WORLDWIDE

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PROTEIN DATA BANK

EMDataBank
Unified Data Resource for 3DEM

wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:05 PM BST

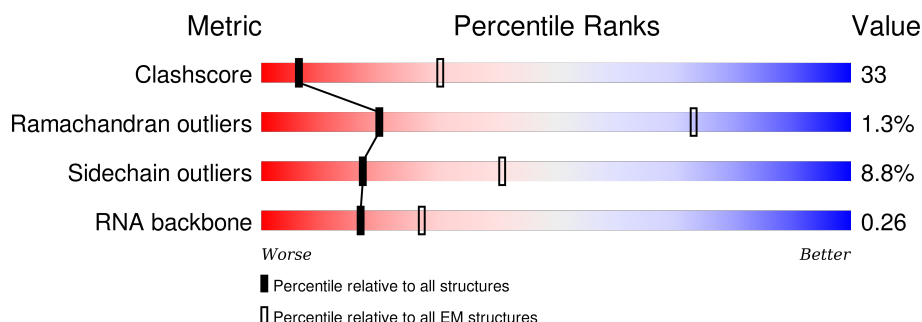|		
PDB ID	:	4CXG
EMDB ID:	:	EMD-2623
Title	:	Regulation of the mammalian elongation cycle by 40S subunit rolling: a eukaryotic-specific ribosome rearrangement
Authors	:	Budkevich, T.V.; Giesebrecht, J.; Behrmann, E.; Loerke, J.; Ramrath, D.J.F.; Mielke, T.; Ismer, J.; Hildebrand, P.; Tung, C.-S.; Nierhaus, K.H.; Sanbonmatsu, K.Y.; Spahn, C.M.T.
Deposited on	:	2014-04-07
Resolution	:	8.70 Å(reported)

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 8.70 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.
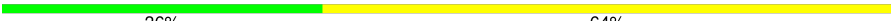
Metric	Percentile Ranks	Value
Clashscore		33
Ramachandran outliers		1.3%
Sidechain outliers		8.8%
RNA backbone		0.26

Worse   *Better*

■ Percentile relative to all structures
▯ Percentile relative to all EM structures

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	1	135	17% 52% 30% •
2	2	50	18% 30% 52%
3	A	437	75% 19% • •
4	X	143	54% 36% • 6%
5	Y	76	14% 22% 54% 9%
6	a	48	33% 65% •
7	b	17	41% 59%
8	c	19	42% 53% 5%

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Mol	Chain	Length	Quality of chain
9	x	28	36% 64%

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
5	2MG	Y	10	-	-	X	-
5	M2G	Y	26	-	-	X	-

2 Entry composition ⓘ

There are 10 unique types of molecules in this entry. The entry contains 12269 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S RRNA - H44.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	135	Total 2890	C 1288	N 527	O 940	P 135	0	0

- Molecule 2 is a RNA chain called 28S RRNA - H89.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	50	Total 1057	C 471	N 176	O 360	P 50	0	0

- Molecule 3 is a protein called ELONGATION FACTOR 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	427	Total 3272	C 2104	N 570	O 585	S 13	0	0

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	134	Total 1046	C 663	N 205	O 176	S 2	0	0

- Molecule 5 is a RNA chain called TRANSFER RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	Y	76	Total 1636	C 737	N 290	O 532	P 76	S 1	0	0

- Molecule 6 is a RNA chain called 18S RRNA - H5-H14.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	48	Total 1024	C 458	N 192	O 326	P 48	0	0

• Molecule 7 is a RNA chain called 18S RRNA - H8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	b	17	363	162	63	121	17	0	0

• Molecule 8 is a RNA chain called 28S RRNA - H95.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	c	19	410	183	78	130	19	0	0

• Molecule 9 is a RNA chain called MESSENGER RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	x	28	560	252	56	224	28	0	0

• Molecule 10 is PHENYLALANINE (three-letter code: PHE) (formula: $C_9H_{11}NO_2$).
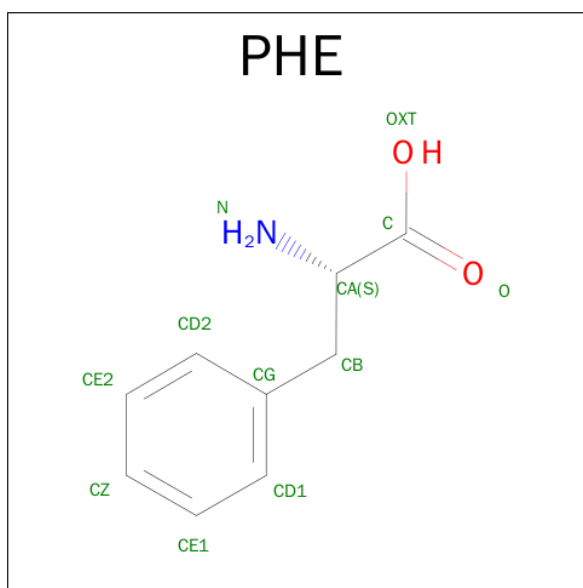
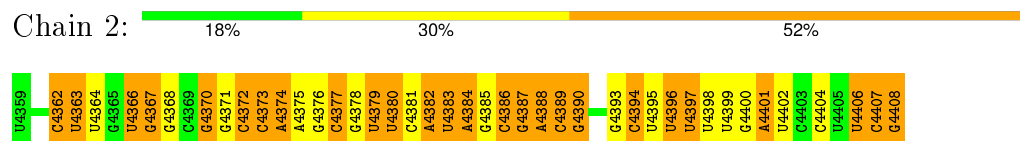| Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
10	Y	1	11	9	1	1	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.
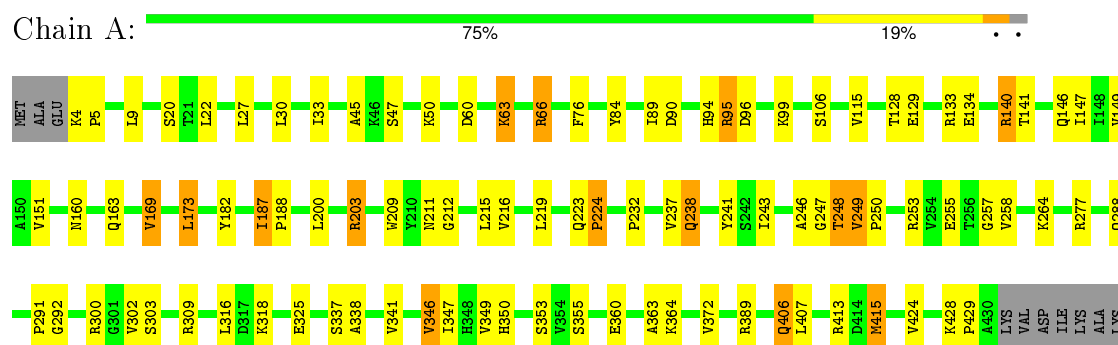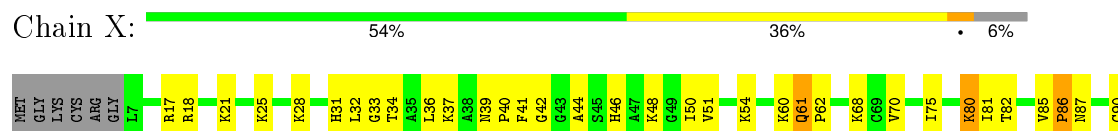
- Molecule 1: 18S RRNA - H44
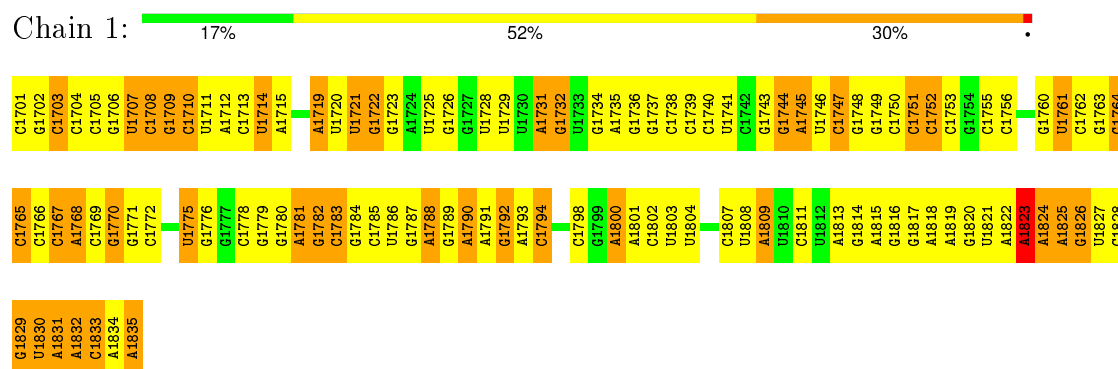
Chain 1:

- Molecule 2: 28S RRNA - H89

Chain 2:

- Molecule 3: ELONGATION FACTOR 1A

Chain A:

- Molecule 4: 40S RIBOSOMAL PROTEIN US12

Chain X:

L91 I94 E95 E96 N97 D98 E99 V100 L101 F105 G106 R107 V112 I115 P116 G117 V118 R119 F120 K121 V122 V123 K124 L130 L131 A132 K138 E139 R140 PRO ARG SER

• Molecule 5: TRANSFER RNA

Chain Y: 14% 22% 54% 9%

G1 C2 G3 G4 A5 U6 U7 U8 A9 G10 C11 U12 C13 A14 G15 U16 U17 G18 G19 G20 A21 G22 A23 G24 C25 C26 C27 C28 U33 A36 A37 A38 G42 G43 A44 G45 G46 U47 C48 C49 U50 G51 U52 G53 U54 U55 C56 G57 A58 U59 C60 C61 A62 C63 A64 G65 A66

A67 U68 U69 C70 G71 C72 A73 C74 C75 A76
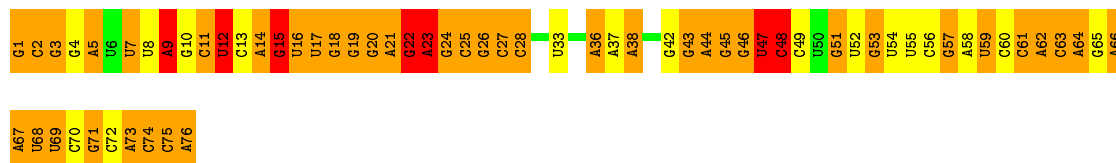
• Molecule 6: 18S RRNA - H5-H14

Chain a: 33% 65% .

A458 C459 A460 C463 A464 A465 G466 G467 A468 C472 A473 U474 C475 A476 G477 G480 C481 G482 A485 A486 U487 U488 A489 C490 C491 C492 A493 C494 U495 C496 C497 C498 G499 A500 C501 C502 C503 G504 G505
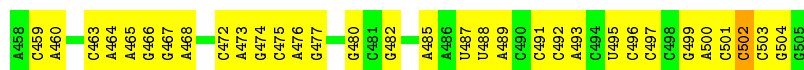
• Molecule 7: 18S RRNA - H8

Chain b: 41% 59%

C151 U152 G153 A158 A159 U160 U161 C162 U163 A164 G165 A166 G167

• Molecule 8: 28S RRNA - H95

Chain c: 42% 53% 5%

C4553 U4557 C4558 A4559 G4560 U4561 A4562 C4563 G4566 A4567 G4568 G4569 A4570 A4571

• Molecule 9: MESSENGER RNA

Chain x: 36% 64%

U34 U35 U36 U37 U38 U39 U40 U41 U42 U43 U44 U45 U46 U49 U52 U53 U54 U55 U56 U57 U58 U59 U60 U61

4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	DEFOCUS GROUP, Not provided	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5   Model quality (i)

5.1   Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, 5MU, H2U, MIA, 2MG, 5MC, 1MA, M2G, 7MG, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#|Z|>2$	RMSZ	$\#|Z|>2$
1	1	0.33	0/3232	0.77	0/5039
2	2	0.34	0/1177	0.81	0/1831
3	A	0.44	0/3346	0.62	0/4542
4	X	0.46	0/1063	0.70	0/1421
5	Y	0.48	1/1550 (0.1%)	1.94	65/2410 (2.7%)
6	a	0.37	0/1145	0.83	1/1782 (0.1%)
7	b	0.35	0/405	0.78	0/629
8	c	0.35	0/459	0.86	1/714 (0.1%)
9	x	0.42	1/615 (0.2%)	1.25	11/948 (1.2%)
All	All	0.40	2/12992 (0.0%)	1.00	78/19316 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
5	Y	1	1
9	x	1	0
All	All	2	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Y	1	G	OP3-P	-5.77	1.54	1.61
9	x	60	U	O3'-P	5.07	1.67	1.61

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	Y	22	G	O4'-C1'-N9	29.56	131.85	108.20
5	Y	21	A	N9-C1'-C2'	-20.07	87.90	114.00
5	Y	22	G	N9-C1'-C2'	-18.97	89.33	114.00
5	Y	71	G	O4'-C1'-N9	-17.30	94.36	108.20
5	Y	48	C	O4'-C1'-N1	15.16	120.33	108.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	Y	36	A	C3'
9	x	58	U	C3'

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	1823	A	Sidechain
5	Y	33	U	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	2890	0	1462	156	0
2	2	1057	0	535	67	0
3	A	3272	0	3292	88	0
4	X	1046	0	1110	48	0
5	Y	1636	0	848	145	0
6	a	1024	0	525	0	0
7	b	363	0	182	0	0
8	c	410	0	207	0	0
9	x	560	0	281	0	0
10	Y	11	0	8	0	0
All	All	12269	0	8450	464	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 33.

The worst 5 of 464 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:A:249:VAL:CG1	5:Y:76:A:N3	1.70	1.51
3:A:249:VAL:HG11	5:Y:76:A:C2	1.58	1.38
3:A:249:VAL:CG1	5:Y:76:A:C2	2.08	1.37
3:A:243:ILE:O	5:Y:76:A:N6	1.62	1.29
3:A:415:MET:CE	5:Y:51:G:H21	1.46	1.28

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	425/437 (97%)	413 (97%)	12 (3%)	0	100	100
4	X	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	2	29
All	All	557/580 (96%)	533 (96%)	17 (3%)	7 (1%)	20	60

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	X	61	GLN
4	X	106	GLY
4	X	107	ARG
4	X	116	PRO
4	X	33	GLY

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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	344/372 (92%)	309 (90%)	35 (10%)	9	37
4	X	108/115 (94%)	103 (95%)	5 (5%)	33	68
All	All	452/487 (93%)	412 (91%)	40 (9%)	17	45

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	187	ILE
3	A	237	VAL
4	X	31	HIS
3	A	211	ASN
3	A	238	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	348	HIS
4	X	77	ASN
4	X	61	GLN
3	A	315	HIS
4	X	31	HIS

5.3.3　RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	134/135 (99%)	57 (42%)	7 (5%)
2	2	49/50 (98%)	28 (57%)	4 (8%)
5	Y	74/76 (97%)	29 (39%)	7 (9%)
6	a	47/48 (97%)	32 (68%)	0
7	b	16/17 (94%)	10 (62%)	0
8	c	18/19 (94%)	11 (61%)	0
9	x	27/28 (96%)	15 (55%)	0
All	All	365/373 (97%)	182 (49%)	18 (4%)

5 of 182 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	1702	G
1	1	1703	C
1	1	1707	U

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Mol	Chain	Res	Type
1	1	1708	C
1	1	1709	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	4387	G
2	2	4388	A
5	Y	22	G
1	1	1834	A
2	2	4374	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
5	2MG	Y	10	5	18,26,27	1.06	1 (5%)	21,38,41	2.94	5 (23%)
5	H2U	Y	16	5	17,21,22	0.90	0	23,30,33	2.60	7 (30%)
5	H2U	Y	17	5	17,21,22	0.74	1 (5%)	23,30,33	1.96	5 (21%)
5	M2G	Y	26	5	18,27,28	1.51	5 (27%)	22,40,43	2.78	7 (31%)
5	OMC	Y	32	5	15,22,23	0.75	0	20,31,34	0.67	1 (5%)
5	MIA	Y	37	5	22,31,32	1.10	3 (13%)	26,44,47	1.71	5 (19%)
5	7MG	Y	46	5	20,26,27	2.26	4 (20%)	23,39,42	2.55	5 (21%)
5	5MC	Y	49	5	14,22,23	1.04	2 (14%)	17,32,35	3.22	5 (29%)
5	5MU	Y	54	5	13,22,23	7.20	3 (23%)	16,32,35	5.98	6 (37%)
5	PSU	Y	55	5	15,21,22	1.67	3 (20%)	16,30,33	4.10	5 (31%)
5	1MA	Y	58	5	15,25,26	1.04	1 (6%)	15,37,40	1.33	2 (13%)

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	2MG	Y	10	5	-	0/5/27/28	0/3/3/3
5	H2U	Y	16	5	-	0/7/38/39	0/2/2/2
5	H2U	Y	17	5	-	0/7/38/39	0/2/2/2
5	M2G	Y	26	5	-	0/7/29/30	0/3/3/3
5	OMC	Y	32	5	-	0/5/27/28	0/2/2/2
5	MIA	Y	37	5	-	0/11/33/34	0/3/3/3
5	7MG	Y	46	5	-	0/7/37/38	0/3/3/3
5	5MC	Y	49	5	-	0/3/25/26	0/2/2/2
5	5MU	Y	54	5	-	0/3/25/26	0/2/2/2
5	PSU	Y	55	5	-	0/7/25/26	0/2/2/2
5	1MA	Y	58	5	-	0/3/25/26	0/3/3/3

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Y	54	5MU	C5M-C5	-25.66	1.02	1.51
5	Y	46	7MG	C8-N9	-5.56	1.37	1.45
5	Y	55	PSU	C5-C1'	-4.24	1.48	1.52
5	Y	55	PSU	C6-C5	-3.13	1.34	1.38
5	Y	46	7MG	C8-N7	-2.79	1.30	1.43

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	Y	54	5MU	C5-C4-N3	-12.79	114.62	125.35
5	Y	49	5MC	CM5-C5-C4	-10.69	110.16	121.47
5	Y	10	2MG	C5-C6-N1	-9.18	111.53	123.52
5	Y	46	7MG	C5-C6-N1	-7.75	111.85	123.39
5	Y	16	H2U	C6-N1-C2	-7.27	110.93	122.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	Y	10	2MG	10	0
5	Y	16	H2U	5	0
5	Y	17	H2U	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	Y	26	M2G	26	0
5	Y	37	MIA	1	0
5	Y	46	7MG	2	0
5	Y	49	5MC	1	0
5	Y	54	5MU	1	0
5	Y	55	PSU	1	0
5	Y	58	1MA	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
10	PHE	Y	77	5	9,11,12	0.59	0	11,13,15	2.03	2 (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
10	PHE	Y	77	5	-	0/4/6/8	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	Y	77	PHE	CG-CB-CA	-4.86	102.92	114.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	Y	77	PHE	O-C-CA	-4.45	113.79	125.72

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.