



wwPDB X-ray Structure Validation Summary Report

Mar 31, 2014 – 06:02 PM BST

PDB ID : 4KBT
Title : 70S ribosome translocation intermediate GDPNP-II containing elongation factor EFG/GDPNP, mRNA, and tRNA bound in the pe^*/E state. This entry contains 30S ribosomal subunit A. The full asymmetric unit also contains PDB entries 4KBU (50S subunit A), 4KBV (30S subunit B), and 4KBW (50S subunit B).
Authors : Zhou, J.; Lancaster, L.; Donohue, J.P.; Noller, H.F.
Deposited on : 2013-04-23
Resolution : 3.86 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

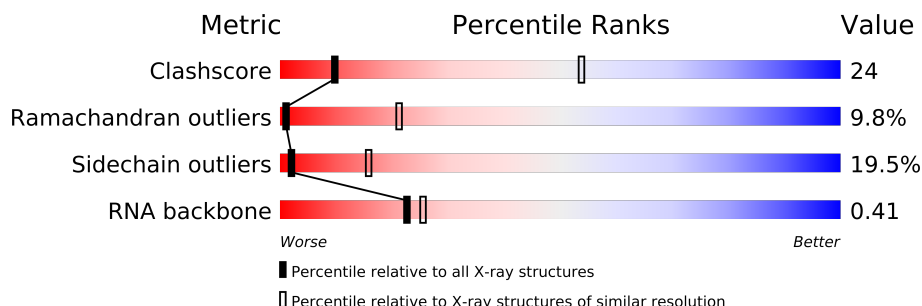
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23004

1 Overall quality at a glance

The reported resolution of this entry is 3.86 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	79885	1145 (4.22-3.50)
Ramachandran outliers	78287	1091 (4.22-3.50)
Sidechain outliers	78261	1081 (4.22-3.50)
RNA backbone	1838	1010 (4.84-2.80)


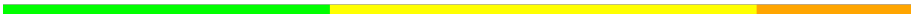
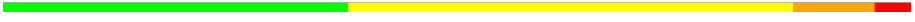

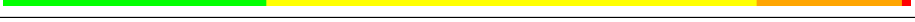

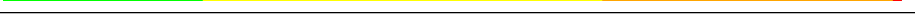

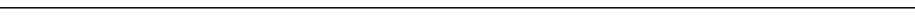
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	B	235	
2	C	207	
3	D	208	
4	E	151	
5	F	101	
6	G	155	
7	H	138	
8	I	127	
9	J	99	
10	K	119	
11	L	125	
12	M	125	
13	N	60	
14	O	88	
15	P	84	

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Mol	Chain	Length	Quality of chain
16	Q	100	
17	R	70	
18	S	79	
19	T	99	
20	A	1511	
21	V	18	
22	W	77	
23	Y	687	
24	U	6	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 58977 atoms, of which 0 are hydrogen and 0 are deuterium.

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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	235	Total	C	N	O	S	0	0	0
			1910	1218	342	345	5			

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	207	Total	C	N	O	S	0	0	0
			1621	1022	315	283	1			

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	151	Total	C	N	O	S	0	0	0
			1156	729	218	205	4			

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	127	Total	C	N	O	S	0	0	0
			1011	639	198	174				

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	99	Total	C	N	O	S	0	0	0
			802	504	157	140	1			

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	K	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	125	Total	C	N	O	S	0	0	0
			976	614	196	165	1			

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	O	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	84	Total	C	N	O	S	0	0	0
			706	446	140	119	1			

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	Q	100	Total	C	N	O	S	0	0	0
			835	534	156	143	2			

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	R	70	Total	C	N	O	S	0	0	0
			574	367	112	95				

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	S	79	Total	C	N	O	S	0	0	0
			634	405	115	112	2			

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	T	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

- Molecule 20 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	A	1511	Total	C	N	O	P	0	0	0
			32474	14455	6015	10494	1510			

- Molecule 21 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	V	18	Total	C	N	O	P	0	0	0
			393	177	81	118	17			

- Molecule 22 is a RNA chain called tRNA-Met.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	W	77	Total	C	N	O	P	0	0	0
			1635	732	291	536	76			

- Molecule 23 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	Y	687	Total	C	N	O	S	0	0	0
			5380	3414	922	1024	20			

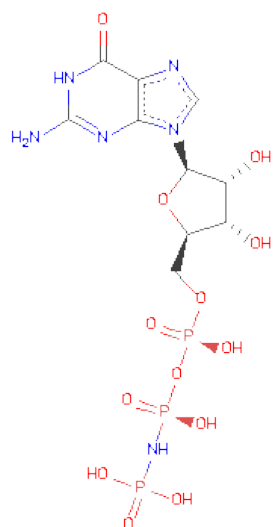
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	129	LYS	HIS	CONFLICT	UNP Q72I01
Y	226	ASN	HIS	CONFLICT	UNP Q72I01

- Molecule 24 is a protein called Viomycin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	U	6	Total	C	N	O	0	0	0
			48	25	13	10			

- Molecule 25 is PHOSPHOAMINOPHOSPHONICACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
25	Y	1	32	10	6	13	3	0	0

- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	Y	1	Total	Mg	0	0
			1	1		

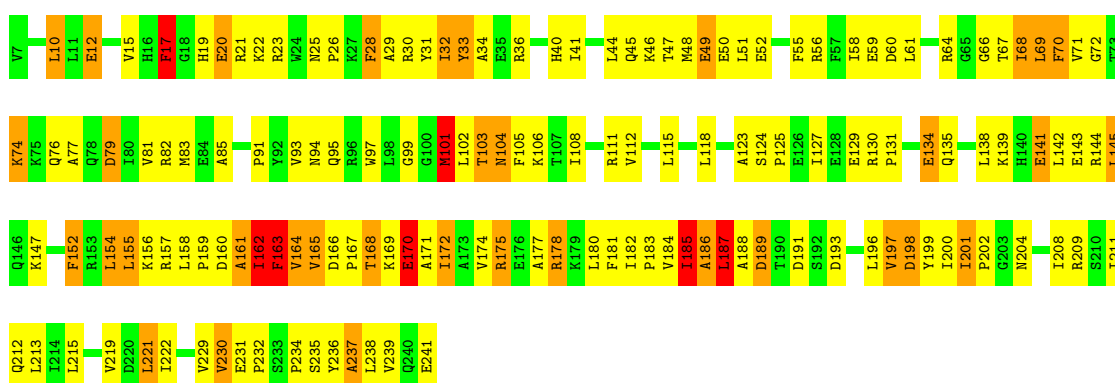
3 Residue-property plots

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

Note EDS was not executed.

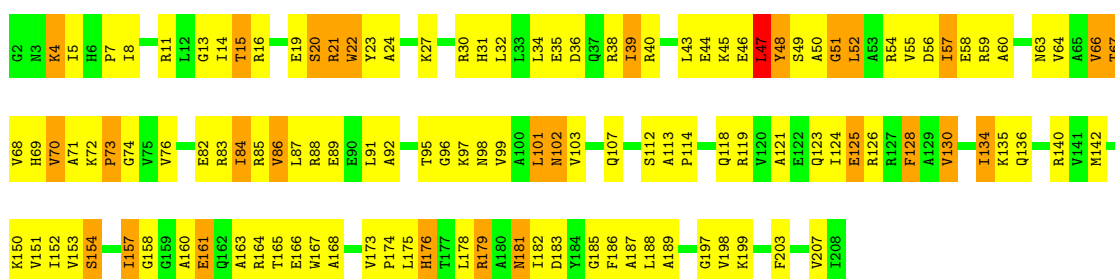
- Molecule 1: 30S ribosomal protein S2

Chain B:



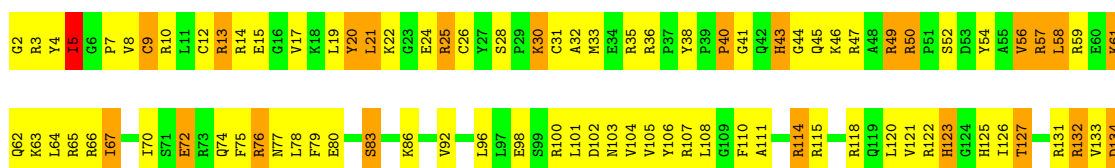
- Molecule 2: 30S ribosomal protein S3

Chain C:



- Molecule 3: 30S ribosomal protein S4

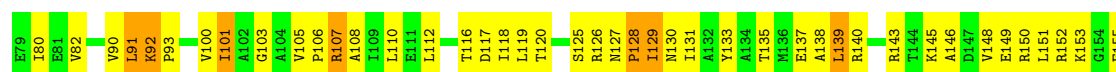
Chain D:





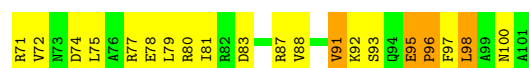
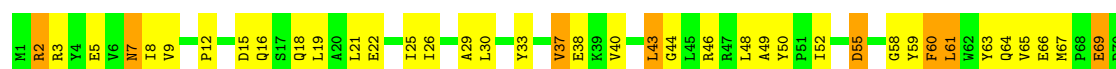
• Molecule 4: 30S ribosomal protein S5

Chain E:



• Molecule 5: 30S ribosomal protein S6

Chain F:



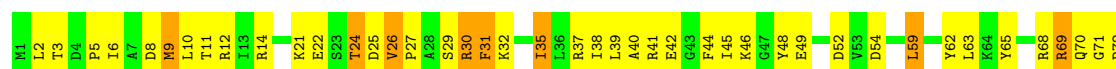
• Molecule 6: 30S ribosomal protein S7

Chain G:



• Molecule 7: 30S ribosomal protein S8

Chain H:



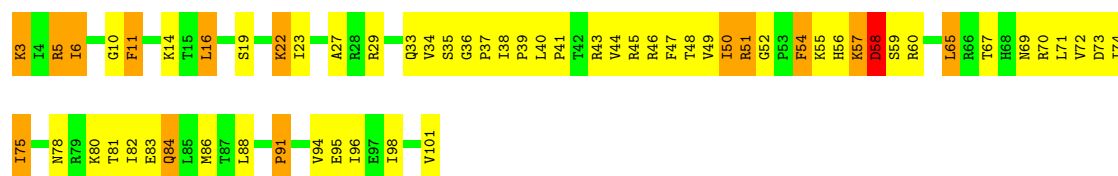
• Molecule 8: 30S ribosomal protein S9

Chain I:



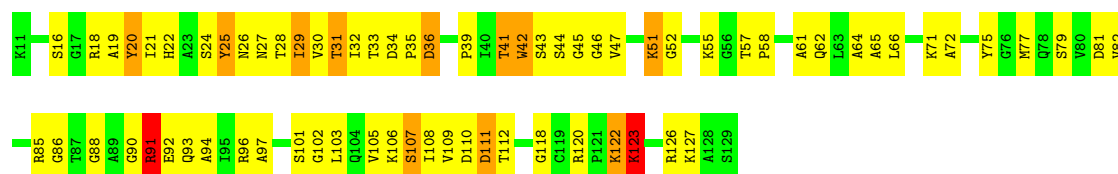
• Molecule 9: 30S ribosomal protein S10

Chain J:



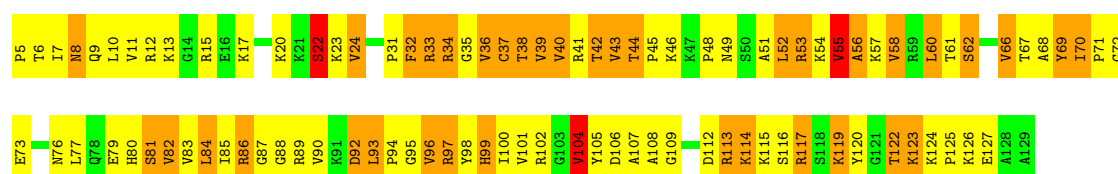
- Molecule 10: 30S ribosomal protein S11

Chain K:



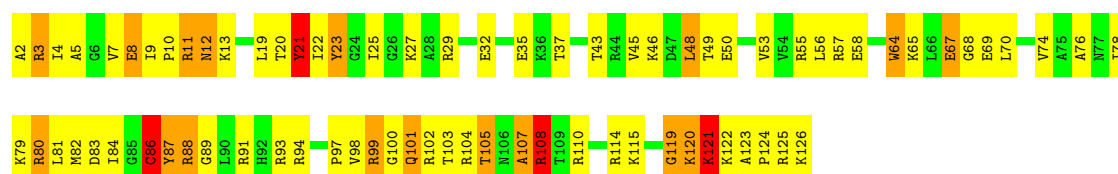
- Molecule 11: 30S ribosomal protein S12

Chain L:



- Molecule 12: 30S ribosomal protein S13

Chain M:



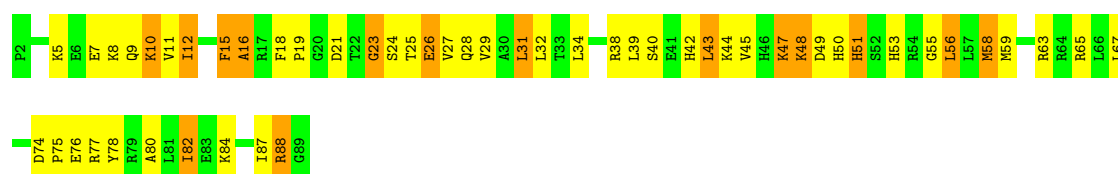
- Molecule 13: 30S ribosomal protein S14 type Z

Chain N:



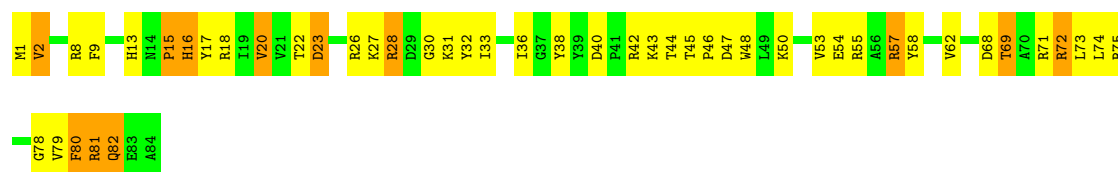
- Molecule 14: 30S ribosomal protein S15

Chain O:



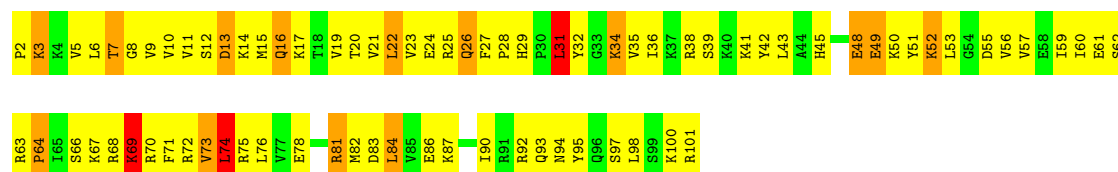
- Molecule 15: 30S ribosomal protein S16

Chain P: 



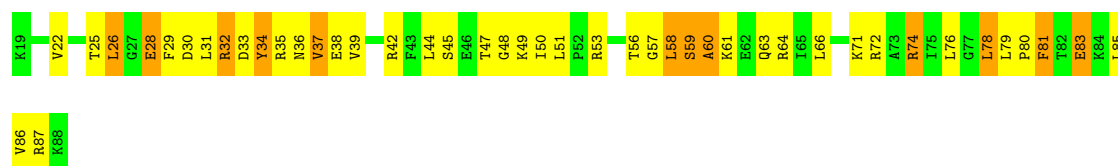
- Molecule 16: 30S ribosomal protein S17

Chain Q: 



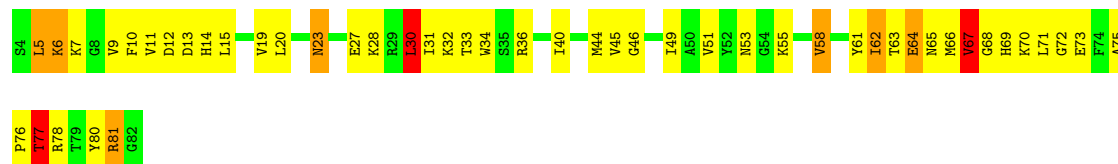
- Molecule 17: 30S ribosomal protein S18

Chain R: 



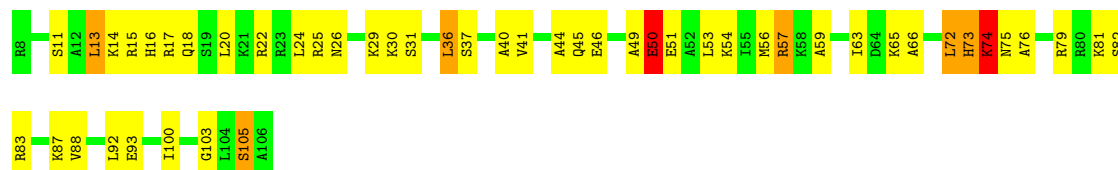
- Molecule 18: 30S ribosomal protein S19

Chain S: 



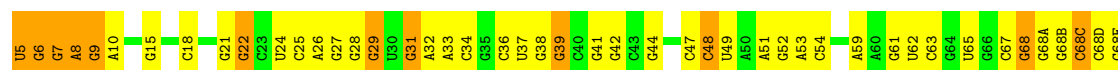
- Molecule 19: 30S ribosomal protein S20

Chain T: 

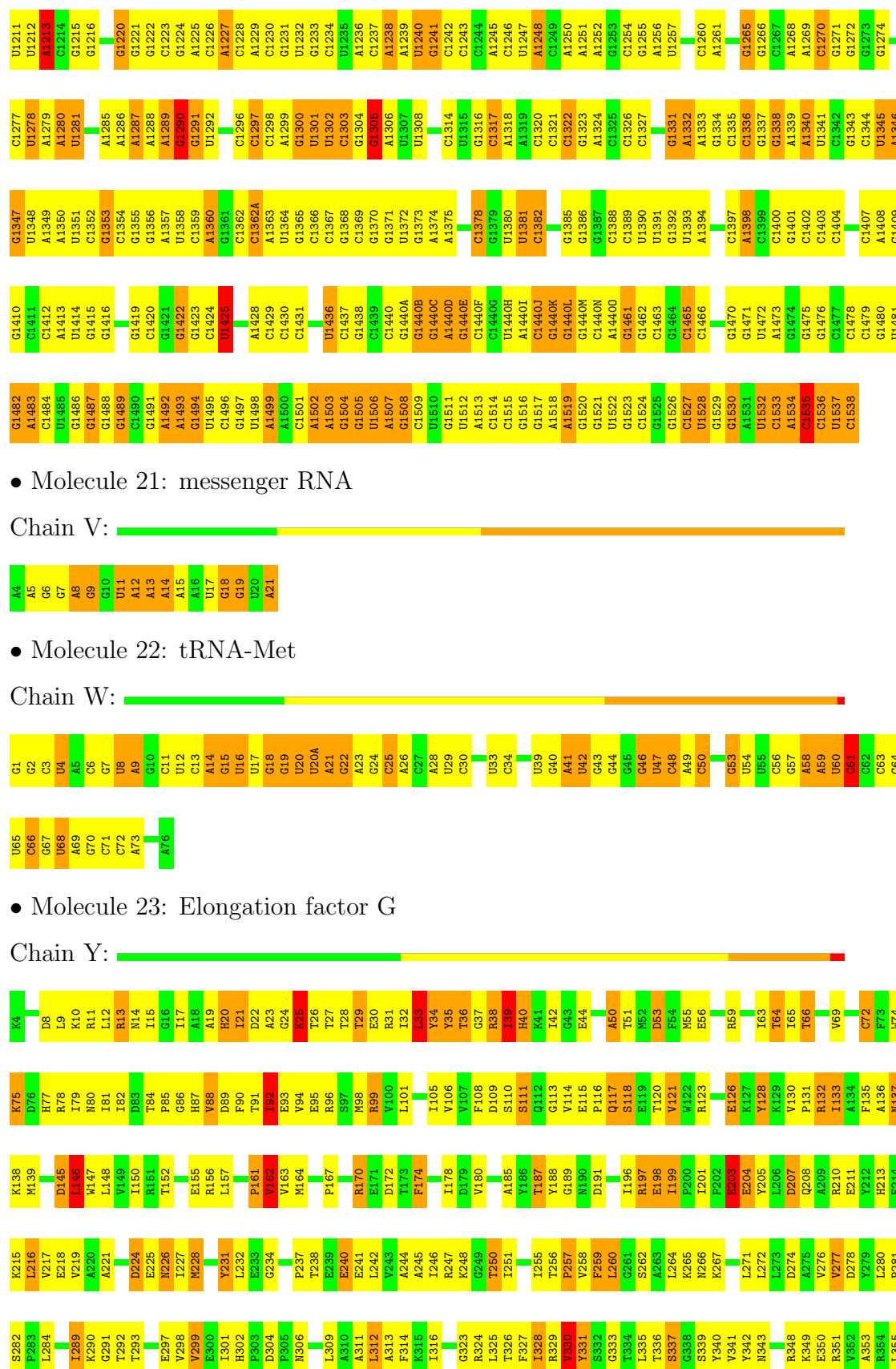


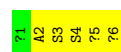
- Molecule 20: 16S ribosomal RNA

Chain A: 









4 Data and refinement statistics

EDS was not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	302.39Å 683.92Å 356.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.86	Depositor
% Data completeness (in resolution range)	(Not available) (40.00-3.86)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.34	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 3.89Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.264 , 0.317	Depositor
Wilson B-factor (Å ²)	76.3	Xtriage
Anisotropy	0.322	Xtriage
Estimated twinning fraction	0.320 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.24$, $\langle L^2 \rangle = 0.09$	Xtriage
Outliers	0 of 432130 reflections	Xtriage
Total number of atoms	58977	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, DPP, MG, KBE, UAL, 5OH

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	B	0.46	0/1945	0.80	9/2621 (0.3%)
2	C	0.30	0/1645	0.60	0/2216
3	D	0.31	0/1733	0.61	0/2318
4	E	0.30	0/1172	0.57	0/1576
5	F	0.29	0/856	0.54	0/1154
6	G	0.29	0/1276	0.54	0/1709
7	H	0.31	0/1136	0.61	0/1527
8	I	0.33	0/1029	0.56	1/1378 (0.1%)
9	J	0.29	0/815	0.56	0/1095
10	K	0.37	0/900	0.71	0/1213
11	L	0.49	0/992	0.91	2/1327 (0.2%)
12	M	0.30	0/1008	0.61	0/1347
13	N	0.30	0/501	0.46	0/664
14	O	0.31	0/745	0.56	0/992
15	P	0.28	0/722	0.54	0/970
16	Q	0.40	0/848	0.71	0/1131
17	R	0.31	0/579	0.64	0/768
18	S	0.30	0/647	0.60	0/870
19	T	0.34	0/764	0.62	0/1006
20	A	0.39	0/36351	1.06	104/56736 (0.2%)
21	V	0.47	0/443	1.09	5/691 (0.7%)
22	W	0.42	0/1827	1.14	7/2845 (0.2%)
23	Y	0.37	0/5481	0.68	8/7418 (0.1%)
24	U	1.08	0/11	1.84	0/13
All	All	0.37	0/63426	0.94	136/93585 (0.1%)

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	B	0	3
11	L	0	1
23	Y	0	4
All	All	0	8

There are no bond length outliers.

The worst 5 of 136 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1535	C	P-O3'-C3'	12.55	134.76	119.70
20	A	1535	C	O3'-P-O5'	-11.58	82.00	104.00
20	A	815	A	N1-C6-N6	-11.01	112.00	118.60
20	A	815	A	C5-C6-N6	10.11	131.79	123.70
20	A	1465	C	C2-N3-C4	-8.95	115.43	119.90

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	170	GLU	Peptide
1	B	185	ILE	Peptide
1	B	68	ILE	Peptide
11	L	32	PHE	Peptide
23	Y	34	TYR	Peptide

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1910	0	1957	119	0
2	C	1621	0	1688	78	0
3	D	1703	0	1763	112	0
4	E	1156	0	1213	57	0
5	F	843	0	857	46	0
6	G	1257	0	1296	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	H	1116	0	1177	77	0
8	I	1011	0	1043	60	0
9	J	802	0	849	54	0
10	K	885	0	904	50	0
11	L	976	0	1062	128	0
12	M	997	0	1072	68	0
13	N	492	0	529	30	0
14	O	734	0	771	41	0
15	P	706	0	725	36	0
16	Q	835	0	906	81	0
17	R	574	0	644	42	0
18	S	634	0	655	35	0
19	T	762	0	859	44	0
20	A	32474	0	16393	1066	0
21	V	393	0	197	18	0
22	W	1635	0	831	65	0
23	Y	5380	0	5435	314	0
24	U	48	0	40	40	0
25	Y	32	0	13	8	0
26	Y	1	0	0	0	0
All	All	58977	0	42879	2428	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 24.

The worst 5 of 2428 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:A:1492:A:H3'	24:U:6:5OH:NP	1.26	1.42
20:A:1492:A:H5'	24:U:6:5OH:CB	1.56	1.34
20:A:1493:A:OP2	24:U:6:5OH:NP	1.60	1.33
20:A:815:A:H2	20:A:1527:C:O2	1.19	1.25
20:A:1492:A:H3'	24:U:6:5OH:CQ	1.68	1.20

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	B	233/235 (99%)	154 (66%)	60 (26%)	19 (8%)	1	27
2	C	205/207 (99%)	140 (68%)	43 (21%)	22 (11%)	1	17
3	D	206/208 (99%)	146 (71%)	46 (22%)	14 (7%)	2	34
4	E	149/151 (99%)	118 (79%)	22 (15%)	9 (6%)	2	38
5	F	99/101 (98%)	82 (83%)	14 (14%)	3 (3%)	7	59
6	G	153/155 (99%)	113 (74%)	27 (18%)	13 (8%)	1	26
7	H	136/138 (99%)	98 (72%)	21 (15%)	17 (12%)	1	14
8	I	125/127 (98%)	98 (78%)	16 (13%)	11 (9%)	1	25
9	J	97/99 (98%)	69 (71%)	22 (23%)	6 (6%)	2	37
10	K	117/119 (98%)	81 (69%)	23 (20%)	13 (11%)	1	17
11	L	123/125 (98%)	55 (45%)	38 (31%)	30 (24%)	0	2
12	M	123/125 (98%)	85 (69%)	21 (17%)	17 (14%)	0	11
13	N	58/60 (97%)	46 (79%)	7 (12%)	5 (9%)	1	26
14	O	86/88 (98%)	59 (69%)	20 (23%)	7 (8%)	1	28
15	P	82/84 (98%)	61 (74%)	14 (17%)	7 (8%)	1	26
16	Q	98/100 (98%)	71 (72%)	14 (14%)	13 (13%)	0	12
17	R	68/70 (97%)	43 (63%)	17 (25%)	8 (12%)	1	15
18	S	77/79 (98%)	45 (58%)	21 (27%)	11 (14%)	0	10
19	T	97/99 (98%)	77 (79%)	16 (16%)	4 (4%)	4	49
23	Y	685/687 (100%)	474 (69%)	144 (21%)	67 (10%)	1	21
24	U	2/6 (33%)	2 (100%)	0	0	100	100
All	All	3019/3063 (99%)	2117 (70%)	606 (20%)	296 (10%)	1	21

5 of 296 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	20	GLU
1	B	67	THR
1	B	76	GLN
1	B	103	THR
1	B	157	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	203/203 (100%)	161 (79%)	42 (21%)	2	13
2	C	161/161 (100%)	124 (77%)	37 (23%)	1	10
3	D	180/180 (100%)	138 (77%)	42 (23%)	1	9
4	E	116/116 (100%)	91 (78%)	25 (22%)	1	11
5	F	90/90 (100%)	72 (80%)	18 (20%)	2	15
6	G	126/126 (100%)	109 (86%)	17 (14%)	6	36
7	H	119/119 (100%)	92 (77%)	27 (23%)	1	10
8	I	98/98 (100%)	79 (81%)	19 (19%)	2	16
9	J	89/89 (100%)	72 (81%)	17 (19%)	2	16
10	K	90/90 (100%)	76 (84%)	14 (16%)	4	28
11	L	104/104 (100%)	83 (80%)	21 (20%)	2	14
12	M	100/100 (100%)	83 (83%)	17 (17%)	3	24
13	N	49/49 (100%)	37 (76%)	12 (24%)	1	8
14	O	79/79 (100%)	63 (80%)	16 (20%)	2	14
15	P	72/72 (100%)	56 (78%)	16 (22%)	1	11
16	Q	95/95 (100%)	77 (81%)	18 (19%)	2	17
17	R	61/61 (100%)	51 (84%)	10 (16%)	3	26
18	S	69/69 (100%)	51 (74%)	18 (26%)	1	7
19	T	76/76 (100%)	66 (87%)	10 (13%)	6	37
23	Y	579/579 (100%)	475 (82%)	104 (18%)	2	19
24	U	2/2 (100%)	2 (100%)	0	100	100
All	All	2558/2558 (100%)	2058 (80%)	500 (20%)	2	16

5 of 500 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	I	128	ARG
12	M	8	GLU
23	Y	428	LEU

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Mol	Chain	Res	Type
9	J	22	LYS
10	K	91	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	84	GLN
11	L	8	ASN
23	Y	14	ASN
7	H	78	GLN
9	J	76	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	A	1511/1511 (100%)	330 (21%)	21 (1%)
21	V	17/18 (94%)	8 (47%)	1 (5%)
22	W	76/77 (98%)	27 (35%)	2 (2%)
All	All	1604/1606 (99%)	365 (22%)	24 (1%)

5 of 365 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	A	6	G
20	A	7	G
20	A	8	A
20	A	9	G
20	A	22	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	A	748	C
20	A	1064	G
22	W	20(A)	U
20	A	792	A
20	A	992	U

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

4 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$
24	KBE	U	1	24	8,8,9	8.66	1 (12%)	6,8,10	1.02	1 (16%)
24	DPP	U	2	24	5,5,6	6.98	1 (20%)	3,5,7	2.65	2 (66%)
24	UAL	U	5	24	7,8,9	1.43	1 (14%)	6,9,11	1.04	0
24	5OH	U	6	24	12,12,13	6.58	3 (25%)	13,16,18	0.85	0

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
24	KBE	U	1	24	-	0/6/7/8	0/0/0/0
24	DPP	U	2	24	-	0/2/4/6	0/0/0/0
24	UAL	U	5	24	-	0/3/7/9	0/0/0/0
24	5OH	U	6	24	-	0/2/18/20	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	U	1	KBE	O-C	24.35	1.28	1.11
24	U	6	5OH	O-C	22.01	1.26	1.11
24	U	2	DPP	O-C	15.38	1.22	1.11
24	U	6	5OH	CQ-NP	5.09	1.40	1.34
24	U	6	5OH	CQ-NR	2.39	1.40	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	U	2	DPP	C-CA-N	3.85	117.68	113.83
24	U	2	DPP	CB-CA-N	-2.50	103.12	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	U	1	KBE	CG-CB-CA	2.14	115.09	111.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates i

There are no carbohydrates in this entry.

5.6 Ligand geometry i

Of 2 ligands modelled in this entry, 1 is 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	$\# Z > 2$
25	GNP	Y	701	26	34,34,34	1.73	6 (17%)	50,54,54	5.60	14 (28%)

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
25	GNP	Y	701	26	-	0/18/38/38	0/1/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	Y	701	GNP	PG-O1G	6.10	1.53	1.46
25	Y	701	GNP	PB-N3B	-4.62	1.60	1.64
25	Y	701	GNP	PA-O3A	-2.67	1.55	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	Y	701	GNP	PB-O3A	-2.30	1.55	1.59
25	Y	701	GNP	PA-O2A	-2.17	1.45	1.55

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Y	701	GNP	C6-C5-N7	-37.40	129.10	134.14
25	Y	701	GNP	PA-O3A-PB	-4.61	116.08	131.81
25	Y	701	GNP	C2-N3-C4	-3.77	109.80	115.09
25	Y	701	GNP	C4'-O4'-C1'	-3.69	105.74	109.75
25	Y	701	GNP	C4-C5-N7	3.54	112.56	109.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.