



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 04:24 AM GMT

PDB ID : 3I21
Title : Crystal structure of the E. coli 70S ribosome in an intermediate state of ratcheting
Authors : Zhang, W.; Dunkle, J.A.; Cate, J.H.D.
Deposited on : 2009-06-28
Resolution : 3.71 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>

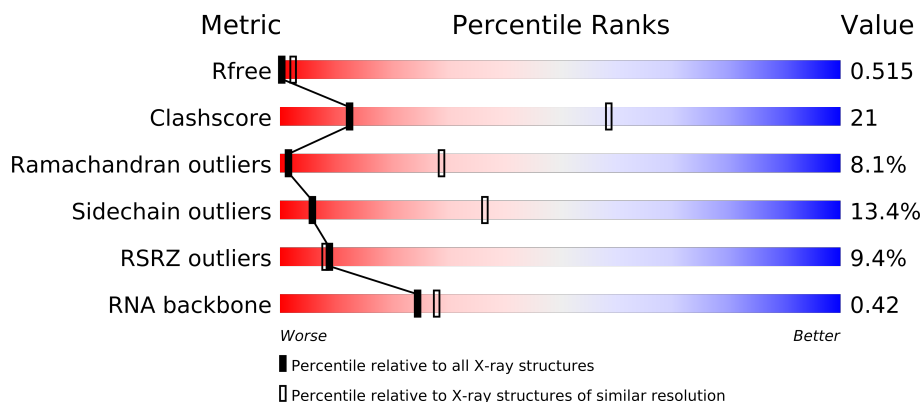
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.71 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.












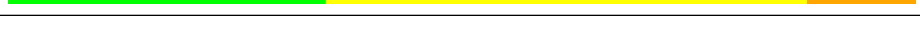

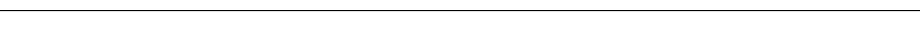
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1103 (4.04-3.40)
Clashscore	79885	1026 (3.98-3.46)
Ramachandran outliers	78287	1082 (4.00-3.44)
Sidechain outliers	78261	1075 (4.00-3.44)
RSRZ outliers	66119	1104 (4.04-3.40)
RNA backbone	1838	1008 (4.52-2.80)

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.

Mol	Chain	Length	Quality of chain
1	B	241	
2	C	233	
3	D	206	
4	E	167	
5	F	135	
6	G	179	
7	H	130	
8	I	130	
9	J	103	
10	K	129	
11	L	124	
12	M	118	

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Mol	Chain	Length	Quality of chain
13	N	101	
14	O	89	
15	P	82	
16	Q	84	
17	R	75	
18	S	92	
19	T	87	
20	U	71	
21	A	1530	
22	V	17	
22	X	17	
23	W	6	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
24	MG	A	1544	-	X
24	MG	A	1549	-	X
24	MG	A	1552	-	X
24	MG	A	1562	-	X
24	MG	A	1570	-	X

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 52443 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	218	Total	C	N	O	S	0	0	0
			1704	1081	305	311	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	206	Total	C	N	O	S	0	0	0
			1624	1028	305	288	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	150	Total	C	N	O	S	0	0	0
			1105	687	211	201	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	100	Total	C	N	O	S	0	0	0
			817	515	148	148	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	150	Total	C	N	O	S	0	0	0
			1174	730	226	214	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- 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
			1022	634	206	179	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	98	Total	C	N	O	S	0	0	0
			786	493	150	142	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	K	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	113	Total	C	N	O	S	0	0	0
			876	541	177	155	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	95	Total	C	N	O	S	0	0	0
			769	480	159	127	3			

- 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
			714	439	144	130	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	80	Total	C	N	O	S	0	0	0
			638	400	126	111	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	Q	80	Total	C	N	O	S	0	0	0
			648	411	121	113	3			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	R	55	Total	C	N	O	0	0	0
			455	288	86	81			

- 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
			637	408	120	107	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	T	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	U	51	Total	C	N	O	S	0	0	0
			425	265	86	73	1			

- Molecule 21 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	A	1530	Total	C	N	O	P	0	0	0
			32831	14642	6024	10635	1530			

- Molecule 22 is a RNA chain called P-site tRNA ASL fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	17	Total	C	N	O	P	0	0	0
			365	163	68	117	17			
22	X	17	Total	C	N	O	P	0	0	0
			365	163	68	117	17			

- Molecule 23 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	6	Total	C	N	O	P	0	0	0
			120	54	12	48	6			

- Molecule 24 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	42	Total	Mg	0	0
			42	42		

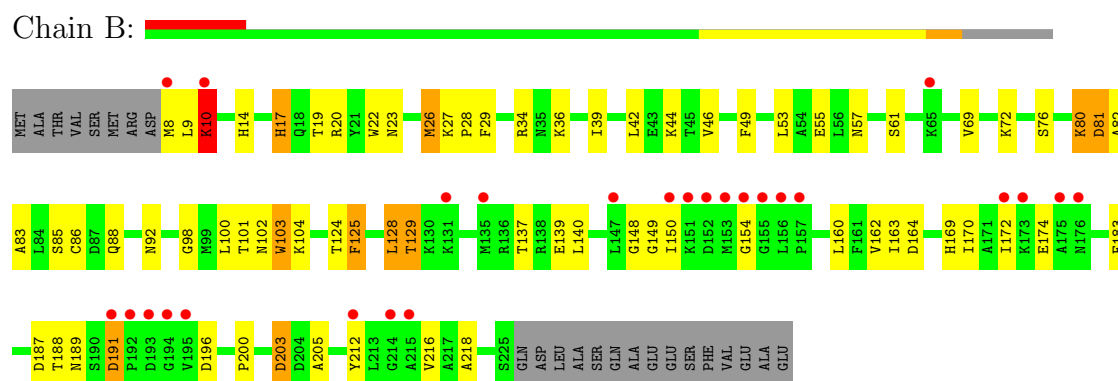
- Molecule 25 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	203	Total	O	0	0
			203	203		
25	N	2	Total	O	0	0
			2	2		
25	T	2	Total	O	0	0
			2	2		

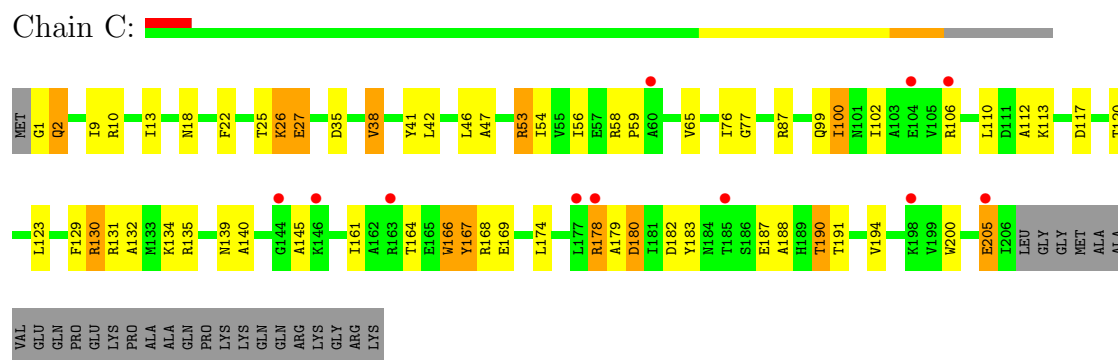
3 Residue-property plots

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

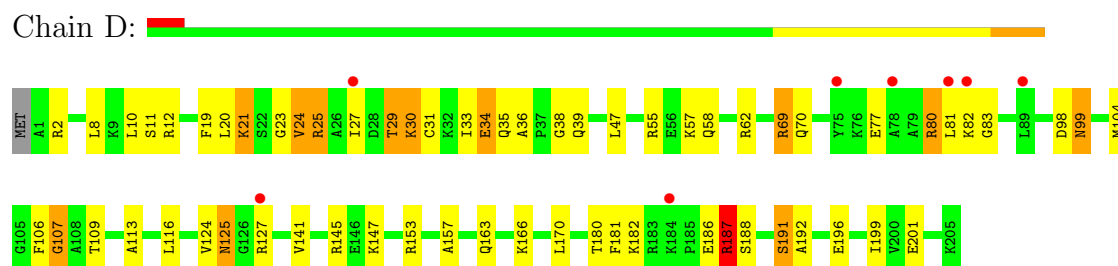
• Molecule 1: 30S ribosomal protein S2



• Molecule 2: 30S ribosomal protein S3

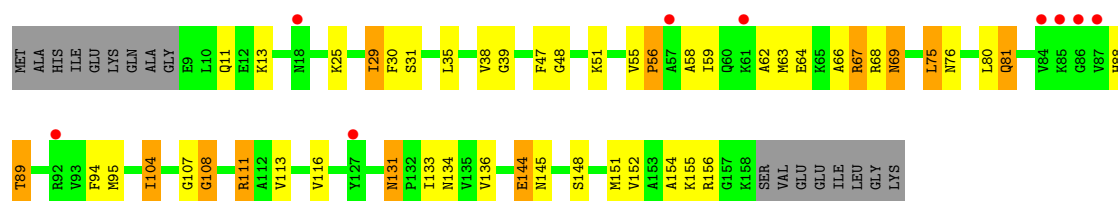


• Molecule 3: 30S ribosomal protein S4



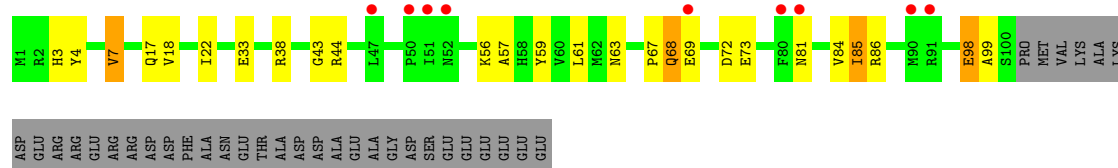
• Molecule 4: 30S ribosomal protein S5





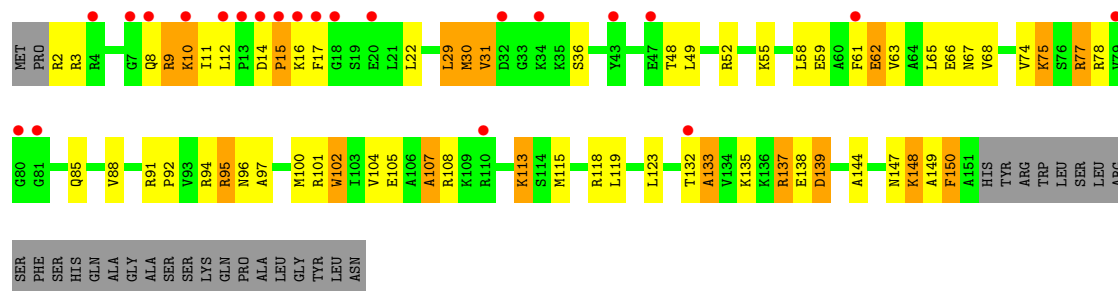
• Molecule 5: 30S ribosomal protein S6

Chain F:



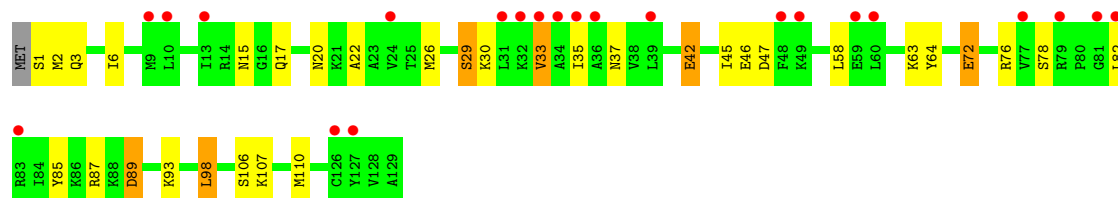
• Molecule 6: 30S ribosomal protein S7

Chain G:



• Molecule 7: 30S ribosomal protein S8

Chain H:



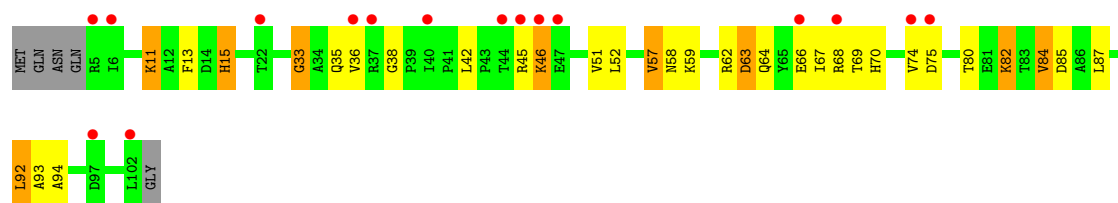
• Molecule 8: 30S ribosomal protein S9

Chain I:



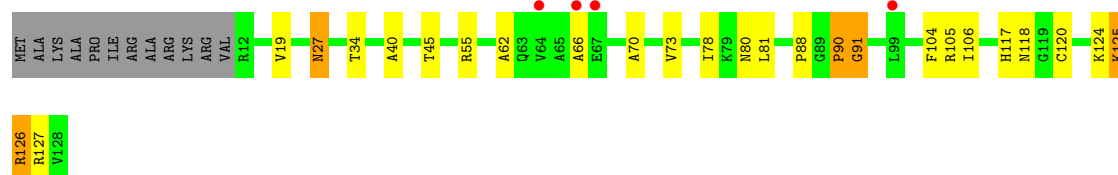
• Molecule 9: 30S ribosomal protein S10

Chain J:



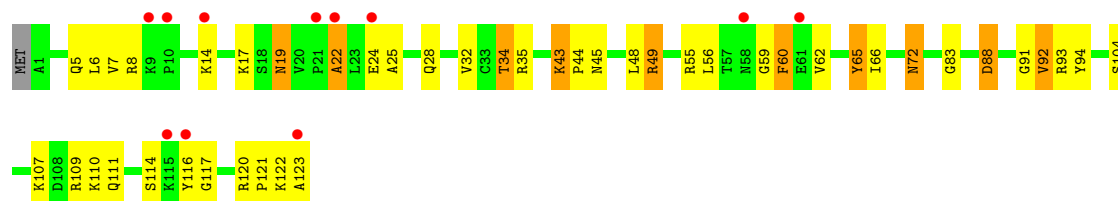
- Molecule 10: 30S ribosomal protein S11

Chain K:



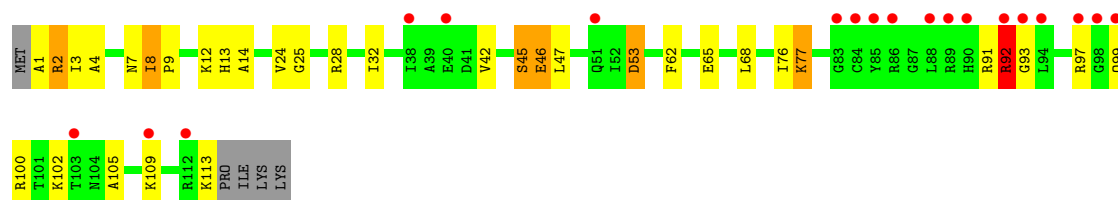
- Molecule 11: 30S ribosomal protein S12

Chain L:



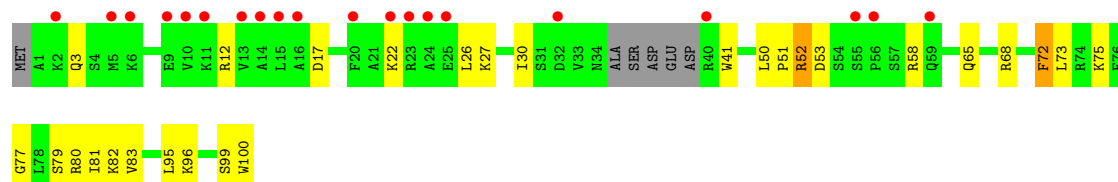
- Molecule 12: 30S ribosomal protein S13

Chain M:



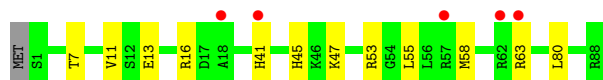
- Molecule 13: 30S ribosomal protein S14

Chain N:



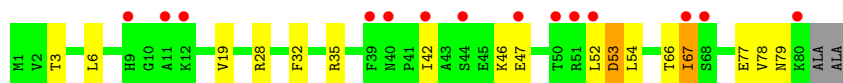
- Molecule 14: 30S ribosomal protein S15

Chain O:



- Molecule 15: 30S ribosomal protein S16

Chain P:



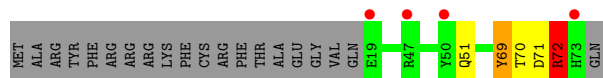
- Molecule 16: 30S ribosomal protein S17

Chain Q:



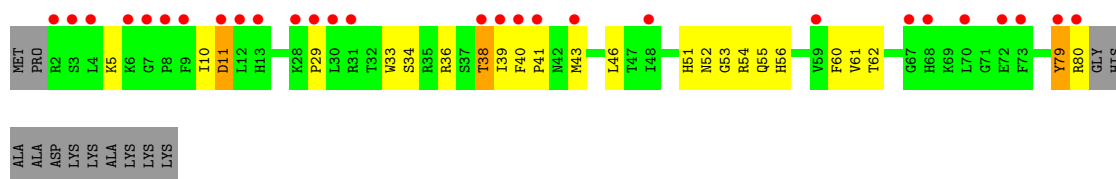
- Molecule 17: 30S ribosomal protein S18

Chain R:



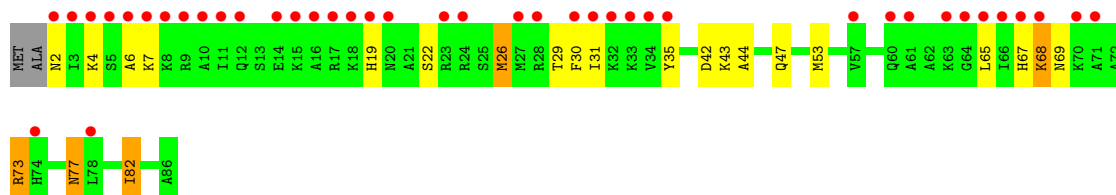
- Molecule 18: 30S ribosomal protein S19

Chain S:



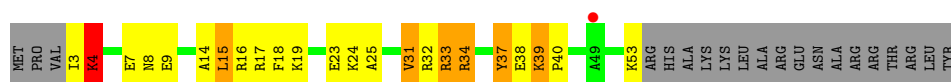
- Molecule 19: 30S ribosomal protein S20

Chain T:



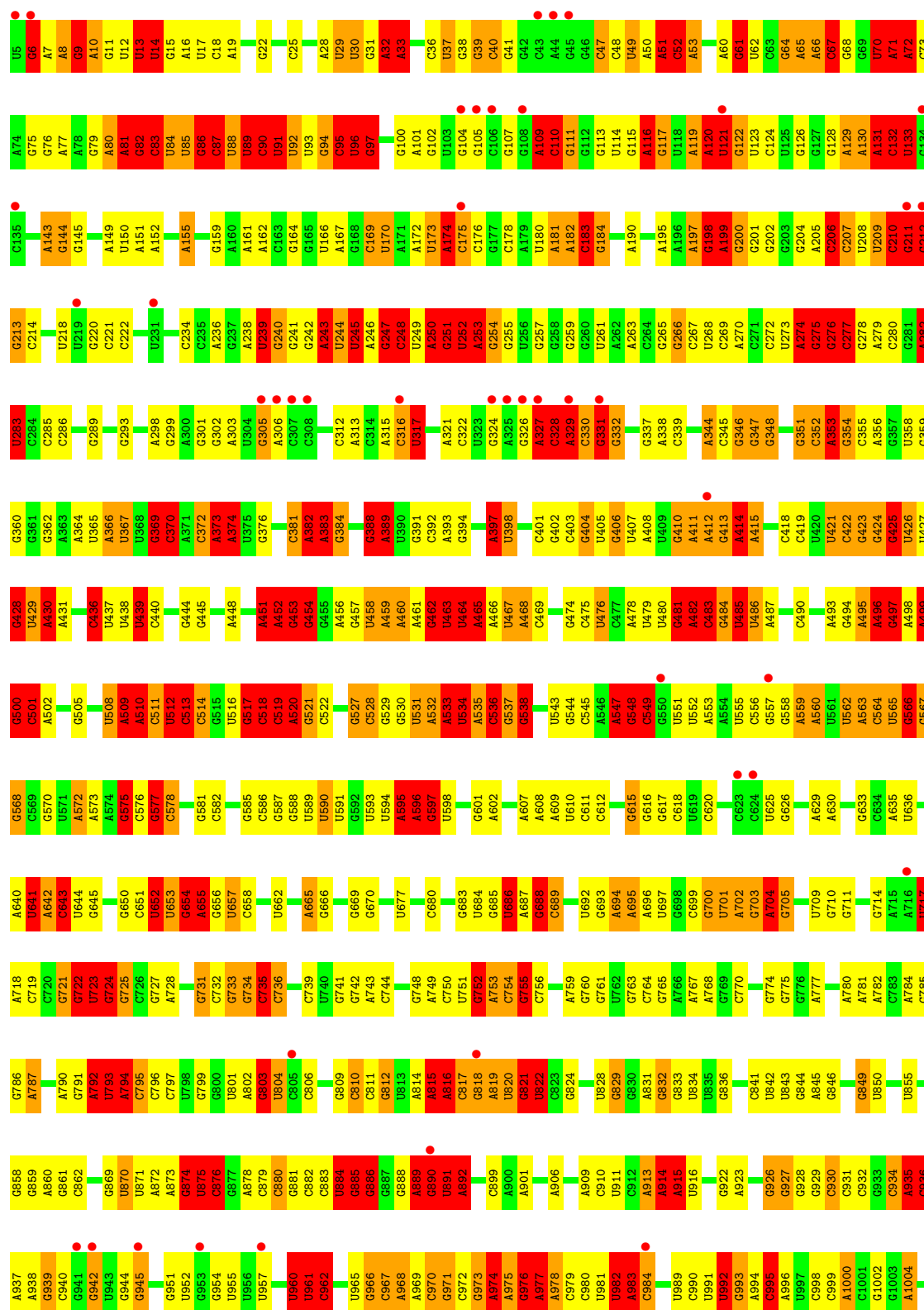
- Molecule 20: 30S ribosomal protein S21

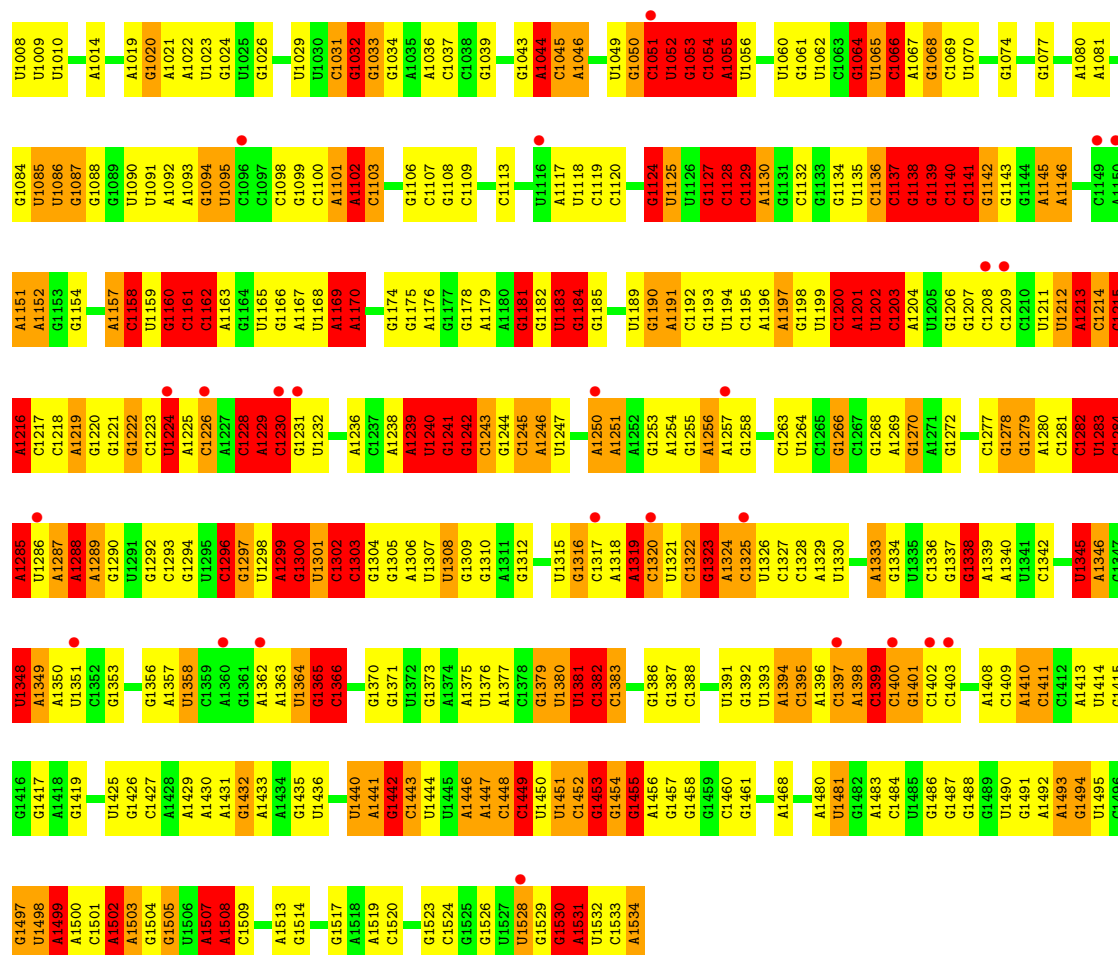
Chain U:



• Molecule 21: 16S rRNA

Chain A:





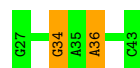
• Molecule 22: P-site tRNA ASL fragment

Chain V:



• Molecule 22: P-site tRNA ASL fragment

Chain X:



• Molecule 23: messenger RNA

Chain W:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.95Å 433.08Å 624.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.44 – 3.71 73.44 – 3.71	Depositor EDS
% Data completeness (in resolution range)	75.7 (73.44-3.71) 75.7 (73.44-3.71)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 3.67Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.227 , 0.268 0.512 , 0.515	Depositor DCC
R_{free} test set	9145 reflections (2.02%)	DCC
Wilson B-factor (Å ²)	109.1	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 52.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 452802 reflections	Xtriage
F_o, F_c correlation	0.56	EDS
Total number of atoms	52443	wwPDB-VP
Average B, all atoms (Å ²)	182.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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: MG

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	0.25	0/1735	0.46	0/2338
2	C	0.26	0/1651	0.47	0/2225
3	D	0.30	0/1665	0.50	0/2227
4	E	0.29	0/1118	0.53	0/1504
5	F	0.26	0/835	0.46	0/1128
6	G	0.27	0/1187	0.50	0/1591
7	H	0.25	0/989	0.47	0/1326
8	I	0.25	0/1034	0.47	0/1375
9	J	0.24	0/796	0.47	0/1077
10	K	0.26	0/893	0.50	0/1205
11	L	0.31	0/969	0.53	0/1300
12	M	0.38	0/884	0.53	0/1181
13	N	0.25	0/780	0.43	0/1036
14	O	0.24	0/722	0.46	0/964
15	P	0.27	0/648	0.47	0/870
16	Q	0.26	0/657	0.46	0/881
17	R	0.27	0/462	0.49	0/621
18	S	0.23	0/652	0.46	0/877
19	T	0.24	0/671	0.44	0/888
20	U	0.29	0/430	0.54	0/570
21	A	0.53	0/36762	1.45	712/57350 (1.2%)
22	V	0.56	0/408	1.14	0/634
22	X	0.41	0/408	0.82	0/634
23	W	0.73	0/131	1.93	7/200 (3.5%)
All	All	0.46	0/56487	1.23	719/84002 (0.9%)

There are no bond length outliers.

The worst 5 of 719 bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	A	590	U	N1-C1'-C2'	-13.65	96.26	114.00
21	A	960	U	O4'-C1'-N1	13.36	118.89	108.20
21	A	1302	C	N1-C1'-C2'	-13.11	96.95	114.00
21	A	512	U	N1-C1'-C2'	-13.00	97.10	114.00
21	A	1345	U	O4'-C1'-N1	12.93	118.55	108.20

There are no chirality outliers.

There are no planarity outliers.

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	1704	0	0	27	0
2	C	1624	0	0	28	0
3	D	1643	0	0	22	0
4	E	1105	0	75	24	0
5	F	817	0	0	6	0
6	G	1174	0	0	27	0
7	H	979	0	0	16	0
8	I	1022	0	0	10	0
9	J	786	0	0	13	0
10	K	877	0	0	9	0
11	L	955	0	0	21	0
12	M	876	0	0	12	0
13	N	769	0	0	11	0
14	O	714	0	0	6	0
15	P	638	0	0	4	0
16	Q	648	0	691	50	0
17	R	455	0	0	2	0
18	S	637	0	0	9	0
19	T	665	0	0	12	0
20	U	425	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	A	32831	0	44	851	0
22	V	365	0	0	12	0
22	X	365	0	0	2	0
23	W	120	0	0	1	0
24	A	42	0	0	0	0
25	A	203	0	0	6	0
25	N	2	0	0	0	0
25	T	2	0	0	0	0
All	All	52443	0	810	1110	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 21.

The worst 5 of 1110 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:A:1213:A:O2'	21:A:1214:C:C5'	2.14	0.95
21:A:499:A:O2'	21:A:500:G:C8	2.25	0.90
21:A:960:U:O2'	21:A:1223:C:C5'	2.29	0.81
21:A:792:A:O2'	21:A:794:A:N7	2.15	0.80
12:M:8:ILE:N	12:M:9:PRO:CD	2.45	0.79

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	216/241 (90%)	144 (67%)	50 (23%)	22 (10%)	1	20
2	C	204/233 (88%)	136 (67%)	52 (26%)	16 (8%)	1	30
3	D	203/206 (98%)	136 (67%)	46 (23%)	21 (10%)	1	20
4	E	148/167 (89%)	100 (68%)	34 (23%)	14 (10%)	1	23
5	F	98/135 (73%)	65 (66%)	27 (28%)	6 (6%)	2	39
6	G	148/179 (83%)	84 (57%)	44 (30%)	20 (14%)	0	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	H	127/130 (98%)	88 (69%)	30 (24%)	9 (7%)	2	34
8	I	125/130 (96%)	88 (70%)	33 (26%)	4 (3%)	6	58
9	J	96/103 (93%)	62 (65%)	22 (23%)	12 (12%)	1	14
10	K	115/129 (89%)	86 (75%)	19 (16%)	10 (9%)	1	26
11	L	121/124 (98%)	86 (71%)	26 (22%)	9 (7%)	2	32
12	M	111/118 (94%)	71 (64%)	28 (25%)	12 (11%)	1	18
13	N	91/101 (90%)	62 (68%)	24 (26%)	5 (6%)	3	42
14	O	86/89 (97%)	67 (78%)	19 (22%)	0	100	100
15	P	78/82 (95%)	52 (67%)	20 (26%)	6 (8%)	1	30
16	Q	78/84 (93%)	57 (73%)	16 (20%)	5 (6%)	2	38
17	R	53/75 (71%)	39 (74%)	11 (21%)	3 (6%)	3	41
18	S	77/92 (84%)	55 (71%)	20 (26%)	2 (3%)	8	63
19	T	83/87 (95%)	59 (71%)	21 (25%)	3 (4%)	5	55
20	U	49/71 (69%)	23 (47%)	17 (35%)	9 (18%)	0	5
All	All	2307/2576 (90%)	1560 (68%)	559 (24%)	188 (8%)	1	29

5 of 188 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	80	LYS
1	B	129	THR
1	B	150	ILE
1	B	188	THR
2	C	87	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	180/199 (90%)	158 (88%)	22 (12%)	7	41
2	C	170/190 (90%)	146 (86%)	24 (14%)	5	34
3	D	172/173 (99%)	152 (88%)	20 (12%)	8	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	113/126 (90%)	100 (88%)	13 (12%)	8	44
5	F	87/116 (75%)	74 (85%)	13 (15%)	4	31
6	G	123/147 (84%)	95 (77%)	28 (23%)	1	10
7	H	104/105 (99%)	91 (88%)	13 (12%)	7	40
8	I	105/107 (98%)	91 (87%)	14 (13%)	6	37
9	J	86/90 (96%)	77 (90%)	9 (10%)	10	49
10	K	90/99 (91%)	80 (89%)	10 (11%)	9	47
11	L	103/104 (99%)	88 (85%)	15 (15%)	5	31
12	M	91/96 (95%)	74 (81%)	17 (19%)	2	17
13	N	79/84 (94%)	68 (86%)	11 (14%)	5	35
14	O	76/77 (99%)	72 (95%)	4 (5%)	32	80
15	P	65/65 (100%)	59 (91%)	6 (9%)	13	57
16	Q	74/78 (95%)	64 (86%)	10 (14%)	6	36
17	R	48/65 (74%)	46 (96%)	2 (4%)	40	84
18	S	70/79 (89%)	59 (84%)	11 (16%)	4	28
19	T	65/66 (98%)	56 (86%)	9 (14%)	5	35
20	U	44/61 (72%)	35 (80%)	9 (20%)	2	13
All	All	1945/2127 (91%)	1685 (87%)	260 (13%)	6	36

5 of 260 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	G	139	ASP
8	I	125	GLN
18	S	62	THR
7	H	29	SER
7	H	110	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
16	Q	49	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	A	1529/1530 (99%)	516 (33%)	245 (16%)
22	V	17/17 (100%)	3 (17%)	1 (5%)
22	X	16/17 (94%)	2 (12%)	0
23	W	5/6 (83%)	1 (20%)	1 (20%)
All	All	1567/1570 (99%)	522 (33%)	247 (15%)

5 of 522 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	A	6	G
21	A	7	A
21	A	8	A
21	A	9	G
21	A	10	A

5 of 247 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	A	537	G
21	A	755	G
21	A	1397	C
21	A	564	C
21	A	654	G

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 42 ligands modelled in this entry, 42 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	B	218/241 (90%)	0.44	26 (11%) 5 6	159, 222, 233, 241	0
2	C	206/233 (88%)	0.22	11 (5%) 25 16	140, 172, 212, 228	0
3	D	205/206 (99%)	0.32	8 (3%) 37 24	112, 131, 152, 165	0
4	E	150/167 (89%)	0.25	9 (6%) 21 15	100, 156, 171, 176	0
5	F	100/135 (74%)	0.43	9 (9%) 10 9	164, 186, 203, 209	0
6	G	150/179 (83%)	0.59	22 (14%) 3 4	142, 194, 228, 244	0
7	H	129/130 (99%)	0.80	22 (17%) 2 3	152, 177, 195, 203	0
8	I	127/130 (97%)	0.52	15 (11%) 5 6	155, 195, 223, 232	0
9	J	98/103 (95%)	0.97	16 (16%) 2 3	155, 196, 230, 240	0
10	K	117/129 (90%)	0.20	4 (3%) 43 27	125, 155, 181, 196	0
11	L	123/124 (99%)	0.43	11 (8%) 10 9	117, 139, 155, 161	0
12	M	113/118 (95%)	0.86	19 (16%) 2 3	195, 269, 309, 322	0
13	N	95/101 (94%)	1.29	20 (21%) 1 2	155, 207, 265, 284	0
14	O	88/89 (98%)	0.33	5 (5%) 23 15	142, 174, 193, 201	0
15	P	80/82 (97%)	1.07	14 (17%) 2 3	151, 180, 203, 207	0
16	Q	80/84 (95%)	0.61	11 (13%) 4 4	99, 123, 145, 163	0
17	R	55/75 (73%)	0.36	4 (7%) 15 11	148, 165, 180, 187	0
18	S	79/92 (85%)	1.60	28 (35%) 1 1	223, 265, 319, 334	0
19	T	85/87 (97%)	2.05	41 (48%) 1 1	194, 242, 275, 283	0
20	U	51/71 (71%)	0.22	1 (1%) 62 39	126, 150, 183, 193	0
21	A	1530/1530 (100%)	0.20	68 (4%) 33 21	109, 171, 272, 362	0
22	V	17/17 (100%)	0.45	2 (11%) 5 6	158, 162, 193, 208	0
22	X	17/17 (100%)	0.16	0 100 100	187, 193, 221, 222	0
23	W	6/6 (100%)	2.28	4 (66%) 0 1	160, 160, 168, 179	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3919/4146 (94%)	0.45	370 (9%) 9 8	99, 175, 270, 362	0

The worst 5 of 370 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	G	16	LYS	11.0
21	A	121	U	9.1
19	T	33	LYS	8.2
12	M	93	GLY	7.8
19	T	19	HIS	6.6

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
24	MG	A	1544	1/1	1.21	50.58	146,146,146,146	0
24	MG	A	1549	1/1	0.44	31.50	135,135,135,135	0
24	MG	A	1552	1/1	0.32	4.48	216,216,216,216	0
24	MG	A	1570	1/1	0.56	3.92	118,118,118,118	0
24	MG	A	1562	1/1	0.83	2.34	210,210,210,210	0
24	MG	A	1566	1/1	0.36	1.23	120,120,120,120	0
24	MG	A	1548	1/1	0.27	1.16	148,148,148,148	0
24	MG	A	1538	1/1	0.25	0.89	121,121,121,121	0
24	MG	A	1541	1/1	0.23	0.18	132,132,132,132	0
24	MG	A	1543	1/1	0.26	0.10	121,121,121,121	0
24	MG	A	1537	1/1	0.24	0.05	134,134,134,134	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
24	MG	A	1553	1/1	0.15	0.05	123,123,123,123	0
24	MG	A	1546	1/1	0.47	-0.01	199,199,199,199	0
24	MG	A	1554	1/1	0.24	-0.07	99,99,99,99	0
24	MG	A	1547	1/1	0.41	-0.19	183,183,183,183	0
24	MG	A	1569	1/1	0.15	-0.37	266,266,266,266	0
24	MG	A	1561	1/1	0.23	-0.49	130,130,130,130	0
24	MG	A	1536	1/1	0.16	-0.49	124,124,124,124	0
24	MG	A	1	1/1	0.15	-0.61	224,224,224,224	0
24	MG	A	1559	1/1	0.20	-0.78	157,157,157,157	0
24	MG	A	1564	1/1	0.20	-0.96	153,153,153,153	0
24	MG	A	1556	1/1	0.29	-1.19	139,139,139,139	0
24	MG	A	4	1/1	0.12	-1.35	117,117,117,117	0
24	MG	A	1572	1/1	0.18	-1.39	170,170,170,170	0
24	MG	A	2	1/1	0.18	-1.55	177,177,177,177	0
24	MG	A	1571	1/1	0.14	-1.75	151,151,151,151	0
24	MG	A	1565	1/1	0.17	-1.80	142,142,142,142	0
24	MG	A	1540	1/1	0.11	-2.00	181,181,181,181	0
24	MG	A	1558	1/1	0.10	-2.31	99,99,99,99	0
24	MG	A	1568	1/1	0.10	-2.57	226,226,226,226	0
24	MG	A	1567	1/1	0.11	-2.58	112,112,112,112	0
24	MG	A	1551	1/1	0.11	-2.61	115,115,115,115	0
24	MG	A	1542	1/1	0.12	-2.72	124,124,124,124	0
24	MG	A	1535	1/1	0.06	-3.23	115,115,115,115	0
24	MG	A	1555	1/1	0.10	-3.38	127,127,127,127	0
24	MG	A	1560	1/1	0.05	-3.39	99,99,99,99	0
24	MG	A	1550	1/1	0.06	-4.32	150,150,150,150	0
24	MG	A	1557	1/1	0.12	-4.52	136,136,136,136	0
24	MG	A	1539	1/1	0.10	-5.34	131,131,131,131	0
24	MG	A	1563	1/1	0.07	-5.41	123,123,123,123	0
24	MG	A	1545	1/1	0.08	-5.63	156,156,156,156	0
24	MG	A	3	1/1	0.05	-9.38	141,141,141,141	0

6.5 Other polymers ⓘ

There are no such residues in this entry.