	Trace		
1	AJ	103	Total 794	C 483	N 158	0 151	${S \over 2}$	0	0

• Molecule 2 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	ΔK	198	Total	С	Ν	0	S	0	0
2 AK	128	923	553	196	171	3		0	

• Molecule 3 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AL	123	Total 923	C 558	N 196	0 165	$\frac{S}{4}$	0	0

• Molecule 4 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues		At	oms	AltConf	Trace		
4	AM	117	Total 876	C 530	N 183	0 160	${ m S} { m 3}$	0	0

• Molecule 5 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues		At	oms	AltConf	Trace		
5	AN	100	Total 771	C 465	N 164	0 139	${ m S} { m 3}$	0	0

• Molecule 6 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues		At	oms	AltConf	Trace		
6	AO	88	Total 690	C 414	N 146	0 129	S 1	0	0



There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AO	79	ARG	GLN	conflict	UNP P0ADZ4

• Molecule 7 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues		At	oms	AltConf	Trace		
7	AP	82	Total 620	C 377	N 128	0 114	S 1	0	0

• Molecule 8 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	AQ	83	Total 657	C 410	N 124	O 120	${ m S} { m 3}$	0	0

• Molecule 9 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues		At	oms	AltConf	Trace		
9	AR	74	Total 603	C 372	N 123	0 107	S 1	0	0

• Molecule 10 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues		At	oms	AltConf	Trace		
10	AS	91	Total 708	C 445	N 139	0 122	${ m S} { m 2}$	0	0

• Molecule 11 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues		Ate	AltConf	Trace			
11	AB	240	Total 1805	C 1113	N 332	O 352	S 8	0	0

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

Mol	Chain	Residues		At	oms	AltConf	Trace		
12	AT	86	Total 636	C 380	N 138	0 115	${ m S} { m 3}$	0	0

• Molecule 13 is a protein called 30S ribosomal protein S21.



Mol	Chain	Residues		Ate	oms			AltConf	Trace
13	AU	70	Total 564	C 340	N 125	O 98	S 1	0	0

• Molecule 14 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues		Ate		AltConf	Trace		
14	AC	232	Total 1761	C 1088	N 346	O 323	$\frac{S}{4}$	0	0

• Molecule 15 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues		At	oms	AltConf	Trace		
15	AD	205	Total 1587	C 970	N 315	0 298	$\frac{S}{4}$	0	0

• Molecule 16 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues		At	oms	AltConf	Trace		
16	AE	166	Total 1182	C 718	N 232	O 226	S 6	0	0

• Molecule 17 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues		At	oms	AltConf	Trace		
17	AF	135	Total 1061	C 637	N 198	O 219	S 7	0	0

• Molecule 18 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues		At	oms	AltConf	Trace		
18	AG	178	Total 1347	C 821	N 269	O 253	$\frac{S}{4}$	0	0

• Molecule 19 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues		At	oms	AltConf	Trace		
19	AH	129	Total 948	C 585	N 173	0 184	S 6	0	0

• Molecule 20 is a protein called 30S ribosomal protein S9.



Mol	Chain	Residues		At	oms	AltConf	Trace		
20	AI	129	Total 1000	C 606	N 208	O 183	${ m S} { m 3}$	0	0

• Molecule 21 is a protein called Tetracycline resistance protein TetO.

Mol	Chain	Residues		At	AltConf	Trace			
21	A1	639	Total 4989	C 3146	N 850	O 966	S 27	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A1	227	ILE	THR	conflict	UNP P10952

• Molecule 22 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues		I	Atoms			AltConf	Trace
22	АА	1542	Total 33089	C 14767	N 6064	O 10717	Р 1541	0	0

• Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues		A	AltConf	Trace			
23	A2	47	Total 993	C 445	N 167	O 335	Р 46	0	0

• Molecule 24 is a RNA chain called P-tRNA.

Mol	Chain	Residues		L	AltConf	Trace				
24	A3	77	Total 1640	С 734	N 297	O 533	Р 75	S 1	0	0

• Molecule 25 is a protein called 50S ribosomal protein L1.

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

• Molecule 26 is a protein called 50S ribosomal protein L10.



Mol	Chain	Residues		At	oms	AltConf	Trace		
26	BJ	164	Total 1233	С 776	N 220	0 231	S 6	0	0

• Molecule 27 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues		At	oms	AltConf	Trace		
27	BK	141	Total 1032	C 651	N 179	O 196	S 6	0	0

• Molecule 28 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues		At	oms	AltConf	Trace		
28	BN	142	Total 1129	С 714	N 212	0 199	$\frac{S}{4}$	0	0

• Molecule 29 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues		At	oms	AltConf	Trace		
29	BO	123	Total 947	C 593	N 181	0 167	S 6	0	0

• Molecule 30 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues		At	AltConf	Trace			
30	BP	144	Total 1053	C 654	N 207	0 190	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 31 is a protein called 50S ribosomal protein L16.

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

• Molecule 32 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues		At	oms	AltConf	Trace		
32	BR	127	Total 1008	C 621	N 204	0 178	${S \atop 5}$	0	0

• Molecule 33 is a protein called 50S ribosomal protein L18.



Mol	Chain	Residues		At	AltConf	Trace			
33	BS	117	Total 900	$\begin{array}{c} \mathrm{C} \\ 557 \end{array}$	N 179	O 163	S 1	0	0

• Molecule 34 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues		At	oms	AltConf	Trace		
34	BT	114	Total 917	С 574	N 179	0 163	S 1	0	0

• Molecule 35 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues		Ate	AltConf	Trace			
35	BD	272	Total 2092	C 1294	N 425	O 366	${ m S} 7$	0	0

• Molecule 36 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
36	BU	117	Total	С	N	0	0	0
			947	604	192	151		

• Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues		At	AltConf	Trace			
37	BV	103	Total 816	C 516	N 153	0 145	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 38 is a protein called 50S ribosomal protein L22.

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

• Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues		At	AltConf	Trace			
39	BX	100	Total 787	C 496	N 146	0 143	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 40 is a protein called 50S ribosomal protein L24.



Mol	Chain	Residues		Ato	ms	AltConf	Trace	
40	BY	103	Total 789	C 498	N 148	0 143	0	0

• Molecule 41 is a protein called 50S ribosomal protein L25.

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

• Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues		At	oms	AltConf	Trace		
42	B0	84	Total 634	C 391	N 129	0 113	S 1	0	0

• Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues		At	oms			AltConf	Trace
43	B1	77	Total 625	C 388	N 129	O 106	${ m S} { m 2}$	0	0

• Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues		Atc	$\mathbf{ms}$	AltConf	Trace		
44	B2	63	Total 509	C 313	N 99	O 95	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 45 is a protein called 50S ribosomal protein L3.

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

• Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues		Ato	$\mathbf{ms}$	AltConf	Trace		
46	B3	58	Total 449	C 281	N 87	O 79	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 47 is a protein called 50S ribosomal protein L31.



Mol	Chain	Residues		At	$\mathbf{oms}$			AltConf	Trace
47	B4	70	Total 549	C 339	N 104	O 100	S 6	0	0

• Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues		Ato	$\mathbf{ms}$	AltConf	Trace		
48	B5	56	Total 444	C 269	N 94	O 80	S 1	0	0

• Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues		Aton	ıs	AltConf	Trace	
49	B6	54	Total 441	C 284	N 81	O 76	0	0

• Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues		Ato	$\mathbf{ms}$		AltConf	Trace	
50	B7	46	Total	С	Ν	0	S	0	0
	21	10	377	228	90	57	2	Ŭ	Ŭ

• Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues		At	oms			AltConf	Trace
51	B8	64	Total 504	C 323	N 105	0 74	${S \over 2}$	0	0

• Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues		Ato	$\mathbf{ms}$			AltConf	Trace
52	B9	38	Total	C	N	0	S	0	0
			302	185	65	48	4		

• Molecule 53 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues		At	oms	AltConf	Trace			
53	BF	201	Total 1552	C 974	N 283	O 290	${f S}{5}$	0	0	

• Molecule 54 is a protein called 50S ribosomal protein L5.



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

• Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues		At	oms	AltConf	Trace		
55	BH	176	Total 1323	C 832	N 243	0 246	${S \over 2}$	0	0

• Molecule 56 is a protein called 50S ribosomal protein L9.

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

• Molecule 57 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues			AltConf	Trace			
57	ВА	2904	Total 62351	C 27824	N 11469	O 20155	Р 2903	0	0

• Molecule 58 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues		A	AltConf	Trace			
58	Ba	120	Total 2566	C 1144	N 468	O 835	Р 119	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 30S ribosomal protein S10





• Molecule 6: 30S ribosomal protein S15 Chain AO: 91% 7% •• • Molecule 7: 30S ribosomal protein S16 Chain AP: 88% 11% . • Molecule 8: 30S ribosomal protein S17 Chain AQ: 93% 6% • H R1 R6 • Molecule 9: 30S ribosomal protein S18 7% Chain AR: 82% 16% •• F4 R5 R6 R7 K8 K8 F9 F9 C1( • Molecule 10: 30S ribosomal protein S19 Chain AS: 87% 13% • Molecule 11: 30S ribosomal protein S2 Chain AB: 95% 5% • Molecule 12: 30S ribosomal protein S20 Chain AT: 93% 7%



#### A1 R9 R23 R24 R28 R28 R28 R28 R28 R28 R38

• Molecule 13: 30S ribosomal protein S21



• Molecule 19: 30S ribosomal protein S8







A432	G433	0435 A435	C436	U437 11/20	0439 U439	C440	A441 G442	C443	G444	6445 CAA6	G447 G447	A448		A451	A452	G455	A456	G457	0458 A760	A460	A461	G462	U463	U464 AA65	A466	U467	A468	C469	0471 U471	U472	0473 CA7A	C475	U476	C477 A478	U479	U480	G481 A460	A402 C483	G484	U485	U486 • • • • 7	A487 C488	C489	C490	G491 C492	A493
G494	A495	G497	A498	A499	C501	A502	C503 C504	G505	G506		A509	<b>A510</b>	C511	U512	C513 C514	G515	U516	G517	C518 C510	A520	G521	C522	A523	G524 CE2E	C526	G527	C528	6259 6530	U531	A532	A533	A535	C536	A539	G540	G541	G542	6544	C545	A546	A547	6549 C549	G550	U551	0552 A553	A554
U555	C556	G558	A559	A560	U562	A563	U565	G5.66	G567	G568 7560	G570	U571	A572	A573	4575 G575	C576	G577	C578	A5/9	G581	C582	A583	G584	G585 7586	0000	U590	U591	1592 1503	U594	A595	A596 CE07	U598	C599	A600 G601	A602	U603	1004	A608	A609	U610	C611	C613	C614	G615 2616	Ge 17	C618
U619	C620	A021 A622	C623	C624	G626	G627	G628 A629	A630	C631	0632	6033 C634	A635	U636	C637	0639 G639	A640	U641	A642	C643	G645	G646	C647	A648	A649	C651		G654	GCOR	C658	<b>U659</b>	C660 C661	U662	A663	G664 A665	G666		G670	U672	A673	G674	A675	Ab/b U677	U678	C679	C680 A681	G682
G683	16.06	0000 A687	G688	C689	0000 0001	U692	6693 A694	A695	A696	7697	C699	<mark>G7 00</mark>	U701	A702	G7 03 A7 04	G7 05	A7 06	U707	C/ 08	G710	G7 11	A712	G713	G714 A715	A7 16	U7 17	A718	C/ 19	G721	G7 22	0723	G725	<mark>C726</mark>	G7 27 A7 28	A729	G730	6731 6730	G733	G734	C735	C736	CT38 CT38	CT39	U740	G742	A743
C744	G745	A747	G748	A749 C760	U751	G752	A / 53 C754	G755	C756	0759 7759	0130 A759	<mark>6760</mark>	G761	0762	G764	G765	A766	A767	A/68	C770	G771	U772	G773	6774 6775	G776	A777	G778	C//9	A781	A782	C783	G785	G786	A787 U788	U789	A790	G791	U793	A794	C795	C796	0797 11798	G799	G800	0801 A802	-
3805	1806 1807	1808	1809	0810 1011	1812	J813	1814 1815	<b>A816</b>	3817	1818 1010	1019 J820	1821	J822	0823 004	1825 1825	3826	J827	1828	1829 1820	831	1832	1833	1834	1835 1026	1837	1838	1839	040 2841	1842	1843	1844 1845	1846	1847	1848 1849		1852	1853 Tec 4	J855	1856	3857	1858	1859 1860	1861	2862	1864 1864	1865
366	367 660	200 200	370	371 570	373 0	374 L	376 I	877 1	878 20		381 1	382	383	384 Ser	386	387	388 1	389		392	393	394 C	395 L	396	398 L	3 <mark>99</mark>	000		903 L	90 <u>4</u>	905 006	07	908 0	909 910	116	912 0	913	915 U		918	919	920 121	922	923	925	926
27 Ct	ë ë		32 U		35 At	36 77		39 39	FO AS			14 C	CC FE			50 61	00 G	AS AS		A5	22 C	56 GE	20	<u>ې د</u>	5 <del>2</del>	51 CC	AS AS		22 25	36 US		AS AS	O AS	1 22 C	3	'4 CS	S AS	7 AS	ø	P AS	SO AS		33	34 AS	2 59 29	37 GS
69			COC		495 A92		A90 A90	69	COC	6.5	00 <sup>4</sup>	<b>G</b> 9	69	A94		A94	19E	165 1011		365	36N	19E	36 <b>0</b>	AUC	60 096	00E	500		006	696		A96	C97	160 160	G97	A97	A97	160 764	A97	C97		36D	96 <b>V</b>	200 C00	GGC CGC	36 <sup>0</sup>
G988	0989 0000	0991	U992	6993	C995	A996	0880	C9 99	A1000	C1 001	A1004	A1005	G1006	U1007	01008 01009	U1010	C1011	A1012	61013 A1014	G1015	A1016	U1017	G1018	ATUIA 00012	A1021	A1022	U1023	61024 111025	G1026	C1027	C1028	U1030	C1031	G1032 G1033	G1034	A1035	A1036	C1038 C1038	G1039	U1040	G1041	A1042 G1043	A1044	C1045	A1 046 G1 047	-
G1050	C1051	G1053	C1054	A1055		C1059	09010	C1 063	G1064	01065 C1066	A1067	G1068	C1069	01070 01070	G1072	U1073	G1074	U1075	01076		A1080	A1081	A1082	01083 01084	U1085	U1086	G1087	G1088	U1090	U1091	A1092	G1094	U1095	C1096 C1097	C1098	G1099	C1100	A1101 A1102	C1103	G1104	A1105	61106 C1107	G1108	C1109	A1110 A1111	C1112
C1113	C1114	U1116 U1116	A1117	U1118	C1120	U1121	U1122 U1123	G1124		C1128	A1130	G1131	C1132	G1133	C1136	C1137	G1138	G1139 G1140	C1140	G1142	G1143	G1144	A1145	A1146 C1147	U1148	C1149	A1150	A1151 A1152	G1153	G1154	A1155 C1156	A1157	C1158	01159 G1160	C1161	C1162	A1163	U1165	G1166	A1167	U1168	Allby All70	A1171	C1172	01173 G1174	G1175
A1176	G1177	A1179	A1180	111 102	G1184 G1184	G1185	G1180 G1187	<mark>A1188</mark>	U1189	61190 A1101	61192 C1192	G1193	<mark>U1194</mark>	C1195	A1196 A1197	G1198	<mark>U1199</mark>	C1200		C1203	A1204	U1205	G1206	G1207	C1209	C1210	U1211	01212	C1214	G1215	A1216	C1218 C1218	A1219	G1220 G1221	G1222	C1223	U1224	A1228 C1226	A1227	C1228	A1229	C1230 G1231	U1232	G1233	U1235	A1236
C1237	A1238	U1240	G1241	G1242	G1244	C1245	A1246 U1247	A1248	C1249	A1250 A1251	A1252	G1253	A1254	G1255	A1257	G1258	C1259	G1260	A1261	C1263	U1264	C1265	G1266	C1 267	A1269	G1270	A1271	612/2 01073	A1274	A1275	G1276	G1278	G1279	A1280 C1281	C1282	U1283	C1284	M1 286	A1287	A1288	A1289	61290 111291	G1292	C1293	01295 U1295	C1296
G1297	U1298	61300	U1301	C1302	G1304	G1305	A1306 U1307	U1308		A1311	U1313	C1314	U1315	G1316	C131/ A1318	A1319	C1320	U1321	C1322	A1324	C1325	U1326	C1327	C1328	N1320	G1331	A1332	A1333	U1335	C1336	G1337	A1339	A1340	U1341 C1342	G1343	C1344	U1345	61347	U1348	A1349	A1350	01351 C1352	G1353	U1354	G1356	A1357









 $\bullet$  Molecule 28: 50S ribosomal protein L13



• Molecule 34: 50S ribosomal protein L19



Chain BT:	89%	11% •
81 K5 K5 K20 R20 R33 R33 R50 R50 G66 G66 G66 G66 G66	R71 R87 R92 R100 E110 E111 N112 N113 N113	
• Molecule 35: 50S ribos	somal protein L2	
Chain BD:	88%	11% •
* - * * -	•••• <b>•</b> •••••	
A1 R12 P31 R42 R42 R47 R47 R47 R51 R51 R51 R51 R51 R51 R51 R51 R51 R51	R68 88 88 80 8100 8100 8100 8100 8155 8155	R176 R181 R181 R181 R202 R212 V212 V212 V212 P217 P217
R257 R268 R268 R268 R271 K272		
• Molecule 36: 50S ribos	somal protein L20	
Chain BU:	85%	13% ·
A1 R2 V3 K4 R5 R2 R12 R2 R12 R2 R12 R12 R12 R12 R12 R1	K63 R54 R57 R63 R63 R63 R91 R91 R91 A117	
• Molecule 37: 50S ribos	somal protein L21	
Chain BV:	88%	12%
M1 R21 F53 F53 R79 R79 R79 R79 R84 R84 R84 R84 R84 R86 R86 R86 R86	R90 1101 S102 A103	
• Molecule 38: 50S ribos	somal protein L22	
Chain BW:	90%	8% •
M1 R11 A21 K28 K28 K28 K28 K28 K28 K28 K28 K38	R9 5 R9 6 R1 10	
• Molecule 39: 50S ribos	somal protein L23	
Chain BX:	94%	5% •
M1 R12 F51 F51 F51 F51 F51 F73 C75 F74 C76 F76 F100		
• Molecule 40: 50S ribos	somal protein L24	
Chain BY:	94%	5%•



• Molecule 41: 50S ribosomal protein L25

Chain BZ:	94%	6%
M1 R9 R19 L42	879 898 998	
• Molecule	42: 50S ribosomal protein L27	
Chain B0:	7% 85%	12% •
A1 A5 G6 G7 S8 T9	R10 R13 R13 R13 R13 R13 R135 R135 R135 R40 R40 R40 R40 R40 R40 R40 R40 R40 R40	
• Molecule	43: 50S ribosomal protein L28	
Chain B1:	87%	10% ·
81 R10 R17 R26 R27	R36 R44 R71 R71 R77 R77	
• Molecule	44: 50S ribosomal protein L29	
Chain B2:	92%	6% •
M1 R7 R23 R47 R48		
• Molecule	45: 50S ribosomal protein L3	
Chain BE:	92%	7%
M1 R13 V37 R46	R17 R13 S113 S113 S113 F116 A119 A119 A119 R128 R128 R128 R128 R128 R128 R128 R128	
$\bullet$ Molecule	46: 50S ribosomal protein L30	
Chain B3:	• 90%	10%
A1 R10 R15 R29 R30	R3 1 R44 4 F56 8 8	

 $\bullet$  Molecule 47: 50S ribosomal protein L31



10%		
Chain B4:	93%	6% ·
M1 R25 R25 R26 R49 R56 R56 R56 R56 R51 R56 R51 R51 R51 R51 R51 R51 R51 R51 R51 R51	K K 2 R 6 4 K 7 0 K 7 0	
• Molecule 48: 50S ribo	somal protein L32	
Chain B5:	82%	18%
A1 K6 R15 R15 R15 R15 R13 R13 R13 R132 R132	R49 R50 R51 F54 A55 K56	
• Molecule 49: 50S ribo	somal protein L33	
Chain B6:	94%	6%
R5 R5 R3 K64		
• Molecule 50: 50S ribo	somal protein L34	
Chain B7:	80%	20%
M1 K2 R12 R12 R14 R14 R14 R36 R33 R33 R34 R41	<mark>. K46</mark>	
• Molecule 51: 50S ribo	somal protein L35	
Chain B8:	89%	9% •
P1 R7 R12 R12 R12 R39 R41 R41 R44 R44 R44		
• Molecule 52: 50S ribo	somal protein L36	
Chain B9:	87%	13%
M1 R4 R12 R16 R16 R16 R16 R24 R24 R24 R24 R24		
• Molecule 53: 50S ribo	somal protein L4	
Chain BF:	92%	7% •
M1 K6 R21 R44 R45 R45 R45 R60 R60 R60 R67 R67	R79 R88 R88 R102 R114 R114 R117 E152 E152 F162 F162 F183 F183 F183	
• Molecule 54: 50S ribo	somal protein L5	

WORLDWIDE PROTEIN DATA BANK

Chain BG:		88%	11% •
A1 R29 L35 L65	R70 R79 R79 G81 G81 C81 R91 R94 R94 R94 R101 I103 R103 R103 R103 R103 R103 R110	K119 R132 E133 E133 C134 R147 V148 R149 R149 R177 K178	
• Molecule 5	5: 50S ribosomal protein I	26	
Chain BH:		92%	6% •
S1 R2 N29 D46 Y57	R68 R94 L104 L104 R151 R152 P153 E154 E166 R152 R152 R152 R175 K175		
• Molecule 5	6: 50S ribosomal protein I	19	
Chain BL:	18%	95%	5%
11 (35 (41 (41		88 197 117 1111 1112 1117 1112 1122 112	1123 1136 ♦ 1147 ♦ 1148 ♦
• Molecule 5	7: 23S ribosomal RNA		
Chain BA:	15%	58% 24%	•
<mark>G 1</mark> G2 U4 A5 G7 C8 C8 C8	A10 U12 U12 A13 A13 A13 C16 C16 C16 C16 C16 C16 C16 C25 C22 C22 C22 C22 C22 C22 C22 C22 C22	6 020 031 032 033 033 033 033 033 033 044 044	451 452 453 453 655 655 658 058 058
61 663 665 66 66 70	71 77 77 77 77 88 88 88 88 88 88 88 88 88	1111 1111 1111 1111 1111 1110 1110 111	1114 1114 1115 1118 1118 1119 121
	A < B C C D C C C D D A < C C D D C A     A	, , , , , , , , , , , , , , , , , , ,	
G122 G123 G124 G124 A125 A126 C128 C128 C128 C120 C120	M33 (1332) (1332	M152 M153 M154 M154 M154 M156 M169 M161 M161 M161 M161 M165 M166 M166 M166	A173 0174 0175 0177 0177 0177 0180 0180 0181 0181
C183 C184 G187 G187 G188 A190 A191 C192	01193 1194 1195 1197 1197 1197 1197 1197 1197 1197	4213 4213 4213 4213 4215 4215 4216 4216 4220 4220 4226 4221 4226 4226 4226 4226 4226 4228 4228 4228	0234 0235 0236 0236 0237 0238 0239 0239 0241 0243 0243
44 48 48 50 50 50 50 50 50 50 50 50 50 50 50 50	555 556 556 557 556 557 556 558 558 558 559 559 559 559 559 559 559	74 76 88 88 88 88 88 88 88 88 88 88 88 88 88	6 8 8 8 8 8 4 8 8 8 8 8 8 8 4 8 8 8 8 8 8
22 23 23 23 23 23 23 23 23 23 23 23 23 2	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 8 9 9 8 9 8 9 8 9 8 9 9 9 9 9 9 9 9 9	2 3 3 3 8 9 8 9 8 8 8 8 8 8 8 8 8 8 8 8 8
U306 G307 G308 A309 A310 A311 C312 G313 C314	6315 6315 6317 6318 6319 6319 6318 6326 6326 6326 6327 6327 6327 6327 6327	C335 C335 C336 C336 C336 C336 C337 C337 C343 C340 C343 C343 C343 C343 C344 C344	C397 C356 C356 C3561 C3661 C3665 C3665 C3665 C3665
G367 A368 A368 G370 G371 G372 U373 A374 A374 G375	6376 6377 6379 6379 6379 6379 6381 6381 6381 6385 6385 6385 6385 6385 6385 6385 6385	6395 6395 0395 0395 0396 0396 0399 0408 0408 0408 0408 0408 0408 0411 0415 0413 0415 0414 0415 0414 0415 0414 0415 0414 0415 0414 0415 0414 0415 0414 0415 0416 0416 0416 0416 0416 0416 0416 0416	C417 C418 C418 C420 C421 C421 A422 A423 G423 G423 G425 C425
U427 A428 A429 A430 U431 U434 U434 C433 C435	0.436 0.438 0.438 0.438 0.440 0.441 0.441 0.444 0.445 0.444 0.445 0.444 0.4450	C455 A457 A457 A456 A456 A456 A456 A466 A466 A466 A473 A472 A472 A472 A472 A472 A472 A472 A472	A4 1 A478 A479 A480 G481 A482 A482 C485 C485 C485 C485
<mark>⊱ 88</mark> 95 0 <del>1</del> 07 09 _ 90	<u>୵୭୭୨</u>	<u>오 년 월 일 김 김 김 국 관 중 년 월 9 월 4 영 9 국 명</u> 6 6 <b>6</b> 6	ល្ <mark>លី 0 ក ល ៧ ៧ ២</mark> ៧ ៧ ២
C46 G46 G46 G46 G49 G49 G49 G49 G49 G49	A44 GGG GGG A55 A55 A55 A55 A55 C51 A55 C51 A51 A51 A51 A51 A51 A51 A51 A51 A51 A		454 655 655 655 754 754 654 054 054 054



322         4670         460         460           733         6673         6613         613           735         6673         6613         613           735         6673         6613         613           736         6673         6613         613           739         6675         6613         613           739         6675         6613         613           743         7675         6613         613           745         6614         6613         613           746         6693         6613         613           746         6693         6613         613           746         6693         6613         613           747         0.6693         6633         623           746         6693         6633         623           746         6693         6633         633           753         6693         633         633           754         0683         633         633           754         6693         633         633           754         6634         633         633           754         6634	C(787         A722         C(660           A788         (723         C(660           U790         (723         C(660           U790         (725         C(660           U791         (725         C(660           U792         (725         C(664           A792         (725         C(664           A793         (725         C(665           A794         (729         C(665           A794         (729         C(665           A794         (729         C(665           A796         (729         C(666           A793         (729         C(666           A794         (729         C(666           A796         (739         C(666           A796         (739         C(666
322         670           733         6670           734         6671           735         6673           736         6674           737         6673           738         6674           739         6674           739         6673           746         6674           739         6674           741         6674           742         6674           743         6674           744         6674           745         6684           746         6684           746         6684           746         6684           755         6691           756         6692           756         6692           756         6693           756         6691           756         6692           756         6700           756         6700           756         6711           771         0702           771         0702           770         0712           771         0714 <trtd>7716           7716</trtd>	C(787 A722 A788 C723 A789 C723 U790 C724 U791 G724 A792 G726 A793 G726 A794 G729 A794 G729 A730 C796 A730 C796 C731
232 233 233 233 233 233 233 233 233 233	C787 A788 U790 C791 A792 A793 A793 C795 C795 C796
00044000000000000000000000000000000000	
A 800 A 800 G 801 G 805 G 815 G 815G 815 G 815	A849 U850 U851 U852 U852 C853 C854 C855 G855 G855 G855 G857 G858 G858
C 2859 C 2859 C 2856 C 2855 C 2855 C 2855 C 2855 C 2855 C 2855 C 2855 C 2855 C 2855 C 2875 C 2855 C 2875 C 2876 C 2875 C 2875 C 2875 C 2875 C 2875 C 2875 C 2875 C 2875 C 2876 C	A909 A910 C911 C913 U913 C914 C915 C915 C915 A918 A918
0919 4920 4922 6923 6923 6926	U970 6971 6973 6973 6974 6975 6975 6976 8979 8981
C982 C982 C985 C985 C985 C986 C986 C986 C986 C986 C986 C991 C992 C992 C992 C992 C993 C995 C994 A1002 C1006 C1006 C1006 C1006 C1006 C1006 C1006 C1006 C1006 C1006 C1005 C1015 C1006 C1015 C1015 C1006 C1025 C105 C1055 C1	41032 U1033 01034 01035 01035 01037 01037 01038 A1039 A1040
C1043 C1044 C1044 C1045 C1045 C1045 C1046 C1046 C1046 C1046 C1055 C1075	<b>G1093</b> 11094 <b>A1095</b> A1095 A1097 G1099 G1099 C1100 C1102 C1102
A103 C104 C104 U105 C104 U1105 C1104 C1106 C1106 C1106 C1108 C1112 C1112 C1112 C1114 C1112 C1114 C1112 C1128 C128 C	C1153 C1155 A1155 A1155 A1155 C1156 C1156 C1158 C1159 C1159 C1161 C1161 C1162 C1161
G1163         G1163           C1164         C1164           C1165         C1166           C1166         C1166           C1167         C1166           G1166         G1166           G1167         C1167           G1170         G1171           G1171         G1173           G1173         G1176           G1174         G1176           G1176         G1177           G1180         G1181           G1181         G1186           G1181         G1181           G1182         G1181           G1184         G1181           G1187         G1186           G1188         G1181           G1189         G1181           G1189         G1180           G1190         G1180           G1191         G1191           G1192         G1193           G1193         G1193           G1194         G1193           G1195         G1193           G1196         G1193           G1197         G1193           G1198         G1193           G1199         G1194           G1190 <td>A1213 A1214 G1216 G1216 G1216 G1218 U1219 C1220 C1221 U1222</td>	A1213 A1214 G1216 G1216 G1216 G1218 U1219 C1220 C1221 U1222
61223 01224 01224 01224 01225 01229 01231 01231 01233 01231 01233 01233 01233 01235 01235 01256 01267 01266 01266 01266 01267 01266 01267 01266 01266 01267 01266 01266 01267 01266 01266 01267 01266 01266 01266 01266 01267 01266 01267 01266 01266 01266 01266 01266 01266 01266 01267 01266 01267 01266 01266 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 01267 01266 0000000000	A1275 A1276 G1277 C1278 G1281 U1282 G1281 A1285 A1285
A 1286 A 1287 A 1287 C 1289 C 1289 C 1292 C 1292 C 1295 C 1395 C 1335 C 1355 C 13555 C 13555 C 13555 C 13555 C 135555 C 135555 C 135555 C 1355	A1336 61337 01340 01341 61341 A1342 01343 01344 01344 01346
A1347 A1347 C1348 C1348 C1348 C1349 C1349 C1357 C1356 G1357 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1356 G1357 G1358 G1358 G1358 G1356 G1358 G1357 G1358 G136 G1358 G	G1401 11402 A1403 C1404 U1406 U1406 G1406 G1400 G1408 G1410 G1410
11441 11445 11445 11445 11445 11445 11445 11445 11445 11442 11422 11422 11422 11422 11422 11423 11423 114445 114445 114445 11445 11445 11445 11445 11445 11445 11445 11445	21463 21464 21465 21465 11467 11467 11467 11470 11470 11471
1473       1475       1476       1476       1476       1476       1476       1476       1476       1448       1458       1458       1518       1518       1518       1518       1518       1518       1518       1518       1518 <th>4525 11526 14528 14528 14531 14531 14531 14531 14532 14532 14533 14533 14533 14533 14533 14533</th>	4525 11526 14528 14528 14531 14531 14531 14531 14532 14532 14533 14533 14533 14533 14533 14533



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	G1537	G1536	01539 01540	C1541	01542 01542	A1544	A1545	G1546 C1547	A1548	A1549	C1550	A1552	A1553	01554	C1556	C1557	C1558	G1560	C1561		C1565	A1566	G1567	41565 A1565	A1570	A1571	G1573	C1574	C1575	C1577	U1578	A1580	G1581	C1582 A1583	U1584	C1585	A1586 C1587	G1586	U1589	A1590 A1591	C1592	A1593	C159E
A1030	A1537 A1598	U1599	C1600 C1601	U1602	A1603	C1605	C1606	C1607 A1608	A1609	A1610	C1611 C1612	G1613	A1614	C1615 A1616	C1617	A1618	G1619	01621	G1622	G1623	01624 C1625	A1626	G1627	61628 U1629	A1630	G1631	G1633	A1634	A1635 111636	A1637	C1638	C1633 A1640	A1641	G1642 G1643	C1644	G1645	C1646 111647	01048 U1648	G1649	A1650 G1651	A1652	G1653	A1004 A1655
01000	C1658	G1659	G1660 G1661	U1662	G1663 A1664	A1004 A1665	G1666	G1667 A1668	A1669	C1670	U1671 A1672	G1673	G1674	C1675 A1676	A10/0 A1677	A1678	A1679 111680	01000 G1681	G1682	U1683	G1685	C1686	G1687	01688 A1689	A1690	C1691	01692 U1693	C1694	G1695	G1697	A1698	A1700	A1701	G1703	C1704	A1705	C1706	C1708	U1709	G1710 A1711	U1712	A1713	U1716
01210 11/14	G1719 G1719	U1720	G1721 A1722	G1723	G1724 111725	C1726	C1727	01728 01729	C1730	G1731	C1732 C1733	G1734	A1735	01736	G1738	A1739	G1740	U1742	G1743	A1744	A1745	U1747	C1748	A1/49 G1750	U1751	C1752	61753 A1754	A1755	G1756 A1757	U1758	A1759	C1761	A1762	G1763 C1764	U1765		C1768 111769	G1770	C1771	A1772 A1773	C1774	U1775	01777
01/10	A1780	U1781	01782 A1783	A1784	A1785 A1786	A1787	C1788	A1789 C1790	A1791	G1792	C1793 A1794	C1795	<mark>U1796</mark>	G1797 111708	01/90 G1799	C1800	A1801	A1602 A1803	C1804	A1805	G1807	A1808	A1809	A1810 G1811	U1812	G1813	41814 A1815	C1816	G1817 111818	01010 A1819	U1820	A1021 C1822	G1823	61824 11825	G1826	U1827	G1828 A1820	C1830	G1831	C1832 C1833	U1834	G1835	C1837
	G1840	U1841	G1842 C1843	C1844	G1845 C1846	A1847	A1848	G1849 G1850	U1851	U1852	A1853 A1854	01855	U1856	G1857 A1050	A1030 U1859	G1860	G1861	G1863	U1864	U1865	G1867	C1868	G1869	C1870 A1871	A1872	G1873	C1875 G1875	A1876	A1877 C1878	C1879	U1880	U1882	U1883	G1884 A1885	01886	C1887	G1888 A1880	A1890	G1891	C1892 C1893	C1894	C1895	61897
01030	A1000	A1901	C1902 G1903	G1904	C1905 C1906	G1907	C1908	C1909 G1910	U1911	A1912	A1913 C1914	3TD1915	A1916	U1917 A1018	A1919 A1919	C1920	G1921	01923 U1923	C1924	C1925	01920 A1927	A1928	G1929	G1930 U1931	A1932	G1933	G1935	A1936	A1937 A1938	N1939 U1939	U1940	C1942	U1943	01944 G1945	01946	C1947	G1948	A1952	A1953	G1954 111955	01956	C1957	61959
DOGT W	C1962	U1963	G1964	C1965 A1966	C1967	G1968 A1969	A1970	U1971	G1973	C1974	G1975	01976 01077	A1978		A1981 114087	20010	C1985	C1986	G1988	G1989	C1990	61992 G1992	U1993	C1994	01995 C1996	C1997	A1998	C2000	C2001	G2002 A2003	G2004	A2005	U2007	C2008	A2009 G2010	U2011	G2012	A2013	A2015	U2016	02017 G2018	A2019	A2020 C2021
22020	G2024	C2025	U2026 G2027	U2028	G2029	A2031	G2032	A2033 112034	G2035	C2036	A2037 G2038	U2039	G2040	U2041	C2043	C2044	C2045	G2040 C2047	G2048	G2049	A2051	A2052	G2053	A2054 C2055	G2056	G2057	A2058 A2059	A2060	G2061 A2062	R2063	C2064	C2066	G2067	02068 G2069	A2070	A2071	C2072 C2073	U2074	U2075	U2076 42077	C2078	U2079	аzuau U2081
2002A	C2084	U2085	U2086 G2087	A2088	C2089	C2091	U2092	G2093 A2094	A2095	C2096	A2097 112098	U2099	G2100	A2101	G2103	C2104	U2105	02100 G2107	A2108	U2109	U2111	G2112	U2113	A2114 G2115	G2116	A2117	02118 A2119	G2120	G2121	77170	A2126	G2128	C2129	U2130 112131	U2132	G2133	A2134 A2135	G2136	U2137	G2138 112139	G2140	G2141	AZ142 C2143
	C2145 C2146	A2147	G2148 U2149	C2150	U2151 62152	C2153	A2154	02155	A2158	G2159	C2160 C2161	G2162	A2163	C2164	U2166	U2167	G2168	A2109 A2170	A2171	U2172	C2174	C2175	A2176	C2177 C2178	C2179	U2180 112181	U2181 U2182	A2183	A2184	G2186	U2187	U2180 U2189	G2190	A2191 112192	G2193 G2193	U2194	U2195 C2196	U2197	A2198	A2199 C2200	G2201	U2202	62204
5022A	C2207	C2208	G2209 U2210	A2211	A2212 112213	C2214 C2214	C2215	62216	U2219	U2220	G2221 C2222	G2223	G2224	A2225	02220 A2227	G2228	U2229	U2231	C2232	U2233	G2235	U2236	G2237	G2238 G2239	U2240	A2241	02243 02243	U2244	U2245 C2246	42247 A2247	C2248	02250 G2250	G2251	G2252 G2253	C2254		C2258	C2260	C2261	U2262 C2263	C2264	U2265	A2267
00774	42270 A2270	G2271	U2272 A2273	A2274	C2275 C2776	G2277	A2278	G2279 G2280	A2281	G2282	C2283	C2285	<mark>G2286</mark>	A2287	G2289	G2290	U2291	G2294	C2295	U2296	A2298 A2298	U2299	C2300	U2301 U2302	G2303	G2304	02306 C2306	G2307	(12308 112308	62310 C2310	A2311 112310	02313 C2313	A2314	40317		U2320	U2321 A7377	G2323	U2324	G2325 C2326	A2327	A2328	02329 G2330
	A2333	U2334	A2335 A2336	G2337	C2338	A2340	G2341	C2342	G2345	A2346	C2347 112348	G2349	<mark>C2350</mark>	G2351	62353	C2354	G2355	02357 G2357	A2358	C2359	G2361	c2362	G2363	C2364 G2365	A2366	G2367	62368 A2369	-	G2373	G2375	A2376	A2371 A2378	G2379	C2380 42381	G2382	G2383	U2384 C7385	A2386	U2387	A2388 G2389	U2390	G2391	A2392 U2393
	62396	G2397	02398 G2399	G2400	U2401	02403 C2403	U2404	G2405 A2406	A2407	U2408	G2409	A2411	A2412	G2413	G2415	C2416	C2417	N2419 U2419	C2420	G2421	U2423	C2424	A2425	A2426 C2427	G2428	G2429	A2430 U2431	A2432	A2433	A2435	G2436	U2438	A2439	C2440	C2442	C2443	G2444 C2445	G2446	G2447	A2448 112449	A2450	A2451	CZ452 A2453



	U2457	G2458	A2459	U2460	A2461	C2462	C2403	C2465	C2466	C2467	A2468	A2469	G2470	A2471	G2472	024/3	C2475	A2476	U2477	A2478	U2479	C2480	G2481	A2482	0.2483	G 2485	C2486	G2487	G2488	02489	112490	U2492	U2493	G2494	G2495	C2496	C:2498	C2499	<b>U2500</b>	C2501	G2502	A2503	U2504	U2505	02900	G2508	G2509	C2510	U2511	C2512	A2513 U2514
C2515	A2516 C2517	A2518	U2519	C2520	C2521	0.2522	COROR	C2527	U2528	G2529	A2530	A2531	G2532	U2533	A2534	62030 77536	112537	C2538	C2539	C2540	A2541	A2542	1	62545	02547 07547	N2548	G2549	<mark>G2550</mark>	C2551	U2552	62553 117554	02555 02555	C2556	G2557	C2558	C2559	112561	U2562	U2563	A2564	A2565	A2566	G2567	02568	02303 02670	U2571	A2572	C2573	G2574	C2575	G2576 A2577
G2578	U2580	G2581	G2582	G2583	02584	0'2585 1175 86	02000 02587	G2588	A2589	A2590	C2591	G2592	U2593	C2594	G2595	A 75 00	62599	A2600	C2601	A2602	G2603	U2604	U2605	C2606	0.2601	02609	C2610	C2611	C2612	02613	A2614 110615	C2616	U2617	G2618	C2619	C2620	12622	G2623	G2624	G2625	C2626	G2627	C2628	U2629	62030 67631	42632 A2632	G2633	A2634	A2635	C2636	0'2637 G2638
A2639	G2640 G2641	G2642	G2643	G2644	G2645	C2646	02041 G2648	C2649	U2650	C2651	C2652	<mark>U2653</mark>	A2654	G2655	U2656	A 2057	02030 02659	A2660	G2661	A2662	G2663	G2664	A2665	0.2666	C2007	62669	A2670	G2671	U2672	G2673	62674 A 7675	C2676	G2677	C2678	A2679	02680	42682	C2683	U2684	G2685	G2686	U2687	G2688	U2689	02030	G2692	G2693	G2694	U2695	U2696	G2697 U2698
C2699	A2100	C2703	C2704	A2705	A2706	02708	00120 C2709	C2710	A2711	C2712	U2713	G2714	C2715	C2716	C2717	01/79	112720	A2721	G2722	C2723	U2724	A2725	A2726	A2727	02/20	C2730	G2731	G2732	A2733	A2734	62735 10736	G2737	A2738	U2739	A2740	A2741	112743	G2744	C2745		A2748	A2749	A2750	62750	02102 A7763	U2754	C2755	U2756	A2757	A2758	G2759 C2760
A2761	G2763	A2764	A2765	A2766	C2767	U2760	02109 C2770	C2771	C2772	C2773	C2774	G2775	A2776	G2777	A2778	07/19	42781	G2782	U2783	U2784	C2785	U2786	C2787	C2/88	112790	G2791	A2792	C2793	C2794	02795	U2796	U2798	A2799	A2800	G2801	G2802	112804	C2805	C2806	U2807	G2808	A2809	A2810	67040	42012 10813	A2814	C2815	G2816	U2817	U2818	G2819 A2820
A2821	42822 A2823	C2824	G2825	A2826	C2827	62828	62029 C2830	G2831	U2832	U2833	G2834	A2835	U2836	A2837	G2838	62839	C2040	G2842	G2843	G2844	U2845	G2846	U2847	6.2848	0.2849 A.2860	A 2030 A 2851	G2852	C2853	G2854	C2855	A2856 C2857	C2858	G2859	A2860	U2861	G2862	62864	U2865	U2866	G2867	A2868	G2869	C2870	17820	A2012	C2874	C2875	G2876	G2877	U2878	A2879 C2880
U2881	A2882 A2883	U2884	G2885	A2886	A2887	0.2888	02009 022890	112891	G2892	A2893	G2894	G2895	C2896	U2897	U2898	A2899	C2901	C2902	U2903	<b>U2904</b>																															
•	М	[0]	le	cι	ıl	е	58	8:		55	3	ri	b	os	0	m	al	[]	RI	N.	A																														
C	hε	ir	1	B	a:	•				18	%																6	4%	)													_	_	17	7%			•	,		
U1 00	C3 C3	C4	NO		80	69	010	C12	G13	U14	A15	G16	C17	G18	C19	620	120	623 G23	G24	U25	C26	C27	C28	A29	C30	U32	<b>G</b> 33	A34	C35	C36	C3/ C38	A39	U40	G41	C42	C43	445 A45	A46	C47	U48	C49	A50	G51	A52 A53	A J J	U55	<b>G56</b>	A57	A58	A59	C60 G61



# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98000	Depositor
Resolution determination method	FSC	Depositor
CTF correction method	group defocus	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose $(e^-/\text{\AA}^2)$	10	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	Not provided	
Maximum map value	253.190	Depositor
Minimum map value	-113.794	Depositor
Average map value	4.829	Depositor
Map value standard deviation	25.951	Depositor
Recommended contour level	22.0	Depositor
Map size (Å)	365.85, 365.85, 365.85	wwPDB
Map dimensions	135, 135, 135	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.71, 2.71, 2.71	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: 5MC, 1MG, UR3, 3TD, OMC, H2U, 2MA, OMG, 5MU, 4SU, PSU, 4OC, 2MG, 7MG, 6MZ, MA6, OMU

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	B	ond lengths	-	Bond angles
	Ullalli	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	AJ	0.75	0/742	1.26	7/941~(0.7%)
2	AK	0.79	0/856	1.39	14/1069~(1.3%)
3	AL	0.79	0/873	1.30	12/1110~(1.1%)
4	AM	0.79	0/817	1.45	20/1022~(2.0%)
5	AN	0.82	0/715	1.37	10/883~(1.1%)
6	AO	0.76	0/646	1.22	8/813~(1.0%)
7	AP	0.83	0/572	1.39	11/711~(1.5%)
8	AQ	0.72	0/636	1.16	6/822~(0.7%)
9	AR	0.92	0/568	1.46	12/713~(1.7%)
10	AS	0.77	0/687	1.27	10/880~(1.1%)
11	AB	0.74	0/1703	1.07	9/2161~(0.4%)
12	AT	0.75	0/574	1.25	12/694~(1.7%)
13	AU	0.94	0/520	1.61	15/636~(2.4%)
14	AC	0.75	0/1669	1.15	16/2122~(0.8%)
15	AD	0.80	0/1497	1.29	19/1890~(1.0%)
16	AE	0.73	0/1110	1.14	9/1405~(0.6%)
17	AF	0.79	0/1001	1.23	11/1268~(0.9%)
18	AG	0.79	0/1263	1.33	16/1590~(1.0%)
19	AH	0.72	0/896	1.11	7/1141~(0.6%)
20	AI	0.85	0/940	1.37	19/1180~(1.6%)
21	A1	0.76	0/4864	1.12	24/6363~(0.4%)
22	AA	1.47	6/36769~(0.0%)	2.38	2673/57354~(4.7%)
23	A2	1.48	0/1108	2.31	71/1724~(4.1%)
24	A3	1.49	0/1717	2.41	129/2675~(4.8%)
25	BC	0.68	0/1748	0.98	4/2355~(0.2%)
26	BJ	0.73	0/1247	1.15	10/1679~(0.6%)
27	BK	0.67	0/1046	1.00	4/1410~(0.3%)
28	BN	0.75	0/1152	1.11	11/1551~(0.7%)
29	BO	0.74	0/956	1.20	$\overline{13/1279}~(1.0\%)$
30	BP	0.79	0/1062	1.36	15/1413~(1.1%)
31	BQ	0.78	0/1093	1.24	13/1460~(0.9%)



Mol	Chain	B	ond lengths		Bond angles
WIOI	Ullalli	RMSZ	# Z  > 5	RMSZ	# Z  > 5
32	BR	0.79	0/1021	1.35	17/1364~(1.2%)
33	BS	0.76	0/910	1.23	14/1219~(1.1%)
34	BT	0.77	0/929	1.25	10/1242~(0.8%)
35	BD	0.75	0/2131	1.25	32/2863~(1.1%)
36	BU	0.80	0/960	1.29	15/1278~(1.2%)
37	BV	0.76	0/829	1.18	9/1107~(0.8%)
38	BW	0.67	0/864	1.10	12/1156~(1.0%)
39	BX	0.69	0/794	1.10	3/1060~(0.3%)
40	BY	0.69	0/797	1.04	4/1062~(0.4%)
41	ΒZ	0.73	0/766	1.11	6/1025~(0.6%)
42	B0	0.79	0/642	1.25	8/848~(0.9%)
43	B1	0.79	0/635	1.37	13/848~(1.5%)
44	B2	0.71	0/510	1.17	6/677~(0.9%)
45	BE	0.72	0/1586	1.14	15/2134~(0.7%)
46	B3	0.72	0/453	1.29	9/605~(1.5%)
47	B4	0.75	0/559	1.06	5/745~(0.7%)
48	B5	0.79	0/450	1.38	9/599~(1.5%)
49	B6	0.73	0/448	1.02	3/594~(0.5%)
50	B7	0.84	0/380	1.47	10/498~(2.0%)
51	B8	0.76	0/513	1.28	9/676~(1.3%)
52	B9	0.71	0/303	1.16	3/397~(0.8%)
53	BF	0.71	0/1571	1.09	13/2113~(0.6%)
54	BG	0.77	0/1444	1.18	10/1937~(0.5%)
55	BH	0.72	$0/1\overline{343}$	1.08	7/1816~(0.4%)
56	BL	0.70	0/1122	1.05	8/1515~(0.5%)
57	BA	1.47	5/69280~(0.0%)	2.39	5083/108078~(4.7%)
58	Ba	1.46	0/2869	2.35	$20\overline{8}/4474~(4.6\%)$
All	All	1.28	11/165156~(0.0%)	2.11	8751/244244 (3.6%)

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
3	AL	0	1
6	AO	0	1
7	AP	0	1
9	AR	0	1
10	AS	0	1
15	AD	0	1
18	AG	0	2



Mol	Chain	#Chirality outliers	#Planarity outliers
21	A1	0	2
22	AA	0	350
23	A2	0	5
24	A3	0	15
26	BJ	0	1
28	BN	0	2
29	BO	0	1
32	BR	0	1
34	BT	0	1
35	BD	0	1
36	BU	0	2
38	BW	0	1
40	BY	0	1
42	B0	0	1
51	B8	0	1
55	BH	0	2
57	BA	0	660
58	Ba	0	15
All	All	0	1070

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The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
22	AA	1223	С	C4-N4	-5.72	1.28	1.33
22	AA	1226	С	O3'-P	-5.66	1.54	1.61
22	AA	1432	G	C2-N2	-5.45	1.29	1.34
57	BA	823	С	C4-N4	-5.35	1.29	1.33
22	AA	1497	G	C2-N2	-5.32	1.29	1.34

The worst 5 of 8751 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
16	AE	111	ARG	NE-CZ-NH1	15.27	127.93	120.30
57	BA	1073	А	N1-C6-N6	-14.45	109.93	118.60
26	BJ	55	ARG	NE-CZ-NH1	14.31	127.46	120.30
57	BA	423	А	N1-C6-N6	-14.03	110.18	118.60
7	AP	70	ARG	NE-CZ-NH1	13.34	126.97	120.30

There are no chirality outliers.

5 of 1070 planarity outliers are listed below:



Mol	Chain	Res	Type	Group
3	AL	109	ARG	Sidechain
6	AO	88	ARG	Sidechain
7	AP	25	ARG	Sidechain
9	AR	2	ARG	Sidechain
10	AS	79	TYR	Sidechain

### 5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AJ	794	0	803	0	0
2	AK	923	0	912	0	0
3	AL	923	0	954	0	0
4	AM	876	0	910	0	0
5	AN	771	0	777	0	0
6	AO	690	0	691	0	0
7	AP	620	0	611	0	0
8	AQ	657	0	687	0	0
9	AR	603	0	602	0	0
10	AS	708	0	732	0	0
11	AB	1805	0	1750	0	0
12	AT	636	0	652	0	0
13	AU	564	0	579	0	0
14	AC	1761	0	1793	0	0
15	AD	1587	0	1596	0	0
16	AE	1182	0	1185	0	0
17	AF	1061	0	971	0	0
18	AG	1347	0	1347	0	0
19	AH	948	0	975	0	0
20	AI	1000	0	1011	0	0
21	A1	4989	0	4915	0	0
22	AA	33089	0	16668	0	0
23	A2	993	0	501	0	0
24	A3	1640	0	845	0	0
25	BC	1733	0	1824	0	0
26	BJ	1233	0	1283	0	0
27	BK	1032	0	1088	0	0
28	BN	1129	0	1162	0	0
29	BO	947	0	1023	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	BP	1053	0	1129	0	0
31	BQ	1074	0	1157	0	0
32	BR	1008	0	1045	0	0
33	BS	900	0	935	0	0
34	BT	917	0	965	0	0
35	BD	2092	0	2170	0	0
36	BU	947	0	1022	0	0
37	BV	816	0	839	0	0
38	BW	857	0	922	0	0
39	BX	787	0	846	0	0
40	BY	789	0	847	0	0
41	BZ	753	0	780	0	0
42	B0	634	0	656	0	0
43	B1	625	0	655	0	0
44	B2	509	0	543	0	0
45	BE	1565	0	1616	0	0
46	B3	449	0	491	0	0
47	B4	549	0	552	0	0
48	B5	444	0	461	0	0
49	B6	441	0	485	0	0
50	B7	377	0	418	0	0
51	B8	504	0	574	0	0
52	B9	302	0	343	0	0
53	BF	1552	0	1619	0	0
54	BG	1420	0	1460	0	0
55	BH	1323	0	1374	0	0
56	BL	1111	0	1148	0	0
57	BA	62351	0	31378	0	0
58	Ba	2566	0	1302	0	0
All	All	154956	0	106579	0	0

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The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.



# 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	AJ	44/103~(43%)	40 (91%)	1 (2%)	3~(7%)	1	15
2	AK	57/128~(44%)	52 (91%)	5~(9%)	0	100	100
3	AL	64/123~(52%)	54 (84%)	8 (12%)	2(3%)	4	27
4	AM	56/117~(48%)	51 (91%)	4 (7%)	1 (2%)	8	40
5	AN	41/100 (41%)	37~(90%)	3 (7%)	1 (2%)	6	33
6	AO	44/88~(50%)	43~(98%)	1 (2%)	0	100	100
7	AP	34/82~(42%)	31 (91%)	3~(9%)	0	100	100
8	AQ	52/83~(63%)	48 (92%)	4 (8%)	0	100	100
9	AR	36/74~(49%)	34 (94%)	2~(6%)	0	100	100
10	AS	54/91~(59%)	53 (98%)	1 (2%)	0	100	100
11	AB	123/240~(51%)	114 (93%)	7 (6%)	2(2%)	9	44
12	AT	32/86~(37%)	30 (94%)	2~(6%)	0	100	100
13	AU	24/70~(34%)	18 (75%)	3 (12%)	3(12%)	0	5
14	AC	126/232~(54%)	122 (97%)	4 (3%)	0	100	100
15	AD	107/205~(52%)	102 (95%)	5(5%)	0	100	100
16	AE	89/166~(54%)	84 (94%)	4 (4%)	1 (1%)	14	52
17	AF	65/135~(48%)	61 (94%)	4 (6%)	0	100	100
18	AG	84/178~(47%)	79~(94%)	5~(6%)	0	100	100
19	AH	77/129~(60%)	70 (91%)	7 (9%)	0	100	100
20	AI	69/129~(54%)	63 (91%)	6 (9%)	0	100	100
21	A1	434/639~(68%)	390 (90%)	38 (9%)	6 (1%)	11	46
25	BC	232/234~(99%)	213 (92%)	18 (8%)	1 (0%)	34	72
26	BJ	162/164~(99%)	158 (98%)	3 (2%)	1 (1%)	25	66
27	BK	139/141~(99%)	133 (96%)	6 (4%)	0	100	100
28	BN	140/142~(99%)	131 (94%)	9 (6%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
29	BO	121/123~(98%)	107 (88%)	11 (9%)	3~(2%)	5	32
30	BP	142/144~(99%)	127~(89%)	13 (9%)	2(1%)	11	46
31	BQ	134/136~(98%)	126 (94%)	6 (4%)	2(2%)	10	46
32	BR	125/127~(98%)	112 (90%)	11 (9%)	2(2%)	9	44
33	BS	115/117~(98%)	115 (100%)	0	0	100	100
34	BT	112/114 (98%)	107 (96%)	3 (3%)	2(2%)	8	40
35	BD	270/272 (99%)	252 (93%)	15 (6%)	3 (1%)	14	52
36	BU	115/117~(98%)	108 (94%)	5 (4%)	2 (2%)	9	42
37	BV	101/103 (98%)	94 (93%)	4 (4%)	3 (3%)	4	28
38	BW	108/110 (98%)	103 (95%)	4 (4%)	1 (1%)	17	57
39	BX	98/100 (98%)	83 (85%)	12 (12%)	3 (3%)	4	27
40	BY	101/103~(98%)	97 (96%)	4 (4%)	0	100	100
41	BZ	92/94~(98%)	90 (98%)	2 (2%)	0	100	100
42	B0	82/84~(98%)	72 (88%)	6 (7%)	4 (5%)	2	20
43	B1	75/77~(97%)	69 (92%)	5 (7%)	1 (1%)	12	48
44	B2	61/63~(97%)	54 (88%)	7 (12%)	0	100	100
45	BE	207/209~(99%)	181 (87%)	20 (10%)	6 (3%)	4	29
46	B3	56/58~(97%)	53 (95%)	3 (5%)	0	100	100
47	B4	68/70~(97%)	62 (91%)	6 (9%)	0	100	100
48	B5	54/56~(96%)	50 (93%)	3 (6%)	1 (2%)	8	38
49	B6	52/54~(96%)	51 (98%)	1 (2%)	0	100	100
50	B7	44/46~(96%)	42 (96%)	2 (4%)	0	100	100
51	B8	62/64~(97%)	61 (98%)	1 (2%)	0	100	100
52	B9	36/38~(95%)	31 (86%)	3 (8%)	2 (6%)	2	19
53	BF	199/201~(99%)	186 (94%)	7 (4%)	6 (3%)	4	28
54	BG	176/178~(99%)	155 (88%)	15 (8%)	6 (3%)	3	26
55	BH	174/176~(99%)	157 (90%)	14 (8%)	3 (2%)	9	42
56	BL	147/149~(99%)	133 (90%)	13 (9%)	1 (1%)	22	63
All	All	5512/7062~(78%)	5089 (92%)	349 (6%)	74 (1%)	16	48

 $5~{\rm of}~74$  Ramachandran outliers are listed below:



Mol	Chain	Res	Type
21	A1	242	THR
21	A1	493	LYS
32	BR	13	ASN
35	BD	140	VAL
42	B0	40	ARG

#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	AJ	90/90~(100%)	88~(98%)	2(2%)	52	71
2	AK	98/98~(100%)	97~(99%)	1 (1%)	76	86
3	AL	103/103~(100%)	102~(99%)	1 (1%)	76	86
4	AM	95/95~(100%)	95~(100%)	0	100	100
5	AN	83/83~(100%)	82~(99%)	1 (1%)	71	83
6	AO	76/76~(100%)	74~(97%)	2(3%)	46	66
7	AP	65/65~(100%)	64~(98%)	1 (2%)	65	80
8	AQ	77/77~(100%)	75~(97%)	2(3%)	46	66
9	AR	64/64~(100%)	62~(97%)	2(3%)	40	62
10	AS	78/78~(100%)	74~(95%)	4(5%)	24	48
11	AB	198/198~(100%)	196~(99%)	2(1%)	76	86
12	AT	65/65~(100%)	65~(100%)	0	100	100
13	AU	60/60~(100%)	58~(97%)	2(3%)	38	61
14	AC	189/189~(100%)	181~(96%)	8 (4%)	30	54
15	AD	172/172~(100%)	168~(98%)	4 (2%)	50	70
16	AE	125/125~(100%)	119~(95%)	6 (5%)	25	51
17	AF	116/116 (100%)	111 (96%)	5 (4%)	29	53
18	AG	146/146~(100%)	143 (98%)	3 (2%)	53	72
19	AH	104/104~(100%)	101 (97%)	3 (3%)	42	64
20	AI	106/106~(100%)	102 (96%)	4 (4%)	33	57



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Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
21	A1	568/568~(100%)	559~(98%)	9 (2%)	62	79
25	BC	181/181~(100%)	174~(96%)	7 (4%)	32	56
26	BJ	122/122~(100%)	120~(98%)	2(2%)	62	79
27	BK	109/109~(100%)	106~(97%)	3~(3%)	43	65
28	BN	116/116~(100%)	110~(95%)	6 (5%)	23	48
29	BO	104/104~(100%)	95~(91%)	9 (9%)	10	31
30	BP	103/103~(100%)	96~(93%)	7 (7%)	16	41
31	BQ	109/109~(100%)	105 (96%)	4 (4%)	34	58
32	BR	103/103~(100%)	100 (97%)	3 (3%)	42	64
33	BS	87/87~(100%)	86~(99%)	1 (1%)	73	84
34	BT	99/99~(100%)	97~(98%)	2 (2%)	55	74
35	BD	217/217~(100%)	212 (98%)	5 (2%)	50	70
36	BU	89/89~(100%)	86 (97%)	3 (3%)	37	60
37	BV	84/84~(100%)	83~(99%)	1 (1%)	71	83
38	BW	93/93~(100%)	90~(97%)	3 (3%)	39	61
39	BX	84/84~(100%)	83~(99%)	1 (1%)	71	83
40	BY	84/84~(100%)	82 (98%)	2 (2%)	49	69
41	BZ	78/78~(100%)	77~(99%)	1 (1%)	69	81
42	B0	62/62~(100%)	56~(90%)	6 (10%)	8	27
43	B1	67/67~(100%)	66~(98%)	1 (2%)	65	80
44	B2	55/55~(100%)	54 (98%)	1 (2%)	59	77
45	BE	164/164~(100%)	163 (99%)	1 (1%)	86	92
46	B3	48/48 (100%)	48 (100%)	0	100	100
47	B4	62/62~(100%)	61 (98%)	1 (2%)	62	79
48	B5	47/47~(100%)	45 (96%)	2 (4%)	29	53
49	B6	48/48 (100%)	48 (100%)	0	100	100
50	B7	38/38~(100%)	37~(97%)	1 (3%)	46	66
51	B8	51/51~(100%)	51 (100%)	0	100	100
52	B9	34/34~(100%)	34 (100%)	0	100	100
53	BF	165/165~(100%)	161 (98%)	4 (2%)	49	69
54	BG	149/149~(100%)	141 (95%)	8 (5%)	22	47



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
55	BH	137/137~(100%)	132~(96%)	5(4%)	35 59
56	BL	114/114~(100%)	114 (100%)	0	100 100
All	All	5781/5781~(100%)	5629~(97%)	152 (3%)	49 66

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5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BW	60	HIS
54	BG	103	ILE
40	BY	46	LYS
45	BE	128	ARG
55	BH	154	GLU

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains identified.

### 5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	AA	1538/1542~(99%)	194 (12%)	57~(3%)
23	A2	46/47~(97%)	13 (28%)	1(2%)
24	A3	75/77~(97%)	12 (16%)	2(2%)
57	BA	2899/2904~(99%)	404 (13%)	115 (3%)
58	Ba	119/120~(99%)	11 (9%)	0
All	All	4677/4690 (99%)	634 (13%)	175 (3%)

5 of 634 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	AA	2	A
22	AA	3	А
22	AA	5	U
22	AA	6	G
22	AA	7	А

 $5~{\rm of}~175$  RNA pucker outliers are listed below:

Mol	Chain	Res	Type
57	BA	1325	U
57	BA	2062	А



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Mol	Chain	Res	Type
57	BA	1393	А
57	BA	1653	G
57	BA	2248	С

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

39 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).

Mol	Tuno	Chain	Dog	Tink	Bo	ond leng	ths	Bond angles		
	туре	Unain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
22	UR3	AA	1498	22	19,22,23	0.71	0	26,32,35	1.01	2 (7%)
24	PSU	A3	56	24	18,21,22	0.84	0	22,30,33	1.12	2 (9%)
24	4SU	A3	8	24	18,21,22	1.39	1 (5%)	26,30,33	1.16	2 (7%)
57	5MU	BA	1939	57	19,22,23	0.72	0	28,32,35	1.31	3 (10%)
57	PSU	BA	2504	57	18,21,22	0.78	0	22,30,33	1.15	2 (9%)
24	OMC	A3	33	24	19,22,23	0.70	0	26,31,34	1.09	1 (3%)
57	6MZ	BA	2030	57	18,25,26	0.92	1 (5%)	16,36,39	1.41	2 (12%)
57	PSU	BA	955	57	18,21,22	0.80	0	22,30,33	1.08	2 (9%)
57	6MZ	BA	1618	57	18,25,26	0.93	0	16,36,39	1.47	2 (12%)
57	PSU	BA	1911	57	18,21,22	0.83	0	22,30,33	1.03	2 (9%)
57	2MA	BA	2503	57	17,25,26	1.21	3 (17%)	17,37,40	1.60	3 (17%)
57	7MG	BA	2069	57	22,26,27	4.62	2 (9%)	29,39,42	1.41	1 (3%)
57	PSU	BA	2605	57	18,21,22	0.87	0	22,30,33	1.27	3 (13%)
22	2MG	AA	1207	22	18,26,27	1.01	2 (11%)	16,38,41	1.11	2 (12%)
57	2MG	BA	2445	57	18,26,27	0.96	2 (11%)	16,38,41	1.31	2 (12%)
57	H2U	BA	2449	57	18,21,22	1.14	2 (11%)	21,30,33	1.07	0
22	5MC	AA	1407	22	18,22,23	0.59	0	26,32,35	1.38	4 (15%)
57	5MC	BA	1962	57	18,22,23	0.57	0	26,32,35	1.51	5 (19%)
24	5MU	A3	55	24	19,22,23	0.67	0	28,32,35	1.33	4 (14%)
57	3TD	BA	1915	57	18,22,23	0.83	0	22,32,35	1.42	3 (13%)



Mal	Tuno	Chain	Dog	Tink	Bo	ond leng	ths	Bond angles		
	туре	Unain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
57	OMG	BA	2251	57	18,26,27	1.01	1 (5%)	19,38,41	1.32	3 (15%)
24	H2U	A3	21	24	18,21,22	1.04	2 (11%)	21,30,33	0.83	0
57	OMU	BA	2552	57	19,22,23	0.60	0	26,31,34	0.91	1 (3%)
22	PSU	AA	516	22	18,21,22	0.81	0	22,30,33	1.24	2 (9%)
57	1MG	BA	745	57	18,26,27	1.08	2 (11%)	19,39,42	1.10	1 (5%)
22	5MC	AA	967	22	18,22,23	0.61	0	26,32,35	1.44	4 (15%)
57	PSU	BA	2457	57	18,21,22	0.79	0	22,30,33	1.14	2 (9%)
22	2MG	AA	1516	22	18,26,27	0.93	1 (5%)	16,38,41	1.14	2 (12%)
57	5MU	BA	747	57	19,22,23	0.72	0	28,32,35	1.34	3 (10%)
57	PSU	BA	746	57	18,21,22	0.80	0	22,30,33	1.22	3 (13%)
22	MA6	AA	1519	22	19,26,27	0.95	2 (10%)	18,38,41	0.93	0
57	PSU	BA	2580	57	18,21,22	0.82	0	22,30,33	1.50	4 (18%)
22	7MG	AA	527	22	22,26,27	4.55	2 (9%)	29,39,42	1.47	2 (6%)
57	2MG	BA	1835	57	18,26,27	0.98	1 (5%)	16,38,41	1.15	2 (12%)
22	MA6	AA	1518	22	19,26,27	0.94	1 (5%)	18,38,41	0.89	0
22	2MG	AA	966	22	18,26,27	1.00	2 (11%)	16,38,41	1.28	2 (12%)
22	4OC	AA	1402	22	20,23,24	0.65	0	26,32,35	1.22	2 (7%)
57	PSU	BA	1917	57	18,21,22	0.78	0	22,30,33	1.13	2 (9%)
57	OMC	BA	2498	57	19,22,23	0.76	0	26,31,34	1.25	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	UR3	AA	1498	22	-	0/7/25/26	0/2/2/2
24	PSU	A3	56	24	-	2/7/25/26	0/2/2/2
24	4SU	A3	8	24	-	0/7/25/26	0/2/2/2
57	5MU	BA	1939	57	-	0/7/25/26	0/2/2/2
57	PSU	BA	2504	57	-	2/7/25/26	0/2/2/2
24	OMC	A3	33	24	-	0/9/27/28	0/2/2/2
57	6MZ	BA	2030	57	-	1/5/27/28	0/3/3/3
57	PSU	BA	955	57	-	0/7/25/26	0/2/2/2
57	6MZ	BA	1618	57	-	0/5/27/28	0/3/3/3
57	PSU	BA	1911	57	-	0/7/25/26	0/2/2/2
57	2MA	BA	2503	57	-	1/3/25/26	0/3/3/3
57	7MG	BA	2069	57	-	0/7/37/38	0/3/3/3



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	PSU	BA	2605	57	-	0/7/25/26	0/2/2/2
22	2MG	AA	1207	22	-	0/5/27/28	0/3/3/3
57	2MG	BA	2445	57	_	0/5/27/28	0/3/3/3
57	H2U	BA	2449	57	_	0/7/38/39	0/2/2/2
22	5MC	AA	1407	22	-	0/7/25/26	0/2/2/2
57	5MC	BA	1962	57	-	0/7/25/26	0/2/2/2
24	5MU	A3	55	24	-	0/7/25/26	0/2/2/2
57	3TD	BA	1915	57	-	1/7/25/26	0/2/2/2
57	OMG	BA	2251	57	-	0/5/27/28	0/3/3/3
24	H2U	A3	21	24	-	1/7/38/39	0/2/2/2
57	OMU	BA	2552	57	-	0/9/27/28	0/2/2/2
22	PSU	AA	516	22	-	0/7/25/26	0/2/2/2
57	1MG	BA	745	57	-	0/3/25/26	0/3/3/3
22	5MC	AA	967	22	-	0/7/25/26	0/2/2/2
57	PSU	BA	2457	57	-	0/7/25/26	0/2/2/2
22	2MG	AA	1516	22	-	0/5/27/28	0/3/3/3
57	5MU	BA	747	57	-	0/7/25/26	0/2/2/2
57	PSU	BA	746	57	-	0/7/25/26	0/2/2/2
22	MA6	AA	1519	22	-	0/7/29/30	0/3/3/3
57	PSU	BA	2580	57	-	0/7/25/26	0/2/2/2
22	7MG	AA	527	22	-	1/7/37/38	0/3/3/3
57	2MG	BA	1835	57	-	0/5/27/28	0/3/3/3
22	MA6	AA	1518	22	-	0/7/29/30	0/3/3/3
22	2MG	AA	966	22	-	0/5/27/28	0/3/3/3
22	4OC	AA	1402	22	-	0/9/29/30	0/2/2/2
57	PSU	BA	1917	57	-	0/7/25/26	0/2/2/2
57	OMC	BA	2498	57	-	1/9/27/28	0/2/2/2

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The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
57	BA	2069	7MG	C8-N9	-21.38	1.34	1.46
22	AA	527	7MG	C8-N9	-21.04	1.34	1.46
24	A3	8	4SU	C5-C4	-4.96	1.36	1.42
57	BA	2449	H2U	C4-N3	-3.07	1.32	1.37
57	BA	2449	H2U	C2-N3	-2.94	1.32	1.38

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
57	BA	2069	7MG	N9-C8-N7	6.06	112.04	103.38
22	AA	527	7MG	N9-C8-N7	5.81	111.68	103.38



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
57	BA	2503	2MA	C5-C6-N1	4.24	121.33	114.02
57	BA	1618	6MZ	C9-N6-C6	4.04	126.35	122.87
57	BA	1915	3TD	C6-C5-C4	3.86	120.89	118.22

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There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A3	56	PSU	O4'-C1'-C5-C4
57	BA	2504	PSU	O4'-C1'-C5-C4
57	BA	2504	PSU	O4'-C4'-C5'-O5'
24	A3	56	PSU	O4'-C1'-C5-C6
57	BA	1915	3TD	O4'-C1'-C5-C6

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)

There are no ligands in this entry.

### 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-5562. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

# 6.1 Orthogonal projections (i)

#### 6.1.1 Primary map



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

### 6.2 Central slices (i)

#### 6.2.1 Primary map



X Index: 67



Y Index: 67



Z Index: 67

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: 70

Y Index: 71

Z Index: 73

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

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

#### 6.4.1 Primary map



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



### 6.5 Orthogonal surface views (i)

#### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 22.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.6 Mask visualisation (i)

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



# 7 Map analysis (i)

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

# 7.1 Map-value distribution (i)



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



# 7.2 Volume estimate (i)



The volume at the recommended contour level is  $3450 \text{ nm}^3$ ; this corresponds to an approximate mass of 3116 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 0.102  ${\rm \AA^{-1}}$ 



# 8 Fourier-Shell correlation (i)

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



# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-5562 and PDB model 4V6V. 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 22.0 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 (22.0).



# 9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (22.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.9700	0.1260
A1	0.9130	0.1120
A2	0.4660	0.0110
A3	0.9840	0.1530
AA	0.9950	0.1430
AB	0.9200	0.1050
AC	0.9110	0.0970
AD	0.9760	0.0960
AE	0.8840	0.0850
AF	0.8220	0.0930
AG	0.9590	0.1070
AH	0.9560	0.1020
AI	0.9750	0.0840
AJ	0.9580	0.0780
AK	0.8950	0.0910
AL	0.9260	0.0940
AM	0.9720	0.1100
AN	0.9470	0.0640
AO	0.9800	0.1040
AP	0.9730	0.0620
AQ	0.9630	0.1070
AR	0.9090	0.0770
AS	0.9540	0.0810
AT	0.9610	0.1110
AU	0.8750	0.0990
B0	0.9000	0.0370
B1	0.9550	0.0880
B2	0.9660	0.1380
B3	0.9660	0.1170
B4	0.8850	0.0850
B5	0.9300	0.0630
B6	0.9540	0.0900
B7	0.9270	0.0670
B8	0.9430	0.0620
B9	0.9520	0.0520



Continued from previous page...

Chain	Atom inclusion	Q-score
BA	0.9930	0.1450
BC	0.8760	0.0490
BD	0.9380	0.0750
BE	0.9420	0.0870
BF	0.9720	0.0950
BG	0.9730	0.0890
BH	0.9810	0.1240
BJ	0.8870	0.0810
BK	0.9790	0.0960
BL	0.7430	0.1000
BN	0.9590	0.0980
BO	0.9100	0.0960
BP	0.9510	0.0750
BQ	0.9500	0.0920
BR	0.9520	0.0900
BS	0.9760	0.0940
BT	0.9350	0.1020
BU	0.9660	0.0980
BV	0.9400	0.0990
BW	0.9250	0.0900
BX	0.9600	0.0890
BY	0.9600	0.1060
BZ	0.9730	0.1180
Ba	0.9960	0.1520

