wwPDB X-ray Structure Validation Summary Report (i)

Nov 7, 2023 – 09:01 PM EST

PDB ID	:	2ZJP
Title	:	Thiopeptide antibiotic Nosiheptide bound to the large ribosomal subunit of Deinococcus radiodurans
Authors	:	Harms, J.M.; Wilson, D.N.; Schluenzen, F.; Connell, S.R.; Stachelhaus, T.; Zaborowska, Z.; Spahn, C.M.T.; Fucini, P.
Deposited on	:	2008-03-07
Resolution	:	3.70 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
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:

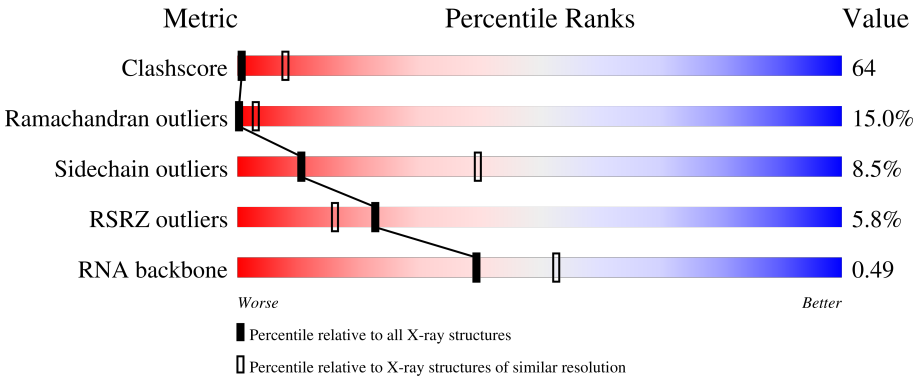
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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))
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)
RNA backbone	3102	1027 (4.40-3.00)

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

Mol	Chain	Length	Quality of chain
1	1	55	71% 95%
2	2	47	89% 96%
3	3	66	86% 92% 5%
4	4	37	8% 30% 65% 5%
5	5	13	23% 54% 23%

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Mol	Chain	Length	Quality of chain
6	A	274	5% 25% 52% 11% 12%
7	B	211	23% 59% 13%
8	C	205	14% 58% 22%
9	D	180	4% 12% 71% 14%
10	E	185	2% 27% 58% 8% 8%
11	F	144	9% 47% 48% 5%
12	G	174	3% 11% 45% 23% 18%
13	H	134	13% 75% 11%
14	I	156	4% 19% 46% 25% 10%
15	J	142	3% 18% 60% 13%
16	K	116	14% 60% 20%
17	L	114	4% 18% 54% 18% 9%
18	M	166	10% 37% 16% 35%
19	N	118	2% 16% 63% 19%
20	O	100	11% 63% 19% 6%
21	P	134	17% 63% 14% 5%
22	Q	95	16% 56% 24%
23	R	115	9% 65% 20%
24	S	237	5% 16% 46% 10% 26%
25	T	91	5% 20% 64% 8% 8%
26	U	81	2% 16% 51% 19% 11%
27	V	67	16% 69% 13%
28	W	55	20% 65% 15%
29	X	2880	4% 10% 52% 24% 7% 7%
30	Y	60	18% 62% 15%

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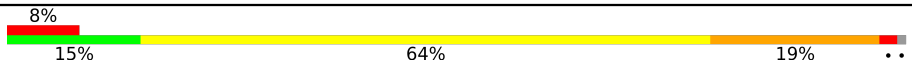
Mol	Chain	Length	Quality of chain
31	Z	123	

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
34	MG	X	2883	-	-	-	X
34	MG	X	2889	-	-	-	X
34	MG	X	2891	-	-	-	X
34	MG	X	2903	-	-	-	X
34	MG	X	2908	-	-	-	X
34	MG	Z	127	-	-	-	X
5	MH6	5	10	-	X	-	-
5	DHA	5	12	-	X	-	-
5	DBU	5	4	-	X	-	-
5	BB9	5	7	-	-	-	X

2 Entry composition (i)

There are 34 unique types of molecules in this entry. The entry contains 84444 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 protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	1	53	Total C 53 53	0	0	53

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	2	46	Total C 46 46	0	0	46

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	3	63	Total C 63 63	0	0	63

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	4	37	Total C N O S 297 179 66 47 5	0	0	0

- Molecule 5 is a protein called NOSIHEPTIDE.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	5	13	Total C N O S 69 40 12 11 6	0	0	1

- Molecule 6 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	A	240	Total C N O S 1826 1137 366 321 2	0	0	0

- Molecule 7 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	B	205	Total	C	N	O	S	0	0	0
			1539	965	295	271	8			

- Molecule 8 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	C	197	Total	C	N	O	S	0	0	0
			1506	935	287	282	2			

- Molecule 9 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	D	177	Total	C	N	O	S	0	0	0
			1400	892	247	254	7			

- Molecule 10 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	E	171	Total	C	N	O	S	0	0	0
			1286	812	237	236	1			

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	F	144	Total	C	N	O	S	0	0	0
			1044	663	179	197	5			

- Molecule 12 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	G	142	Total	C	N	O	S	0	0	0
			1114	704	209	198	3			

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	H	134	Total	C	N	O	S	0	0	0
			997	614	198	180	5			

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	I	141	Total 1067	C 655	N 216	O 196	0	0	0

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	J	136	Total 1090	C 696	N 202	O 185	S 7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	MET	-	initiating methionine	UNP Q9RXJ5

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	K	113	Total 878	C 541	N 178	O 157	S 2	0	0	0

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	L	104	Total 779	C 476	N 161	O 142	0	0	0

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	M	108	Total 871	C 543	N 172	O 156	0	0	0

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	N	117	Total 978	C 608	N 210	O 159	S 1	0	0	0

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	O	94	Total	C	N	O	0	0	0
			741	465	139	137			

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	P	127	Total	C	N	O	S	0	0	0
			1014	639	199	174	2			

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	Q	93	Total	C	N	O	S	0	0	0
			726	458	136	130	2			

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	R	110	Total	C	N	O	S	0	0	0
			825	513	160	151	1			

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	S	175	Total	C	N	O	S	0	0	0
			1345	849	236	254	6			

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	T	84	Total	C	N	O	S	0	0	0
			625	393	122	109	1			

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
26	U	72	Total	C	N	O	0	0	0
			552	341	116	95			

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	V	66	Total	C	N	O	S	0	0	0
			533	327	107	96	3			

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	W	55	Total	C	N	O	S	0	0	0
			424	264	82	76	2			

- Molecule 29 is a RNA chain called RIBOSOMAL 23S RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	X	2686	Total	C	N	O	P	0	0	0
			57651	25718	10642	18606	2685			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	Y	58	Total	C	N	O	S	0	0	0
			457	281	94	77	5			

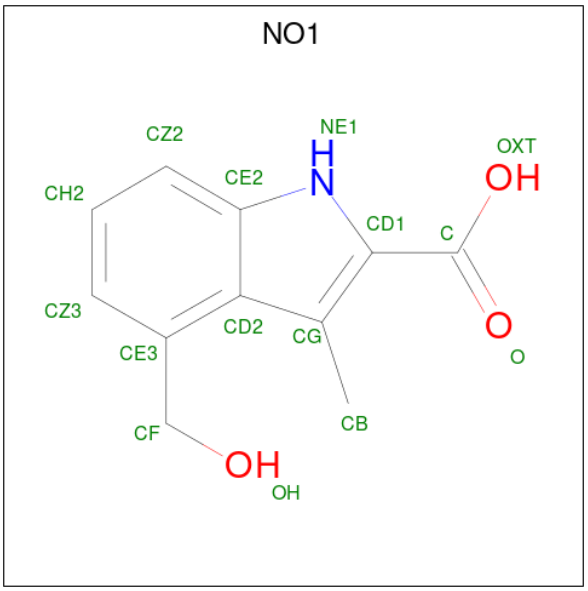
- Molecule 31 is a RNA chain called RIBOSOMAL 5S RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	Z	122	Total	C	N	O	P	0	0	0
			2598	1161	476	840	121			

- Molecule 32 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	4	1	Total	Zn	0	0
			1	1		
32	Y	1	Total	Zn	0	0
			1	1		

- Molecule 33 is 4-(hydroxymethyl)-3-methyl-1H-indole-2-carboxylic acid (three-letter code: NO1) (formula: $C_{11}H_{11}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	5	1	Total C N O 13 11 1 1	0	0

- Molecule 34 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

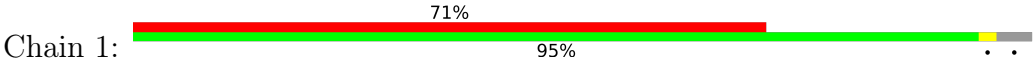
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	M	1	Total Mg 1 1	0	0
34	X	28	Total Mg 28 28	0	0
34	Z	6	Total Mg 6 6	0	0

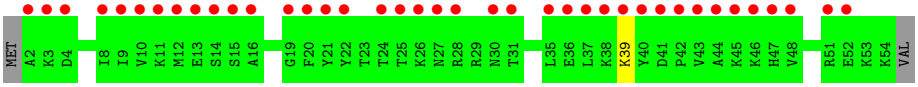
3 Residue-property plots (i)

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 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: 50S RIBOSOMAL PROTEIN L33

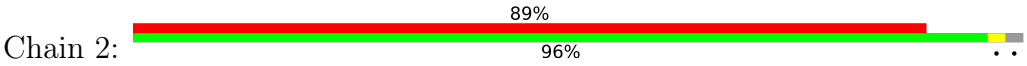
Chain 1:

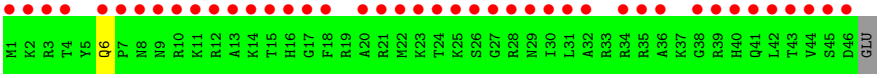




• Molecule 2: 50S RIBOSOMAL PROTEIN L34

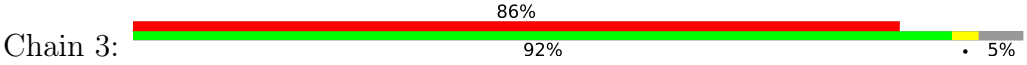
Chain 2:

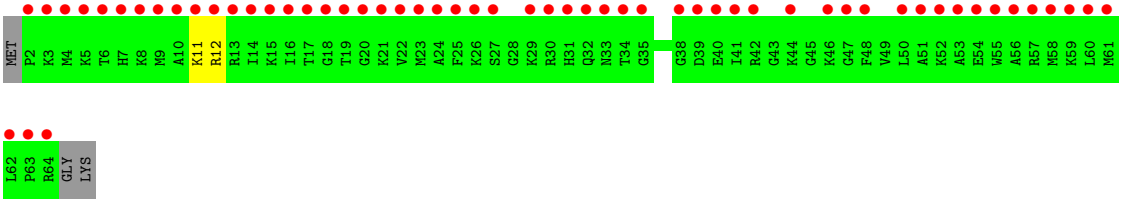




• Molecule 3: 50S RIBOSOMAL PROTEIN L35

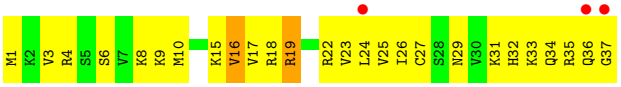
Chain 3:





• Molecule 4: 50S RIBOSOMAL PROTEIN L36

Chain 4:

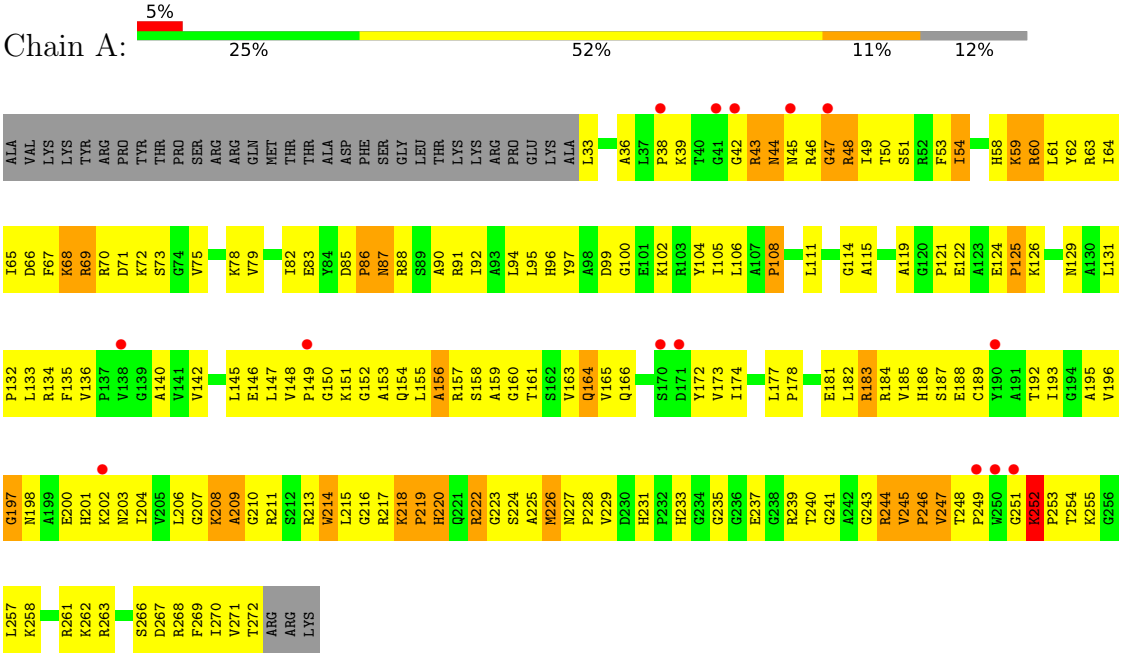


• Molecule 5: NOSIHEPTIDE

Chain 5:

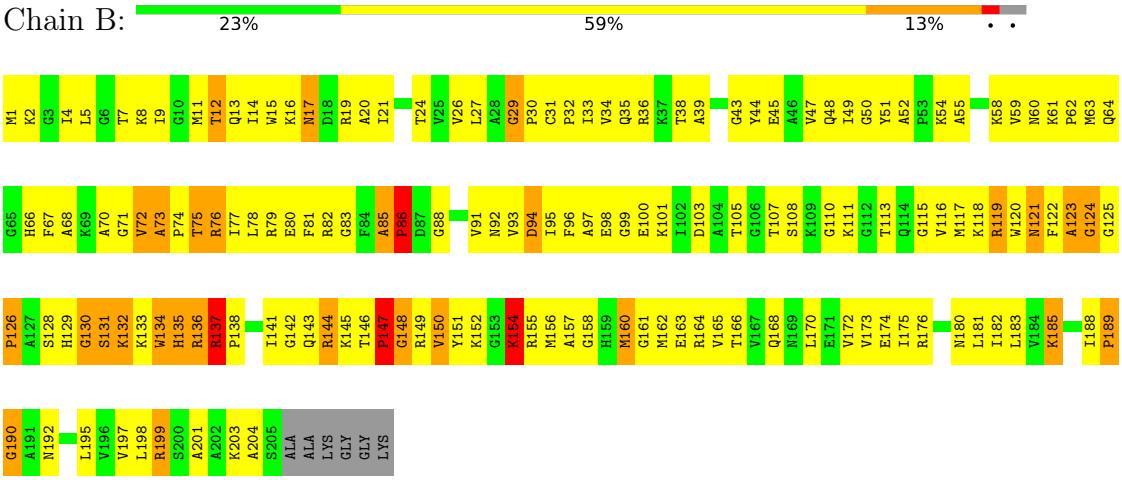
• Molecule 6: 50S RIBOSOMAL PROTEIN L2

Chain A:



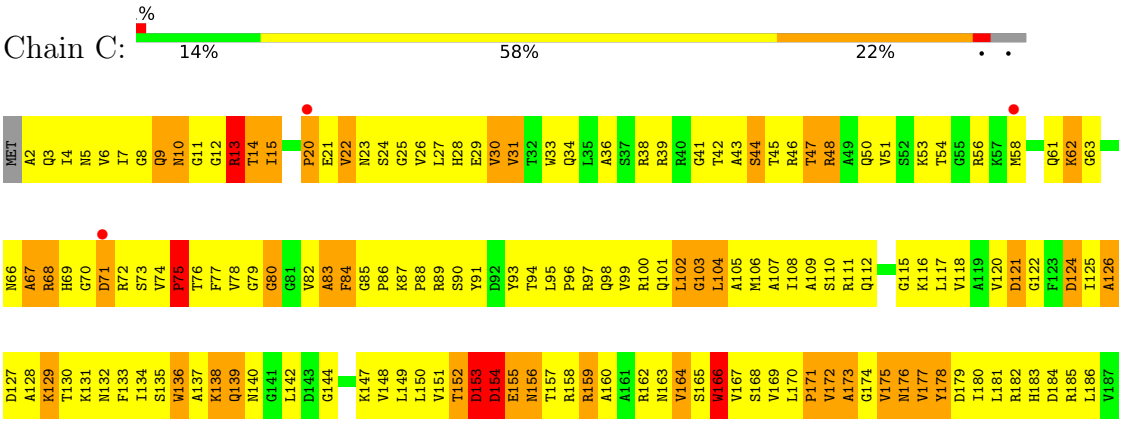
• Molecule 7: 50S RIBOSOMAL PROTEIN L3

Chain B:

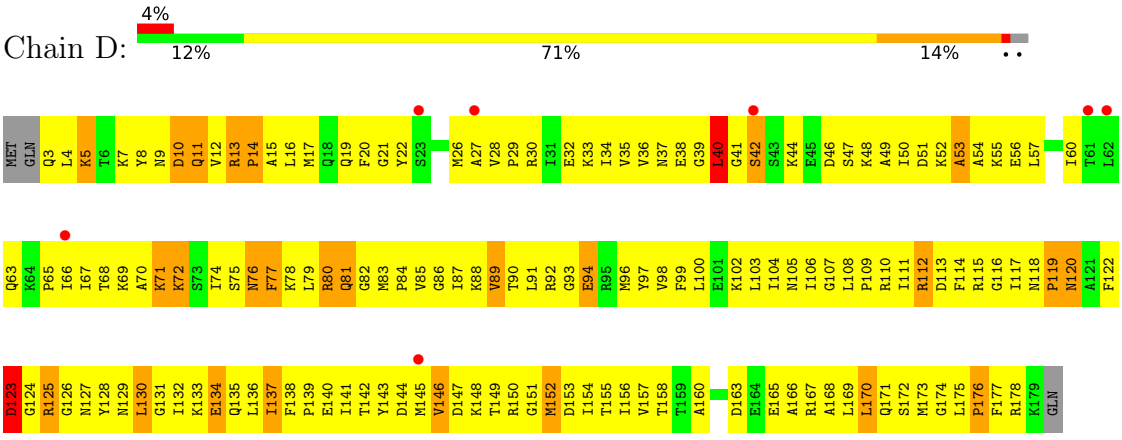


• Molecule 8: 50S RIBOSOMAL PROTEIN L4

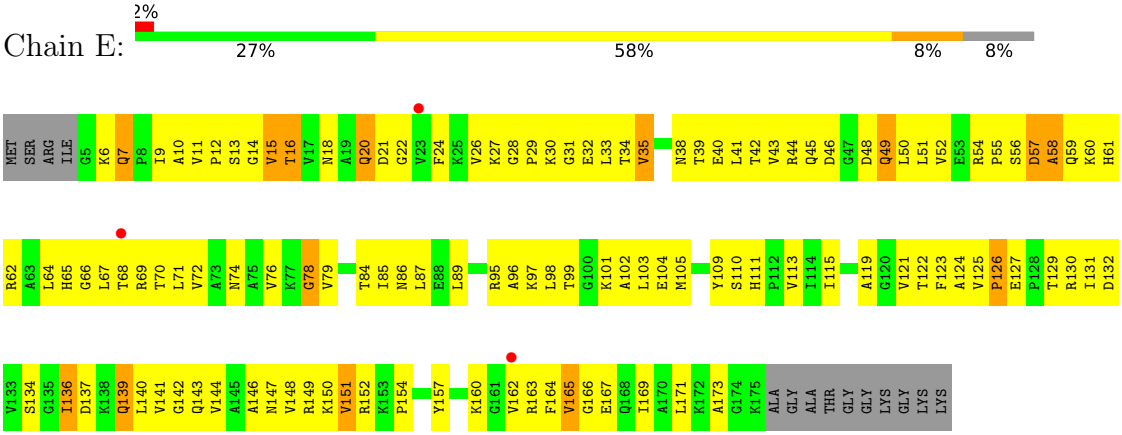
Chain C:



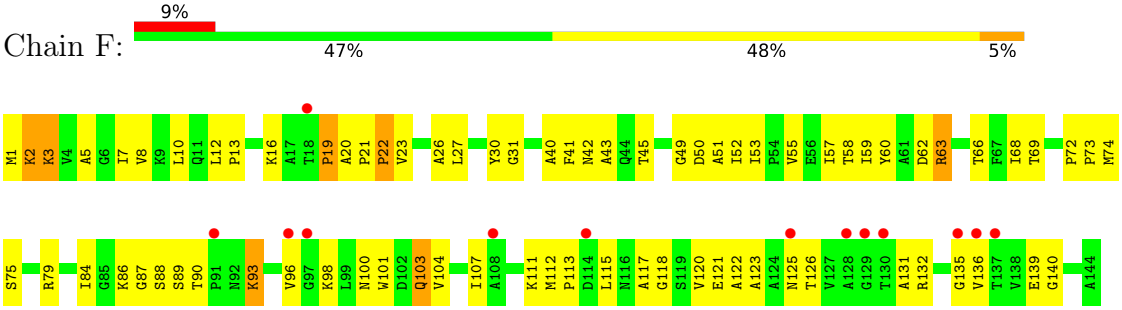
• Molecule 9: 50S RIBOSOMAL PROTEIN L5



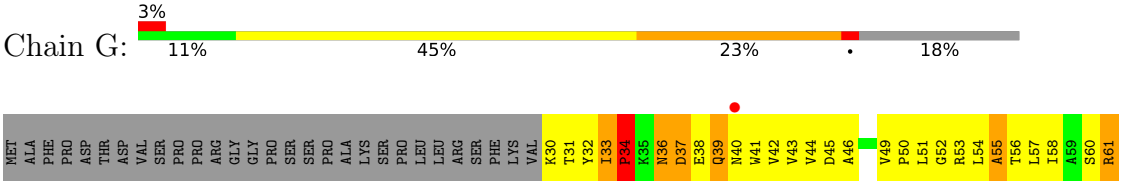
• Molecule 10: 50S RIBOSOMAL PROTEIN L6

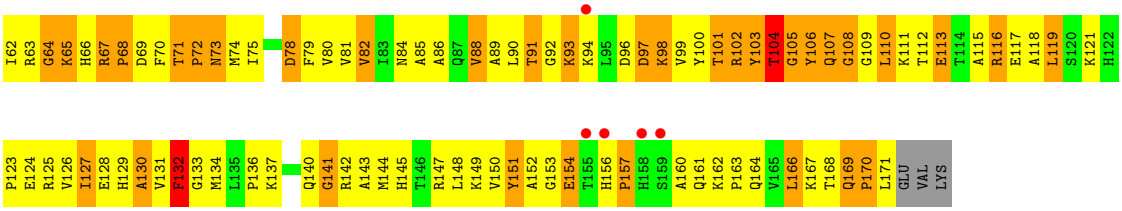


• Molecule 11: 50S RIBOSOMAL PROTEIN L11



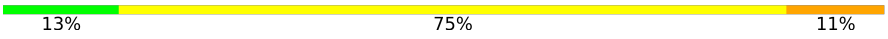
• Molecule 12: 50S RIBOSOMAL PROTEIN L13





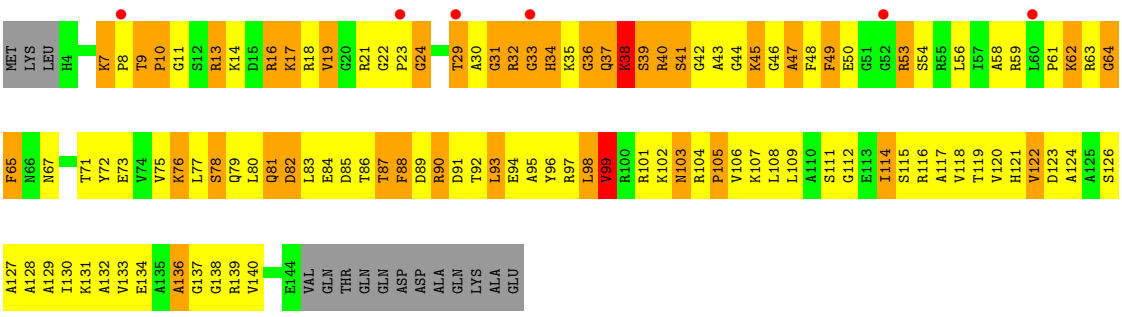
• Molecule 13: 50S RIBOSOMAL PROTEIN L14

Chain H:



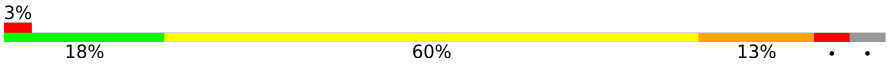
• Molecule 14: 50S RIBOSOMAL PROTEIN L15

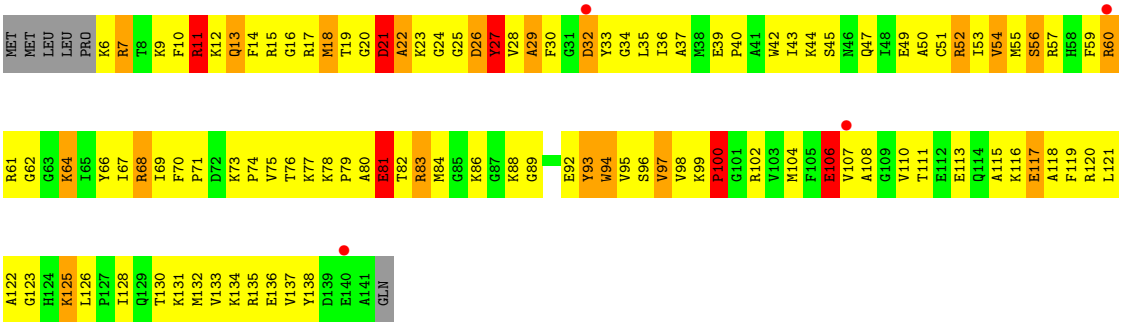
Chain I:



• Molecule 15: 50S RIBOSOMAL PROTEIN L16

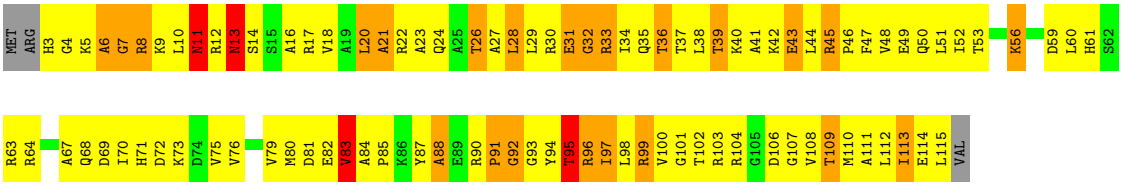
Chain J:

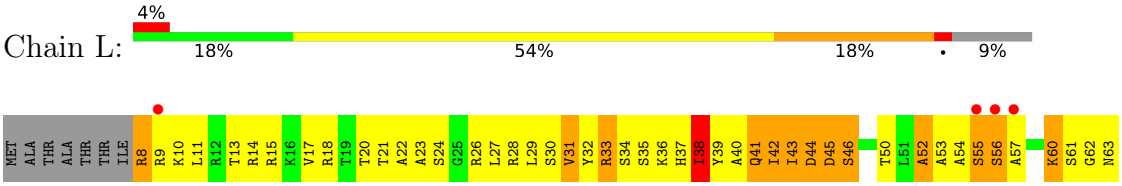




• Molecule 16: 50S RIBOSOMAL PROTEIN L17

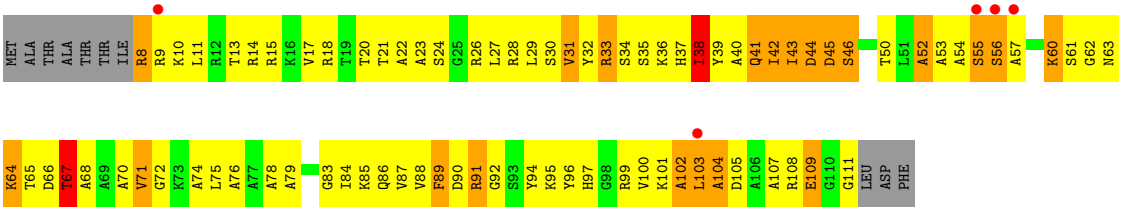
Chain K:





• Molecule 17: 50S RIBOSOMAL PROTEIN L18

Chain L:

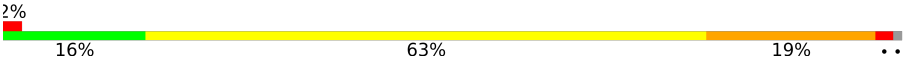


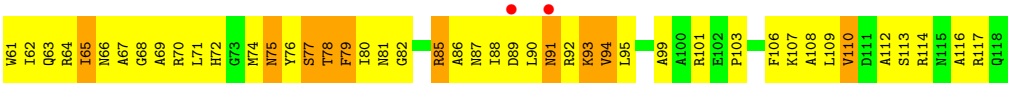
• Molecule 18: 50S RIBOSOMAL PROTEIN L19

Chain M:

• Molecule 19: 50S RIBOSOMAL PROTEIN L20

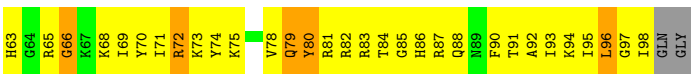
Chain N:





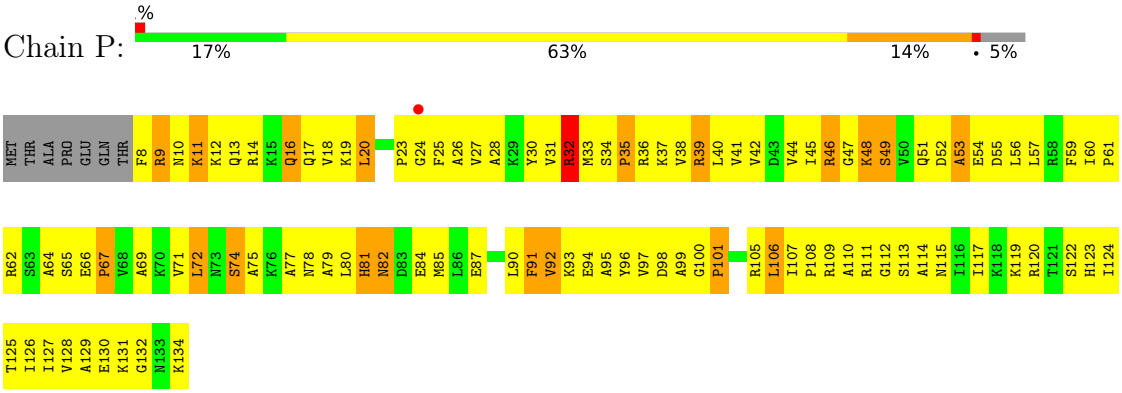
• Molecule 20: 50S RIBOSOMAL PROTEIN L21

Chain O:



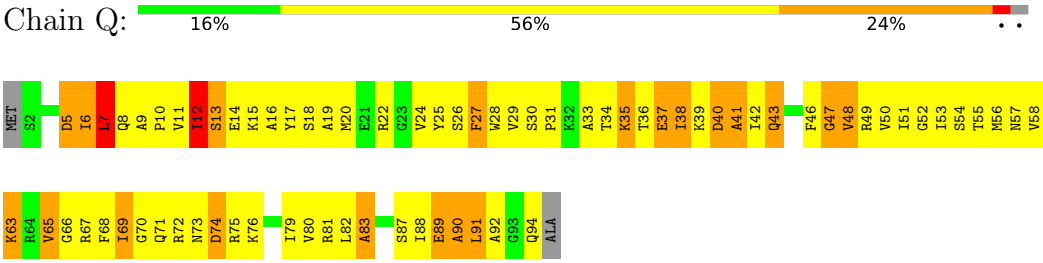
• Molecule 21: 50S RIBOSOMAL PROTEIN L22

Chain P:



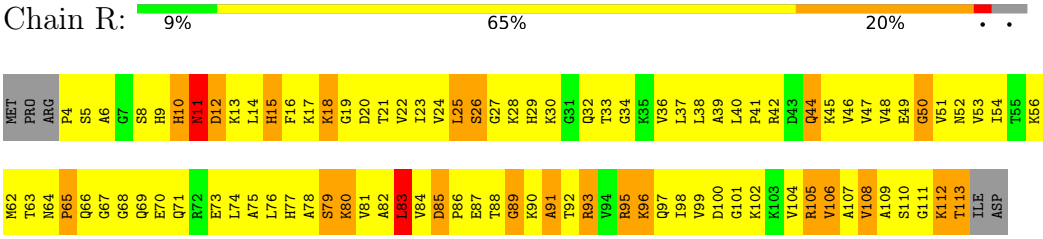
• Molecule 22: 50S RIBOSOMAL PROTEIN L23

Chain Q:



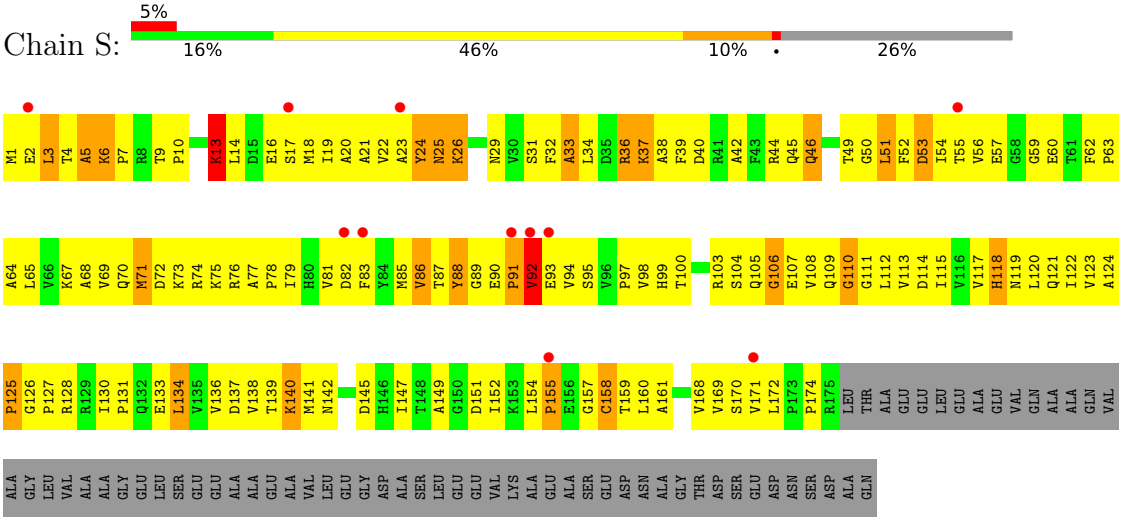
• Molecule 23: 50S RIBOSOMAL PROTEIN L24

Chain R:



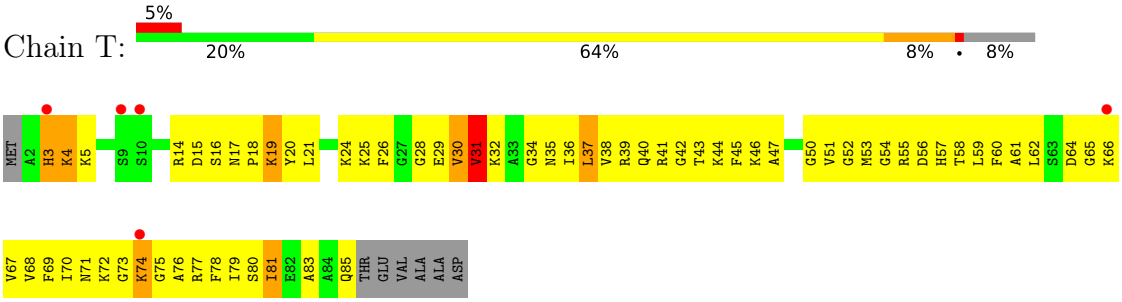
• Molecule 24: 50S RIBOSOMAL PROTEIN L25

Chain S:



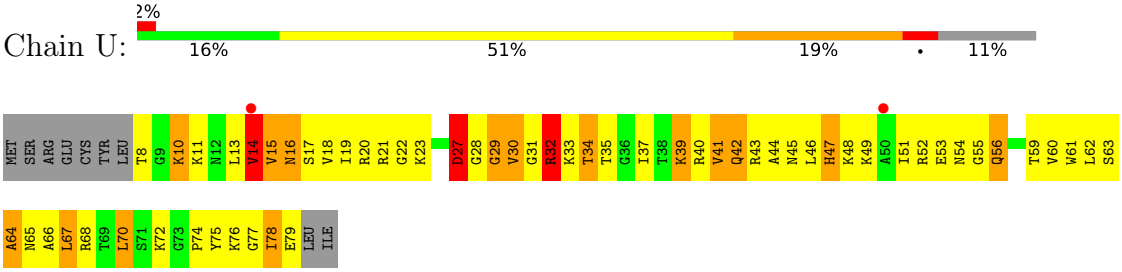
• Molecule 25: 50S RIBOSOMAL PROTEIN L27

Chain T:



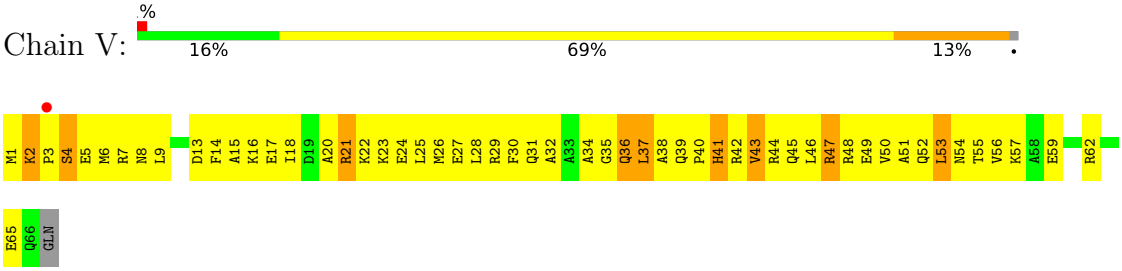
• Molecule 26: 50S RIBOSOMAL PROTEIN L28

Chain U:



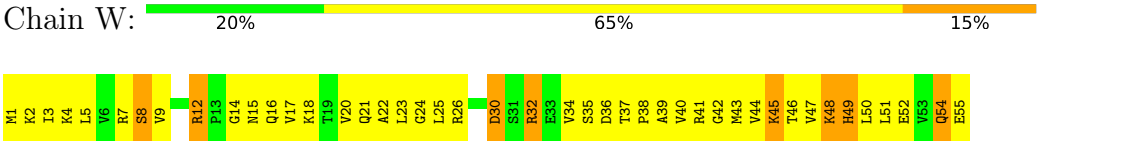
• Molecule 27: 50S RIBOSOMAL PROTEIN L29

Chain V:



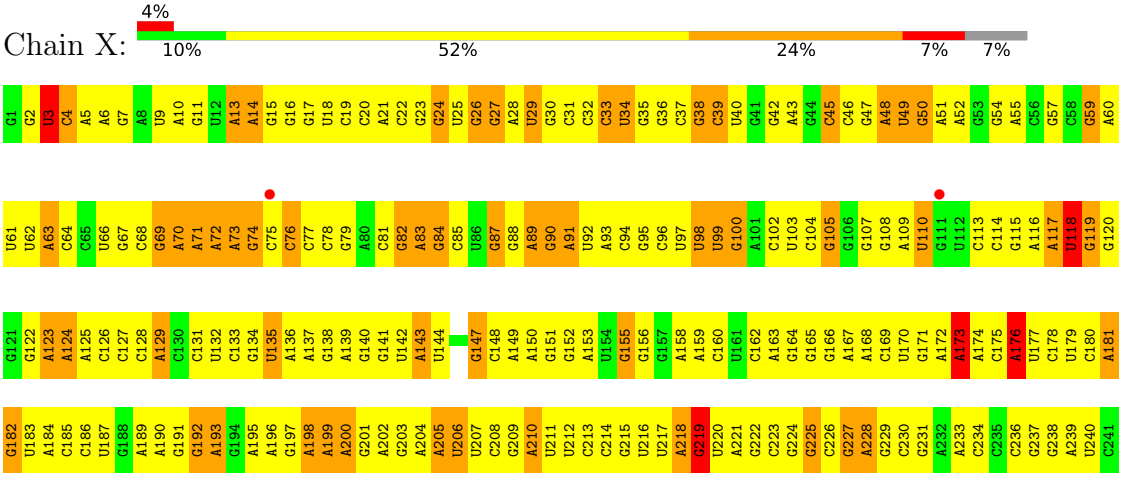
• Molecule 28: 50S RIBOSOMAL PROTEIN L30

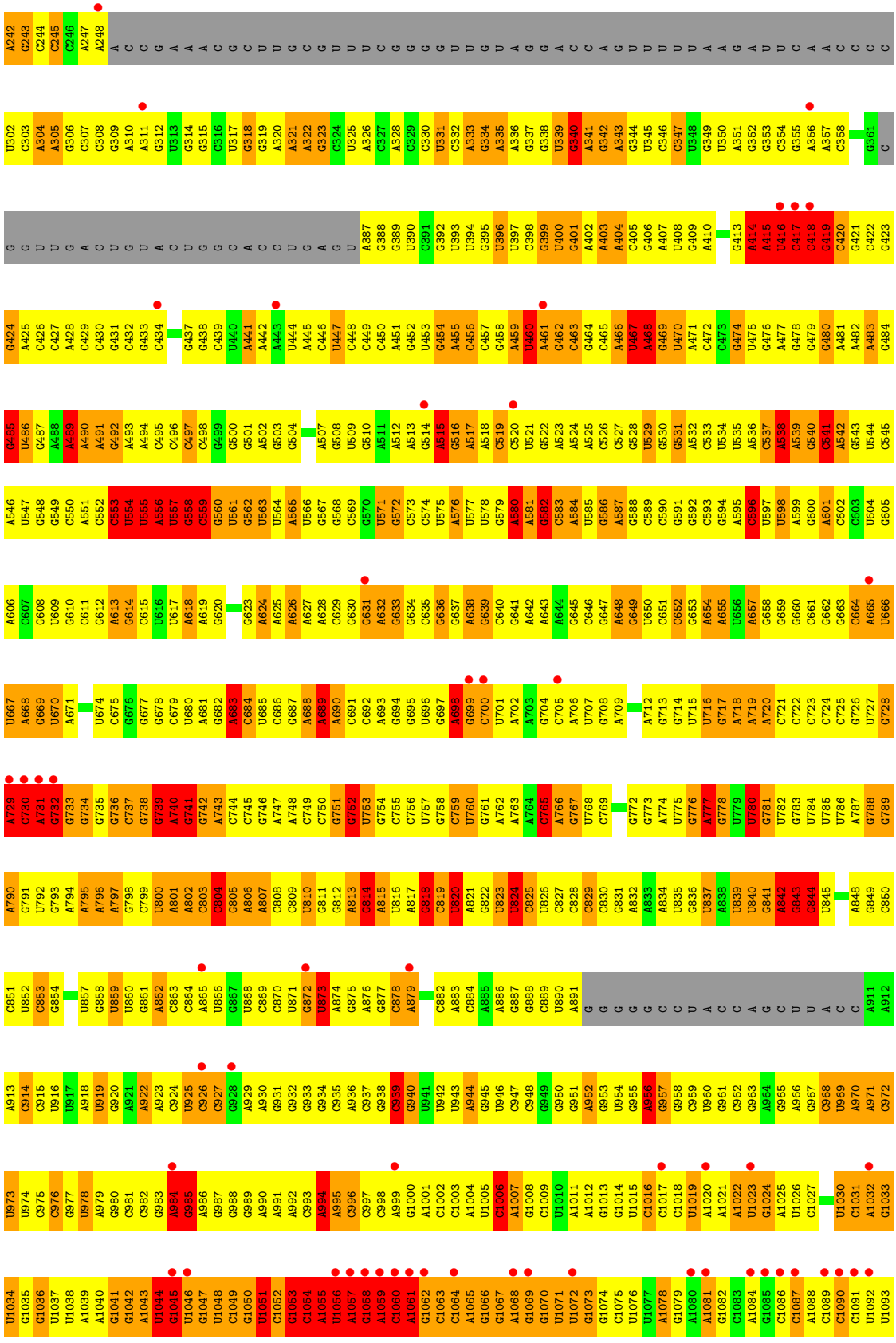
Chain W:

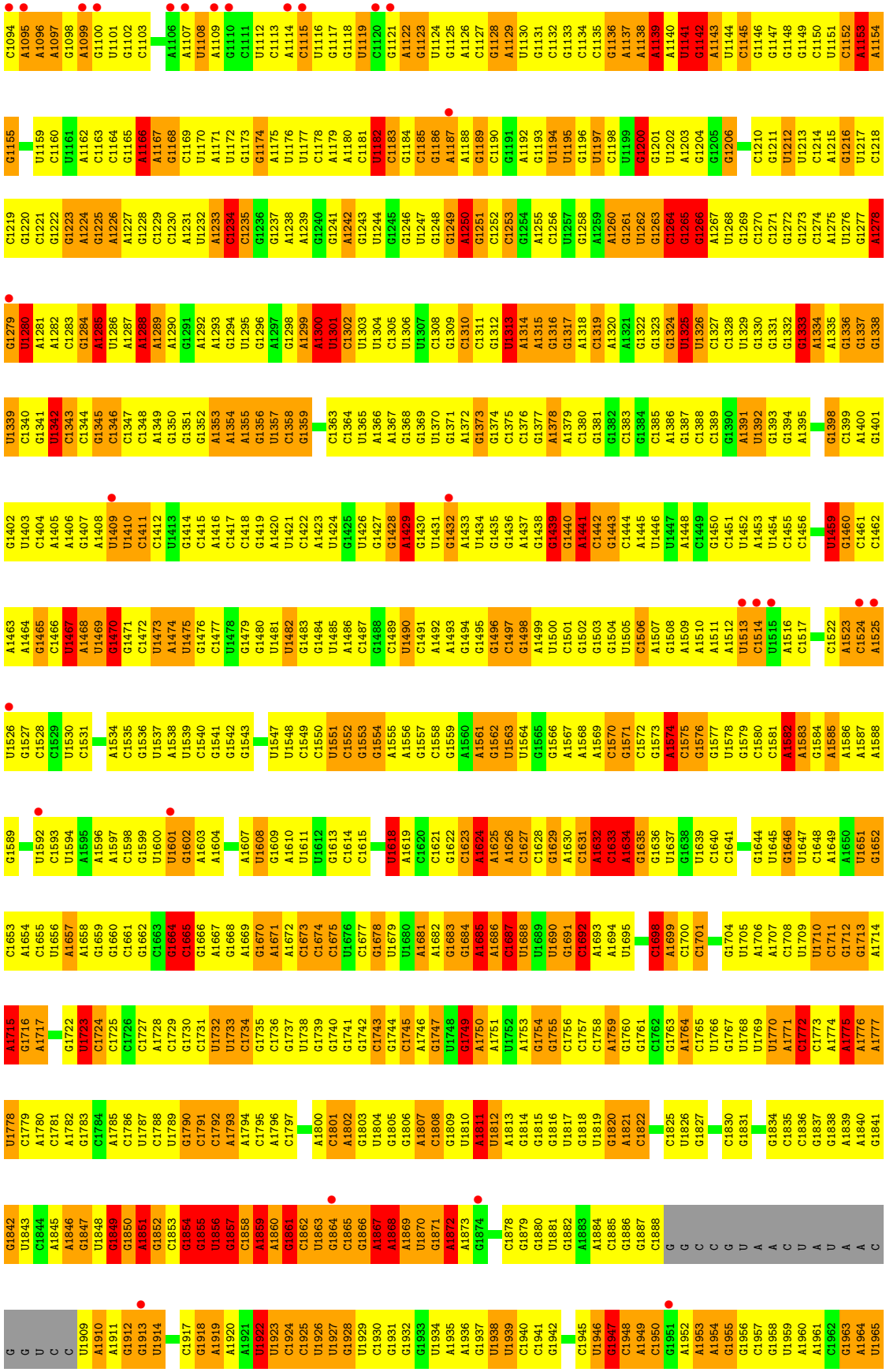


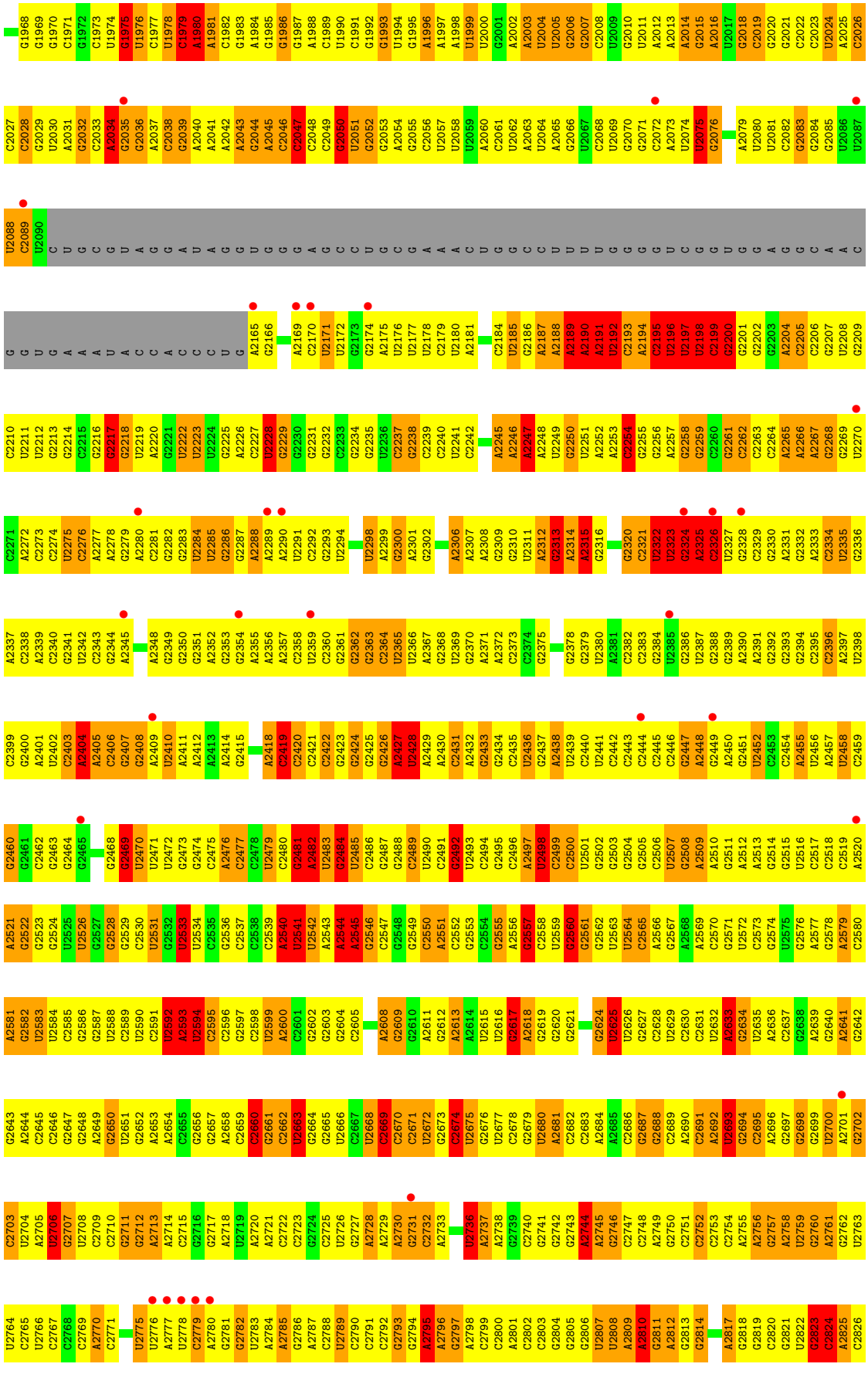
• Molecule 29: RIBOSOMAL 23S RNA

Chain X:



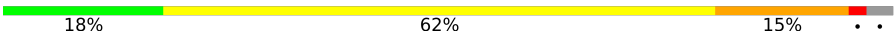


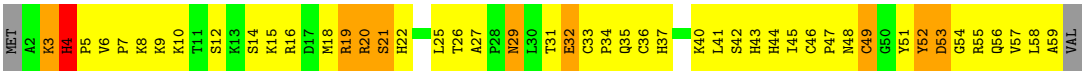




• Molecule 30: 50S RIBOSOMAL PROTEIN L32

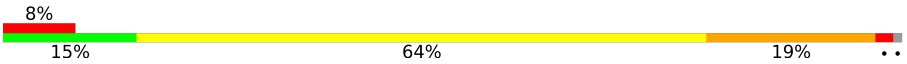
Chain Y:

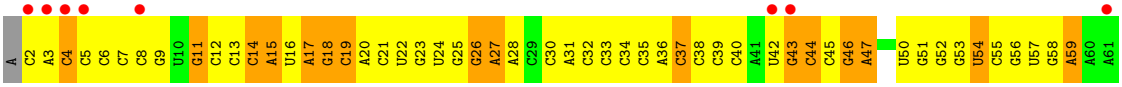




• Molecule 31: RIBOSOMAL 5S RNA

Chain Z:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	169.90Å 408.90Å 694.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.70 29.75 – 3.61	Depositor EDS
% Data completeness (in resolution range)	85.6 (30.00-3.70) 87.2 (29.75-3.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 3.65Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.300 , 0.340 0.323 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	109.2	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.19 , 129.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.83	EDS
Total number of atoms	84444	wwPDB-VP
Average B, all atoms (Å^2)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: DHA, BB9, MH6, NO1, ZN, 3GL, DBU, MG, NH2

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
4	4	0.48	0/298	0.63	0/390
5	5	3.86	2/12 (16.7%)	2.59	1/12 (8.3%)
6	A	0.46	0/1862	0.66	0/2510
7	B	0.73	0/1567	0.93	0/2105
8	C	0.54	0/1529	0.75	0/2070
9	D	0.40	0/1419	0.62	0/1903
10	E	0.42	0/1308	0.64	0/1771
11	F	0.42	0/1063	0.57	0/1440
12	G	0.57	0/1138	0.79	1/1539 (0.1%)
13	H	0.81	0/1007	1.03	1/1352 (0.1%)
14	I	0.51	0/1081	0.76	0/1448
15	J	0.60	0/1113	0.82	1/1486 (0.1%)
16	K	0.84	0/886	1.07	0/1188
17	L	0.48	0/785	0.72	0/1048
18	M	0.76	0/884	1.03	1/1186 (0.1%)
19	N	0.60	0/994	0.79	1/1323 (0.1%)
20	O	0.55	0/750	0.79	0/1000
21	P	0.72	0/1027	0.95	1/1373 (0.1%)
22	Q	0.52	0/737	0.70	0/988
23	R	0.47	0/835	0.76	0/1121
24	S	0.46	0/1370	0.66	0/1862
25	T	0.50	0/633	0.72	0/838
26	U	0.46	0/556	0.75	0/741
27	V	0.46	0/537	0.62	0/714
28	W	0.59	0/426	0.83	0/568
29	X	0.84	68/64561 (0.1%)	1.00	396/100708 (0.4%)
30	Y	0.69	0/469	0.95	1/629 (0.2%)
31	Z	0.58	1/2904 (0.0%)	0.76	0/4525
All	All	0.77	71/91751 (0.1%)	0.95	404/137838 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	5	1	0
19	N	0	1
29	X	1	199
30	Y	0	1
31	Z	0	4
All	All	2	205

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	5	1	SER	CA-CB	-10.07	1.37	1.52
29	X	2533	U	N1-C2	9.78	1.47	1.38
29	X	2492	G	C5-C6	-9.33	1.33	1.42
29	X	2533	U	C4-C5	8.27	1.50	1.43
29	X	2424	G	C5-C6	-7.50	1.34	1.42

The worst 5 of 404 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	X	1055	A	N9-C1'-C2'	-28.05	77.53	114.00
29	X	557	U	N1-C1'-C2'	19.61	139.50	114.00
29	X	417	C	N1-C1'-C2'	17.87	137.23	114.00
29	X	558	G	C3'-C2'-C1'	-13.92	90.37	101.50
29	X	556	A	N9-C1'-C2'	12.66	130.46	114.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	5	1	SER	CA
29	X	2592	U	C1'

5 of 205 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	N	32	TYR	Sidechain
29	X	228	A	Sidechain
29	X	24	G	Sidechain
29	X	26	G	Sidechain
29	X	321	A	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	1	53	0	0	2	0
2	2	46	0	0	1	0
3	3	63	0	0	2	0
4	4	297	0	328	63	0
5	5	69	0	34	3	0
6	A	1826	0	1885	312	0
7	B	1539	0	1600	305	0
8	C	1506	0	1525	334	0
9	D	1400	0	1481	313	0
10	E	1286	0	1336	201	0
11	F	1044	0	1088	101	0
12	G	1114	0	1144	278	0
13	H	997	0	1046	205	0
14	I	1067	0	1103	244	0
15	J	1090	0	1125	258	0
16	K	878	0	930	205	0
17	L	779	0	820	180	0
18	M	871	0	894	218	0
19	N	978	0	1020	200	0
20	O	741	0	756	191	0
21	P	1014	0	1096	200	0
22	Q	726	0	753	142	0
23	R	825	0	881	212	0
24	S	1345	0	1372	221	0
25	T	625	0	655	118	0
26	U	552	0	604	150	0
27	V	533	0	558	88	0
28	W	424	0	470	67	0
29	X	57651	0	29048	4666	0
30	Y	457	0	460	109	0
31	Z	2598	0	1328	176	0
32	4	1	0	0	0	0
32	Y	1	0	0	0	0
33	5	13	0	7	0	0
34	M	1	0	0	0	0
34	X	28	0	0	0	0
34	Z	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	84444	0	55347	8931	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 64.

The worst 5 of 8931 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)
18:M:108:ARG:O	18:M:109:GLU:HG3	1.25	1.33
29:X:1854:G:O2'	29:X:1855:G:H5'	1.31	1.28
29:X:1053:G:H2'	29:X:1054:C:C6	1.71	1.25
29:X:1386:A:H5"	29:X:2191:A:N6	1.48	1.25
29:X:2196:U:H2'	29:X:2197:U:O4'	1.31	1.23

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
4	4	35/37 (95%)	20 (57%)	12 (34%)	3 (9%)	1 10
5	5	2/13 (15%)	1 (50%)	1 (50%)	0	100 100
6	A	238/274 (87%)	166 (70%)	51 (21%)	21 (9%)	1 10
7	B	203/211 (96%)	143 (70%)	33 (16%)	27 (13%)	0 4
8	C	195/205 (95%)	94 (48%)	55 (28%)	46 (24%)	0 0
9	D	175/180 (97%)	99 (57%)	50 (29%)	26 (15%)	0 3
10	E	169/185 (91%)	110 (65%)	40 (24%)	19 (11%)	0 5
11	F	142/144 (99%)	101 (71%)	33 (23%)	8 (6%)	2 19
12	G	140/174 (80%)	76 (54%)	34 (24%)	30 (21%)	0 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
13	H	132/134 (98%)	106 (80%)	18 (14%)	8 (6%)	1 18
14	I	139/156 (89%)	60 (43%)	41 (30%)	38 (27%)	0 0
15	J	134/142 (94%)	76 (57%)	41 (31%)	17 (13%)	0 4
16	K	111/116 (96%)	70 (63%)	23 (21%)	18 (16%)	0 3
17	L	102/114 (90%)	65 (64%)	23 (22%)	14 (14%)	0 3
18	M	106/166 (64%)	64 (60%)	22 (21%)	20 (19%)	0 1
19	N	115/118 (98%)	65 (56%)	30 (26%)	20 (17%)	0 2
20	O	92/100 (92%)	52 (56%)	23 (25%)	17 (18%)	0 1
21	P	125/134 (93%)	84 (67%)	26 (21%)	15 (12%)	0 5
22	Q	91/95 (96%)	45 (50%)	25 (28%)	21 (23%)	0 0
23	R	108/115 (94%)	61 (56%)	28 (26%)	19 (18%)	0 2
24	S	173/237 (73%)	96 (56%)	50 (29%)	27 (16%)	0 3
25	T	82/91 (90%)	56 (68%)	16 (20%)	10 (12%)	0 4
26	U	70/81 (86%)	34 (49%)	19 (27%)	17 (24%)	0 0
27	V	64/67 (96%)	44 (69%)	12 (19%)	8 (12%)	0 4
28	W	53/55 (96%)	36 (68%)	13 (24%)	4 (8%)	1 13
30	Y	56/60 (93%)	35 (62%)	15 (27%)	6 (11%)	0 6
All	All	3052/3404 (90%)	1859 (61%)	734 (24%)	459 (15%)	0 3

5 of 459 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	A	54	ILE
6	A	59	LYS
7	B	76	ARG
7	B	85	ALA
7	B	86	PRO

5.3.2 Protein sidechains (i)

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	
4	4	35/35 (100%)	35 (100%)	0	100	100
5	5	2/3 (67%)	2 (100%)	0	100	100
6	A	185/215 (86%)	170 (92%)	15 (8%)	11	41
7	B	155/157 (99%)	145 (94%)	10 (6%)	17	48
8	C	157/163 (96%)	146 (93%)	11 (7%)	15	45
9	D	153/156 (98%)	145 (95%)	8 (5%)	23	55
10	E	136/144 (94%)	133 (98%)	3 (2%)	52	72
11	F	107/107 (100%)	103 (96%)	4 (4%)	34	61
12	G	118/146 (81%)	100 (85%)	18 (15%)	2	17
13	H	103/103 (100%)	94 (91%)	9 (9%)	10	38
14	I	108/121 (89%)	99 (92%)	9 (8%)	11	40
15	J	110/116 (95%)	94 (86%)	16 (14%)	3	18
16	K	90/93 (97%)	74 (82%)	16 (18%)	2	12
17	L	74/82 (90%)	62 (84%)	12 (16%)	2	15
18	M	94/134 (70%)	79 (84%)	15 (16%)	2	15
19	N	96/97 (99%)	91 (95%)	5 (5%)	23	55
20	O	75/79 (95%)	70 (93%)	5 (7%)	16	47
21	P	109/115 (95%)	101 (93%)	8 (7%)	14	44
22	Q	75/76 (99%)	68 (91%)	7 (9%)	9	35
23	R	91/96 (95%)	79 (87%)	12 (13%)	4	22
24	S	149/192 (78%)	141 (95%)	8 (5%)	22	54
25	T	62/67 (92%)	59 (95%)	3 (5%)	25	56
26	U	57/66 (86%)	50 (88%)	7 (12%)	4	24
27	V	54/55 (98%)	52 (96%)	2 (4%)	34	61
28	W	48/48 (100%)	44 (92%)	4 (8%)	11	40
30	Y	51/53 (96%)	46 (90%)	5 (10%)	8	33
All	All	2494/2719 (92%)	2282 (92%)	212 (8%)	10	40

5 of 212 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	K	97	ILE
18	M	90	GLN
26	U	70	LEU

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Mol	Chain	Res	Type
17	L	8	ARG
17	L	91	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
24	S	146	HIS
25	T	57	HIS
30	Y	29	ASN
14	I	34	HIS
13	H	79	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	X	2680/2880 (93%)	653 (24%)	239 (8%)
31	Z	121/123 (98%)	24 (19%)	1 (0%)
All	All	2801/3003 (93%)	677 (24%)	240 (8%)

5 of 677 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	X	4	C
29	X	13	A
29	X	14	A
29	X	27	G
29	X	29	U

5 of 240 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	X	1299	A
29	X	2660	C
29	X	1632	A
29	X	2593	A
29	X	2848	A

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

Of 10 non-standard protein/DNA/RNA residues modelled in this entry, 1 is modelled with single atom - leaving 9 for Mogul analysis.

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	$\#\|Z\| > 2$
5	DBU	5	4	5	4,4,6	4.92	4 (100%)	4,4,7	2.20	1 (25%)
5	BB9	5	9	5	2,4,6	1.52	1 (50%)	3,4,7	2.11	2 (66%)
5	MH6	5	10	5	3,4,6	3.22	1 (33%)	2,4,7	3.95	2 (100%)
5	BB9	5	5	5	3,5,6	4.14	1 (33%)	1,5,7	0.14	0
5	DHA	5	12	5	4,4,5	4.99	2 (50%)	2,4,6	2.86	2 (100%)
5	BB9	5	7	5	3,5,6	3.15	2 (66%)	1,5,7	4.72	1 (100%)
5	BB9	5	11	5	3,5,6	0.69	0	1,5,7	1.85	0
5	BB9	5	2	5	3,5,6	6.54	2 (66%)	1,5,7	5.98	1 (100%)
5	3GL	5	6	5,33	8,8,10	4.24	6 (75%)	10,10,13	1.36	1 (10%)

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
5	DBU	5	4	5	-	1/1/2/6	-
5	BB9	5	9	5	-	0/0/2/6	-
5	MH6	5	10	5	-	1/1/2/6	-
5	BB9	5	5	5	-	0/0/4/6	-
5	DHA	5	12	5	-	0/0/2/4	-
5	BB9	5	7	5	-	0/0/4/6	-
5	BB9	5	11	5	-	0/0/4/6	-
5	BB9	5	2	5	-	0/0/4/6	-
5	3GL	5	6	5,33	-	0/8/8/12	-

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	5	2	BB9	C-CA	10.97	1.62	1.45
5	5	12	DHA	C-CA	9.31	1.60	1.45
5	5	6	3GL	CG-CD	8.81	1.65	1.52
5	5	5	BB9	C-CA	7.11	1.56	1.45
5	5	4	DBU	CA-N	6.37	1.49	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	5	2	BB9	O-C-CA	-5.98	117.79	125.39
5	5	7	BB9	O-C-CA	-4.72	119.39	125.39
5	5	10	MH6	OG-CB-CA	4.21	120.27	112.19
5	5	10	MH6	C-CA-CB	3.67	126.14	118.30
5	5	4	DBU	C-CA-N	-3.67	112.42	116.53

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	5	10	MH6	C-CA-CB-OG
5	5	4	DBU	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	5	4	DBU	1	0
5	5	7	BB9	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 38 ligands modelled in this entry, 37 are monoatomic - leaving 1 for Mogul analysis.

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	$\#\|Z\| > 2$
33	NO1	5	14	5	11,14,16	4.69	6 (54%)	12,20,23	4.52	9 (75%)

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
33	NO1	5	14	5	-	0/0/2/6	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	5	14	NO1	CE3-CD2	10.42	1.61	1.44
33	5	14	NO1	CF-CE3	-7.89	1.36	1.51
33	5	14	NO1	CH2-CZ3	6.13	1.51	1.38
33	5	14	NO1	CZ3-CE3	-4.06	1.29	1.37
33	5	14	NO1	CD1-C	-2.31	1.46	1.48

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	5	14	NO1	CE3-CD2-CE2	-9.91	106.80	122.70
33	5	14	NO1	CZ2-CE2-CD2	7.96	135.30	120.76
33	5	14	NO1	CF-CE3-CD2	-5.37	114.51	124.37
33	5	14	NO1	CH2-CZ2-CE2	-4.22	114.00	120.08
33	5	14	NO1	CZ2-CE2-NE1	-3.05	121.93	130.78

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, 95^{th} 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	1	53/55 (96%)	3.66	39 (73%) 0 0	91, 120, 138, 158	0
2	2	46/47 (97%)	5.49	42 (91%) 0 0	42, 90, 116, 151	0
3	3	63/66 (95%)	4.98	57 (90%) 0 0	52, 106, 135, 145	0
4	4	37/37 (100%)	0.53	3 (8%) 12 9	73, 124, 148, 152	0
5	5	3/13 (23%)	-0.10	0 100 100	84, 84, 84, 84	0
6	A	240/274 (87%)	0.28	14 (5%) 23 16	36, 129, 160, 198	0
7	B	205/211 (97%)	-0.53	0 100 100	13, 85, 130, 161	0
8	C	197/205 (96%)	-0.28	3 (1%) 73 63	24, 110, 147, 170	0
9	D	177/180 (98%)	-0.02	7 (3%) 38 28	101, 136, 160, 179	0
10	E	171/185 (92%)	-0.23	3 (1%) 68 57	79, 131, 158, 176	0
11	F	144/144 (100%)	0.62	13 (9%) 9 7	117, 148, 172, 188	0
12	G	142/174 (81%)	0.02	6 (4%) 36 27	30, 112, 143, 169	0
13	H	134/134 (100%)	-0.69	0 100 100	13, 67, 106, 127	0
14	I	141/156 (90%)	0.18	6 (4%) 35 26	13, 128, 156, 181	0
15	J	136/142 (95%)	-0.03	4 (2%) 51 39	25, 112, 155, 202	0
16	K	113/116 (97%)	-0.67	0 100 100	13, 57, 111, 148	0
17	L	104/114 (91%)	0.18	5 (4%) 30 22	73, 125, 149, 167	0
18	M	108/166 (65%)	-0.56	0 100 100	13, 76, 121, 150	0
19	N	117/118 (99%)	-0.30	2 (1%) 70 59	16, 104, 144, 182	0
20	O	94/100 (94%)	-0.15	1 (1%) 80 71	28, 117, 151, 160	0
21	P	127/134 (94%)	-0.61	1 (0%) 86 78	13, 76, 126, 155	0
22	Q	93/95 (97%)	-0.34	0 100 100	35, 114, 152, 159	0
23	R	110/115 (95%)	-0.41	0 100 100	53, 118, 145, 161	0
24	S	175/237 (73%)	0.25	11 (6%) 20 13	78, 136, 159, 184	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
25	T	84/91 (92%)	0.20	5 (5%) 21 15	75, 117, 145, 181	0
26	U	72/81 (88%)	0.27	2 (2%) 53 40	60, 130, 160, 180	0
27	V	66/67 (98%)	-0.42	1 (1%) 73 63	83, 126, 158, 168	0
28	W	55/55 (100%)	-0.20	0 100 100	35, 105, 140, 169	0
29	X	2686/2880 (93%)	0.25	116 (4%) 35 26	13, 114, 186, 250	0
30	Y	58/60 (96%)	-0.66	0 100 100	13, 70, 119, 132	0
31	Z	122/123 (99%)	0.67	10 (8%) 11 9	38, 143, 188, 205	0
All	All	6073/6575 (92%)	0.18	351 (5%) 23 16	13, 116, 174, 250	0

The worst 5 of 351 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	2	6	GLN	16.9
3	3	35	GLY	13.4
3	3	7	HIS	13.4
2	2	8	ASN	13.2
3	3	33	ASN	11.9

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. 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	B-factors(Å^2)	Q<0.9
5	BB9	5	7	6/7	0.74	0.43	83,83,83,83	0
5	3GL	5	6	9/11	0.77	0.36	83,83,83,83	0
5	DHA	5	12	5/6	0.81	0.50	83,83,83,83	0
5	BB9	5	9	5/7	0.84	0.26	83,83,83,83	0
5	BB9	5	2	6/7	0.84	0.18	83,83,83,83	0
5	DBU	5	4	5/7	0.85	0.26	83,83,83,83	0
5	MH6	5	10	5/7	0.86	0.27	83,83,83,83	0
5	BB9	5	5	6/7	0.86	0.26	83,83,83,83	0
5	BB9	5	11	6/7	0.91	0.34	83,83,83,83	0
5	NH2	5	13	1/1	0.95	0.42	83,83,83,83	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
34	MG	X	2908	1/1	0.69	1.05	83,83,83,83	0
34	MG	X	2889	1/1	0.70	0.83	131,131,131,131	0
34	MG	X	2891	1/1	0.74	0.52	84,84,84,84	0
34	MG	X	2903	1/1	0.74	2.21	82,82,82,82	0
34	MG	X	2883	1/1	0.74	1.51	104,104,104,104	0
34	MG	Z	127	1/1	0.78	0.91	98,98,98,98	0
34	MG	X	2902	1/1	0.81	1.36	76,76,76,76	0
34	MG	X	2881	1/1	0.81	0.70	77,77,77,77	0
34	MG	Z	128	1/1	0.81	0.26	110,110,110,110	0
34	MG	X	2892	1/1	0.82	0.57	109,109,109,109	0
34	MG	Z	125	1/1	0.82	1.00	83,83,83,83	0
34	MG	X	2882	1/1	0.82	0.35	112,112,112,112	0
34	MG	X	2885	1/1	0.82	0.69	98,98,98,98	0
33	NO1	5	14	13/15	0.83	0.28	83,83,83,83	0
34	MG	X	2895	1/1	0.83	0.22	81,81,81,81	0
34	MG	Z	129	1/1	0.83	0.86	101,101,101,101	0
34	MG	Z	126	1/1	0.84	1.16	122,122,122,122	0
34	MG	X	2896	1/1	0.85	1.48	86,86,86,86	0
34	MG	X	2893	1/1	0.88	1.13	85,85,85,85	0
34	MG	X	2901	1/1	0.89	0.54	100,100,100,100	0
32	ZN	4	38	1/1	0.89	0.05	125,125,125,125	0
34	MG	X	2888	1/1	0.89	2.17	73,73,73,73	0
32	ZN	Y	61	1/1	0.91	0.08	118,118,118,118	0
34	MG	M	167	1/1	0.91	1.30	68,68,68,68	0
34	MG	Z	124	1/1	0.92	0.63	113,113,113,113	0
34	MG	X	2906	1/1	0.93	1.36	82,82,82,82	0
34	MG	X	2907	1/1	0.94	0.38	66,66,66,66	0
34	MG	X	2886	1/1	0.94	0.20	80,80,80,80	0
34	MG	X	2905	1/1	0.95	0.57	123,123,123,123	0
34	MG	X	2897	1/1	0.95	0.95	100,100,100,100	0
34	MG	X	2898	1/1	0.96	0.57	57,57,57,57	0
34	MG	X	2900	1/1	0.97	0.12	104,104,104,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
34	MG	X	2904	1/1	0.97	0.79	81,81,81,81	0
34	MG	X	2890	1/1	0.97	0.22	58,58,58,58	0
34	MG	X	2899	1/1	0.97	0.65	57,57,57,57	0
34	MG	X	2894	1/1	0.98	0.60	57,57,57,57	0
34	MG	X	2884	1/1	0.98	0.28	98,98,98,98	0
34	MG	X	2887	1/1	0.98	0.75	98,98,98,98	0

6.5 Other polymers (i)

There are no such residues in this entry.