wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 02:09 PM BST

PDB ID	:	4A2I
EMDB ID:	:	EMD-1895
Title	:	Cryo-electron Microscopy Structure of the 30S Subunit in Complex with the YjeQ Biogenesis Factor
Authors	:	Jomaa, A.; Stewart, G.; Mears, J.A.; Kireeva, I.; Brown, E.D.; Ortega, J.
Deposited on	:	2011-09-27
Resolution	:	16.50 Å(reported)
Based on PDB ID	:	2AVY,2RCN

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

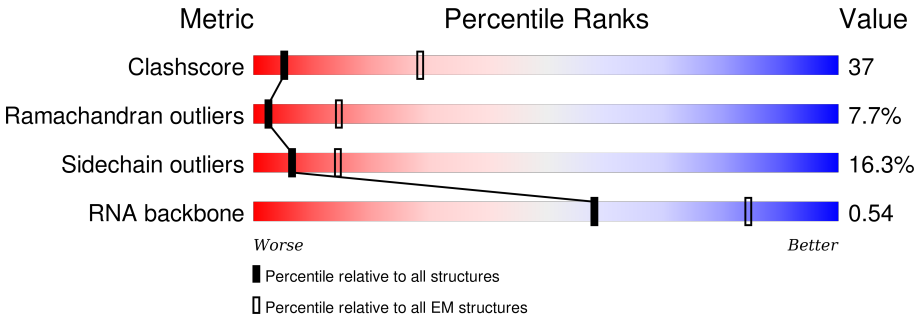
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 16.50 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)	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	A	1530	25% 61% 14%
2	B	218	23% 56% 20%
3	C	206	30% 54% 15%
4	D	205	28% 53% 18%
5	E	150	33% 55% 11%
6	F	100	32% 50% 15%
7	G	150	32% 53% 14%
8	H	129	42% 49% 9%

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Mol	Chain	Length	Quality of chain
9	I	127	24% 53% 23%
10	J	98	27% 53% 17%
11	K	117	27% 53% 18%
12	L	123	22% 60% 18%
13	M	114	26% 55% 18%
14	N	100	24% 57% 14%
15	O	88	43% 50% 6%
16	P	82	35% 54% 11%
17	Q	80	23% 59% 19%
18	R	55	31% 60% 9%
19	S	79	29% 58% 10%
20	T	85	40% 49% 8%
21	U	51	20% 37% 39%
22	V	277	62% 35%

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 53533 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 16S RIBOSOMAL RNA.

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

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	218	1704	1081	305	311	7	0	0

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S21.

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

- Molecule 22 is a protein called PUTATIVE RIBOSOME BIOGENESIS GTPASE RSGA.

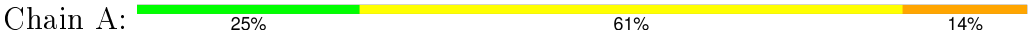
Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	277	Total	C	N	O	S	0	0
			2164	1364	382	408	10		

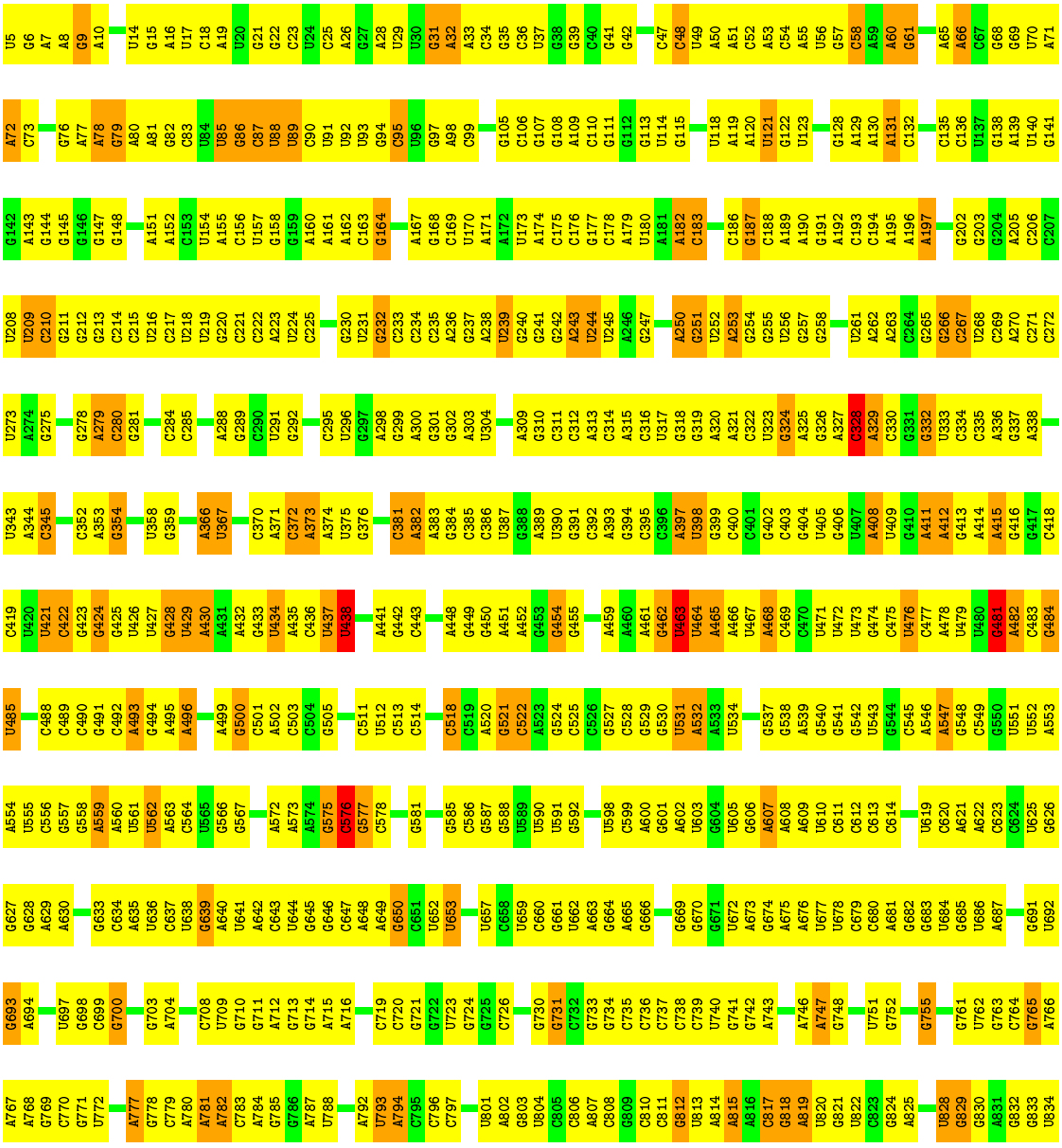
3 Residue-property plots (i)

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.

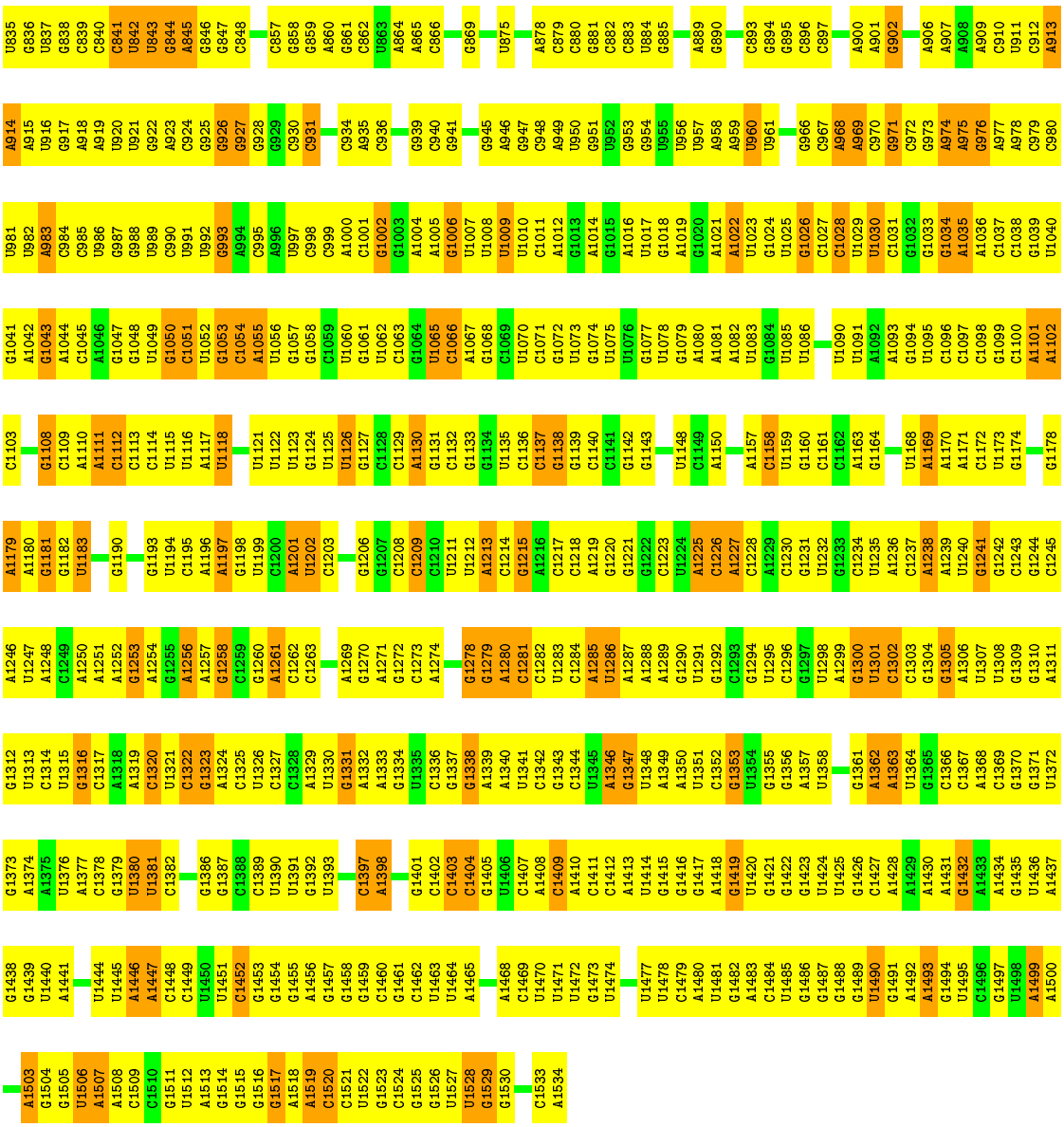
- Molecule 1: 16S RIBOSOMAL RNA

Chain A:



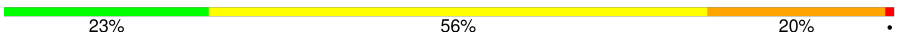


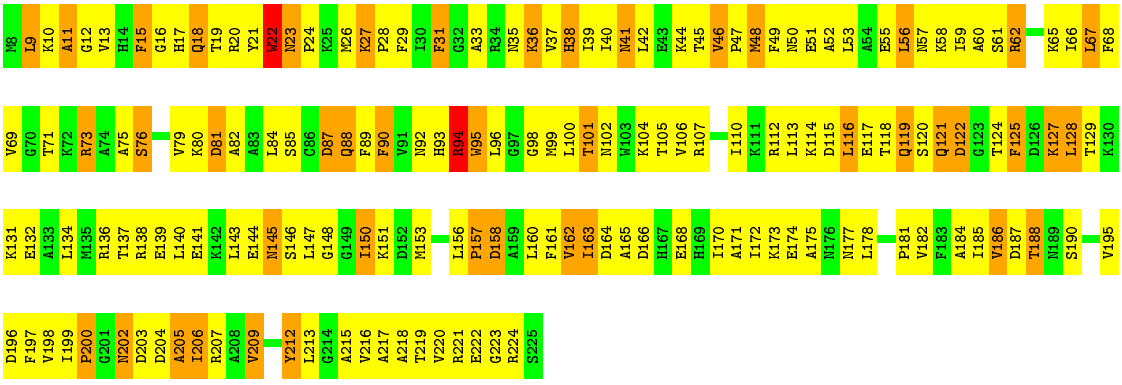
WORLDWIDE PDB PROTEIN DATA BANK
EMDataBank Unified Data Resource for 3DEM



- Molecule 2: 30S RIBOSOMAL PROTEIN S2

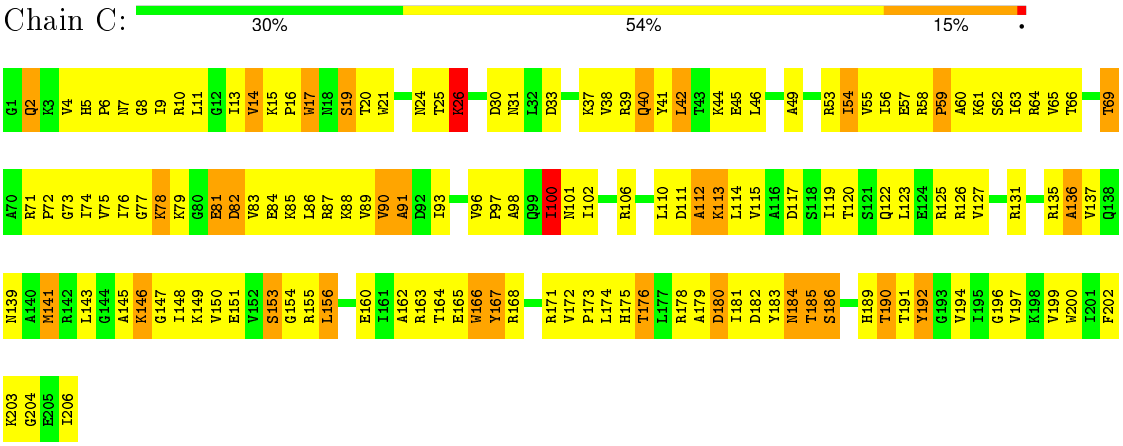
Chain B:





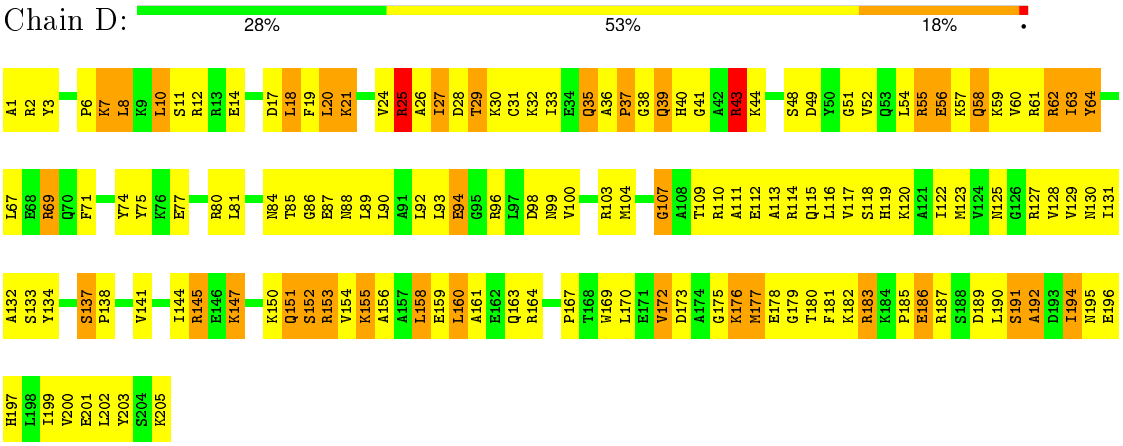
- Molecule 3: 30S RIBOSOMAL PROTEIN S3

Chain C:



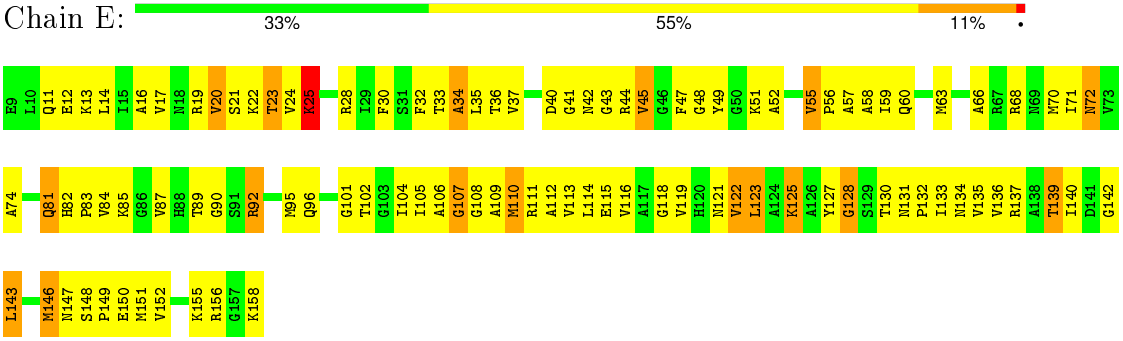
- Molecule 4: 30S RIBOSOMAL PROTEIN S4

Chain D:



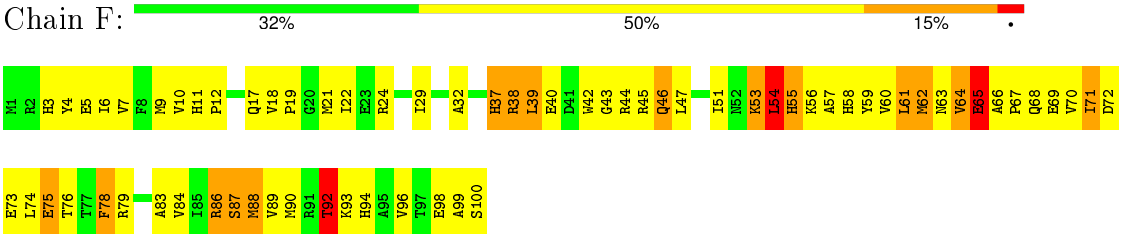
- Molecule 5: 30S RIBOSOMAL PROTEIN S5

Chain E:



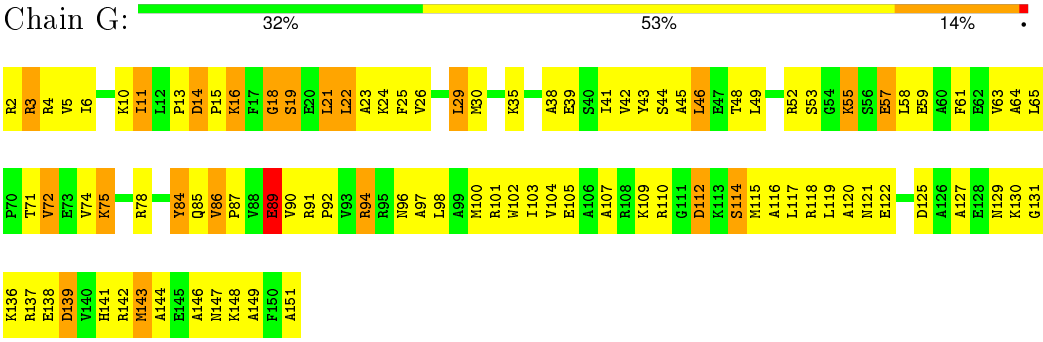
- Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain F:



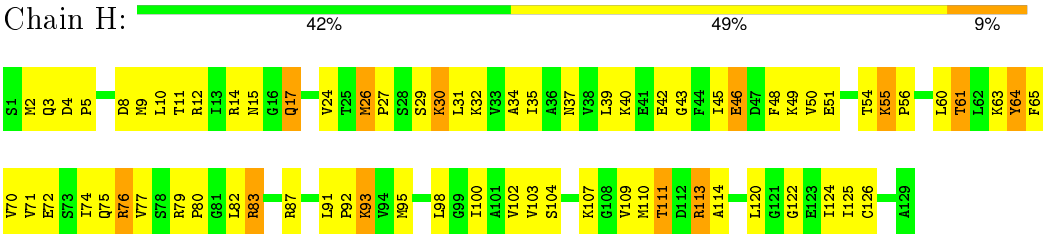
- Molecule 7: 30S RIBOSOMAL PROTEIN S7

Chain G:



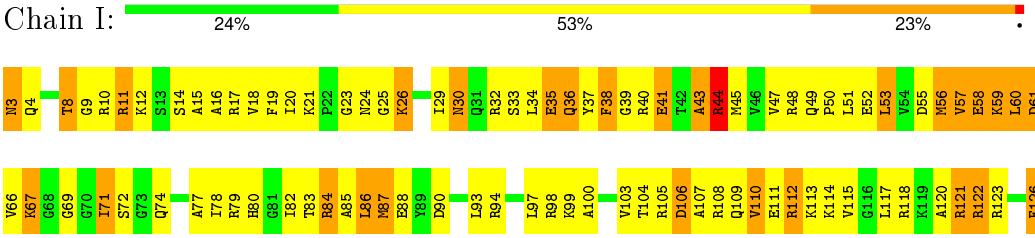
- Molecule 8: 30S RIBOSOMAL PROTEIN S8

Chain H:



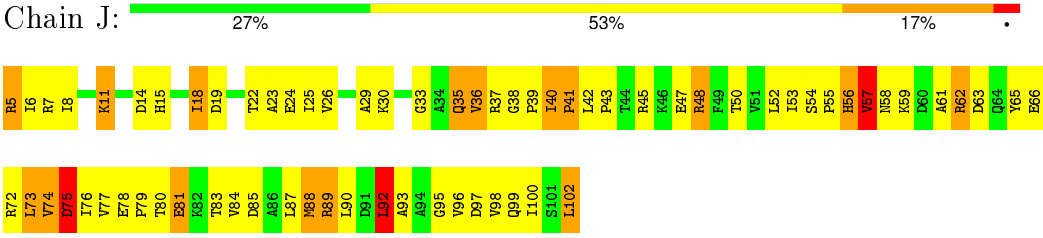
- Molecule 9: 30S RIBOSOMAL PROTEIN S9

Chain I:



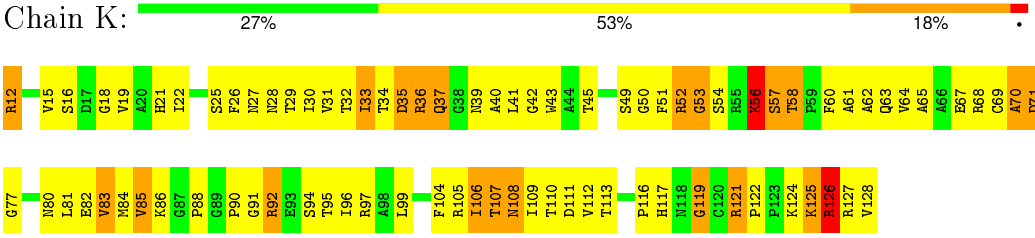
- Molecule 10: 30S RIBOSOMAL PROTEIN S10

Chain J:



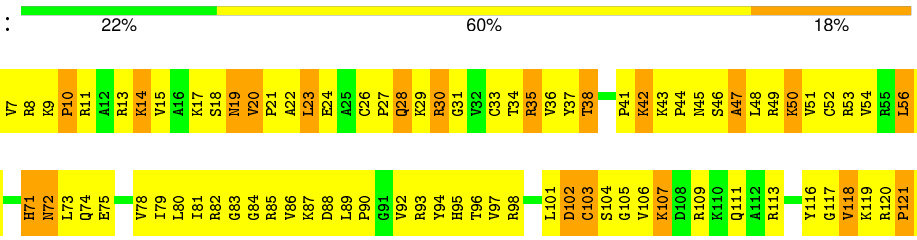
- Molecule 11: 30S RIBOSOMAL PROTEIN S11

Chain K:



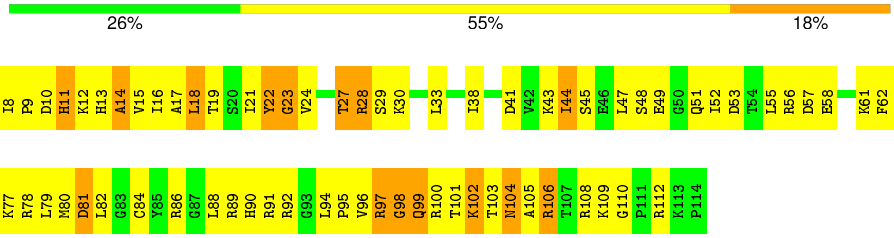
- Molecule 12: 30S RIBOSOMAL PROTEIN S12

Chain L:



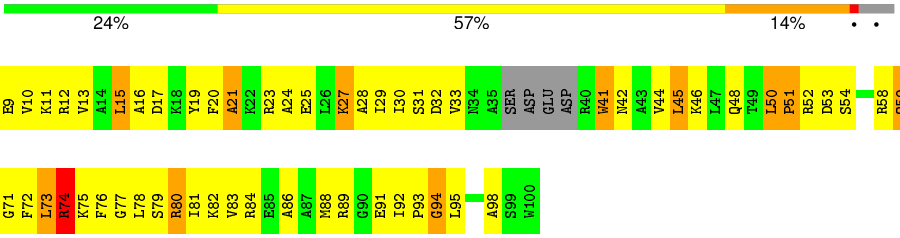
- Molecule 13: 30S RIBOSOMAL PROTEIN S13

Chain M:



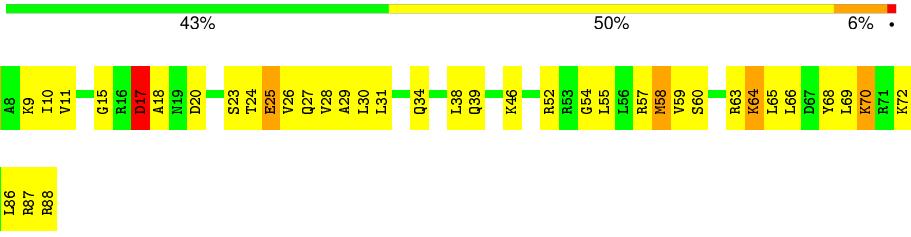
- Molecule 14: 30S RIBOSOMAL PROTEIN S14

Chain N:



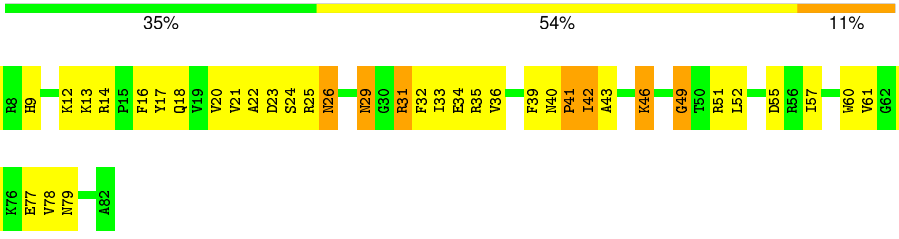
- Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain O:



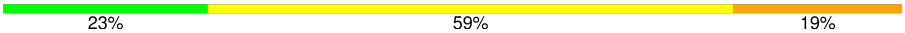
- Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain P:



- Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain Q:

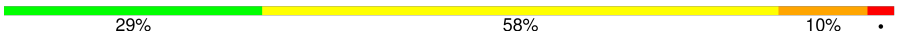


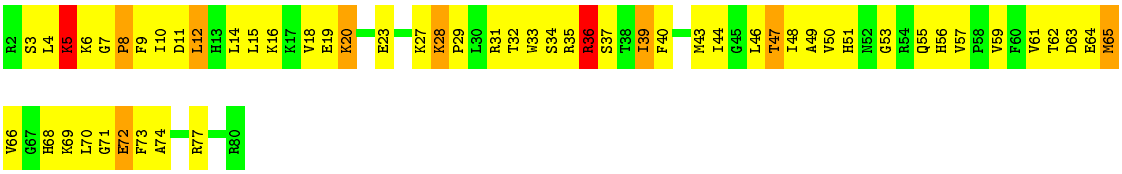
• Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain R:

• Molecule 19: 30S RIBOSOMAL PROTEIN S19

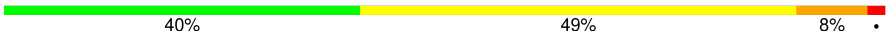
Chain S:

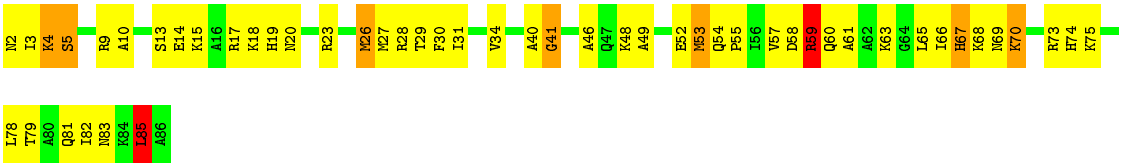




• Molecule 20: 30S RIBOSOMAL PROTEIN S20

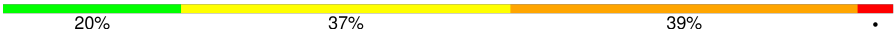
Chain T:

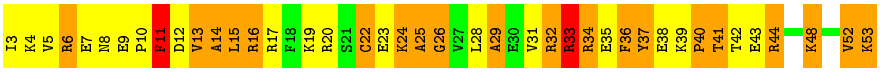




• Molecule 21: 30S RIBOSOMAL PROTEIN S21

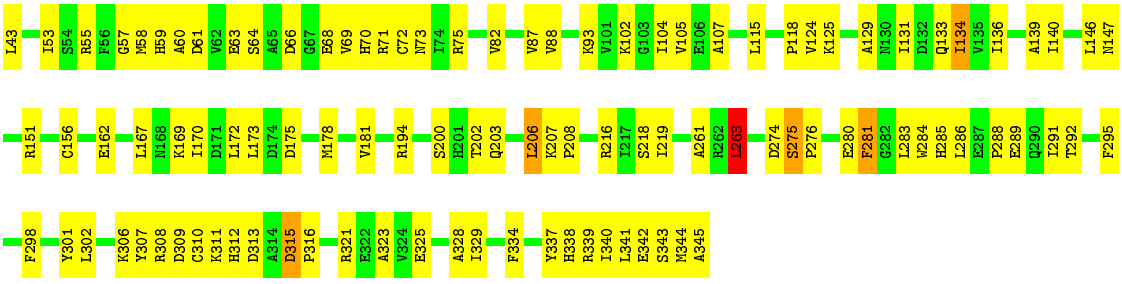
Chain U:





• Molecule 22: PUTATIVE RIBOSOME BIOGENESIS GTPASE RSGA

Chain V:



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	EACH MICROGRAPH	Depositor
Microscope	JEOL 2010F	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	15	Depositor
Minimum defocus (nm)	650	Depositor
Maximum defocus (nm)	3900	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality

5.1 Standard geometry

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	A	0.26	1/36762 (0.0%)	0.75	7/57350 (0.0%)
10	J	0.23	0/796	0.49	0/1077
11	K	0.24	0/893	0.46	0/1205
12	L	0.22	0/969	0.47	0/1300
13	M	0.21	0/892	0.48	0/1193
14	N	0.24	0/785	0.46	0/1043
15	O	0.23	0/724	0.45	0/966
16	P	0.26	0/659	0.44	0/884
17	Q	0.23	0/657	0.46	0/881
18	R	0.23	0/462	0.46	0/621
19	S	0.25	0/652	0.46	0/877
2	B	0.25	0/1735	0.47	0/2338
20	T	0.24	0/671	0.41	0/888
21	U	1.01	4/430 (0.9%)	0.74	2/570 (0.4%)
22	V	0.30	0/2200	0.59	1/2974 (0.0%)
3	C	0.23	0/1651	0.45	0/2225
4	D	0.23	0/1665	0.46	0/2227
5	E	0.23	0/1118	0.45	0/1504
6	F	0.25	0/835	0.48	0/1128
7	G	0.23	0/1187	0.45	0/1591
8	H	0.23	0/989	0.45	0/1326
9	I	0.24	0/1034	0.45	0/1375
All	All	0.27	5/57766 (0.0%)	0.67	10/85543 (0.0%)

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	A	0	16
21	U	0	1
All	All	0	17

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	U	15	LEU	C-N	-15.04	0.99	1.34
21	U	25	ALA	C-N	-9.32	1.16	1.33
1	A	463	U	O3'-P	-6.66	1.53	1.61
21	U	29	ALA	C-N	6.60	1.49	1.34
21	U	11	PHE	C-N	-5.41	1.21	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	765	G	N9-C1'-C2'	-8.23	102.94	112.00
1	A	438	U	N1-C1'-C2'	-6.31	105.06	112.00
22	V	263	LEU	CA-CB-CG	6.29	129.77	115.30
1	A	232	G	C5'-C4'-C3'	-6.20	106.09	116.00
1	A	66	A	N9-C1'-C2'	-5.98	105.42	112.00

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	187	G	Sidechain
1	A	281	G	Sidechain
1	A	437	U	Sidechain
1	A	438	U	Sidechain
1	A	58	C	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	A	32831	0	16507	1529	0
2	B	1704	0	1732	196	0
3	C	1624	0	1699	161	0
4	D	1643	0	1710	167	0
5	E	1105	0	1148	110	0
6	F	817	0	808	78	0
7	G	1174	0	1230	97	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	979	0	1034	78	0
9	I	1022	0	1070	141	0
10	J	786	0	828	94	0
11	K	877	0	887	109	0
12	L	955	0	1019	103	0
13	M	883	0	944	83	0
14	N	774	0	827	97	0
15	O	716	0	742	52	0
16	P	649	0	666	77	0
17	Q	648	0	691	79	0
18	R	455	0	478	39	0
19	S	637	0	665	75	0
20	T	665	0	714	54	0
21	U	425	0	447	98	0
22	V	2164	0	2131	447	0
All	All	53533	0	37977	3345	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 37.

The worst 5 of 3345 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)
1:A:1415:G:H21	22:V:285:HIS:CE1	1.06	1.69
1:A:1418:A:C6	22:V:312:HIS:CD2	1.77	1.68
1:A:1485:U:H4'	22:V:286:LEU:CD1	1.22	1.61
1:A:1485:U:C4'	22:V:286:LEU:HD12	1.22	1.59
1:A:1418:A:C6	22:V:312:HIS:HD2	0.88	1.54

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
2	B	216/218 (99%)	145 (67%)	53 (24%)	18 (8%)	1 18
3	C	204/206 (99%)	135 (66%)	49 (24%)	20 (10%)	1 14
4	D	203/205 (99%)	131 (64%)	54 (27%)	18 (9%)	1 17
5	E	148/150 (99%)	107 (72%)	34 (23%)	7 (5%)	3 32
6	F	98/100 (98%)	69 (70%)	23 (24%)	6 (6%)	2 26
7	G	148/150 (99%)	103 (70%)	37 (25%)	8 (5%)	2 29
8	H	127/129 (98%)	105 (83%)	19 (15%)	3 (2%)	7 47
9	I	125/127 (98%)	86 (69%)	28 (22%)	11 (9%)	1 17
10	J	96/98 (98%)	63 (66%)	21 (22%)	12 (12%)	0 8
11	K	115/117 (98%)	75 (65%)	27 (24%)	13 (11%)	0 10
12	L	121/123 (98%)	74 (61%)	30 (25%)	17 (14%)	0 6
13	M	112/114 (98%)	87 (78%)	14 (12%)	11 (10%)	1 14
14	N	92/100 (92%)	59 (64%)	24 (26%)	9 (10%)	1 14
15	O	86/88 (98%)	66 (77%)	18 (21%)	2 (2%)	8 48
16	P	80/82 (98%)	59 (74%)	17 (21%)	4 (5%)	3 31
17	Q	78/80 (98%)	48 (62%)	26 (33%)	4 (5%)	2 30
18	R	53/55 (96%)	27 (51%)	19 (36%)	7 (13%)	0 7
19	S	77/79 (98%)	57 (74%)	14 (18%)	6 (8%)	1 20
20	T	83/85 (98%)	69 (83%)	8 (10%)	6 (7%)	1 22
21	U	49/51 (96%)	22 (45%)	12 (24%)	15 (31%)	0 0
22	V	265/277 (96%)	256 (97%)	7 (3%)	2 (1%)	24 69
All	All	2576/2634 (98%)	1843 (72%)	534 (21%)	199 (8%)	2 20

5 of 199 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	19	THR
2	B	22	TRP
2	B	163	ILE
2	B	186	VAL
3	C	2	GLN

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
2	B	180/180 (100%)	142 (79%)	38 (21%)	1 9
3	C	170/170 (100%)	142 (84%)	28 (16%)	3 19
4	D	172/172 (100%)	140 (81%)	32 (19%)	2 14
5	E	113/113 (100%)	92 (81%)	21 (19%)	2 14
6	F	87/87 (100%)	68 (78%)	19 (22%)	1 9
7	G	123/123 (100%)	102 (83%)	21 (17%)	2 17
8	H	104/104 (100%)	87 (84%)	17 (16%)	3 20
9	I	105/105 (100%)	83 (79%)	22 (21%)	1 9
10	J	86/86 (100%)	66 (77%)	20 (23%)	1 7
11	K	90/90 (100%)	70 (78%)	20 (22%)	1 9
12	L	103/103 (100%)	88 (85%)	15 (15%)	4 24
13	M	92/92 (100%)	70 (76%)	22 (24%)	1 7
14	N	79/83 (95%)	67 (85%)	12 (15%)	3 22
15	O	76/76 (100%)	69 (91%)	7 (9%)	11 43
16	P	65/65 (100%)	56 (86%)	9 (14%)	4 27
17	Q	74/74 (100%)	60 (81%)	14 (19%)	2 13
18	R	48/48 (100%)	45 (94%)	3 (6%)	22 59
19	S	70/70 (100%)	60 (86%)	10 (14%)	4 25
20	T	65/65 (100%)	56 (86%)	9 (14%)	4 27
21	U	44/44 (100%)	36 (82%)	8 (18%)	2 15
22	V	235/235 (100%)	227 (97%)	8 (3%)	44 75
All	All	2181/2185 (100%)	1826 (84%)	355 (16%)	6 20

5 of 355 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	17	GLN
10	J	5	ARG

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Mol	Chain	Res	Type
19	S	72	GLU
8	H	55	LYS
9	I	35	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
7	G	121	ASN
9	I	36	GLN
20	T	60	GLN
9	I	24	ASN
9	I	109	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1529/1530 (99%)	277 (18%)	25 (1%)

5 of 277 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	A
1	A	9	G
1	A	14	U
1	A	31	G
1	A	32	A

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	913	A
1	A	975	A
1	A	1397	C
1	A	960	U
1	A	1025	U

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.