wwPDB X-ray Structure Validation Summary Report (i)

Oct 10, 2023 – 08:19 AM EDT

PDB ID	:	5DM7
Title	:	Crystal structure of the 50S ribosomal subunit from Deinococcus radiodurans in complex with hygromycin A
Authors	:	Kaminishi, T.; Schedlbauer, A.; Ochoa-Lizarralde, B.; Connell, S.R.; Fucini, P.
Deposited on	:	2015-09-08
Resolution	:	3.00 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 (i)) were used in the production of this report:

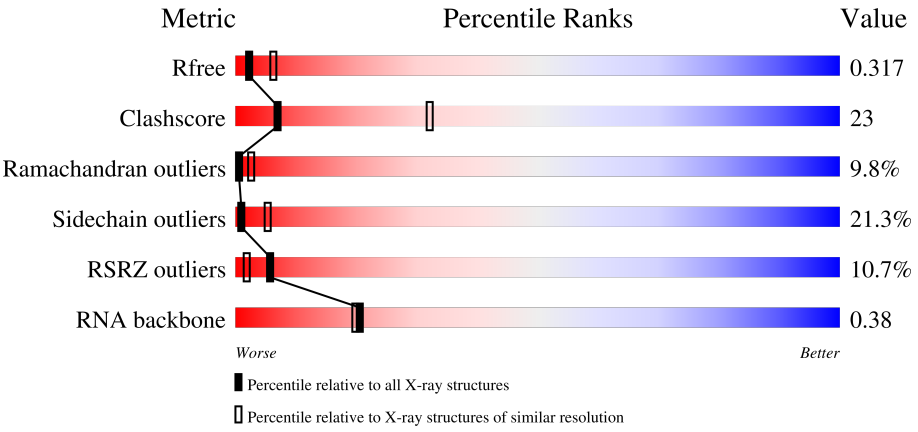
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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	0	224	80% 54% 39% 6%
2	A	274	14% 43% 47% 9%
3	B	205	2% 33% 50% 17%

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Mol	Chain	Length	Quality of chain
4	C	197	5% 30% 50% 17%
5	D	177	8% 38% 49% 13%
6	E	171	6% 46% 44% 9%
7	F	144	42% 60% 33% 6%
8	G	142	6% 47% 45% 6%
9	H	134	3% 29% 46% 23%
10	I	141	24% 43% 43% 11%
11	J	136	18% 39% 44% 15%
12	K	113	5% 29% 51% 17%
13	L	104	25% 29% 46% 24%
14	M	109	3% 32% 44% 23%
15	N	117	9% 30% 62% 8%
16	O	94	6% 38% 45% 16%
17	P	127	5% 31% 53% 15%
18	Q	93	13% 46% 39% 14%
19	R	110	7% 34% 41% 25%
20	S	175	14% 41% 43% 13%
21	T	84	20% 42% 46% 11%
22	U	72	29% 24% 51% 17% 8%
23	V	66	18% 61% 32% 8%
24	W	55	11% 38% 56% 5%
25	Z	57	5% 30% 51% 18%
26	1	54	43% 46% 39% 13%
27	2	47	4% 40% 47% 13%
28	3	65	40% 17% 60% 20%

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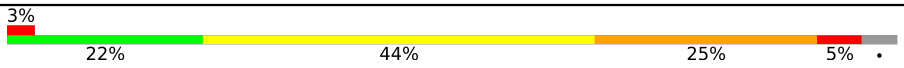
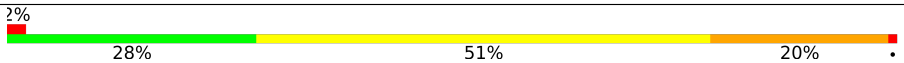
Mol	Chain	Length	Quality of chain
29	X	2881	
30	Y	122	

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
31	MG	X	6006	-	-	-	X
31	MG	X	6035	-	-	-	X
31	MG	X	6051	-	-	-	X
31	MG	X	6076	-	-	-	X
31	MG	X	6099	-	-	-	X
31	MG	X	6101	-	-	-	X
31	MG	X	6111	-	-	-	X
31	MG	X	6114	-	-	-	X
31	MG	X	6116	-	-	-	X
31	MG	X	6118	-	-	-	X
31	MG	X	6124	-	-	-	X
31	MG	X	6125	-	-	-	X
31	MG	X	6127	-	-	-	X
31	MG	X	6135	-	-	-	X
31	MG	X	6139	-	-	-	X
31	MG	X	6140	-	-	-	X
31	MG	X	6149	-	-	-	X
31	MG	X	6150	-	-	-	X
31	MG	X	6159	-	-	-	X
31	MG	X	6160	-	-	-	X
31	MG	X	6162	-	-	-	X
31	MG	X	6168	-	-	-	X
31	MG	X	6169	-	-	-	X
31	MG	X	6176	-	-	-	X
31	MG	Y	205	-	-	-	X

2 Entry composition (i)

There are 32 unique types of molecules in this entry. The entry contains 89361 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 L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	224	Total	C	N	O	S	0	0	0
			1651	1031	302	313	5			

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	274	Total	C	N	O	S	0	0	0
			2107	1313	423	368	3			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	LYS	ARG	conflict	UNP Q9RXJ9
A	25	ALA	THR	conflict	UNP Q9RXJ9
A	270	LEU	ILE	conflict	UNP Q9RXJ9

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	205	Total	C	N	O	S	0	0	0
			1540	965	295	272	8			

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	197	Total	C	N	O	S	0	0	0
			1507	935	287	283	2			

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	177	Total	C	N	O	S	0	0	0
			1401	892	247	255	7			

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	E	171	Total	C	N	O	S	0	0	0
			1287	812	237	237	1			

- Molecule 7 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	F	144	Total	C	N	O	S	0	0	0
			1048	663	183	197	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	2	ARG	LYS	conflict	UNP Q9RSS7
F	3	ARG	LYS	conflict	UNP Q9RSS7

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	G	142	Total	C	N	O	S	0	0	0
			1115	704	209	199	3			

- Molecule 9 is a protein called 50S ribosomal protein L14.

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

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	I	141	Total	C	N	O	0	0	0
			1068	655	216	197			

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	J	136	Total	C	N	O	S	0	0	0
			1091	696	202	186	7			

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	K	113	Total	C	N	O	S	0	0	0
			879	541	178	158	2			

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	L	104	Total	C	N	O	0	0	0
			778	476	159	143			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	26	LYS	ARG	conflict	UNP Q9RSL2

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	M	109	Total	C	N	O	0	0	0
			867	540	171	156			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	?	-	LEU	deletion	UNP Q9RWB4
M	?	-	ARG	deletion	UNP Q9RWB4
M	?	-	GLU	deletion	UNP Q9RWB4
M	?	-	LEU	deletion	UNP Q9RWB4

- Molecule 15 is a protein called 50S ribosomal protein L20.

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

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	O	94	Total	C	N	O	0	0	0
			742	465	139	138			

- Molecule 17 is a protein called 50S ribosomal protein L22.

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

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	Q	93	Total	C	N	O	S	0	0	0
			727	458	136	131	2			

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	R	110	Total	C	N	O	S	0	0	0
			826	513	160	152	1			

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	S	175	Total	C	N	O	S	0	0	0
			1346	849	236	255	6			

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	T	84	Total	C	N	O	S	0	0	0
			626	393	122	110	1			

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	U	72	Total	C	N	O	0	0	0
			553	341	116	96			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	67	ILE	LEU	conflict	UNP Q9RRG8

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	V	66	Total	C	N	O	S	0	0	0
			534	327	107	97	3			

- Molecule 24 is a protein called 50S ribosomal protein L30.

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

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	Z	57	Total	C	N	O	S	0	0	0
			453	278	93	77	5			

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	1	54	Total	C	N	O	S	0	0	0
			404	256	73	74	1			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	0	ALA	-	insertion	UNP Q9RSS4
1	1	ALA	-	insertion	UNP Q9RSS4
1	3	GLY	LYS	conflict	UNP Q9RSS4
1	4	ALA	ASP	conflict	UNP Q9RSS4
1	5	ALA	GLY	conflict	UNP Q9RSS4
1	45	ALA	LYS	conflict	UNP Q9RSS4
1	46	HIS	LYS	conflict	UNP Q9RSS4
1	47	VAL	HIS	conflict	UNP Q9RSS4
1	49	PHE	VAL	conflict	UNP Q9RSS4
1	50	ALA	PHE	conflict	UNP Q9RSS4
1	51	ALA	-	insertion	UNP Q9RSS4
1	52	ALA	-	insertion	UNP Q9RSS4
1	53	ALA	-	insertion	UNP Q9RSS4

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	2	47	Total	C	N	O	S	0	0	0
			393	235	92	64	2			

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	3	65	Total	C	N	O	S	0	0	0
			509	320	104	80	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	X	2780	Total	C	N	O	P	0	0	0
			59673	26617	11011	19265	2780			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	1526	U	UNK	conflict	GB 11612676

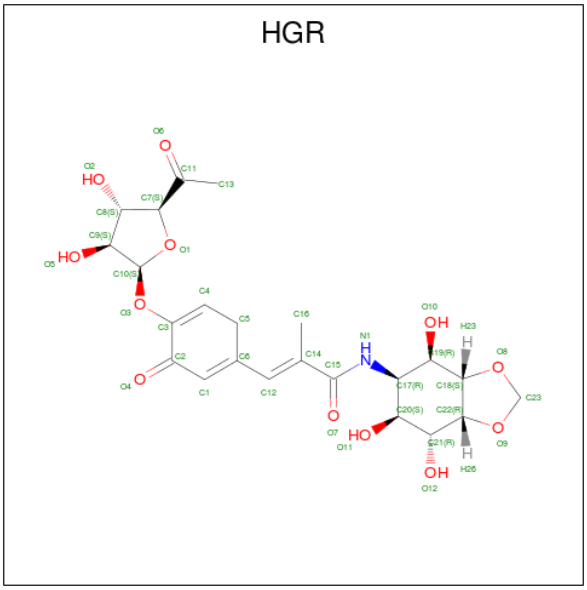
- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	Y	122	Total	C	N	O	P	0	0	0
			2601	1161	476	842	122			

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
31	A	1	Total	Mg	0	0
			1	1		
31	H	1	Total	Mg	0	0
			1	1		
31	M	1	Total	Mg	0	0
			1	1		
31	N	1	Total	Mg	0	0
			1	1		
31	X	177	Total	Mg	0	0
			177	177		
31	Y	5	Total	Mg	0	0
			5	5		

- Molecule 32 is Hygromycin A (three-letter code: HGR) (formula: $C_{23}H_{29}NO_{12}$).



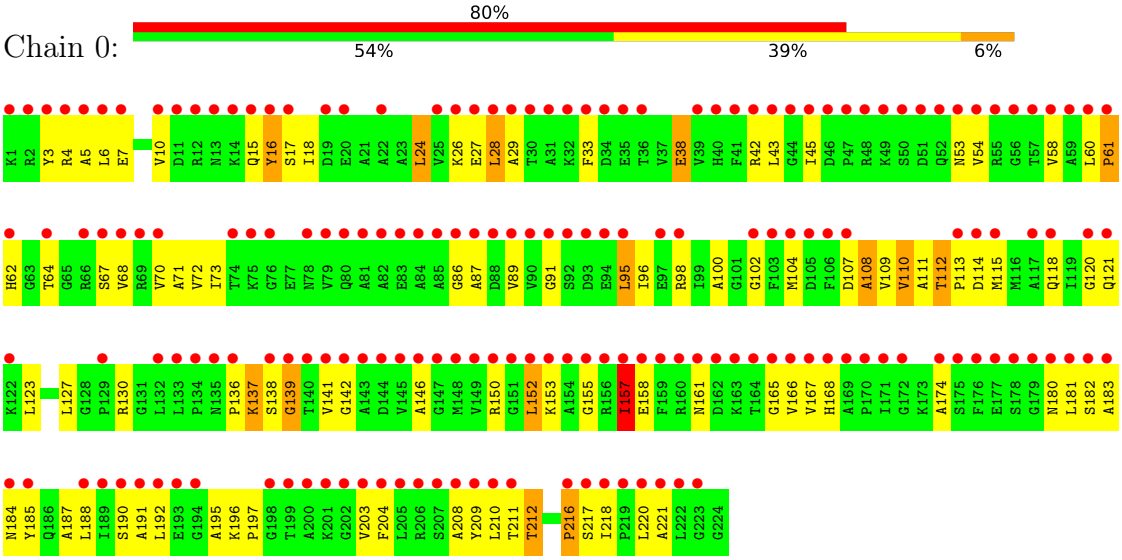
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	X	1	Total C N O 36 23 1 12	0	0

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.

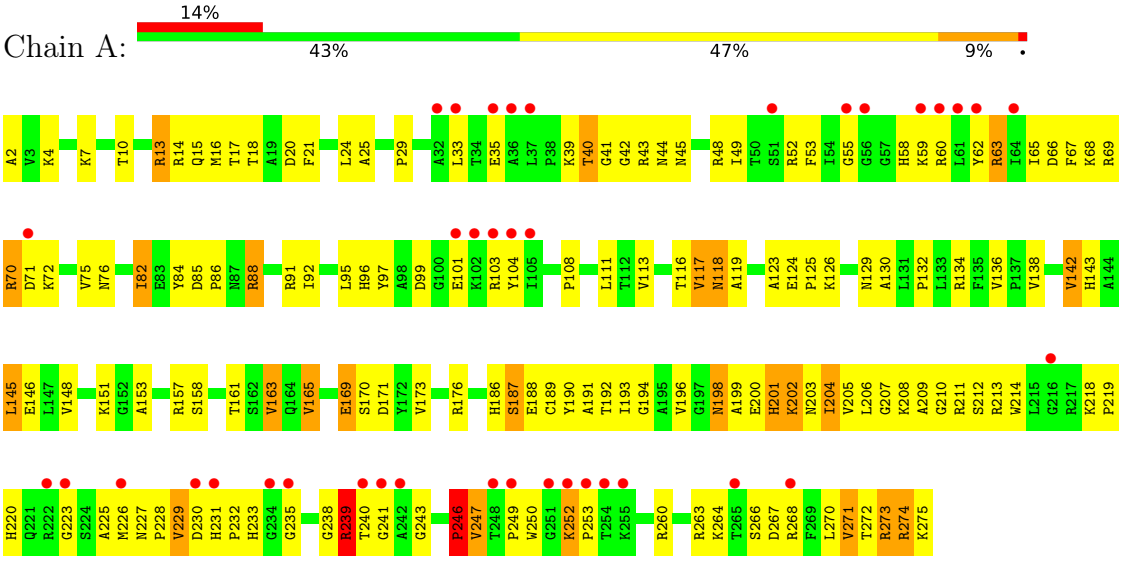
• Molecule 1: 50S ribosomal protein L1

Chain 0:



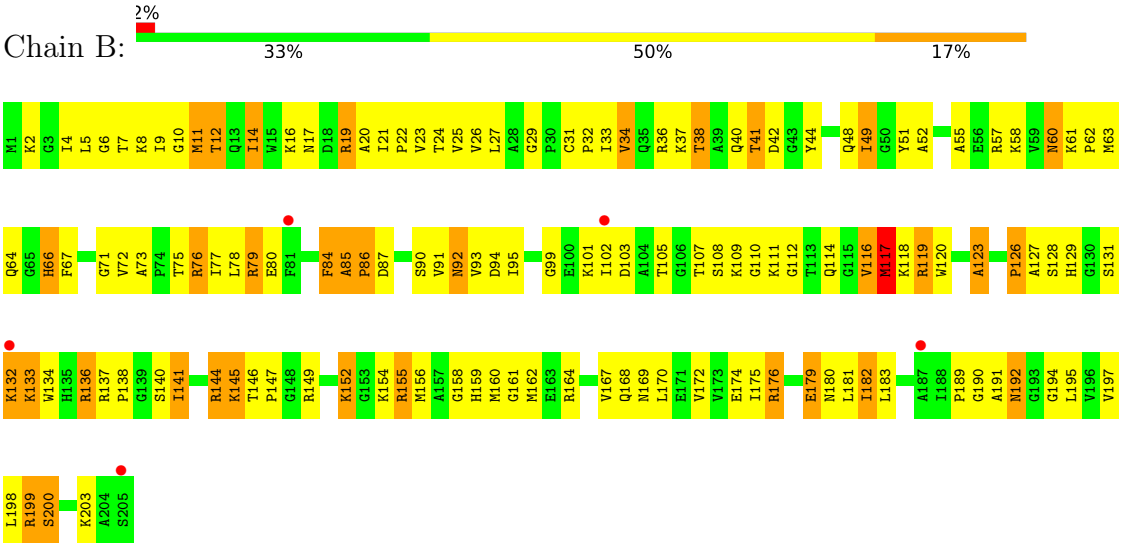
• Molecule 2: 50S ribosomal protein L2

Chain A:



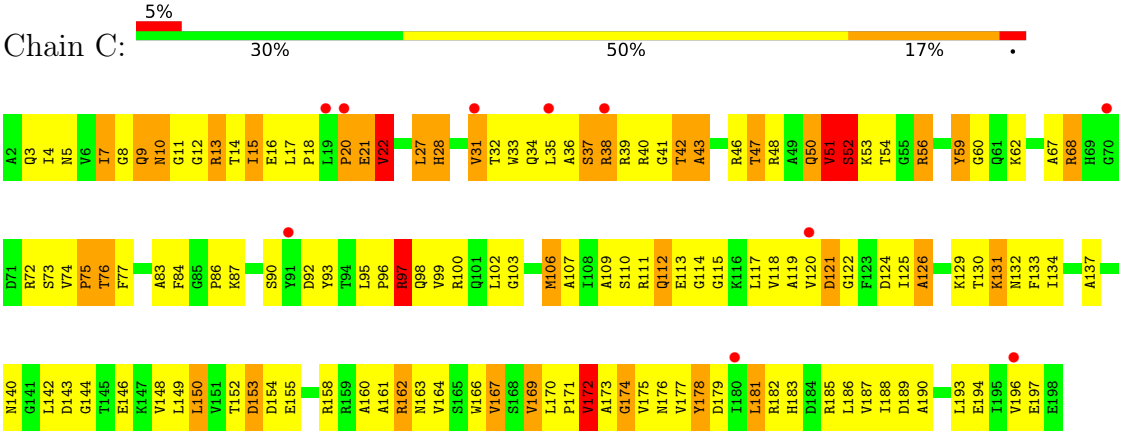
• Molecule 3: 50S ribosomal protein L3

Chain B:



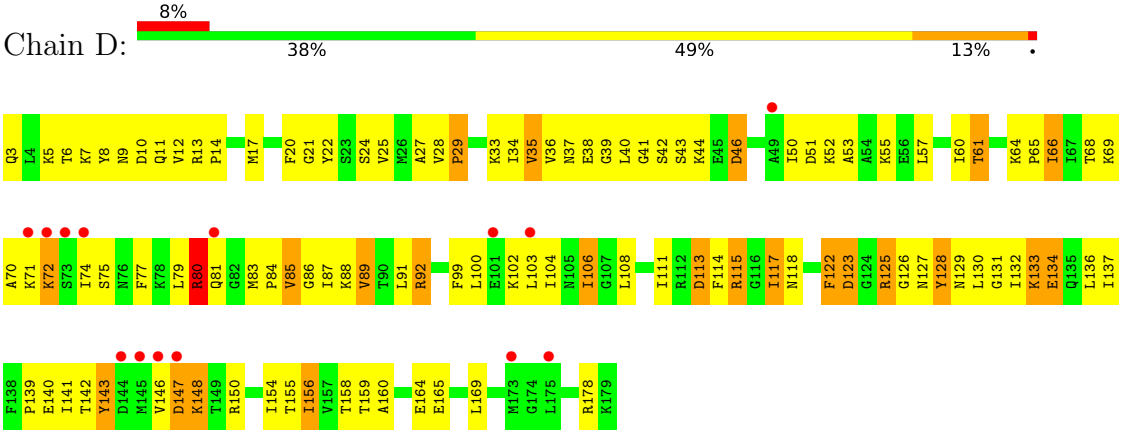
• Molecule 4: 50S ribosomal protein L4

Chain C:



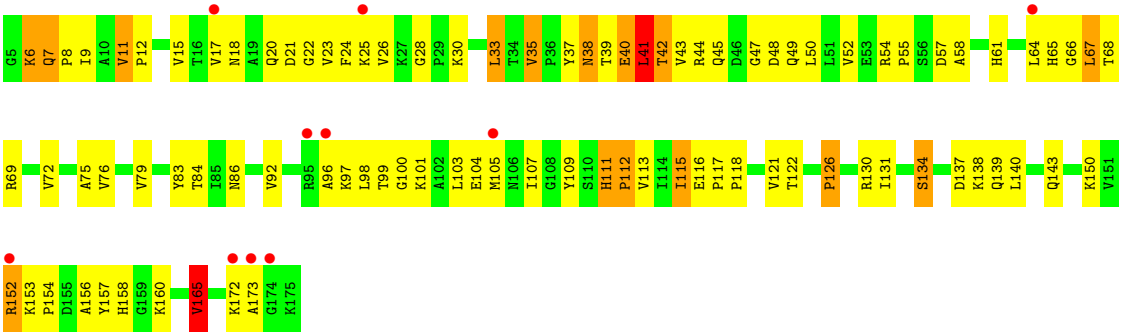
• Molecule 5: 50S ribosomal protein L5

Chain D:

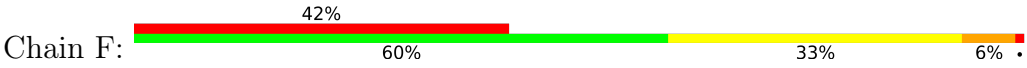


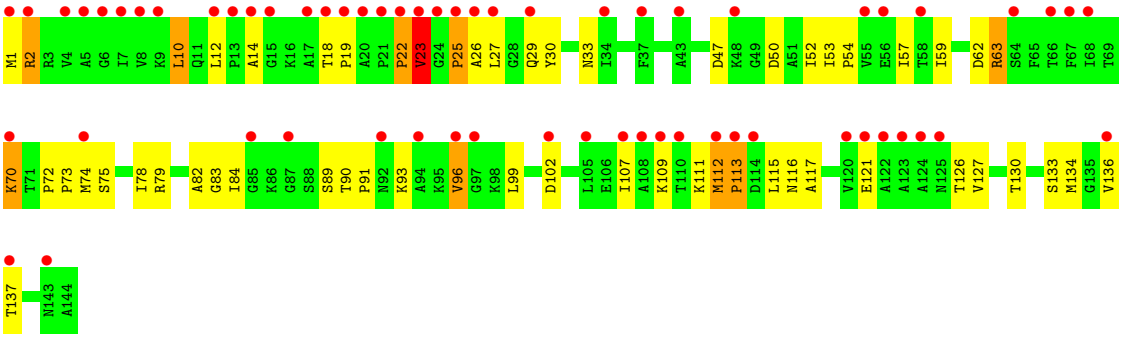
• Molecule 6: 50S ribosomal protein L6

Chain E:

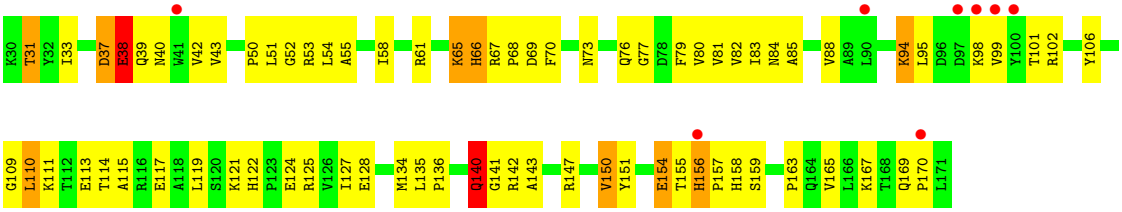


• Molecule 7: 50S ribosomal protein L11

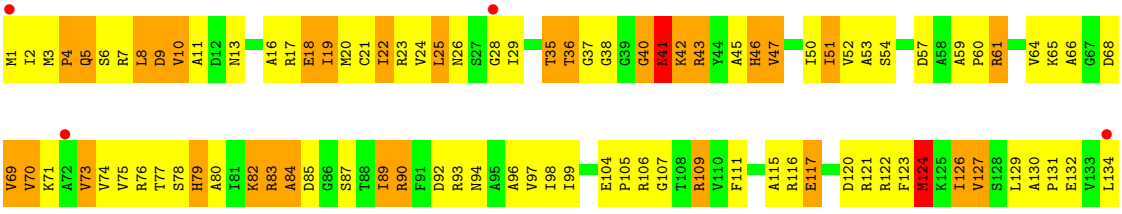




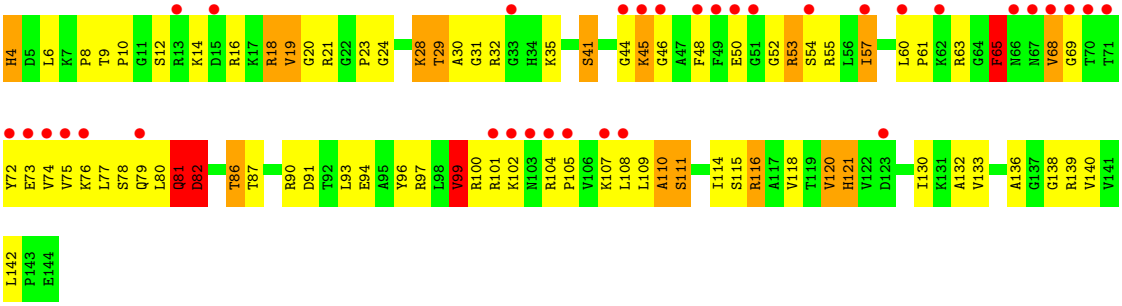
• Molecule 8: 50S ribosomal protein L13



• Molecule 9: 50S ribosomal protein L14

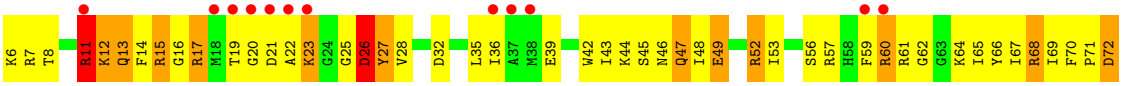


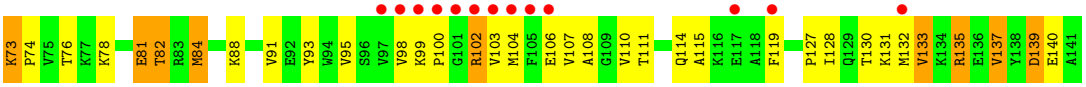
• Molecule 10: 50S ribosomal protein L15



• Molecule 11: 50S ribosomal protein L16

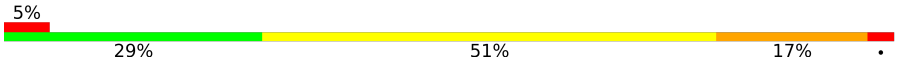
Chain J:

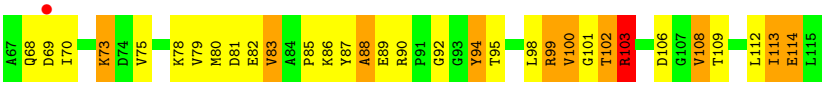




• Molecule 12: 50S ribosomal protein L17

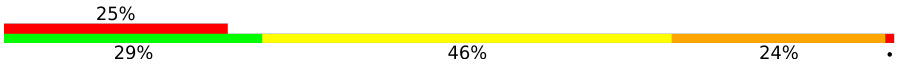
Chain K:

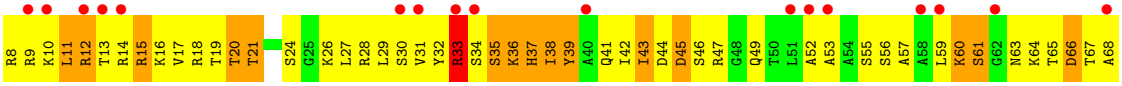


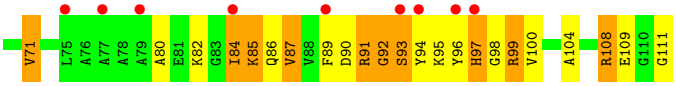


• Molecule 13: 50S ribosomal protein L18

Chain L:

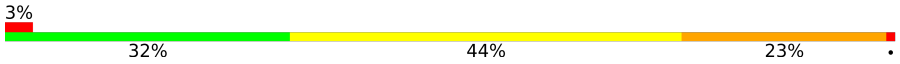


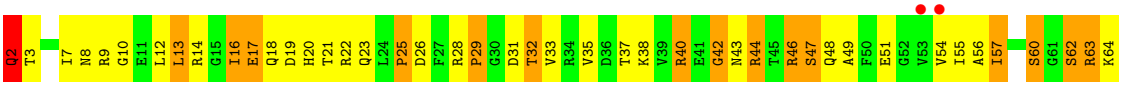


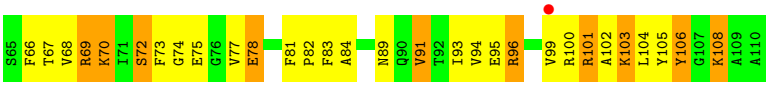


• Molecule 14: 50S ribosomal protein L19

Chain M:

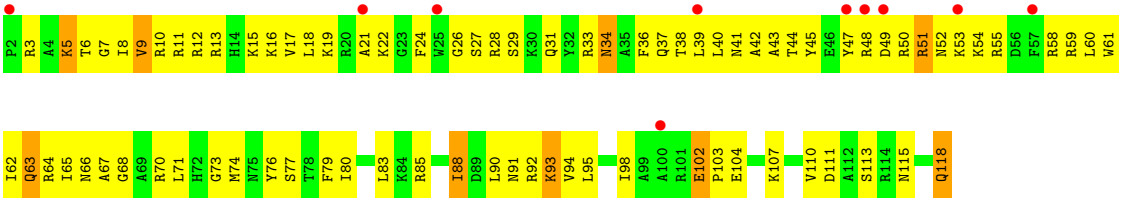






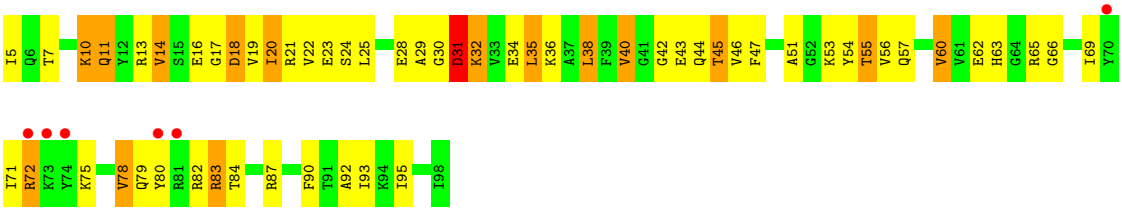
• Molecule 15: 50S ribosomal protein L20

Chain N:



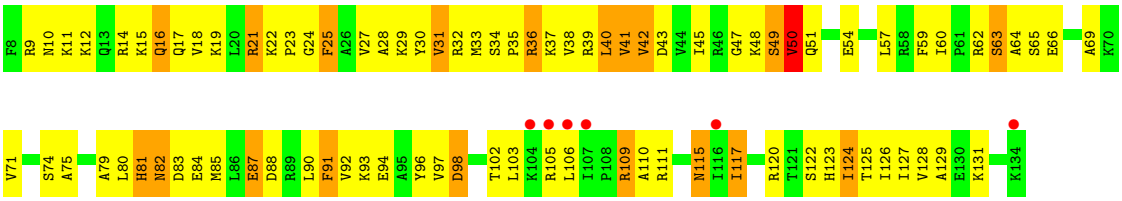
• Molecule 16: 50S ribosomal protein L21

Chain O:



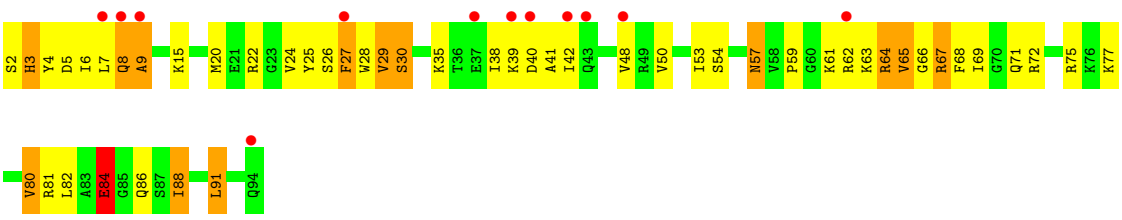
• Molecule 17: 50S ribosomal protein L22

Chain P:



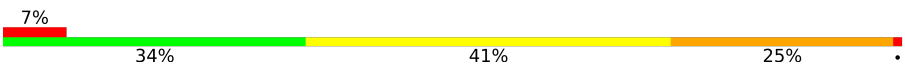
• Molecule 18: 50S ribosomal protein L23

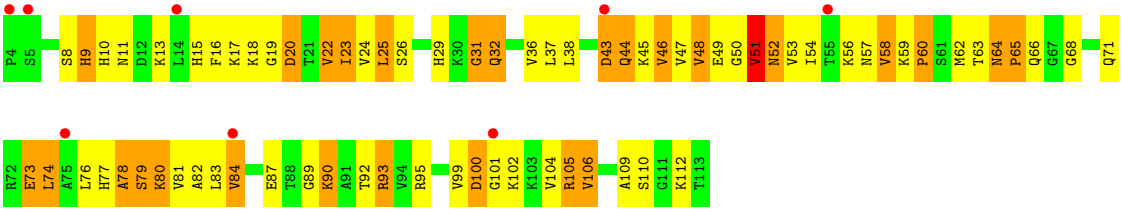
Chain Q:



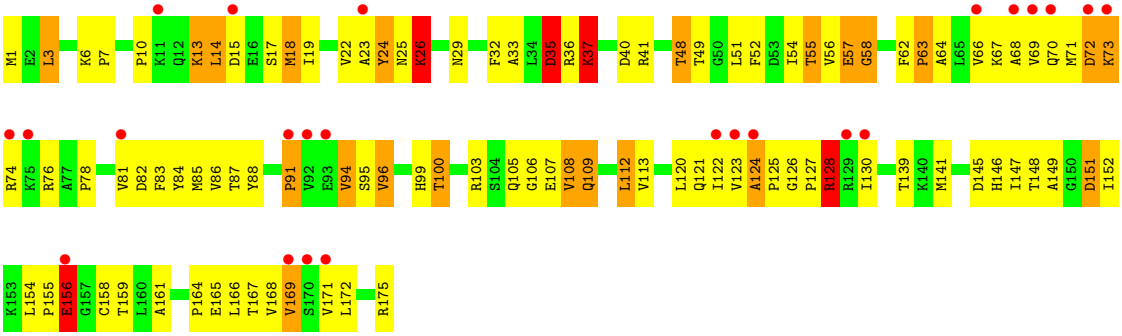
• Molecule 19: 50S ribosomal protein L24

Chain R:

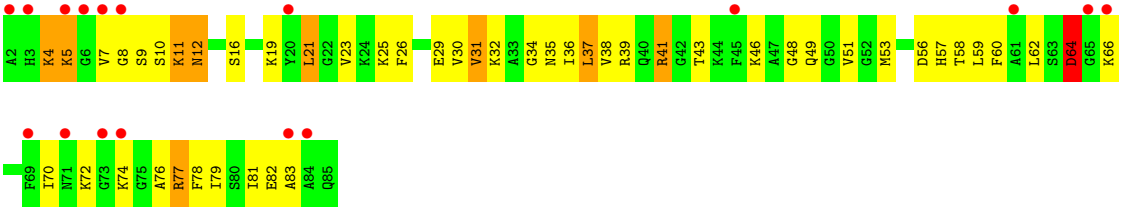




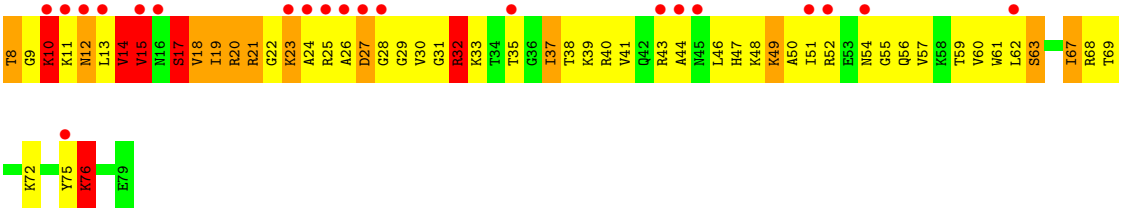
• Molecule 20: 50S ribosomal protein L25



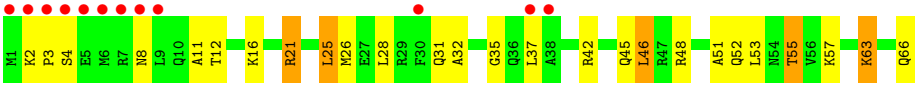
• Molecule 21: 50S ribosomal protein L27



• Molecule 22: 50S ribosomal protein L28

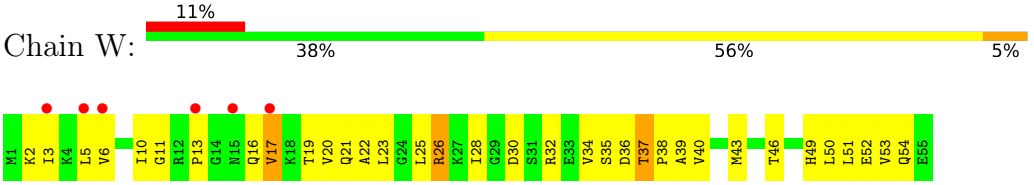


• Molecule 23: 50S ribosomal protein L29



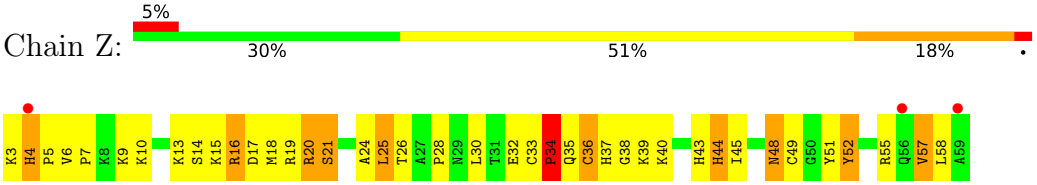
• Molecule 24: 50S ribosomal protein L30

Chain W:



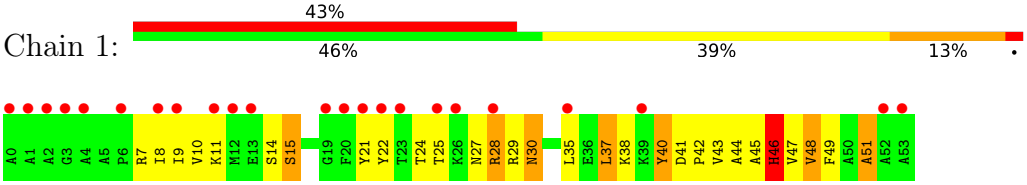
• Molecule 25: 50S ribosomal protein L32

Chain Z:



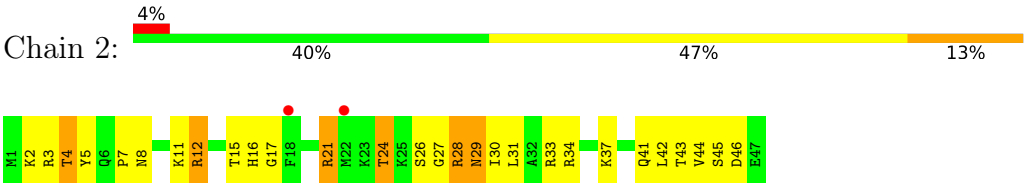
• Molecule 26: 50S ribosomal protein L33

Chain 1:



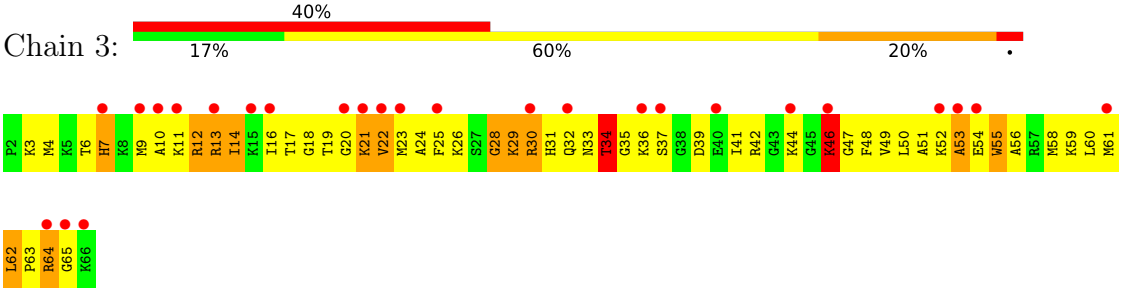
• Molecule 27: 50S ribosomal protein L34

Chain 2:



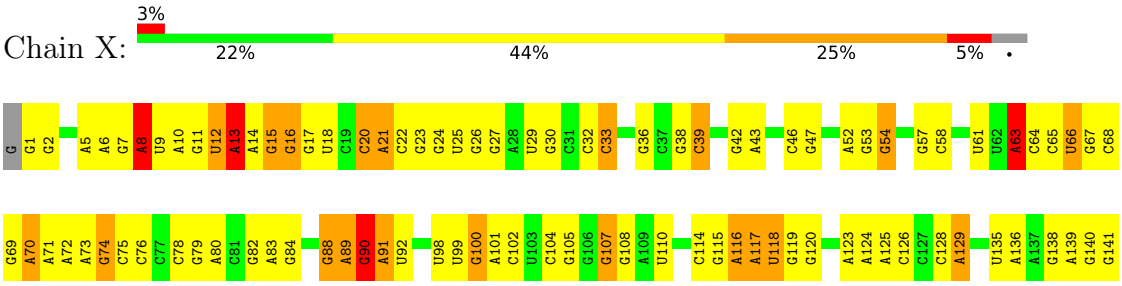
• Molecule 28: 50S ribosomal protein L35

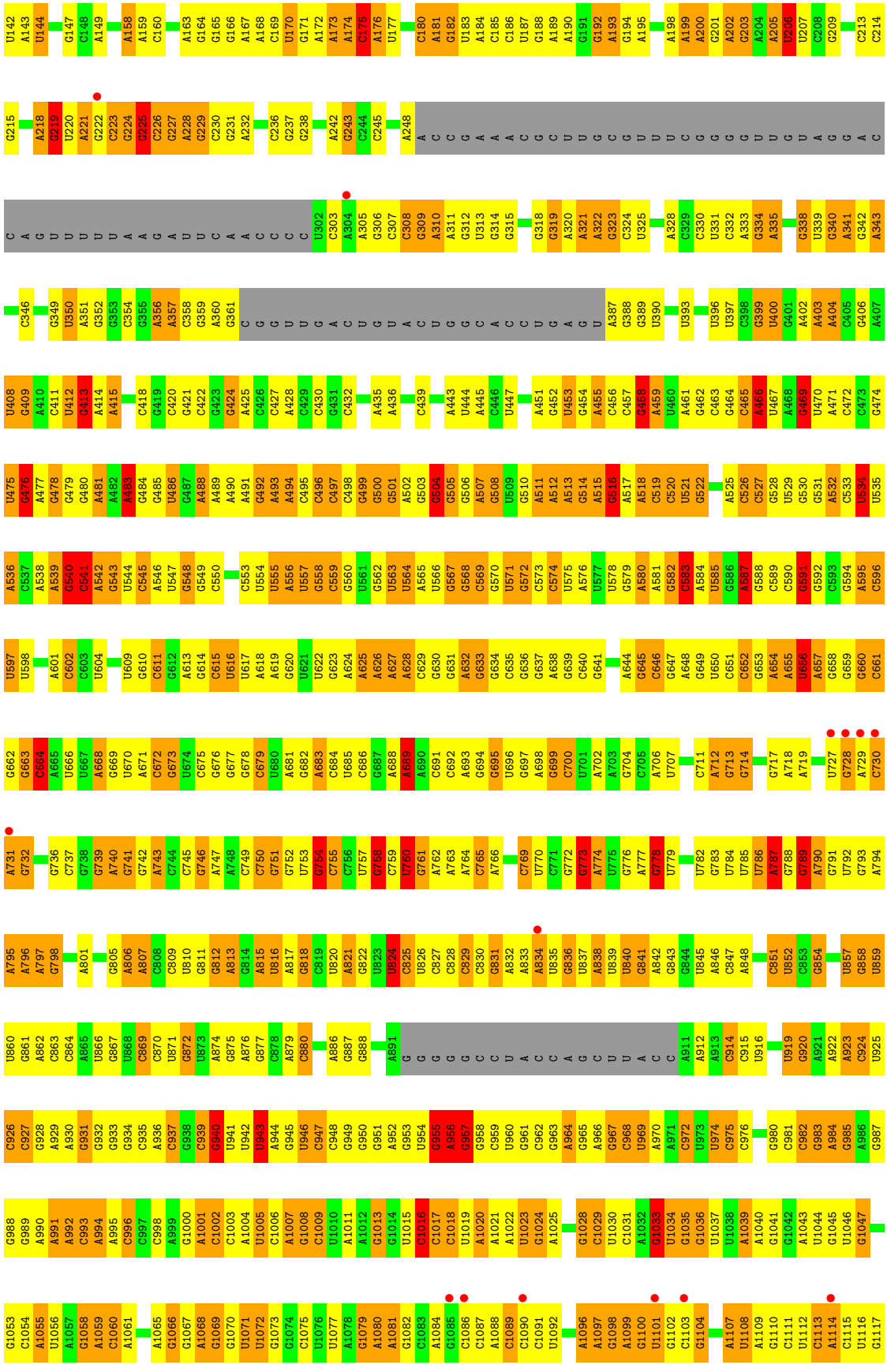
Chain 3:

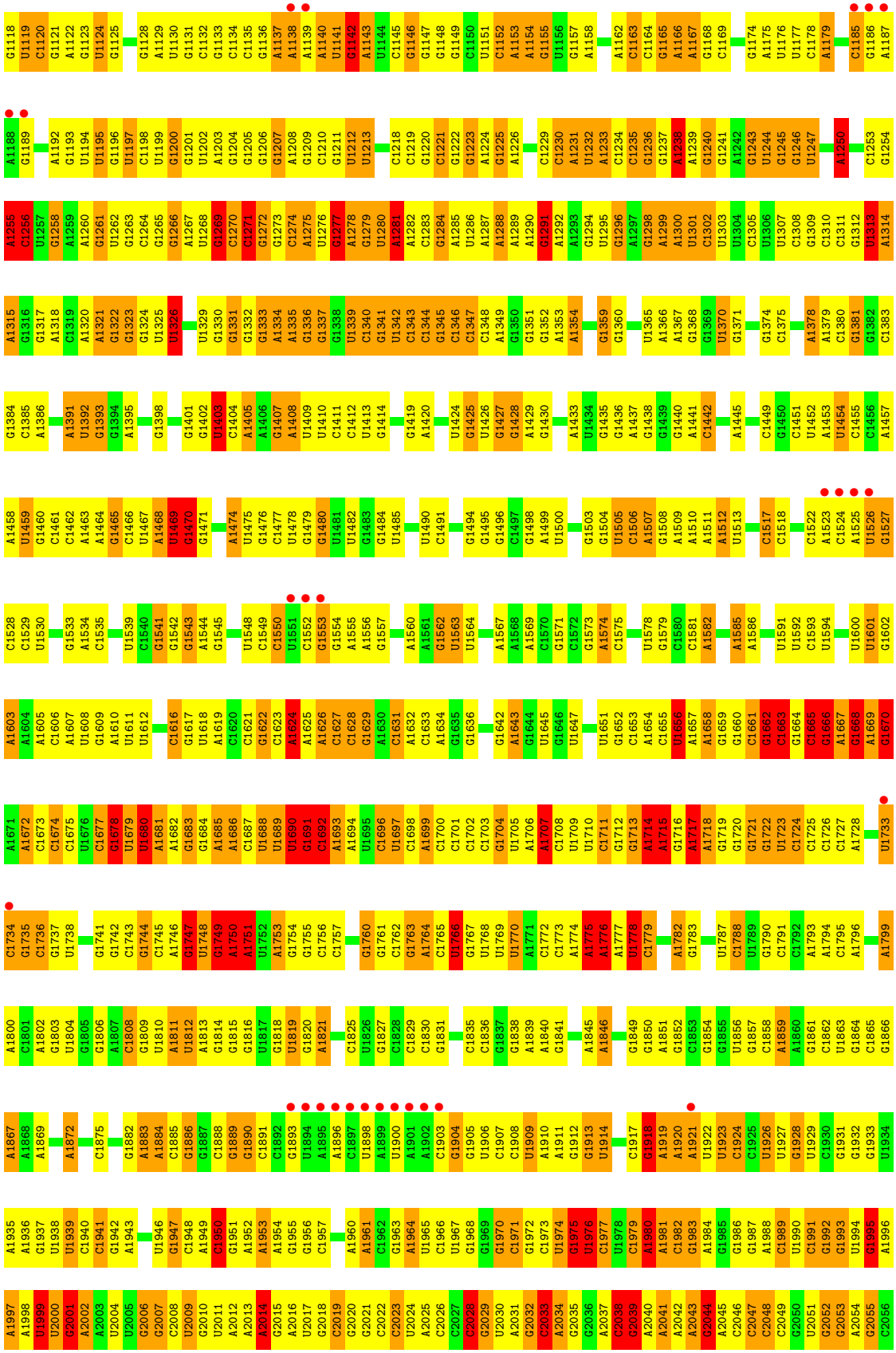


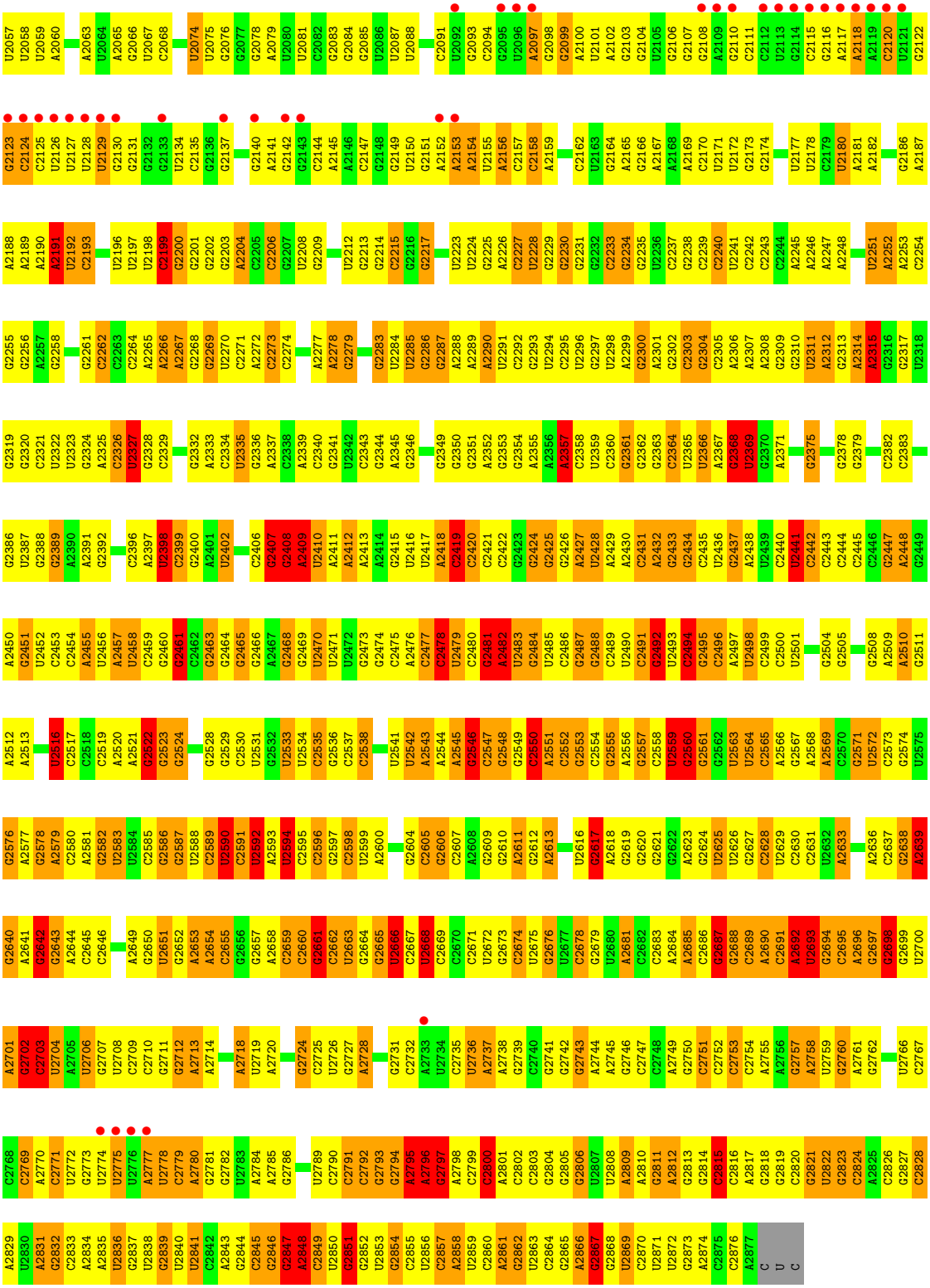
• Molecule 29: 23S ribosomal RNA

Chain X:



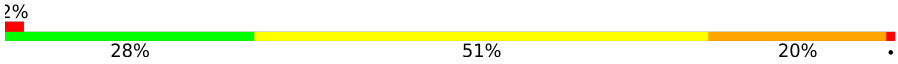


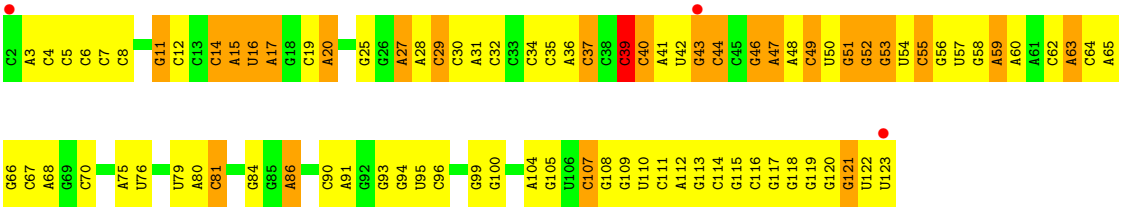




• Molecule 30: 5S ribosomal RNA

Chain Y:




C2 A3 C4 C5 C6 C7 C8 G11 C12 C13 C14 A15 U16 A17 G18 C19 A20 G25 G26 A27 A28 C29 C30 A31 C32 C33 C34 C35 A36 C37 C38 C39 C40 A41 U42 G43 C44 C45 G46 A47 A48 C49 U50 G51 G52 G53 U54 C55 G56 U57 G58 A59 A60 A61 C62 A63 C64 A65
G66 C67 A68 G69 C70 A75 U76 U79 A80 C81 G84 G85 A86 C90 A91 G92 G93 G94 U95 C96 G99 G100 A104 G105 U106 C107 G108 G109 U110 C111 A112 G113 C114 G115 C116 G117 G118 G119 G120 G121 U122 U123

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	169.82Å 411.54Å 695.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.02 – 3.00 59.03 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.9 (57.02-3.00) 76.2 (59.03-3.00)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.27 (at 3.01Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.284 , 0.326 0.272 , 0.317	Depositor DCC
R_{free} test set	22814 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å^2)	67.3	Xtriage
Anisotropy	0.451	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.16 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	89361	wwPDB-VP
Average B, all atoms (Å^2)	142.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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: MG, HGR

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	0.25	0/1674	0.46	0/2257
2	A	0.40	0/2149	0.62	0/2890
3	B	0.66	0/1568	0.92	2/2105 (0.1%)
4	C	0.50	0/1530	0.75	0/2070
5	D	0.36	0/1420	0.59	0/1903
6	E	0.39	0/1309	0.61	0/1771
7	F	0.30	0/1067	0.55	0/1446
8	G	0.47	0/1139	0.74	0/1539
9	H	0.72	0/1007	1.02	1/1352 (0.1%)
10	I	0.49	0/1082	0.78	0/1448
11	J	0.60	0/1114	0.83	1/1486 (0.1%)
12	K	0.81	0/887	1.11	4/1188 (0.3%)
13	L	0.54	0/784	0.79	1/1045 (0.1%)
14	M	0.76	0/880	1.02	3/1179 (0.3%)
15	N	0.65	0/994	0.77	0/1323
16	O	0.54	0/751	0.75	0/1000
17	P	0.75	0/1027	0.93	0/1373
18	Q	0.46	0/738	0.63	0/988
19	R	0.58	0/836	0.87	0/1121
20	S	0.40	0/1371	0.68	0/1862
21	T	0.52	0/634	0.70	0/838
22	U	0.52	0/557	0.88	1/741 (0.1%)
23	V	0.40	0/538	0.58	0/714
24	W	0.51	0/426	0.74	0/568
25	Z	0.67	0/465	0.99	1/622 (0.2%)
26	1	0.47	0/411	0.68	0/554
27	2	0.47	0/397	0.70	0/521
28	3	0.56	0/516	0.75	0/673
29	X	0.79	28/66826 (0.0%)	1.38	1078/104247 (1.0%)
30	Y	0.61	0/2907	1.12	10/4529 (0.2%)
All	All	0.73	28/97004 (0.0%)	1.25	1102/145353 (0.8%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	B	0	1
9	H	0	1
10	I	0	1
13	L	0	1
14	M	0	2
19	R	0	1
All	All	0	7

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	X	774	A	N3-C4	7.61	1.39	1.34
29	X	774	A	C5-C4	7.18	1.43	1.38
29	X	1682	A	N7-C5	-6.86	1.35	1.39
29	X	1975	G	N7-C5	6.29	1.43	1.39
29	X	2823	G	N9-C8	-6.08	1.33	1.37

The worst 5 of 1102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	X	1678	G	C8-N9-C4	14.96	112.38	106.40
29	X	1292	A	C8-N9-C4	14.80	111.72	105.80
29	X	774	A	N1-C6-N6	13.97	126.98	118.60
29	X	1679	U	C5-C6-N1	-13.00	116.20	122.70
29	X	1678	G	N7-C8-N9	-12.95	106.62	113.10

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	85	ALA	Peptide
9	H	36	THR	Peptide
10	I	52	GLY	Peptide
13	L	87	VAL	Peptide
14	M	2	GLN	Peptide

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	0	1651	0	1693	51	0
2	A	2107	0	2190	133	0
3	B	1540	0	1600	117	0
4	C	1507	0	1525	115	0
5	D	1401	0	1481	81	0
6	E	1287	0	1336	53	0
7	F	1048	0	1088	35	0
8	G	1115	0	1144	50	0
9	H	997	0	1046	81	0
10	I	1068	0	1103	68	0
11	J	1091	0	1125	66	0
12	K	879	0	930	79	0
13	L	778	0	820	57	0
14	M	867	0	890	64	0
15	N	978	0	1020	95	0
16	O	742	0	756	37	0
17	P	1014	0	1096	80	0
18	Q	727	0	753	31	0
19	R	826	0	881	65	0
20	S	1346	0	1372	71	0
21	T	626	0	655	38	0
22	U	553	0	604	50	0
23	V	534	0	558	13	0
24	W	424	0	470	24	0
25	Z	453	0	455	49	0
26	1	404	0	416	25	0
27	2	393	0	420	24	0
28	3	509	0	565	56	0
29	X	59673	0	30060	1967	0
30	Y	2601	0	1327	91	0
31	A	1	0	0	0	0
31	H	1	0	0	0	0
31	M	1	0	0	0	0
31	N	1	0	0	0	0
31	X	177	0	0	1	0
31	Y	5	0	0	0	0
32	X	36	0	29	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	89361	0	59408	3326	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 23.

The worst 5 of 3326 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)
3:B:14:ILE:HB	14:M:20:HIS:HD2	1.16	1.11
12:K:79:VAL:HA	12:K:83:VAL:HG13	1.35	1.06
29:X:1225:G:H1'	29:X:1250:A:H61	1.21	1.03
29:X:517:A:H5"	29:X:518:A:H5'	1.37	1.02
29:X:2690:A:OP1	29:X:2692:A:OP2	1.78	0.99

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
1	0	222/224 (99%)	139 (63%)	58 (26%)	25 (11%)	0 2
2	A	272/274 (99%)	206 (76%)	50 (18%)	16 (6%)	1 9
3	B	203/205 (99%)	152 (75%)	33 (16%)	18 (9%)	1 3
4	C	195/197 (99%)	123 (63%)	50 (26%)	22 (11%)	0 2
5	D	175/177 (99%)	117 (67%)	42 (24%)	16 (9%)	1 3
6	E	169/171 (99%)	119 (70%)	33 (20%)	17 (10%)	0 2
7	F	142/144 (99%)	100 (70%)	27 (19%)	15 (11%)	0 2
8	G	140/142 (99%)	111 (79%)	19 (14%)	10 (7%)	1 5
9	H	132/134 (98%)	96 (73%)	18 (14%)	18 (14%)	0 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
10	I	139/141 (99%)	93 (67%)	30 (22%)	16 (12%)	0 2
11	J	134/136 (98%)	97 (72%)	28 (21%)	9 (7%)	1 6
12	K	111/113 (98%)	81 (73%)	18 (16%)	12 (11%)	0 2
13	L	102/104 (98%)	68 (67%)	18 (18%)	16 (16%)	0 1
14	M	107/109 (98%)	83 (78%)	14 (13%)	10 (9%)	0 3
15	N	115/117 (98%)	90 (78%)	19 (16%)	6 (5%)	2 12
16	O	92/94 (98%)	69 (75%)	13 (14%)	10 (11%)	0 2
17	P	125/127 (98%)	102 (82%)	17 (14%)	6 (5%)	2 13
18	Q	91/93 (98%)	67 (74%)	16 (18%)	8 (9%)	1 3
19	R	108/110 (98%)	63 (58%)	28 (26%)	17 (16%)	0 1
20	S	173/175 (99%)	123 (71%)	32 (18%)	18 (10%)	0 2
21	T	82/84 (98%)	68 (83%)	8 (10%)	6 (7%)	1 5
22	U	70/72 (97%)	39 (56%)	15 (21%)	16 (23%)	0 0
23	V	64/66 (97%)	54 (84%)	9 (14%)	1 (2%)	9 40
24	W	53/55 (96%)	36 (68%)	13 (24%)	4 (8%)	1 5
25	Z	55/57 (96%)	36 (66%)	13 (24%)	6 (11%)	0 2
26	1	52/54 (96%)	31 (60%)	13 (25%)	8 (15%)	0 1
27	2	45/47 (96%)	38 (84%)	6 (13%)	1 (2%)	6 31
28	3	63/65 (97%)	38 (60%)	17 (27%)	8 (13%)	0 1
All	All	3431/3487 (98%)	2439 (71%)	657 (19%)	335 (10%)	0 2

5 of 335 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	17	SER
1	0	61	PRO
1	0	157	ILE
1	0	216	PRO
2	A	25	ALA

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
1	0	167/167 (100%)	150 (90%)	17 (10%)	7 28
2	A	214/214 (100%)	177 (83%)	37 (17%)	2 10
3	B	155/155 (100%)	123 (79%)	32 (21%)	1 6
4	C	157/157 (100%)	117 (74%)	40 (26%)	0 3
5	D	153/153 (100%)	126 (82%)	27 (18%)	2 10
6	E	136/136 (100%)	111 (82%)	25 (18%)	1 9
7	F	107/107 (100%)	94 (88%)	13 (12%)	5 21
8	G	118/118 (100%)	97 (82%)	21 (18%)	2 9
9	H	103/103 (100%)	73 (71%)	30 (29%)	0 2
10	I	108/108 (100%)	88 (82%)	20 (18%)	1 8
11	J	110/110 (100%)	82 (74%)	28 (26%)	0 3
12	K	90/90 (100%)	68 (76%)	22 (24%)	0 3
13	L	74/74 (100%)	46 (62%)	28 (38%)	0 0
14	M	92/92 (100%)	58 (63%)	34 (37%)	0 0
15	N	96/96 (100%)	82 (85%)	14 (15%)	3 15
16	O	75/75 (100%)	59 (79%)	16 (21%)	1 5
17	P	109/109 (100%)	85 (78%)	24 (22%)	1 4
18	Q	75/75 (100%)	57 (76%)	18 (24%)	0 3
19	R	91/91 (100%)	71 (78%)	20 (22%)	1 4
20	S	149/149 (100%)	119 (80%)	30 (20%)	1 6
21	T	62/62 (100%)	42 (68%)	20 (32%)	0 1
22	U	57/57 (100%)	38 (67%)	19 (33%)	0 1
23	V	54/54 (100%)	45 (83%)	9 (17%)	2 11
24	W	48/48 (100%)	38 (79%)	10 (21%)	1 5
25	Z	51/51 (100%)	43 (84%)	8 (16%)	2 13
26	1	38/38 (100%)	33 (87%)	5 (13%)	4 18
27	2	40/40 (100%)	32 (80%)	8 (20%)	1 7
28	3	51/51 (100%)	34 (67%)	17 (33%)	0 1
All	All	2780/2780 (100%)	2188 (79%)	592 (21%)	1 5

5 of 592 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	R	90	LYS
27	2	29	ASN
20	S	55	THR
19	R	84	VAL
22	U	15	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
26	1	30	ASN
28	3	7	HIS
7	F	11	GLN
13	L	37	HIS
14	M	48	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	X	2776/2881 (96%)	839 (30%)	30 (1%)
30	Y	121/122 (99%)	35 (28%)	1 (0%)
All	All	2897/3003 (96%)	874 (30%)	31 (1%)

5 of 874 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	X	8	A
29	X	13	A
29	X	15	G
29	X	54	G
29	X	63	A

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	X	1506	C
29	X	2758	A
29	X	1602	G
29	X	2854	G
29	X	2551	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 187 ligands modelled in this entry, 186 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	$\#\|Z\| > 2$
32	HGR	X	6178	-	39,39,39	1.81	7 (17%)	50,58,58	1.72	9 (18%)

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
32	HGR	X	6178	-	-	4/20/79/79	0/4/4/4

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	X	6178	HGR	C5-C6	-4.19	1.42	1.50
32	X	6178	HGR	C1-C6	4.15	1.41	1.35
32	X	6178	HGR	C12-C14	4.14	1.43	1.33
32	X	6178	HGR	C12-C6	3.87	1.55	1.44
32	X	6178	HGR	C3-C2	-3.78	1.41	1.48

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	X	6178	HGR	C10-O3-C3	4.73	126.09	115.36
32	X	6178	HGR	C4-C5-C6	4.24	121.49	112.36
32	X	6178	HGR	C23-O8-C18	-4.00	100.22	106.31
32	X	6178	HGR	C4-C3-C2	-3.98	118.17	121.83
32	X	6178	HGR	O3-C3-C2	3.09	118.43	112.56

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	X	6178	HGR	C2-C3-O3-C10
32	X	6178	HGR	C13-C11-C7-O1
32	X	6178	HGR	C13-C11-C7-C8
32	X	6178	HGR	O6-C11-C7-C8

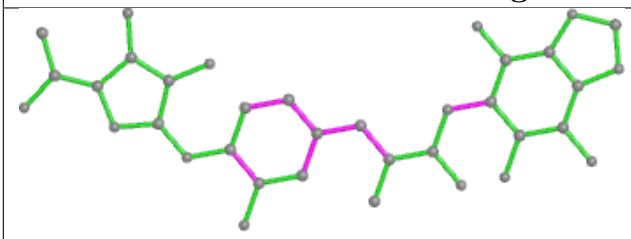
There are no ring outliers.

1 monomer is involved in 2 short contacts:

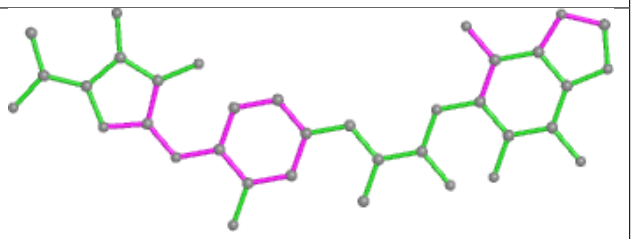
Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	X	6178	HGR	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

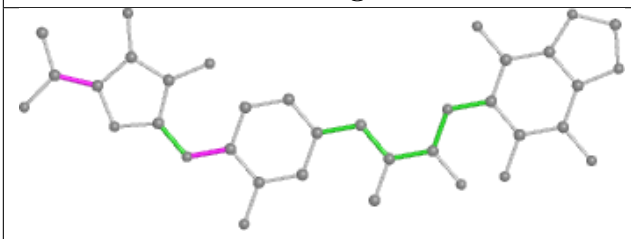
Ligand HGR X 6178



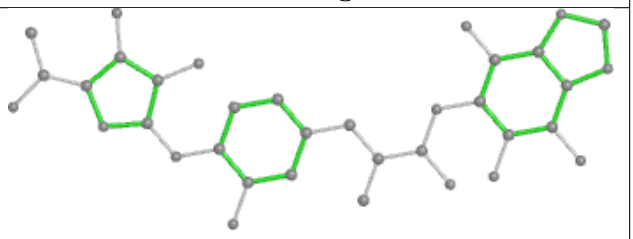
Bond lengths



Bond angles



Torsions



Rings

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	0	224/224 (100%)	4.90	179 (79%) 0 0	291, 311, 319, 322	0
2	A	274/274 (100%)	0.62	39 (14%) 2 1	108, 151, 172, 185	0
3	B	205/205 (100%)	0.04	5 (2%) 59 30	67, 102, 129, 146	0
4	C	197/197 (100%)	0.12	10 (5%) 28 10	93, 133, 158, 177	0
5	D	177/177 (100%)	0.30	14 (7%) 12 4	165, 183, 200, 214	0
6	E	171/171 (100%)	0.09	10 (5%) 23 7	116, 167, 191, 198	0
7	F	144/144 (100%)	2.34	61 (42%) 0 0	233, 259, 275, 281	0
8	G	142/142 (100%)	0.28	8 (5%) 24 8	87, 125, 139, 169	0
9	H	134/134 (100%)	-0.10	4 (2%) 50 22	70, 92, 108, 118	0
10	I	141/141 (100%)	1.05	34 (24%) 0 0	98, 150, 173, 182	0
11	J	136/136 (100%)	0.94	25 (18%) 1 0	107, 126, 156, 159	0
12	K	113/113 (100%)	0.22	6 (5%) 26 10	63, 82, 95, 99	0
13	L	104/104 (100%)	1.12	26 (25%) 0 0	126, 147, 162, 173	0
14	M	109/109 (100%)	-0.06	3 (2%) 53 25	72, 89, 117, 147	0
15	N	117/117 (100%)	0.36	10 (8%) 10 3	90, 118, 144, 153	0
16	O	94/94 (100%)	-0.28	6 (6%) 19 6	103, 129, 156, 173	0
17	P	127/127 (100%)	0.16	6 (4%) 31 11	81, 96, 120, 180	0
18	Q	93/93 (100%)	0.59	12 (12%) 3 1	108, 137, 160, 176	0
19	R	110/110 (100%)	0.37	8 (7%) 15 4	111, 131, 166, 180	0
20	S	175/175 (100%)	0.48	24 (13%) 3 1	134, 167, 185, 193	0
21	T	84/84 (100%)	1.16	17 (20%) 1 0	111, 130, 148, 171	0
22	U	72/72 (100%)	1.51	21 (29%) 0 0	134, 163, 177, 182	0
23	V	66/66 (100%)	0.82	12 (18%) 1 0	147, 163, 190, 201	0
24	W	55/55 (100%)	0.66	6 (10%) 5 2	112, 124, 142, 157	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
25	Z	57/57 (100%)	0.05	3 (5%) 26 10	82, 97, 120, 130	0
26	1	54/54 (100%)	1.72	23 (42%) 0 0	140, 153, 179, 189	0
27	2	47/47 (100%)	0.17	2 (4%) 35 13	108, 121, 132, 134	0
28	3	65/65 (100%)	1.63	26 (40%) 0 0	115, 132, 143, 153	0
29	X	2780/2881 (96%)	-0.16	79 (2%) 53 25	59, 127, 241, 397	0
30	Y	122/122 (100%)	-0.36	3 (2%) 57 29	110, 157, 182, 203	0
All	All	6389/6490 (98%)	0.37	682 (10%) 6 2	59, 134, 276, 397	0

The worst 5 of 682 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	0	204	PHE	18.3
1	0	200	ALA	18.1
1	0	205	LEU	17.5
1	0	85	ALA	15.5
1	0	47	PRO	15.3

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

There are no non-standard protein/DNA/RNA residues in this entry.

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, 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
31	MG	X	6101	1/1	0.05	1.26	138,138,138,138	0
31	MG	X	6135	1/1	0.44	1.17	129,129,129,129	0
31	MG	X	6140	1/1	0.45	0.42	97,97,97,97	0
31	MG	X	6103	1/1	0.49	0.23	126,126,126,126	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
31	MG	X	6168	1/1	0.55	0.67	100,100,100,100	0
31	MG	X	6152	1/1	0.57	0.30	158,158,158,158	0
31	MG	X	6099	1/1	0.58	0.86	120,120,120,120	0
31	MG	X	6114	1/1	0.62	0.70	93,93,93,93	0
31	MG	X	6118	1/1	0.62	0.41	82,82,82,82	0
31	MG	X	6093	1/1	0.66	0.34	96,96,96,96	0
31	MG	X	6124	1/1	0.68	0.58	100,100,100,100	0
31	MG	X	6161	1/1	0.69	0.23	113,113,113,113	0
31	MG	X	6176	1/1	0.69	0.55	73,73,73,73	0
31	MG	X	6139	1/1	0.71	0.42	113,113,113,113	0
31	MG	X	6111	1/1	0.71	0.41	98,98,98,98	0
31	MG	X	6125	1/1	0.72	0.49	109,109,109,109	0
31	MG	X	6112	1/1	0.72	0.33	80,80,80,80	0
31	MG	X	6051	1/1	0.73	0.54	83,83,83,83	0
31	MG	A	301	1/1	0.73	0.35	108,108,108,108	0
31	MG	X	6163	1/1	0.74	0.34	82,82,82,82	0
31	MG	X	6160	1/1	0.74	0.72	108,108,108,108	0
31	MG	X	6174	1/1	0.74	0.30	117,117,117,117	0
31	MG	X	6076	1/1	0.74	0.55	73,73,73,73	0
31	MG	X	6149	1/1	0.75	0.40	99,99,99,99	0
31	MG	Y	205	1/1	0.75	0.64	123,123,123,123	0
31	MG	X	6162	1/1	0.76	0.76	104,104,104,104	0
31	MG	X	6035	1/1	0.76	0.46	80,80,80,80	0
31	MG	N	201	1/1	0.77	0.38	74,74,74,74	0
31	MG	X	6169	1/1	0.78	0.48	91,91,91,91	0
31	MG	X	6172	1/1	0.78	0.34	88,88,88,88	0
31	MG	X	6006	1/1	0.78	0.56	70,70,70,70	0
31	MG	X	6116	1/1	0.78	0.67	99,99,99,99	0
31	MG	X	6049	1/1	0.78	0.40	91,91,91,91	0
31	MG	X	6141	1/1	0.79	0.38	87,87,87,87	0
31	MG	X	6159	1/1	0.79	1.13	109,109,109,109	0
31	MG	X	6131	1/1	0.80	0.39	80,80,80,80	0
31	MG	X	6090	1/1	0.80	0.46	72,72,72,72	0
31	MG	X	6150	1/1	0.80	0.46	97,97,97,97	0
31	MG	X	6075	1/1	0.80	0.26	85,85,85,85	0
31	MG	Y	203	1/1	0.80	0.76	96,96,96,96	0
31	MG	X	6127	1/1	0.80	0.62	81,81,81,81	0
31	MG	X	6070	1/1	0.81	0.47	69,69,69,69	0
31	MG	X	6014	1/1	0.81	0.47	99,99,99,99	0
31	MG	X	6144	1/1	0.81	0.26	132,132,132,132	0
31	MG	X	6133	1/1	0.81	0.48	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
31	MG	Y	201	1/1	0.81	0.41	96,96,96,96	0
31	MG	X	6052	1/1	0.81	0.43	86,86,86,86	0
31	MG	X	6078	1/1	0.81	0.36	89,89,89,89	0
31	MG	X	6173	1/1	0.82	0.14	87,87,87,87	0
31	MG	X	6155	1/1	0.82	0.79	108,108,108,108	0
31	MG	X	6156	1/1	0.82	0.25	91,91,91,91	0
31	MG	X	6085	1/1	0.82	0.41	66,66,66,66	0
31	MG	X	6003	1/1	0.82	0.31	72,72,72,72	0
31	MG	X	6030	1/1	0.82	0.33	101,101,101,101	0
31	MG	X	6033	1/1	0.83	0.69	76,76,76,76	0
31	MG	X	6020	1/1	0.83	0.44	76,76,76,76	0
31	MG	X	6061	1/1	0.83	0.23	100,100,100,100	0
31	MG	X	6087	1/1	0.83	0.62	85,85,85,85	0
31	MG	X	6047	1/1	0.83	0.25	79,79,79,79	0
31	MG	X	6015	1/1	0.83	0.27	74,74,74,74	0
31	MG	X	6170	1/1	0.83	0.37	97,97,97,97	0
31	MG	X	6074	1/1	0.84	0.39	89,89,89,89	0
31	MG	X	6022	1/1	0.84	0.58	92,92,92,92	0
31	MG	X	6137	1/1	0.84	0.47	136,136,136,136	0
31	MG	X	6148	1/1	0.85	0.31	104,104,104,104	0
31	MG	X	6002	1/1	0.85	0.32	91,91,91,91	0
31	MG	X	6171	1/1	0.85	0.32	118,118,118,118	0
31	MG	X	6064	1/1	0.85	0.48	77,77,77,77	0
31	MG	X	6046	1/1	0.85	0.58	76,76,76,76	0
31	MG	X	6017	1/1	0.86	0.45	54,54,54,54	0
31	MG	X	6079	1/1	0.86	0.33	99,99,99,99	0
31	MG	X	6012	1/1	0.86	0.24	78,78,78,78	0
31	MG	X	6058	1/1	0.86	0.34	70,70,70,70	0
31	MG	X	6175	1/1	0.86	0.54	121,121,121,121	0
31	MG	X	6164	1/1	0.86	0.23	86,86,86,86	0
31	MG	X	6042	1/1	0.86	1.02	96,96,96,96	0
31	MG	X	6130	1/1	0.86	0.41	132,132,132,132	0
31	MG	X	6062	1/1	0.86	0.72	87,87,87,87	0
31	MG	X	6045	1/1	0.87	0.72	94,94,94,94	0
31	MG	X	6065	1/1	0.87	0.28	93,93,93,93	0
31	MG	X	6158	1/1	0.87	0.20	76,76,76,76	0
31	MG	X	6098	1/1	0.88	0.20	71,71,71,71	0
31	MG	X	6091	1/1	0.88	0.27	72,72,72,72	0
31	MG	X	6153	1/1	0.88	0.30	114,114,114,114	0
31	MG	X	6126	1/1	0.88	0.41	114,114,114,114	0
31	MG	X	6083	1/1	0.88	0.28	83,83,83,83	0
31	MG	Y	204	1/1	0.88	0.59	116,116,116,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
31	MG	X	6120	1/1	0.88	0.27	78,78,78,78	0
31	MG	H	201	1/1	0.89	0.14	104,104,104,104	0
31	MG	X	6071	1/1	0.89	0.34	99,99,99,99	0
31	MG	X	6001	1/1	0.89	0.72	67,67,67,67	0
31	MG	X	6037	1/1	0.89	0.40	65,65,65,65	0
31	MG	X	6165	1/1	0.89	0.44	88,88,88,88	0
31	MG	X	6146	1/1	0.89	0.15	125,125,125,125	0
31	MG	X	6039	1/1	0.90	0.39	79,79,79,79	0
31	MG	X	6157	1/1	0.90	0.56	96,96,96,96	0
31	MG	X	6129	1/1	0.90	0.45	89,89,89,89	0
31	MG	X	6117	1/1	0.90	0.42	130,130,130,130	0
31	MG	X	6097	1/1	0.90	0.52	122,122,122,122	0
31	MG	X	6105	1/1	0.90	0.40	86,86,86,86	0
31	MG	X	6122	1/1	0.90	0.36	84,84,84,84	0
31	MG	X	6059	1/1	0.90	0.24	88,88,88,88	0
31	MG	X	6177	1/1	0.90	0.49	125,125,125,125	0
31	MG	X	6011	1/1	0.90	0.39	104,104,104,104	0
31	MG	X	6154	1/1	0.90	0.66	96,96,96,96	0
31	MG	X	6167	1/1	0.90	1.06	97,97,97,97	0
31	MG	X	6100	1/1	0.90	0.42	111,111,111,111	0
32	HGR	X	6178	36/36	0.90	0.24	79,99,109,111	0
31	MG	X	6142	1/1	0.91	0.56	106,106,106,106	0
31	MG	X	6119	1/1	0.91	0.41	89,89,89,89	0
31	MG	X	6010	1/1	0.91	0.49	64,64,64,64	0
31	MG	X	6025	1/1	0.91	0.65	76,76,76,76	0
31	MG	X	6041	1/1	0.91	0.41	64,64,64,64	0
31	MG	X	6115	1/1	0.91	0.30	133,133,133,133	0
31	MG	X	6029	1/1	0.91	0.40	82,82,82,82	0
31	MG	X	6069	1/1	0.91	0.34	65,65,65,65	0
31	MG	X	6110	1/1	0.91	0.21	84,84,84,84	0
31	MG	X	6077	1/1	0.92	0.56	80,80,80,80	0
31	MG	X	6028	1/1	0.92	0.30	75,75,75,75	0
31	MG	X	6132	1/1	0.92	0.56	84,84,84,84	0
31	MG	X	6060	1/1	0.92	0.65	80,80,80,80	0
31	MG	X	6092	1/1	0.92	0.72	97,97,97,97	0
31	MG	Y	202	1/1	0.92	0.17	130,130,130,130	0
31	MG	X	6056	1/1	0.92	0.32	81,81,81,81	0
31	MG	X	6013	1/1	0.92	0.49	76,76,76,76	0
31	MG	X	6107	1/1	0.92	0.22	76,76,76,76	0
31	MG	X	6108	1/1	0.92	0.52	108,108,108,108	0
31	MG	X	6044	1/1	0.93	0.42	66,66,66,66	0
31	MG	X	6138	1/1	0.93	0.15	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
31	MG	X	6123	1/1	0.93	0.55	89,89,89,89	0
31	MG	X	6019	1/1	0.93	0.48	75,75,75,75	0
31	MG	X	6043	1/1	0.93	0.39	106,106,106,106	0
31	MG	X	6073	1/1	0.93	0.30	105,105,105,105	0
31	MG	X	6066	1/1	0.93	0.39	105,105,105,105	0
31	MG	X	6104	1/1	0.93	0.54	89,89,89,89	0
31	MG	X	6147	1/1	0.93	1.06	93,93,93,93	0
31	MG	X	6095	1/1	0.93	0.58	78,78,78,78	0
31	MG	X	6106	1/1	0.93	0.50	100,100,100,100	0
31	MG	X	6096	1/1	0.93	0.33	99,99,99,99	0
31	MG	X	6166	1/1	0.93	0.12	76,76,76,76	0
31	MG	X	6068	1/1	0.93	0.38	111,111,111,111	0
31	MG	X	6121	1/1	0.93	0.60	85,85,85,85	0
31	MG	X	6113	1/1	0.94	0.59	143,143,143,143	0
31	MG	M	201	1/1	0.94	0.67	71,71,71,71	0
31	MG	X	6084	1/1	0.94	0.29	124,124,124,124	0
31	MG	X	6151	1/1	0.94	0.16	88,88,88,88	0
31	MG	X	6040	1/1	0.94	0.54	63,63,63,63	0
31	MG	X	6031	1/1	0.94	0.61	85,85,85,85	0
31	MG	X	6134	1/1	0.94	0.12	100,100,100,100	0
31	MG	X	6089	1/1	0.94	0.27	89,89,89,89	0
31	MG	X	6027	1/1	0.94	0.72	65,65,65,65	0
31	MG	X	6034	1/1	0.94	0.27	69,69,69,69	0
31	MG	X	6021	1/1	0.94	0.26	91,91,91,91	0
31	MG	X	6036	1/1	0.94	0.35	70,70,70,70	0
31	MG	X	6094	1/1	0.94	0.37	95,95,95,95	0
31	MG	X	6109	1/1	0.94	0.36	92,92,92,92	0
31	MG	X	6009	1/1	0.94	0.31	50,50,50,50	0
31	MG	X	6145	1/1	0.94	0.39	84,84,84,84	0
31	MG	X	6080	1/1	0.94	0.69	82,82,82,82	0
31	MG	X	6082	1/1	0.94	0.68	105,105,105,105	0
31	MG	X	6008	1/1	0.95	0.26	58,58,58,58	0
31	MG	X	6048	1/1	0.95	0.57	66,66,66,66	0
31	MG	X	6038	1/1	0.95	0.08	82,82,82,82	0
31	MG	X	6136	1/1	0.95	0.68	84,84,84,84	0
31	MG	X	6018	1/1	0.95	0.78	86,86,86,86	0
31	MG	X	6024	1/1	0.95	0.37	100,100,100,100	0
31	MG	X	6053	1/1	0.95	0.36	85,85,85,85	0
31	MG	X	6102	1/1	0.95	0.30	98,98,98,98	0
31	MG	X	6032	1/1	0.95	0.36	86,86,86,86	0
31	MG	X	6057	1/1	0.95	0.68	92,92,92,92	0
31	MG	X	6004	1/1	0.96	0.28	93,93,93,93	0

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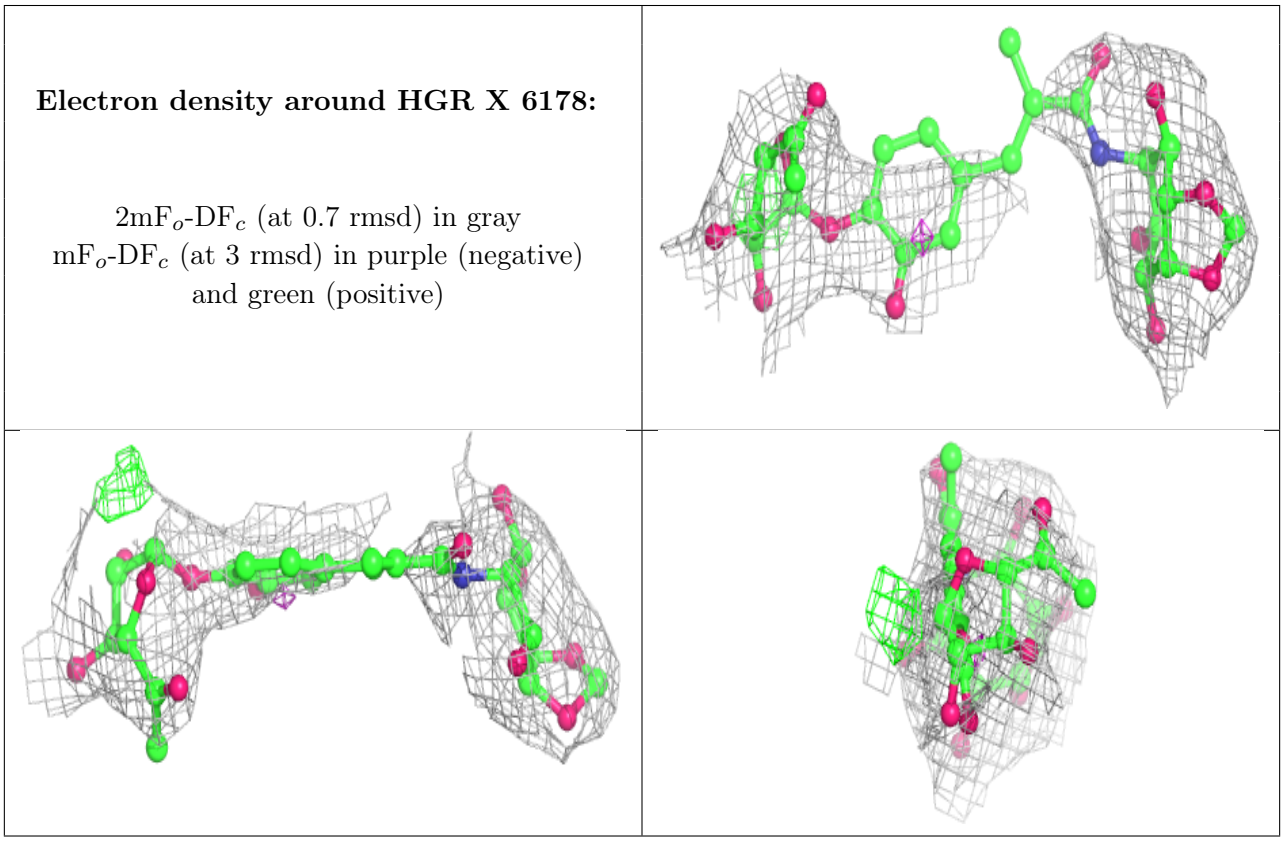
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
31	MG	X	6128	1/1	0.96	0.21	131,131,131,131	0
31	MG	X	6054	1/1	0.96	0.39	79,79,79,79	0
31	MG	X	6086	1/1	0.96	0.17	104,104,104,104	0
31	MG	X	6007	1/1	0.96	0.39	78,78,78,78	0
31	MG	X	6081	1/1	0.96	0.34	90,90,90,90	0
31	MG	X	6016	1/1	0.96	0.35	74,74,74,74	0
31	MG	X	6072	1/1	0.96	0.51	101,101,101,101	0
31	MG	X	6055	1/1	0.97	0.45	85,85,85,85	0
31	MG	X	6026	1/1	0.97	0.34	79,79,79,79	0
31	MG	X	6063	1/1	0.97	0.31	87,87,87,87	0
31	MG	X	6023	1/1	0.97	0.37	83,83,83,83	0
31	MG	X	6143	1/1	0.97	0.63	99,99,99,99	0
31	MG	X	6050	1/1	0.98	0.44	91,91,91,91	0
31	MG	X	6067	1/1	0.98	0.18	72,72,72,72	0
31	MG	X	6005	1/1	0.98	0.55	58,58,58,58	0
31	MG	X	6088	1/1	0.99	0.29	88,88,88,88	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HGR X 6178:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.