



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:58 PM GMT

PDB ID : 1YJ9
Title : Crystal Structure Of The Mutant 50S Ribosomal Subunit Of Haloarcula Marismortui Containing a three residue deletion in L22
Authors : Tu, D.; Blaha, G.; Moore, P.B.; Steitz, T.A.
Deposited on : 2005-01-13
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

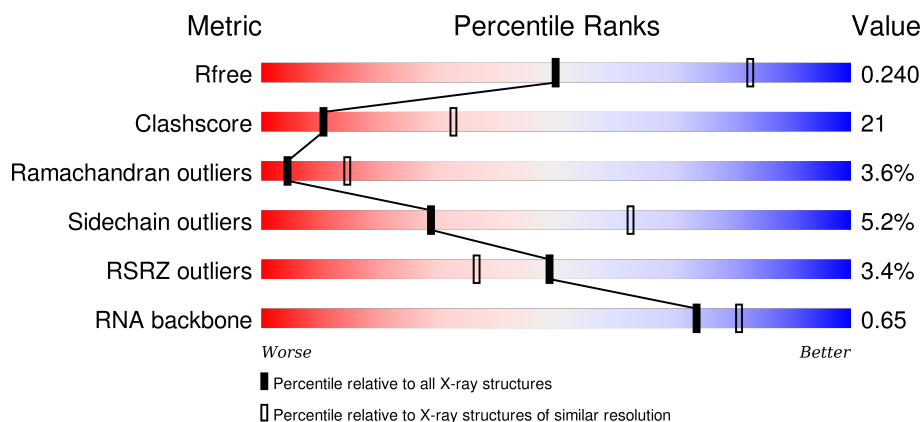
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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




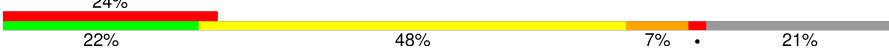

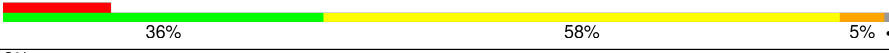
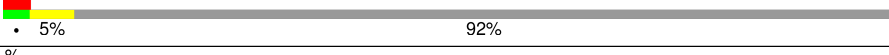
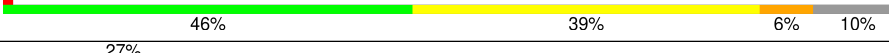



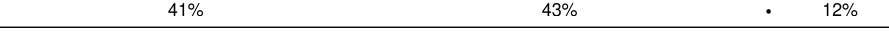
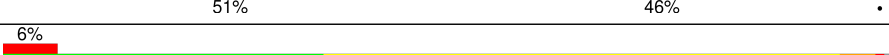


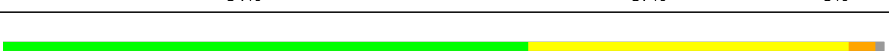

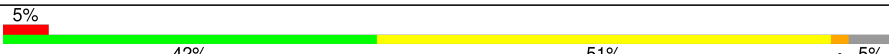
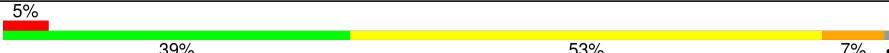




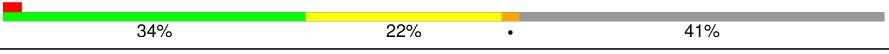



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)
RNA backbone	2183	1091 (3.20-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	2922	<div> <div>51%</div> <div>38%</div> <div>5%</div> <div>6%</div> </div>
2	9	122	<div>2%</div> <div>38%</div> <div>53%</div> <div>8%</div> <div>.</div>
3	A	240	<div>4%</div> <div>50%</div> <div>41%</div> <div>7%</div> <div>.</div>
4	B	338	<div>%</div> <div>43%</div> <div>49%</div> <div>8%</div>

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	177	
11	I	162	
12	J	145	
13	K	132	
14	L	165	
15	M	195	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	152	
21	S	85	
22	T	120	
23	U	66	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	83	
29	1	57	

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Mol	Chain	Length	Quality of chain
30	2	50	
31	3	92	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
32	MG	0	8038	-	-	-	X
32	MG	0	8064	-	-	-	X
33	K	0	8401	-	-	-	X
34	NA	0	8502	-	-	-	X
34	NA	0	8503	-	-	-	X
34	NA	0	8510	-	-	-	X
34	NA	0	8521	-	-	-	X
34	NA	0	8526	-	-	-	X
34	NA	0	8529	-	-	-	X
34	NA	0	8531	-	-	-	X
34	NA	0	8532	-	-	-	X
34	NA	0	8535	-	-	-	X
34	NA	0	8550	-	-	-	X
34	NA	0	8555	-	-	-	X
34	NA	0	8556	-	-	-	X
34	NA	0	8559	-	-	-	X
34	NA	0	8561	-	-	-	X
34	NA	0	8562	-	-	-	X
34	NA	0	8565	-	-	-	X
34	NA	0	8566	-	-	-	X
34	NA	0	8568	-	-	-	X
34	NA	0	8571	-	-	-	X
34	NA	0	8573	-	-	-	X
34	NA	0	8574	-	-	-	X
34	NA	0	8576	-	-	-	X
34	NA	0	8578	-	-	-	X
34	NA	0	8579	-	-	-	X
34	NA	0	8582	-	-	-	X
34	NA	9	8583	-	-	-	X
34	NA	L	8580	-	-	-	X
34	NA	M	8547	-	-	-	X
34	NA	R	8586	-	-	-	X
35	CL	0	8805	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	CL	0	8815	-	-	-	X
35	CL	0	8816	-	-	-	X
35	CL	B	8819	-	-	-	X
35	CL	J	8801	-	-	X	-
35	CL	J	8802	-	-	X	-
35	CL	O	8808	-	-	-	X

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 99031 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	1	0
			59041	26358	10875	19062	2746			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	628	1MA	A	MODIFIED RESIDUE	GB 55229667
0	2587	OMU	U	MODIFIED RESIDUE	GB 55229667
0	2588	OMG	G	MODIFIED RESIDUE	GB 55229667
0	2619	UR3	U	MODIFIED RESIDUE	GB 55229667
0	2621	PSU	U	MODIFIED RESIDUE	GB 55229667

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

- Molecule 3 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 4 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 5 is a protein called 50S ribosomal protein L4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

- Molecule 6 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 7 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 8 is a protein called 50S ribosomal protein L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 9 is a protein called ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	29	Total	C	N	O	S	0	0	0
			240	149	39	51	1			

- Molecule 10 is a protein called 50S RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 12 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 13 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	CONFLICT	UNP P22450

- Molecule 14 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	145	Total	C	N	O	S	0	0	0
			1118	670	222	226				

- Molecule 15 is a protein called 50S Ribosomal Protein L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	194	Total	C	N	O	S	0	0	0
			1558	942	332	283	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	CONFLICT	GB 55231501

- Molecule 16 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 17 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	O	115	Total	C	N	O	S	0	0	0
			865	529	161	175				

- Molecule 18 is a protein called 50S ribosomal protein L19E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	P	143	Total	C	N	O	0	0	0
			1136	683	229	224			

- Molecule 19 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	Q	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 20 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	147	Total	C	N	O	S	0	0	0
			1123	699	204	216	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	?	-	GLN	DELETION	UNP P10970
R	?	-	GLN	DELETION	UNP P10970
R	?	-	GLY	DELETION	UNP P10970

- Molecule 21 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	S	81	Total	C	N	O	S	0	0	0
			641	389	111	138	3			

- Molecule 22 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	T	119	Total	C	N	O	0	0	0
			950	568	180	202			

- Molecule 23 is a protein called 50S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 24 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 25 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 26 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 27 is a protein called 50S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y	142	Total	C	N	O	S	0	0	0
			1130	686	228	216				

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	CONFLICT	GB 55231162

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	49	Total	C	N	O	S	0	0	0
			421	254	93	73	1			

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	107	Total	Mg	0	0
			107	107		
32	Y	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	B	1	Total	Mg	0	0
			1	1		
32	A	2	Total	Mg	0	0
			2	2		
32	T	1	Total	Mg	0	0
			1	1		
32	2	1	Total	Mg	0	0
			1	1		
32	9	1	Total	Mg	0	0
			1	1		
32	3	1	Total	Mg	0	0
			1	1		

- Molecule 33 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	2	Total	K	0	0
			2	2		

- Molecule 34 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	74	Total	Na	0	0
			74	74		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	J	1	Total 1	Na 1	0	0
34	Q	1	Total 1	Na 1	0	0
34	C	1	Total 1	Na 1	0	0
34	A	1	Total 1	Na 1	0	0
34	T	1	Total 1	Na 1	0	0
34	R	2	Total 2	Na 2	0	0
34	9	2	Total 2	Na 2	0	0
34	L	1	Total 1	Na 1	0	0
34	S	1	Total 1	Na 1	0	0
34	M	1	Total 1	Na 1	0	0

- Molecule 35 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	9	Total 9	Cl 9	0	0
35	J	3	Total 3	Cl 3	0	0
35	Q	1	Total 1	Cl 1	0	0
35	B	1	Total 1	Cl 1	0	0
35	A	1	Total 1	Cl 1	0	0
35	N	1	Total 1	Cl 1	0	0
35	O	1	Total 1	Cl 1	0	0
35	R	1	Total 1	Cl 1	0	0
35	Y	1	Total 1	Cl 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	L	1	Total 1	Cl 1	0	0
35	3	1	Total 1	Cl 1	0	0
35	M	1	Total 1	Cl 1	0	0

- Molecule 36 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	O	1	Total 1	Cd 1	0	0
36	Z	1	Total 1	Cd 1	0	0
36	1	1	Total 1	Cd 1	0	0
36	3	1	Total 1	Cd 1	0	0
36	U	1	Total 1	Cd 1	0	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	0	5866	Total 5866	O 5866	0	0
37	9	143	Total 143	O 143	0	0
37	A	119	Total 119	O 119	0	0
37	B	148	Total 148	O 148	0	0
37	C	180	Total 180	O 180	0	0
37	D	46	Total 46	O 46	0	0
37	E	45	Total 45	O 45	0	0
37	F	27	Total 27	O 27	0	0
37	G	19	Total 19	O 19	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	H	69	Total 69	O 69	0	0
37	I	9	Total 9	O 9	0	0
37	J	57	Total 57	O 57	0	0
37	K	54	Total 54	O 54	0	0
37	L	84	Total 84	O 84	0	0
37	M	130	Total 130	O 130	0	0
37	N	64	Total 64	O 64	0	0
37	O	45	Total 45	O 45	0	0
37	P	64	Total 64	O 64	0	0
37	Q	53	Total 53	O 53	0	0
37	R	58	Total 58	O 58	0	0
37	S	34	Total 34	O 34	0	0
37	T	32	Total 32	O 32	0	0
37	U	26	Total 26	O 26	0	0
37	V	14	Total 14	O 14	0	0
37	W	72	Total 72	O 72	0	0
37	X	24	Total 24	O 24	0	0
37	Y	104	Total 104	O 104	0	0
37	Z	34	Total 34	O 34	0	0
37	1	63	Total 63	O 63	0	0
37	2	32	Total 32	O 32	0	0

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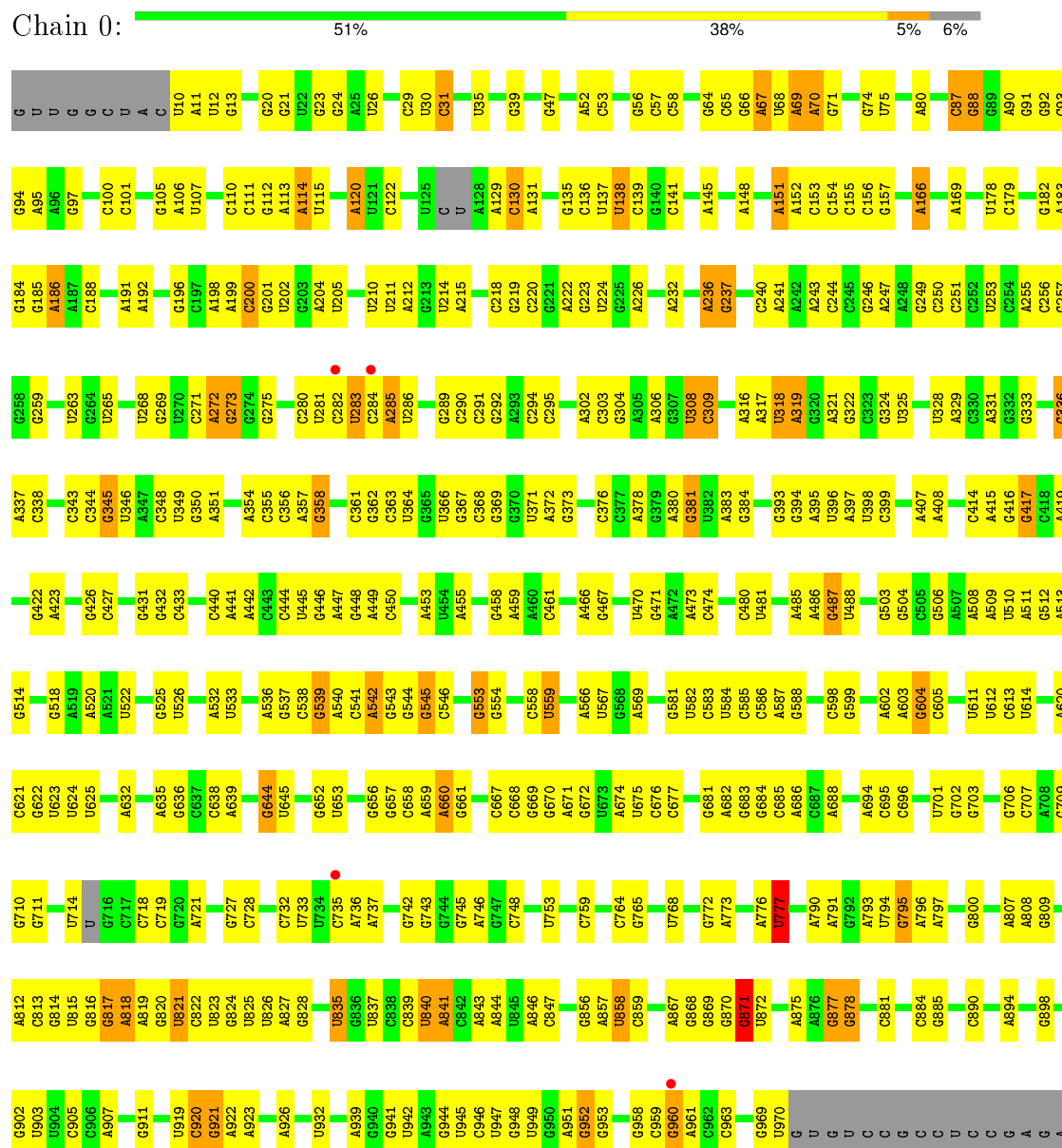
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	3	69	Total	O	0	0
			69	69		

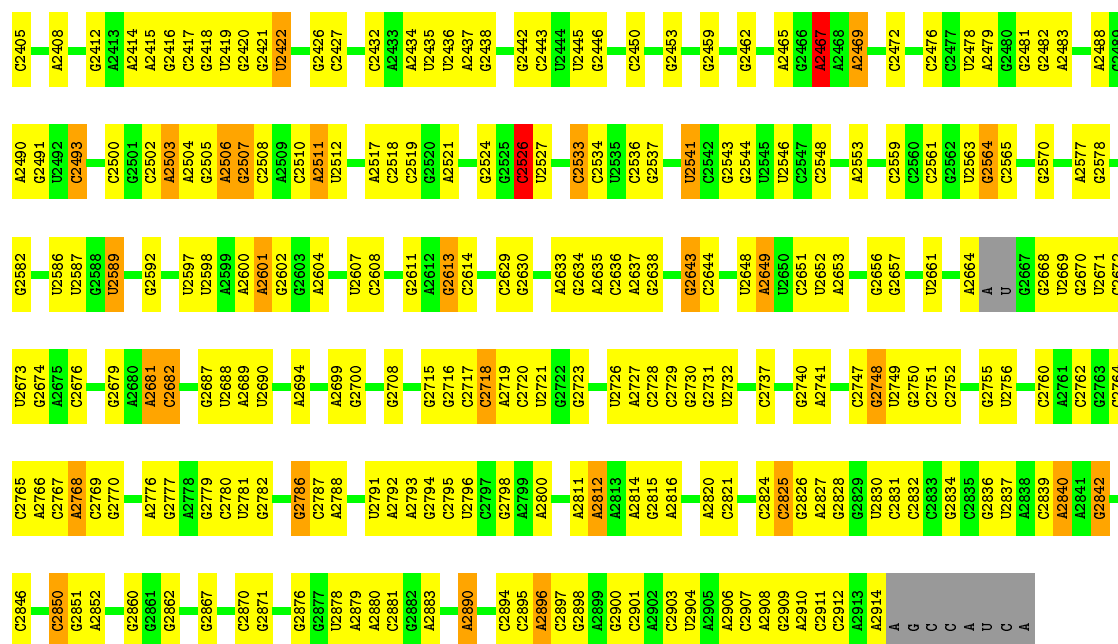
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

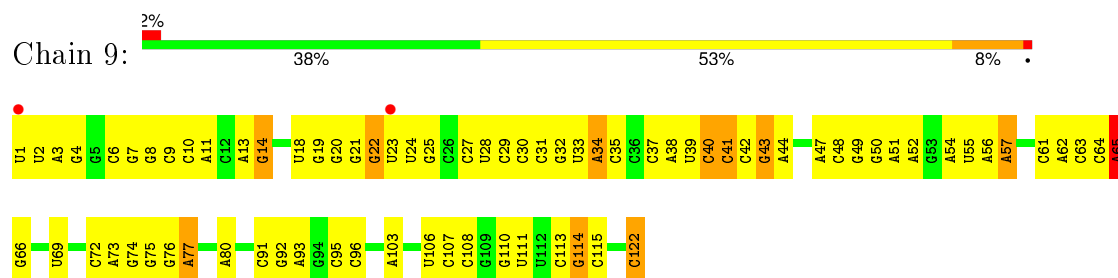
• Molecule 1: 23S Ribosomal RNA



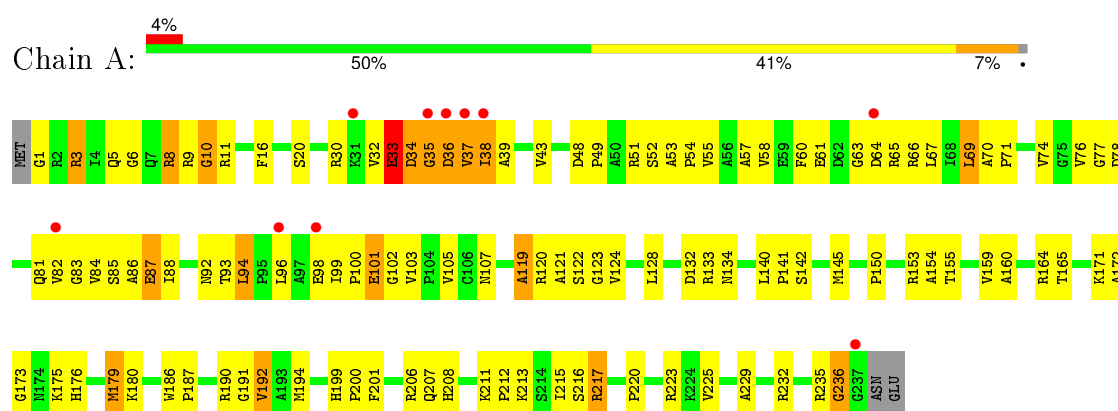




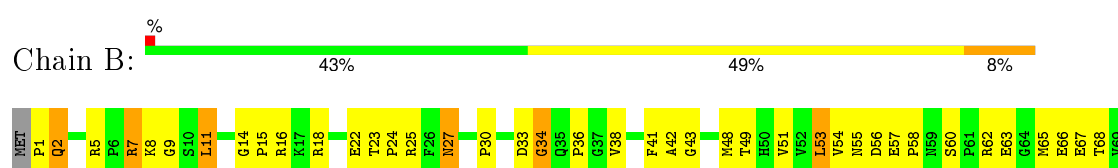
• Molecule 2: 5S Ribosomal RNA

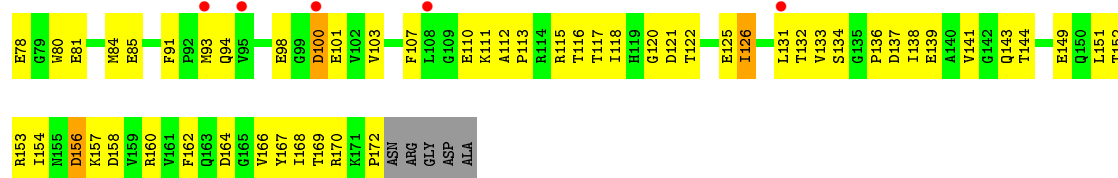


• Molecule 3: 50S ribosomal protein L2P

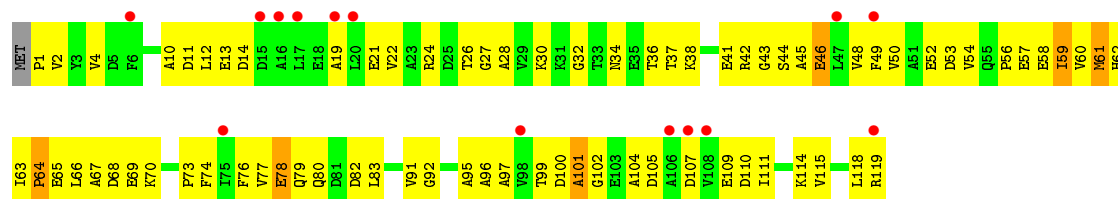


• Molecule 4: 50S ribosomal protein L3P

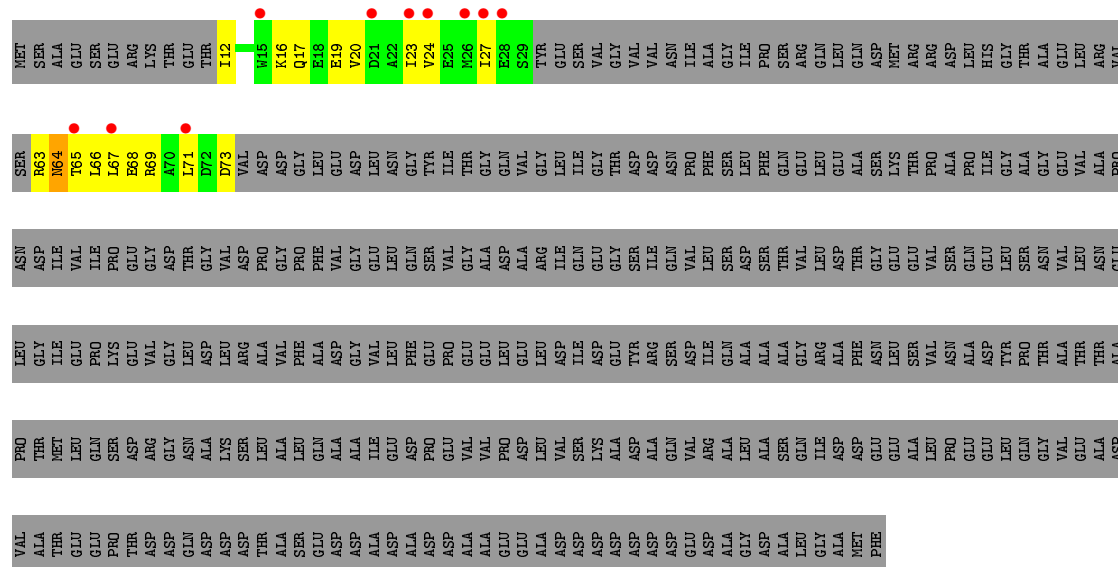




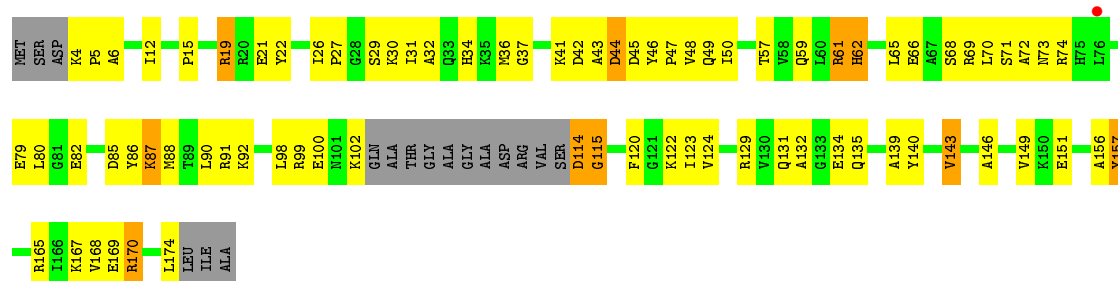
• Molecule 8: 50S ribosomal protein L7AE



• Molecule 9: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG



• Molecule 10: 50S RIBOSOMAL PROTEIN L10E

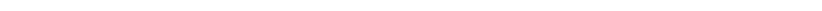


[illegible]

Chain J:

50% 43% 5%

MET SER VAL A4 E5 D7 A8 I11 G17 I18 M19 G20 R21 S24 G33 E34 T35 V36 V39 M40 A41 E42 R43 A44 V45 I46 T47 E51 Q52 I53 V54 E55 E58 M65 V69 F70 R74 P75 D76 G77 I78 F79 R80 R81 T82 I83 R84 Q85 M86

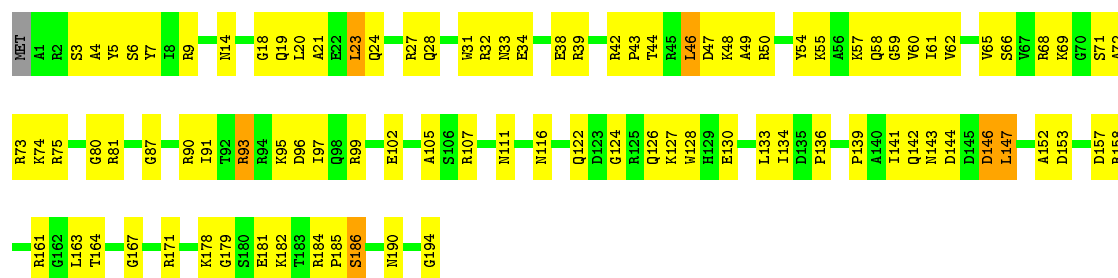
Chain K: 

Chain L:

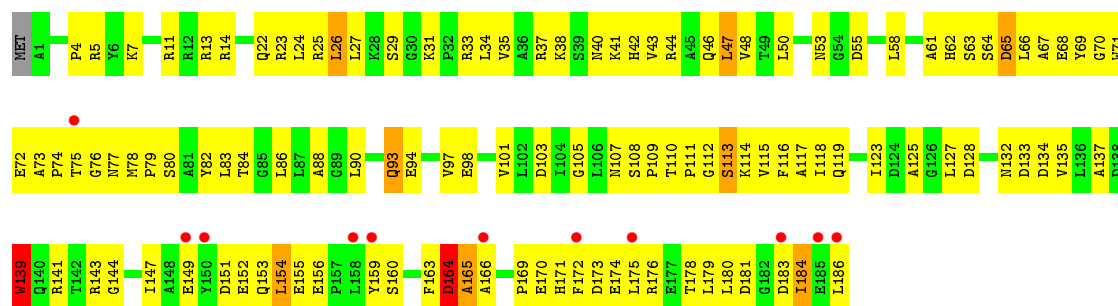
7% 41% 43% 12%

THR, GLU, ASP, ALA, ASP, ASP, ASP, ASP, ASP, GLU, MET, T1, K4, K5, R6, S17, H18, K19, R22, G25, H26, R30, G34, R35, D36, F40, H41, H42, H43, G50, P51, K52, R53, P54, K55, K56, V57, Q58, E59, E60, A61, D65, R66, R67, R68, I69, D70, E71, I72, V73, T74, L75, L76, A77, A78, D79, D80, V81, A82, E83, K132, V133, E134, G135, A136, G137, G138, S139, V140, E141, L142, T143, D144, G146, E147, E148, R149, Q150, ALA, GLU, ALA, GLU

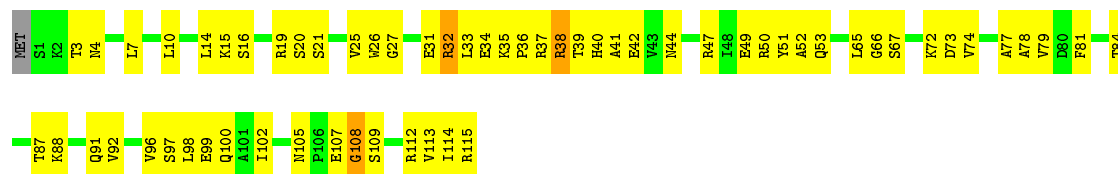
Chain M: 51% 46%



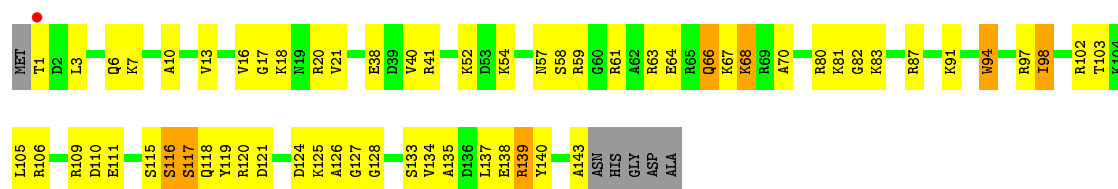
• Molecule 16: 50S ribosomal protein L18P



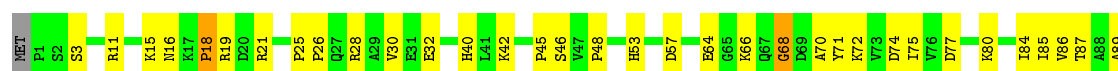
• Molecule 17: 50S ribosomal protein L18e

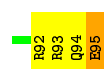


• Molecule 18: 50S ribosomal protein L19E

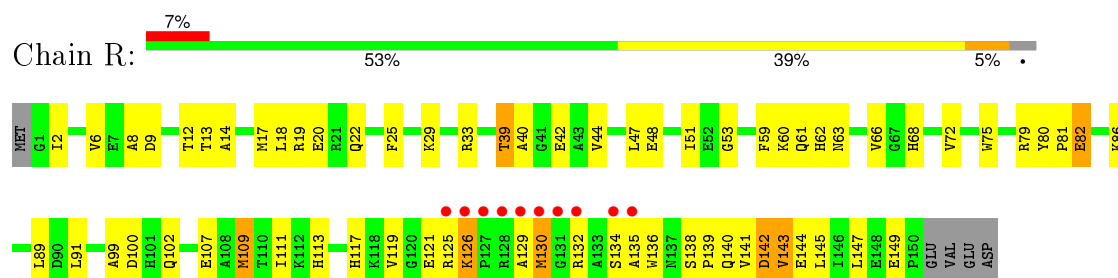


• Molecule 19: 50S ribosomal protein L21e

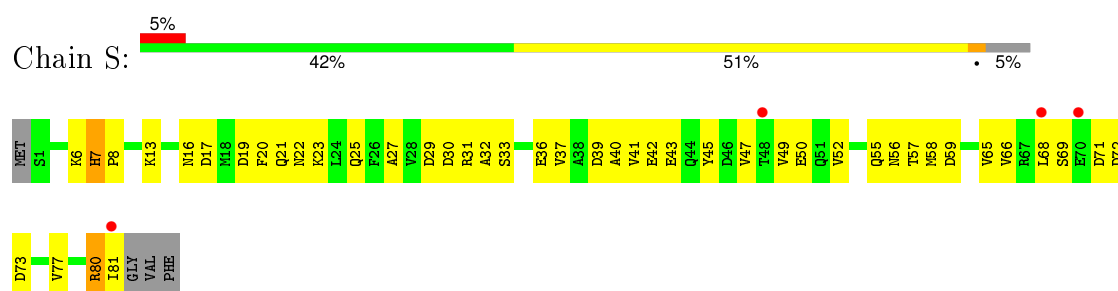




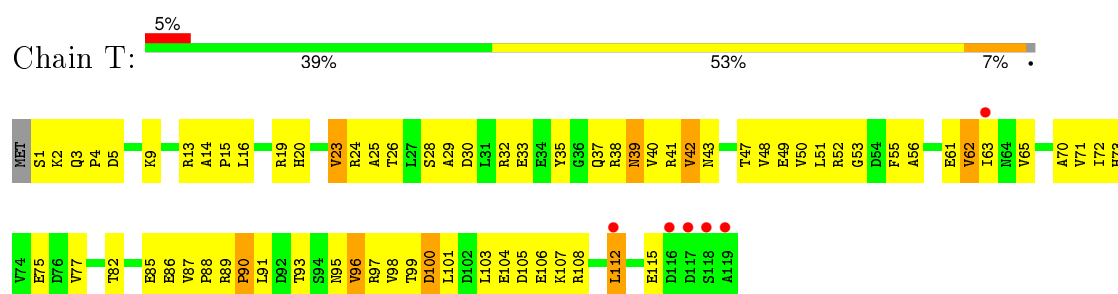
- Molecule 20: 50S ribosomal protein L22P



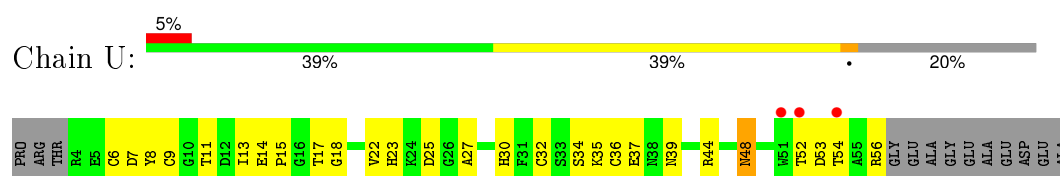
- Molecule 21: 50S ribosomal protein L23P



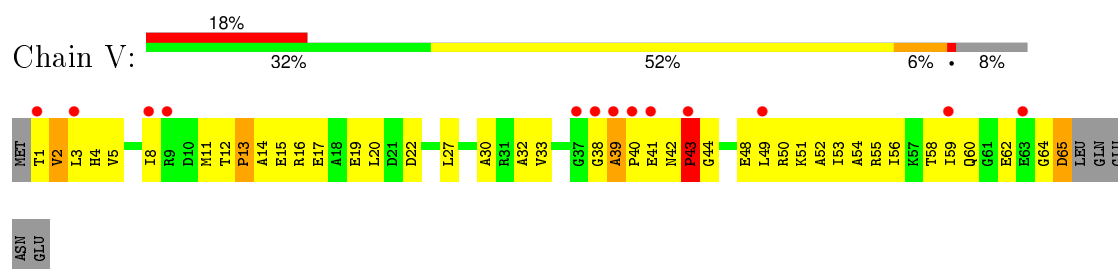
- Molecule 22: 50S ribosomal protein L24P



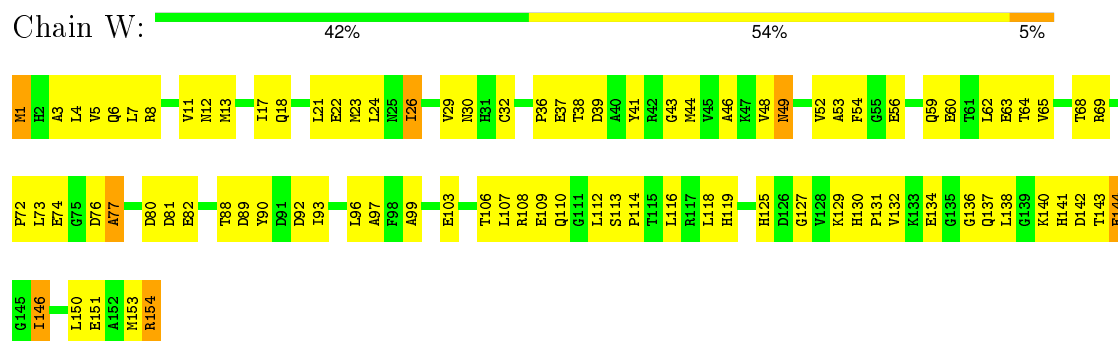
- Molecule 23: 50S ribosomal protein L24E



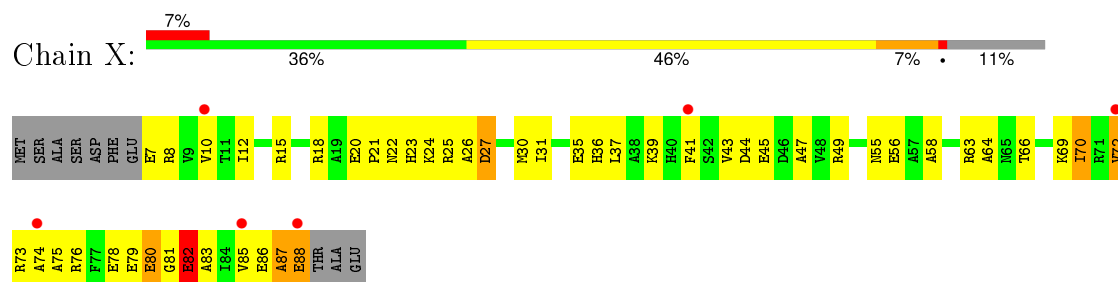
- Molecule 24: 50S ribosomal protein L29P



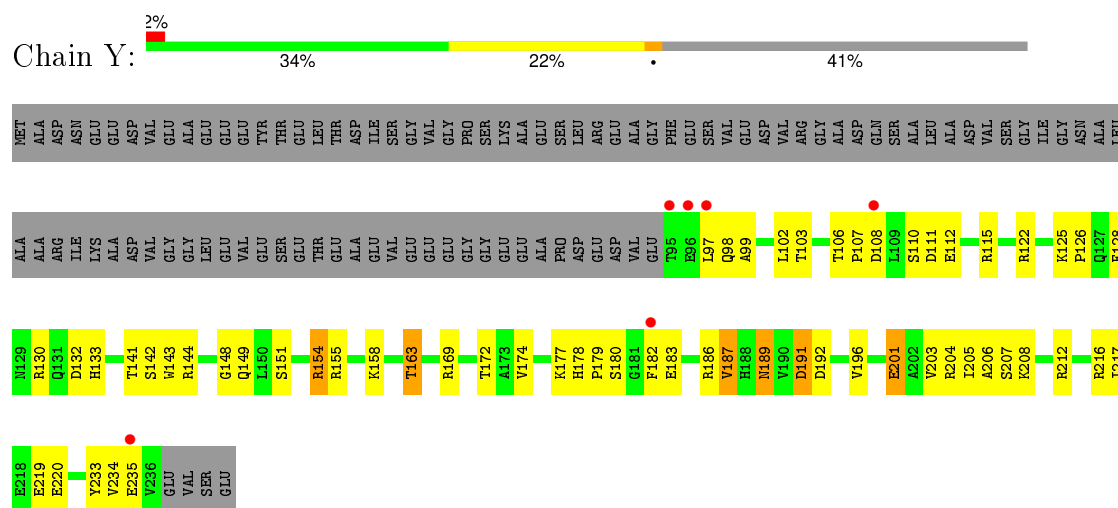
- Molecule 25: 50S ribosomal protein L30P



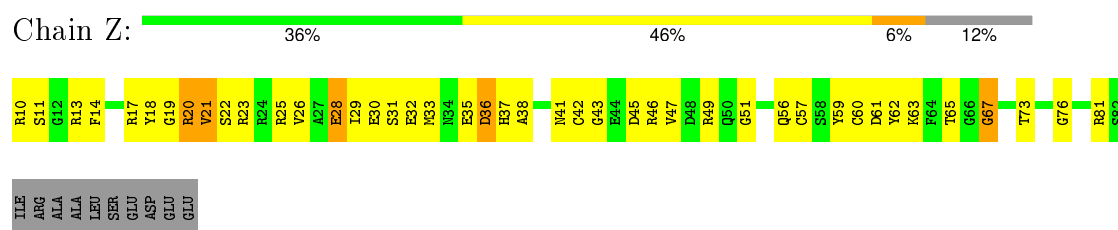
- Molecule 26: 50S ribosomal protein L31e



- Molecule 27: 50S ribosomal protein L32E



- Molecule 28: 50S ribosomal protein L37Ae

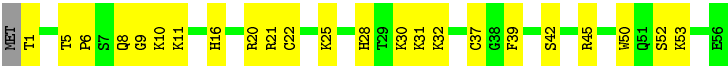


- Molecule 29: 50S ribosomal protein L37e

Chain 1:

58%

40%



- Molecule 30: 50S ribosomal protein L39e

Chain 2:

6%

48%

46%



- Molecule 31: 50S ribosomal protein L44E

Chain 3:

%

63%

34%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	213.08Å 300.75Å 575.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.94 – 2.80 49.56 – 2.80	Depositor EDS
% Data completeness (in resolution range)	89.3 (29.94-2.80) 89.2 (49.56-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.184 , 0.242 0.185 , 0.240	Depositor DCC
R_{free} test set	3986 reflections (1.00%)	DCC
Wilson B-factor (Å ²)	55.8	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 63.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 400940 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	99031	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, NA, K, CD, OMU, UR3, 1MA, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.42	0/65980	0.69	13/102903 (0.0%)
2	9	0.38	0/2904	0.70	1/4526 (0.0%)
3	A	0.35	0/1786	0.66	0/2408
4	B	0.35	0/2690	0.66	0/3652
5	C	0.39	0/1884	0.66	0/2551
6	D	0.33	0/1111	0.57	0/1498
7	E	0.35	0/1382	0.59	0/1880
8	F	0.34	0/901	0.59	0/1224
9	G	0.31	0/241	0.53	0/324
10	H	0.38	0/1302	0.70	1/1743 (0.1%)
11	I	0.31	0/526	0.59	0/716
12	J	0.40	0/1136	0.61	0/1530
13	K	0.37	0/1001	0.69	0/1347
14	L	0.36	0/1130	0.65	0/1509
15	M	0.36	0/1582	0.62	1/2117 (0.0%)
16	N	0.32	0/1474	0.64	0/1999
17	O	0.35	0/874	0.58	0/1181
18	P	0.37	0/1147	0.55	0/1528
19	Q	0.40	0/749	0.74	1/1005 (0.1%)
20	R	0.42	0/1146	0.63	0/1544
21	S	0.36	0/648	0.59	0/875
22	T	0.34	0/958	0.64	0/1289
23	U	0.34	0/417	0.58	0/562
24	V	0.31	0/502	0.56	0/675
25	W	0.37	0/1219	0.65	0/1655
26	X	0.36	0/664	0.62	0/895
27	Y	0.38	0/1146	0.65	0/1536
28	Z	0.38	0/589	0.63	0/787
29	1	0.40	0/438	0.64	0/578
30	2	0.41	0/427	0.61	0/566
31	3	0.40	0/771	0.58	0/1024
All	All	0.40	0/98725	0.68	17/147627 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	46
2	9	0	1
All	All	0	47

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1942	A	C5'-C4'-C3'	7.17	127.47	116.00
1	0	1504	A	C1'-O4'-C4'	-6.38	104.80	109.90
1	0	2291	A	N9-C1'-C2'	6.19	122.05	114.00
19	Q	68	GLY	N-CA-C	-5.89	98.36	113.10
1	0	1504	A	N9-C1'-C2'	5.75	121.48	114.00

There are no chirality outliers.

5 of 47 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	148	A	Sidechain
1	0	26	U	Sidechain
1	0	333	G	Sidechain
1	0	398	U	Sidechain
1	0	458	G	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59041	0	29817	1161	0
2	9	2599	0	1325	86	0
3	A	1753	0	1766	148	0
4	B	2625	0	2533	200	0
5	C	1859	0	1816	160	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	1094	0	1085	138	0
7	E	1357	0	1266	77	0
8	F	890	0	843	79	0
9	G	240	0	231	22	0
10	H	1282	0	1292	95	0
11	I	519	0	500	63	0
12	J	1120	0	1098	80	0
13	K	992	0	1031	77	0
14	L	1118	0	1076	81	0
15	M	1558	0	1566	98	0
16	N	1445	0	1401	147	0
17	O	865	0	873	62	0
18	P	1136	0	1123	71	0
19	Q	735	0	729	37	0
20	R	1123	0	1099	69	0
21	S	641	0	605	39	0
22	T	950	0	923	99	0
23	U	410	0	364	31	0
24	V	499	0	511	44	0
25	W	1196	0	1137	120	0
26	X	654	0	653	57	0
27	Y	1130	0	1133	66	0
28	Z	578	0	539	39	0
29	1	431	0	426	36	0
30	2	421	0	437	35	0
31	3	755	0	728	31	0
32	0	107	0	0	0	0
32	2	1	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	2	0	0	0	0
34	0	74	0	0	0	0
34	9	2	0	0	0	0
34	A	1	0	0	0	0
34	C	1	0	0	0	0
34	J	1	0	0	0	0
34	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	M	1	0	0	0	0
34	Q	1	0	0	0	0
34	R	2	0	0	0	0
34	S	1	0	0	0	0
34	T	1	0	0	0	0
35	0	9	0	0	1	0
35	3	1	0	0	0	0
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	J	3	0	0	4	0
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	N	1	0	0	1	0
35	O	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	Y	1	0	0	0	0
36	1	1	0	0	0	0
36	3	1	0	0	0	0
36	O	1	0	0	0	0
36	U	1	0	0	0	0
36	Z	1	0	0	0	0
37	0	5866	0	0	246	0
37	1	63	0	0	8	0
37	2	32	0	0	2	0
37	3	69	0	0	8	0
37	9	143	0	0	12	0
37	A	119	0	0	21	0
37	B	148	0	0	31	0
37	C	180	0	0	34	0
37	D	46	0	0	17	0
37	E	45	0	0	10	0
37	F	27	0	0	8	0
37	G	19	0	0	2	0
37	H	69	0	0	12	0
37	I	9	0	0	5	0
37	J	57	0	0	8	0
37	K	54	0	0	10	0
37	L	84	0	0	17	0
37	M	130	0	0	10	0
37	N	64	0	0	22	0
37	O	45	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	P	64	0	0	10	0
37	Q	53	0	0	7	0
37	R	58	0	0	5	0
37	S	34	0	0	3	0
37	T	32	0	0	9	0
37	U	26	0	0	3	0
37	V	14	0	0	5	0
37	W	72	0	0	12	0
37	X	24	0	0	5	0
37	Y	104	0	0	15	0
37	Z	34	0	0	3	0
All	All	99031	0	59926	3232	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

The worst 5 of 3232 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:127:ARG:NH2	5:C:225:PRO:HG2	1.66	1.09
5:C:236:THR:HG22	5:C:239:ALA:H	0.95	1.08
1:O:1160:G:H5'	1:O:1161:A:H5'	1.13	1.07
4:B:264:GLU:HG2	4:B:267:LYS:HE2	1.36	1.04
29:1:25:LYS:HD2	30:2:49:GLU:H	1.20	1.03

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	235/240 (98%)	191 (81%)	31 (13%)	13 (6%)	2 6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	335/338 (99%)	291 (87%)	35 (10%)	9 (3%)	6	21
5	C	244/246 (99%)	201 (82%)	32 (13%)	11 (4%)	3	10
6	D	134/177 (76%)	85 (63%)	31 (23%)	18 (13%)	0	1
7	E	170/178 (96%)	150 (88%)	15 (9%)	5 (3%)	6	19
8	F	117/120 (98%)	93 (80%)	17 (14%)	7 (6%)	2	5
9	G	25/348 (7%)	23 (92%)	2 (8%)	0	100	100
10	H	156/177 (88%)	134 (86%)	17 (11%)	5 (3%)	5	17
11	I	68/162 (42%)	49 (72%)	14 (21%)	5 (7%)	1	3
12	J	140/145 (97%)	121 (86%)	14 (10%)	5 (4%)	4	14
13	K	130/132 (98%)	111 (85%)	17 (13%)	2 (2%)	13	40
14	L	141/165 (86%)	114 (81%)	25 (18%)	2 (1%)	14	42
15	M	192/195 (98%)	169 (88%)	20 (10%)	3 (2%)	12	38
16	N	184/187 (98%)	149 (81%)	23 (12%)	12 (6%)	1	4
17	O	113/116 (97%)	102 (90%)	8 (7%)	3 (3%)	6	21
18	P	141/149 (95%)	125 (89%)	12 (8%)	4 (3%)	6	21
19	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	8	28
20	R	145/152 (95%)	122 (84%)	18 (12%)	5 (3%)	5	16
21	S	79/85 (93%)	69 (87%)	9 (11%)	1 (1%)	15	44
22	T	117/120 (98%)	92 (79%)	19 (16%)	6 (5%)	2	8
23	U	51/66 (77%)	43 (84%)	7 (14%)	1 (2%)	9	30
24	V	63/71 (89%)	50 (79%)	9 (14%)	4 (6%)	2	4
25	W	152/154 (99%)	136 (90%)	14 (9%)	2 (1%)	15	44
26	X	80/92 (87%)	69 (86%)	8 (10%)	3 (4%)	4	13
27	Y	140/241 (58%)	138 (99%)	2 (1%)	0	100	100
28	Z	71/83 (86%)	56 (79%)	10 (14%)	5 (7%)	1	3
29	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
30	2	47/50 (94%)	44 (94%)	1 (2%)	2 (4%)	3	10
31	3	90/92 (98%)	84 (93%)	6 (7%)	0	100	100
All	All	3707/4434 (84%)	3148 (85%)	424 (11%)	135 (4%)	4	14

5 of 135 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	34	ASP
4	B	34	GLY
4	B	139	ASP
4	B	206	THR
5	C	8	LEU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	179/182 (98%)	171 (96%)	8 (4%)	34	68
4	B	282/283 (100%)	258 (92%)	24 (8%)	13	36
5	C	193/193 (100%)	182 (94%)	11 (6%)	25	58
6	D	117/148 (79%)	109 (93%)	8 (7%)	20	49
7	E	152/156 (97%)	147 (97%)	5 (3%)	45	79
8	F	93/94 (99%)	90 (97%)	3 (3%)	46	80
9	G	27/283 (10%)	26 (96%)	1 (4%)	41	76
10	H	134/145 (92%)	125 (93%)	9 (7%)	20	50
11	I	58/130 (45%)	55 (95%)	3 (5%)	29	62
12	J	118/121 (98%)	111 (94%)	7 (6%)	24	57
13	K	106/106 (100%)	104 (98%)	2 (2%)	65	91
14	L	113/127 (89%)	108 (96%)	5 (4%)	35	69
15	M	158/159 (99%)	151 (96%)	7 (4%)	35	69
16	N	149/150 (99%)	143 (96%)	6 (4%)	38	73
17	O	93/94 (99%)	88 (95%)	5 (5%)	27	60
18	P	113/117 (97%)	107 (95%)	6 (5%)	28	61
19	Q	79/80 (99%)	77 (98%)	2 (2%)	55	86
20	R	114/120 (95%)	109 (96%)	5 (4%)	35	69
21	S	71/74 (96%)	66 (93%)	5 (7%)	19	47
22	T	105/106 (99%)	99 (94%)	6 (6%)	25	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	44/52 (85%)	41 (93%)	3 (7%)	20	49
24	V	51/57 (90%)	48 (94%)	3 (6%)	24	57
25	W	130/130 (100%)	125 (96%)	5 (4%)	40	74
26	X	66/74 (89%)	60 (91%)	6 (9%)	12	33
27	Y	120/196 (61%)	114 (95%)	6 (5%)	30	64
28	Z	60/68 (88%)	58 (97%)	2 (3%)	45	79
29	1	46/47 (98%)	46 (100%)	0	100	100
30	2	45/46 (98%)	42 (93%)	3 (7%)	20	50
31	3	79/79 (100%)	75 (95%)	4 (5%)	29	63
All	All	3095/3617 (86%)	2935 (95%)	160 (5%)	29	62

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	J	46	ILE
15	M	93	ARG
27	Y	187	VAL
12	J	74	ARG
14	L	18	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
15	M	24	GLN
18	P	66	GLN
30	2	16	ASN
15	M	58	GLN
16	N	107	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2744/2922 (93%)	247 (9%)	26 (0%)
2	9	121/122 (99%)	17 (14%)	1 (0%)
All	All	2865/3044 (94%)	264 (9%)	27 (0%)

5 of 264 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1352	A
1	0	1506	U
1	0	2718	C
1	0	1377	C
1	0	857	A

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

5 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMU	0	2587	1	12,22,23	0.96	1 (8%)	19,31,34	3.16	2 (10%)
1	OMG	0	2588	1	17,26,27	1.05	1 (5%)	21,38,41	2.55	3 (14%)
1	UR3	0	2619	1	12,22,23	0.80	0	16,32,35	0.75	0
1	PSU	0	2621	1	13,21,22	1.45	2 (15%)	18,30,33	6.12	3 (16%)
1	1MA	0	628	1	14,25,26	1.02	1 (7%)	15,37,40	1.12	1 (6%)

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
1	OMU	0	2587	1	-	0/5/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	0	2588	1	-	0/5/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/3/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	1	-	0/3/25/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C5-C1'	-4.25	1.48	1.52
1	0	2587	OMU	C4-N3	2.13	1.37	1.33
1	0	2621	PSU	C4-N3	2.53	1.37	1.33
1	0	628	1MA	C6-N6	2.76	1.34	1.29
1	0	2588	OMG	C6-N1	3.22	1.39	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	N1-C2-N3	-21.54	114.59	128.33
1	0	2588	OMG	C5-C6-N1	-8.69	111.71	123.59
1	0	628	1MA	C2-N3-C4	-3.60	110.82	116.40
1	0	2587	OMU	C5-C4-N3	-3.27	114.73	123.12
1	0	2588	OMG	N3-C2-N1	-2.35	123.87	127.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 231 ligands modelled in this entry, 231 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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.21	10 (0%) 93 90	29, 55, 100, 157	0
2	9	122/122 (100%)	-0.20	2 (1%) 74 66	44, 68, 95, 159	0
3	A	237/240 (98%)	0.13	10 (4%) 40 28	34, 62, 95, 116	0
4	B	337/338 (99%)	-0.05	5 (1%) 76 68	32, 64, 90, 97	0
5	C	246/246 (100%)	-0.19	1 (0%) 93 90	29, 58, 81, 90	0
6	D	140/177 (79%)	1.30	43 (30%) 1 0	62, 107, 129, 138	0
7	E	172/178 (96%)	0.60	12 (6%) 19 11	52, 75, 97, 101	0
8	F	119/120 (99%)	0.66	14 (11%) 6 3	65, 84, 105, 117	0
9	G	29/348 (8%)	1.83	10 (34%) 0 0	76, 98, 106, 107	0
10	H	160/177 (90%)	-0.01	1 (0%) 90 86	40, 61, 96, 107	0
11	I	70/162 (43%)	2.77	44 (62%) 0 0	112, 126, 144, 147	0
12	J	142/145 (97%)	-0.19	1 (0%) 89 84	43, 58, 82, 95	0
13	K	132/132 (100%)	-0.04	0 100 100	40, 61, 84, 89	0
14	L	145/165 (87%)	0.30	12 (8%) 14 7	29, 75, 115, 126	0
15	M	194/195 (99%)	-0.23	0 100 100	40, 55, 69, 79	0
16	N	186/187 (99%)	0.26	11 (5%) 26 16	46, 71, 115, 125	0
17	O	115/116 (99%)	-0.04	0 100 100	47, 65, 81, 83	0
18	P	143/149 (95%)	0.21	1 (0%) 89 84	44, 66, 80, 86	0
19	Q	95/96 (98%)	-0.11	0 100 100	39, 51, 64, 79	0
20	R	147/152 (96%)	0.25	10 (6%) 20 12	41, 56, 114, 128	0
21	S	81/85 (95%)	0.23	4 (4%) 33 22	52, 72, 88, 95	0
22	T	119/120 (99%)	0.53	6 (5%) 32 21	51, 69, 94, 111	0
23	U	53/66 (80%)	0.15	3 (5%) 27 17	51, 64, 79, 85	0
24	V	65/71 (91%)	1.02	13 (20%) 1 1	63, 85, 118, 122	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	-0.19	0 100 100	41, 56, 76, 85	0
26	X	82/92 (89%)	0.39	6 (7%) 18 10	49, 66, 87, 101	0
27	Y	142/241 (58%)	0.06	6 (4%) 40 28	31, 53, 79, 95	0
28	Z	73/83 (87%)	-0.10	0 100 100	53, 69, 86, 102	0
29	1	56/57 (98%)	-0.41	0 100 100	35, 43, 49, 58	0
30	2	49/50 (98%)	0.22	3 (6%) 25 15	40, 66, 94, 104	0
31	3	92/92 (100%)	0.09	1 (1%) 82 74	42, 63, 76, 91	0
All	All	6646/7478 (88%)	0.03	229 (3%) 49 36	29, 61, 106, 159	0

The worst 5 of 229 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
24	V	1	THR	9.8
20	R	131	GLY	7.4
22	T	119	ALA	6.8
6	D	69	ILE	6.5
20	R	134	SER	6.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	UR3	0	2619	21/22	0.98	0.14	-	40,42,43,46	0
1	OMG	0	2588	24/25	0.98	0.14	-	40,42,44,44	0
1	1MA	0	628	23/24	0.99	0.16	-	32,37,39,39	0
1	PSU	0	2621	20/21	0.98	0.14	-	40,41,43,44	0
1	OMU	0	2587	21/22	0.98	0.14	-	39,42,43,46	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
34	NA	9	8583	1/1	0.89	0.64	67.19	71,71,71,71	0
35	CL	0	8815	1/1	0.71	0.75	64.08	112,112,112,112	0
34	NA	0	8578	1/1	0.94	0.59	43.70	77,77,77,77	0
34	NA	0	8568	1/1	0.49	0.45	43.24	84,84,84,84	0
34	NA	0	8574	1/1	0.93	0.80	40.37	63,63,63,63	0
34	NA	0	8526	1/1	0.65	0.82	37.47	78,78,78,78	0
34	NA	L	8580	1/1	0.85	0.71	36.83	72,72,72,72	0
34	NA	0	8556	1/1	0.70	0.68	33.92	58,58,58,58	0
34	NA	0	8559	1/1	0.93	0.40	31.66	66,66,66,66	0
33	K	0	8401	1/1	0.96	0.41	27.93	91,91,91,91	0
34	NA	0	8521	1/1	0.95	0.39	27.33	73,73,73,73	0
34	NA	0	8571	1/1	0.75	0.27	23.84	61,61,61,61	0
34	NA	0	8532	1/1	0.88	0.37	23.68	47,47,47,47	0
34	NA	0	8573	1/1	0.94	0.65	21.94	73,73,73,73	0
35	CL	B	8819	1/1	0.91	0.41	21.05	74,74,74,74	0
34	NA	0	8502	1/1	0.97	0.23	19.92	49,49,49,49	0
34	NA	0	8579	1/1	0.92	0.27	16.21	62,62,62,62	0
34	NA	0	8561	1/1	0.94	0.34	15.97	50,50,50,50	0
35	CL	0	8805	1/1	0.89	0.23	15.80	77,77,77,77	0
34	NA	0	8562	1/1	0.96	0.31	14.43	81,81,81,81	0
34	NA	0	8550	1/1	0.94	0.27	10.08	56,56,56,56	0
34	NA	R	8586	1/1	0.61	0.50	9.09	81,81,81,81	0
35	CL	0	8816	1/1	0.87	0.45	8.51	79,79,79,79	0
34	NA	0	8566	1/1	0.91	0.32	8.04	68,68,68,68	0
34	NA	0	8510	1/1	0.93	0.24	7.95	40,40,40,40	0
34	NA	0	8582	1/1	0.86	0.25	6.56	78,78,78,78	0
34	NA	0	8503	1/1	0.97	0.22	6.06	70,70,70,70	0
32	MG	0	8038	1/1	0.84	0.21	5.77	38,38,38,38	0
32	MG	0	8064	1/1	0.97	0.20	4.70	43,43,43,43	0
34	NA	0	8565	1/1	0.98	0.30	3.38	49,49,49,49	0
34	NA	0	8531	1/1	0.98	0.17	3.21	55,55,55,55	0
34	NA	M	8547	1/1	0.94	0.22	2.93	45,45,45,45	0
34	NA	0	8529	1/1	0.93	0.15	2.88	79,79,79,79	0
35	CL	O	8808	1/1	0.95	0.39	2.86	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
34	NA	0	8535	1/1	0.94	0.20	2.76	73,73,73,73	0
34	NA	0	8555	1/1	0.99	0.23	2.52	67,67,67,67	0
34	NA	0	8576	1/1	0.95	0.18	2.25	51,51,51,51	0
34	NA	0	8564	1/1	0.83	0.17	1.80	40,40,40,40	0
35	CL	3	8804	1/1	0.92	0.29	1.71	74,74,74,74	0
34	NA	0	8505	1/1	0.96	0.17	1.56	49,49,49,49	0
32	MG	0	8044	1/1	0.95	0.16	1.02	51,51,51,51	0
32	MG	0	8053	1/1	0.97	0.14	0.53	47,47,47,47	0
34	NA	0	8554	1/1	0.96	0.15	0.42	38,38,38,38	0
32	MG	0	8057	1/1	0.98	0.18	0.31	67,67,67,67	0
35	CL	M	8818	1/1	0.98	0.19	0.16	60,60,60,60	0
34	NA	0	8533	1/1	0.94	0.14	-0.01	49,49,49,49	0
34	NA	Q	8548	1/1	0.95	0.17	-0.27	49,49,49,49	0
32	MG	0	8013	1/1	0.98	0.16	-0.35	54,54,54,54	0
34	NA	T	8543	1/1	0.96	0.14	-0.48	43,43,43,43	0
32	MG	0	8091	1/1	0.96	0.13	-0.66	53,53,53,53	0
35	CL	0	8812	1/1	0.97	0.14	-0.73	65,65,65,65	0
36	CD	Z	8703	1/1	0.99	0.11	-0.79	71,71,71,71	0
34	NA	0	8509	1/1	0.96	0.12	-0.81	37,37,37,37	0
36	CD	3	8704	1/1	0.93	0.08	-0.95	72,72,72,72	0
32	MG	T	8073	1/1	0.91	0.21	-1.19	68,68,68,68	0
32	MG	0	8086	1/1	0.98	0.07	-1.37	46,46,46,46	0
33	K	0	8402	1/1	0.96	0.13	-1.37	69,69,69,69	0
32	MG	0	8060	1/1	0.99	0.13	-1.37	50,50,50,50	0
36	CD	U	8701	1/1	0.99	0.10	-1.39	76,76,76,76	0
32	MG	Y	8108	1/1	0.95	0.15	-1.52	48,48,48,48	0
36	CD	1	8702	1/1	1.00	0.07	-1.53	68,68,68,68	0
32	MG	0	8033	1/1	0.97	0.13	-1.56	37,37,37,37	0
32	MG	0	8113	1/1	0.95	0.12	-1.56	49,49,49,49	0
34	NA	0	8527	1/1	0.97	0.13	-1.56	69,69,69,69	0
34	NA	0	8517	1/1	0.96	0.10	-1.60	52,52,52,52	0
34	NA	0	8538	1/1	0.88	0.09	-2.20	61,61,61,61	0
32	MG	0	8027	1/1	0.96	0.09	-2.31	63,63,63,63	0
35	CL	J	8821	1/1	0.97	0.10	-2.56	54,54,54,54	0
32	MG	0	8008	1/1	0.97	0.08	-2.61	35,35,35,35	0
34	NA	J	8546	1/1	0.98	0.11	-2.61	48,48,48,48	0
32	MG	0	8012	1/1	0.99	0.10	-2.63	33,33,33,33	0
34	NA	0	8553	1/1	0.99	0.10	-2.65	36,36,36,36	0
32	MG	0	8074	1/1	0.97	0.06	-2.75	40,40,40,40	0
32	MG	3	8078	1/1	0.97	0.07	-2.85	43,43,43,43	0
32	MG	0	8004	1/1	0.96	0.07	-2.92	43,43,43,43	0
34	NA	A	8545	1/1	0.96	0.10	-3.02	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8056	1/1	0.99	0.11	-3.06	49,49,49,49	0
32	MG	0	8015	1/1	0.95	0.06	-3.20	41,41,41,41	0
32	MG	0	8047	1/1	0.98	0.09	-3.24	59,59,59,59	0
34	NA	0	8544	1/1	0.97	0.07	-3.28	33,33,33,33	0
34	NA	0	8525	1/1	0.97	0.10	-3.29	50,50,50,50	0
32	MG	0	8088	1/1	0.96	0.10	-3.42	34,34,34,34	0
32	MG	0	8077	1/1	0.98	0.07	-3.60	32,32,32,32	0
32	MG	0	8010	1/1	0.98	0.10	-3.61	45,45,45,45	0
32	MG	0	8032	1/1	0.98	0.07	-3.80	32,32,32,32	0
32	MG	0	8017	1/1	0.99	0.04	-3.92	33,33,33,33	0
32	MG	0	8101	1/1	0.97	0.09	-3.95	70,70,70,70	0
32	MG	A	8065	1/1	0.99	0.08	-3.96	43,43,43,43	0
32	MG	0	8054	1/1	0.99	0.10	-4.28	43,43,43,43	0
32	MG	B	8055	1/1	0.99	0.06	-4.29	46,46,46,46	0
34	NA	0	8539	1/1	0.97	0.10	-4.32	26,26,26,26	0
32	MG	0	8111	1/1	0.94	0.07	-4.50	48,48,48,48	0
32	MG	0	8084	1/1	0.99	0.07	-5.00	54,54,54,54	0
34	NA	0	8523	1/1	0.96	0.10	-5.36	37,37,37,37	0
32	MG	0	8052	1/1	0.96	0.06	-5.55	44,44,44,44	0
32	MG	0	8001	1/1	0.99	0.09	-5.87	33,33,33,33	0
32	MG	0	8106	1/1	0.99	0.09	-6.15	38,38,38,38	0
32	MG	0	8058	1/1	1.00	0.09	-6.19	46,46,46,46	0
32	MG	0	8003	1/1	0.96	0.10	-6.39	47,47,47,47	0
32	MG	0	8080	1/1	0.99	0.09	-6.85	47,47,47,47	0
32	MG	0	8020	1/1	1.00	0.06	-7.55	31,31,31,31	0
32	MG	0	8006	1/1	0.99	0.06	-7.69	37,37,37,37	0
32	MG	0	8019	1/1	0.99	0.03	-7.83	39,39,39,39	0
32	MG	0	8035	1/1	0.98	0.03	-8.14	58,58,58,58	0
34	NA	0	8520	1/1	0.98	0.07	-8.17	33,33,33,33	0
32	MG	0	8007	1/1	0.97	0.09	-8.66	29,29,29,29	0
32	MG	0	8002	1/1	0.99	0.06	-10.31	35,35,35,35	0
32	MG	0	8109	1/1	0.95	0.05	-10.36	33,33,33,33	0
32	MG	0	8067	1/1	1.00	0.07	-10.54	54,54,54,54	0
34	NA	0	8516	1/1	0.96	0.23	-	61,61,61,61	0
35	CL	0	8814	1/1	0.94	0.17	-	71,71,71,71	0
34	NA	0	8558	1/1	0.97	0.70	-	107,107,107,107	0
34	NA	R	8537	1/1	0.87	0.13	-	51,51,51,51	0
32	MG	0	8048	1/1	0.96	0.09	-	62,62,62,62	0
32	MG	0	8036	1/1	0.98	0.08	-	44,44,44,44	0
34	NA	0	8570	1/1	0.93	0.16	-	66,66,66,66	0
32	MG	0	8025	1/1	0.97	0.12	-	58,58,58,58	0
35	CL	0	8803	1/1	0.94	0.20	-	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8031	1/1	0.70	0.19	-	34,34,34,34	0
32	MG	0	8079	1/1	0.99	0.11	-	43,43,43,43	0
34	NA	0	8567	1/1	0.86	0.17	-	70,70,70,70	0
32	MG	0	8026	1/1	0.99	0.09	-	28,28,28,28	0
34	NA	9	8551	1/1	0.85	0.18	-	46,46,46,46	0
32	MG	0	8081	1/1	0.97	0.14	-	74,74,74,74	0
32	MG	0	8034	1/1	0.99	0.10	-	36,36,36,36	0
34	NA	0	8524	1/1	0.86	0.26	-	68,68,68,68	0
36	CD	O	8705	1/1	0.98	0.08	-	98,98,98,98	0
34	NA	0	8542	1/1	0.97	0.20	-	51,51,51,51	0
32	MG	0	8100	1/1	0.96	0.14	-	66,66,66,66	0
35	CL	0	8822	1/1	0.92	0.20	-	79,79,79,79	0
34	NA	0	8563	1/1	0.79	0.46	-	51,51,51,51	0
35	CL	Q	8811	1/1	0.96	0.17	-	72,72,72,72	0
32	MG	0	8005	1/1	0.99	0.09	-	45,45,45,45	0
32	MG	0	8021	1/1	0.99	0.10	-	31,31,31,31	0
34	NA	0	8508	1/1	0.89	0.23	-	73,73,73,73	0
34	NA	0	8557	1/1	0.94	0.11	-	65,65,65,65	0
32	MG	0	8022	1/1	0.98	0.06	-	42,42,42,42	0
32	MG	0	8085	1/1	0.91	0.13	-	62,62,62,62	0
32	MG	0	8039	1/1	1.00	0.07	-	44,44,44,44	0
35	CL	0	8817	1/1	0.89	0.16	-	74,74,74,74	0
32	MG	0	8042	1/1	0.95	0.11	-	55,55,55,55	0
34	NA	0	8581	1/1	0.91	0.14	-	52,52,52,52	0
32	MG	0	8011	1/1	0.98	0.11	-	32,32,32,32	0
32	MG	A	8066	1/1	0.98	0.06	-	88,88,88,88	0
34	NA	C	8504	1/1	0.89	0.34	-	48,48,48,48	0
32	MG	0	8093	1/1	0.95	0.19	-	50,50,50,50	0
32	MG	0	8043	1/1	0.88	0.12	-	62,62,62,62	0
32	MG	0	8110	1/1	0.98	0.04	-	59,59,59,59	0
32	MG	0	8089	1/1	0.94	0.08	-	69,69,69,69	0
32	MG	0	8040	1/1	0.90	0.12	-	57,57,57,57	0
34	NA	S	8512	1/1	0.92	0.14	-	48,48,48,48	0
32	MG	0	8041	1/1	0.87	0.22	-	59,59,59,59	0
32	MG	0	8092	1/1	0.92	0.23	-	80,80,80,80	0
34	NA	0	8507	1/1	0.82	0.46	-	61,61,61,61	0
35	CL	0	8813	1/1	0.97	0.10	-	67,67,67,67	0
35	CL	N	8807	1/1	0.88	0.33	-	74,74,74,74	0
32	MG	0	8059	1/1	0.96	0.10	-	44,44,44,44	0
34	NA	0	8501	1/1	0.97	0.11	-	29,29,29,29	0
34	NA	0	8577	1/1	0.96	0.20	-	72,72,72,72	0
32	MG	0	8046	1/1	0.97	0.06	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8016	1/1	0.97	0.13	-	48,48,48,48	0
32	MG	0	8045	1/1	0.98	0.10	-	59,59,59,59	0
32	MG	0	8051	1/1	0.96	0.15	-	67,67,67,67	0
32	MG	0	8009	1/1	0.99	0.04	-	36,36,36,36	0
34	NA	0	8536	1/1	0.96	0.09	-	52,52,52,52	0
34	NA	0	8560	1/1	0.93	0.64	-	61,61,61,61	0
34	NA	0	8518	1/1	0.97	0.18	-	32,32,32,32	0
32	MG	0	8099	1/1	0.88	0.14	-	62,62,62,62	0
32	MG	0	8096	1/1	0.97	0.11	-	53,53,53,53	0
32	MG	0	8098	1/1	0.99	0.11	-	30,30,30,30	0
32	MG	0	8062	1/1	0.93	0.14	-	65,65,65,65	0
34	NA	0	8528	1/1	0.89	0.74	-	61,61,61,61	0
34	NA	0	8522	1/1	0.88	0.19	-	68,68,68,68	0
32	MG	0	8082	1/1	0.91	0.10	-	76,76,76,76	0
34	NA	0	8506	1/1	0.88	0.71	-	51,51,51,51	0
34	NA	0	8575	1/1	0.96	0.25	-	58,58,58,58	0
34	NA	0	8569	1/1	0.91	0.59	-	66,66,66,66	0
34	NA	0	8515	1/1	0.95	0.26	-	65,65,65,65	0
35	CL	J	8801	1/1	0.95	0.10	-	67,67,67,67	0
34	NA	0	8541	1/1	0.87	0.23	-	53,53,53,53	0
35	CL	R	8806	1/1	0.89	0.18	-	63,63,63,63	0
32	MG	0	8070	1/1	0.94	0.12	-	54,54,54,54	0
34	NA	0	8513	1/1	0.60	0.17	-	72,72,72,72	0
34	NA	0	8572	1/1	0.85	0.31	-	69,69,69,69	0
32	MG	0	8115	1/1	0.91	0.14	-	70,70,70,70	0
32	MG	0	8023	1/1	0.99	0.08	-	42,42,42,42	0
32	MG	0	8075	1/1	0.98	0.09	-	54,54,54,54	0
32	MG	0	8083	1/1	0.98	0.04	-	52,52,52,52	0
32	MG	0	8107	1/1	0.89	0.19	-	65,65,65,65	0
32	MG	0	8087	1/1	0.96	0.10	-	81,81,81,81	0
32	MG	0	8114	1/1	0.90	0.16	-	47,47,47,47	0
34	NA	0	8584	1/1	0.94	0.17	-	70,70,70,70	0
34	NA	0	8549	1/1	0.95	0.16	-	54,54,54,54	0
32	MG	0	8049	1/1	0.90	0.31	-	70,70,70,70	0
35	CL	A	8809	1/1	0.94	0.23	-	82,82,82,82	0
32	MG	0	8105	1/1	0.97	0.08	-	63,63,63,63	0
32	MG	0	8030	1/1	0.99	0.13	-	34,34,34,34	0
34	NA	0	8540	1/1	0.93	0.24	-	40,40,40,40	0
32	MG	0	8072	1/1	0.99	0.11	-	61,61,61,61	0
34	NA	0	8530	1/1	0.86	0.30	-	72,72,72,72	0
32	MG	0	8028	1/1	0.98	0.06	-	48,48,48,48	0
32	MG	0	8102	1/1	0.97	0.19	-	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8071	1/1	0.99	0.07	-	80,80,80,80	0
32	MG	0	8103	1/1	0.92	0.16	-	67,67,67,67	0
32	MG	2	8076	1/1	0.92	0.16	-	69,69,69,69	0
34	NA	0	8552	1/1	0.73	0.65	-	62,62,62,62	0
32	MG	0	8116	1/1	0.97	0.08	-	39,39,39,39	0
35	CL	J	8802	1/1	0.92	0.12	-	75,75,75,75	0
32	MG	0	8068	1/1	0.96	0.05	-	70,70,70,70	0
32	MG	9	8095	1/1	0.82	0.09	-	54,54,54,54	0
32	MG	0	8104	1/1	0.78	0.29	-	61,61,61,61	0
32	MG	0	8090	1/1	0.99	0.10	-	59,59,59,59	0
32	MG	0	8061	1/1	0.99	0.10	-	36,36,36,36	0
34	NA	0	8585	1/1	0.86	0.53	-	60,60,60,60	0
34	NA	0	8514	1/1	0.95	0.09	-	39,39,39,39	0
32	MG	0	8037	1/1	0.98	0.08	-	51,51,51,51	0
32	MG	0	8094	1/1	0.97	0.04	-	67,67,67,67	0
32	MG	0	8024	1/1	0.95	0.14	-	45,45,45,45	0
35	CL	Y	8820	1/1	0.92	0.14	-	55,55,55,55	0
34	NA	0	8534	1/1	0.97	0.11	-	55,55,55,55	0
34	NA	0	8519	1/1	0.97	0.07	-	34,34,34,34	0
32	MG	0	8097	1/1	0.87	0.19	-	51,51,51,51	0
32	MG	0	8014	1/1	0.96	0.10	-	20,20,20,20	0
35	CL	L	8810	1/1	0.94	0.13	-	73,73,73,73	0
32	MG	0	8018	1/1	0.98	0.11	-	50,50,50,50	0
34	NA	0	8511	1/1	0.92	0.13	-	43,43,43,43	0
32	MG	0	8112	1/1	0.94	0.18	-	64,64,64,64	0
32	MG	0	8029	1/1	0.98	0.11	-	55,55,55,55	0
32	MG	K	8069	1/1	0.95	0.09	-	62,62,62,62	0
32	MG	0	8063	1/1	0.96	0.23	-	73,73,73,73	0
32	MG	0	8050	1/1	0.80	0.12	-	97,97,97,97	0

6.5 Other polymers ⓘ

There are no such residues in this entry.