



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:17 PM BST

PDB ID : 5GAO  
EMDB ID: : EMD-8013  
Title : Head region of the yeast spliceosomal U4/U6.U5 tri-snRNP  
Authors : Nguyen, T.H.D.; Galej, W.P.; Bai, X.C.; Oubridge, C.; Scheres, S.H.W.; Newman, A.J.; Nagai, K.  
Deposited on : 2015-12-15  
Resolution : 3.60 Å(reported)  
Based on PDB ID : 4BGD

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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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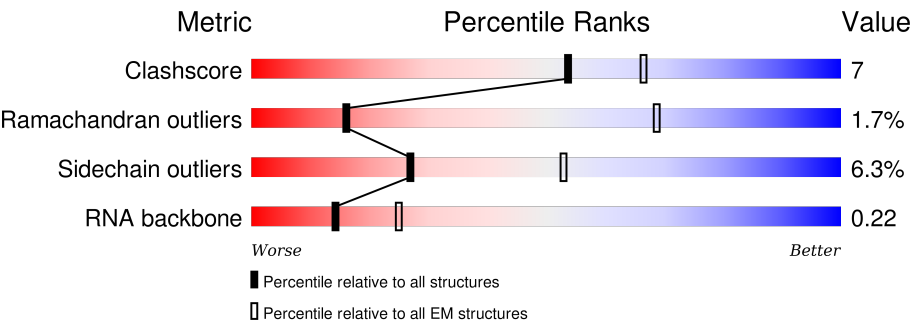
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 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 3.60 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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	k	196	<div><div>39%</div><div>.</div><div>59%</div></div>
2	l	146	<div><div>60%</div><div>.</div><div>38%</div></div>
3	m	110	<div><div>80%</div><div>5%</div><div>15%</div></div>
4	n	101	<div><div>79%</div><div>.</div><div>19%</div></div>
5	p	94	<div><div>76%</div><div>5%</div><div>19%</div></div>
6	q	86	<div><div>83%</div><div>.</div><div>16%</div></div>
7	r	77	<div><div>86%</div><div>.</div><div>10%</div></div>
8	E	338	<div><div>98%</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
9	B	2163	<div><div></div><div>59%</div><div>18%</div><div>•</div><div>21%</div></div>
10	V	96	<div><div></div><div>17%</div><div>35%</div><div>7%</div><div>41%</div></div>
11	A	267	<div><div></div><div>76%</div><div>17%</div><div>•</div><div>•</div></div>

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 23073 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 protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	k	80	Total	C	N	O	S	0	0
			635	406	115	111	3		

- Molecule 2 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	l	91	Total	C	N	O	S	0	0
			720	455	129	134	2		

- Molecule 3 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	m	94	Total	C	N	O	S	0	0
			737	474	140	119	4		

- Molecule 4 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	n	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

- Molecule 5 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	p	76	Total	C	N	O	S	0	0
			580	382	93	102	3		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	q	72	Total	C	N	O	S	0	0
			573	368	101	103	1		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	r	69	Total	C	N	O	S	0	0
			526	336	93	95	2		

- Molecule 8 is a protein called Snu66.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	338	Total	C	N	O		0	0
			1763	1063	352	348			

- Molecule 9 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	1710	Total	C	N	O	S	1	0
			13690	8772	2283	2579	56		

- Molecule 10 is a RNA chain called Saccharomyces cerevisiae strain UOA\_M2 chromosome 5 sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	57	Total	C	N	O	P	0	0
			1209	542	212	398	57		

- Molecule 11 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	255	Total	C	N	O	S	0	0
			2015	1300	329	380	6		

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- Molecule 1: Small nuclear ribonucleoprotein-associated protein B





Y543	V651	L815	L979	N1095	P1200	E1295	G1482	Y1637	Y1770	L1880	T2011	G
K556	T854	D818	L981	I1098	K1201	N1296	Y1493	Y1641	F1773	S1884	V2012	A
V558	T854	V827	L981	V1099	M1202	M1297	G1485	Y1641	T1774	S1884	V2013	A
A561	R666	T831	E885	F1100	A1208	F1302	A1486	D1648	L1781	V1887	D2018	U
P562	I688	A632	E885	V1099	P1210	F1317	Y1488	T1651	R1782	L1894	D2024	U
L566	G669	T833	E885	A1105	V1215	T1331	E1489	V1652	H1783	P1910	L2030	A73
V567	S671	A836	E885	L1109	M1216	G1335	L1491	L1655	N1784	P1910	L2031	U74
V571	L874	S864	E885	F1113	F1218	K1346	S1493	Y1656	P1786	T1917	L2037	U75
F574	F683	D870	E885	G1122	N1219	K1346	R1494	V1683	S1787	V1922	L2038	A76
R577	L684	T871	E885	H1123	I1220	F1367	I1498	I1666	Y1789	V1926	V2041	A77
F707	F707	L872	E885	P1124	A1224	V1368	A1499	I1666	G1790	F1927	V2041	A78
C708	C708	A875	E885	T1125	L1236	S1370	T1500	C1670	V1791	L1928	F2044	A79
G709	G709	T889	E885	L1128	L1240	K1372	S1542	C1675	I1799	L1929	V2048	C82
K717	K717	T890	E885	L1129	L1241	R1394	N1513	T1677	L1803	L1930	V2048	A83
C726	C726	D891	E885	L1130	L1243	A1395	L1515	I1682	C1810	Y1933	Y2091	A84
V730	V730	T897	E885	L1131	T1246	V1396	N1517	I1682	N1812	L1939	S2098	A85
I740	I740	T898	E885	L1132	D1249	M1399	R1519	L1687	Y1815	F1943	L2103	C86
V744	V744	T901	E885	L1133	I1251	S1401	F1521	I1688	F1819	L1947	A2113	C87
H745	H745	L902	E885	L1134	I1252	S1401	F1521	D1689	T1819	L1947	V2117	C88
H768	H768	T912	E885	L1135	Y1253	I1405	Y1533	D1689	T1819	L1947	V2117	C89
K769	K769	L916	E885	L1136	L1257	D1411	F1535	K1694	T1825	V1954	V2118	U91
L770	L770	T917	E885	L1137	F1258	M1426	R1540	T1695	GLU	V1955	L2119	U94
T771	T771	T920	E885	L1138	I1259	N1426	R1540	M1696	ALA	V1955	L2119	U94
K772	K772	L920	E885	L1139	P1261	P1432	L1544	P1697	GLU	V1960	L2128	G98
D774	D774	T921	E885	L1140	D1262	L1438	L1545	GLU	VAL	V1960	E2129	C101
T778	T778	T924	E885	L1141	V1156	L1438	L1546	I1700	THR	V1964	F2130	A102
K778	K778	T928	E885	L1142	I1157	S1442	L1546	I1700	ALA	I1964	D2131	A103
K782	K782	T931	E885	L1143	K1158	S1442	L1546	L1703	GLU	I1964	L2140	H194
E784	E784	T932	E885	L1144	R1159	S1442	L1546	L1704	ASN	I1972	L2149	U
V788	V788	T933	E885	L1145	F1268	L1445	L1546	L1705	GLY	T1975	L2160	C
L789	L789	T934	E885	L1146	L1270	L1445	L1546	M1706	GLY	Q1981	V2163	C
D790	D790	T936	E885	L1147	S1271	L1445	L1546	G1708	ASP	M1982		C
P791	P791	T942	E885	L1148	F1272	L1445	L1546	I1722	ASP	L1983		C
S792	S792	T943	E885	L1149	T1273	L1445	L1546	L1724	ASP	G1986		C
L793	L793	T944	E885	L1150	L1276	L1445	L1546	T1724	ALA	V1987		C
H804	H804	T945	E885	L1151	K1277	L1445	L1546	F1735	ALA	D1991		C
L808	L808	T946	E885	L1152	N1280	L1445	L1546	L1740	ALA	L1994		C
T809	T809	T947	E885	L1153	L1284	L1445	L1546	E1743	ALA	F2000		C
R813	R813	T948	E885	L1154	L1284	L1445	L1546	Y1745	ALA	N2001		C
S814	S814	T949	E885	L1155	L1284	L1445	L1546	L1746	ALA	N2002		C
		T950	E885	L1156	L1284	L1445	L1546	I1750	ALA	L2005		C
		T951	E885	L1157	L1284	L1445	L1546	H1751	ALA	C2008		C
		T952	E885	L1158	L1284	L1445	L1546		ALA			C
		T953	E885	L1159	L1284	L1445	L1546		ALA			C
		T954	E885	L1160	L1284	L1445	L1546		ALA			C
		T955	E885	L1161	L1284	L1445	L1546		ALA			C
		T956	E885	L1162	L1284	L1445	L1546		ALA			C
		T957	E885	L1163	L1284	L1445	L1546		ALA			C
		T958	E885	L1164	L1284	L1445	L1546		ALA			C
		T959	E885	L1165	L1284	L1445	L1546		ALA			C
		T960	E885	L1166	L1284	L1445	L1546		ALA			C
		T961	E885	L1167	L1284	L1445	L1546		ALA			C
		T962	E885	L1168	L1284	L1445	L1546		ALA			C
		T963	E885	L1169	L1284	L1445	L1546		ALA			C
		T964	E885	L1170	L1284	L1445	L1546		ALA			C
		T965	E885	L1171	L1284	L1445	L1546		ALA			C
		T966	E885	L1172	L1284	L1445	L1546		ALA			C
		T967	E885	L1173	L1284	L1445	L1546		ALA			C
		T968	E885	L1174	L1284	L1445	L1546		ALA			C
		T969	E885	L1175	L1284	L1445	L1546		ALA			C
		T970	E885	L1176	L1284	L1445	L1546		ALA			C
		T971	E885	L1177	L1284	L1445	L1546		ALA			C
		T972	E885	L1178	L1284	L1445	L1546		ALA			C
		T973	E885	L1179	L1284	L1445	L1546		ALA			C
		T974	E885	L1180	L1284	L1445	L1546		ALA			C
		T975	E885	L1181	L1284	L1445	L1546		ALA			C
		T976	E885	L1182	L1284	L1445	L1546		ALA			C
		T977	E885	L1183	L1284	L1445	L1546		ALA			C
		T978	E885	L1184	L1284	L1445	L1546		ALA			C
		T979	E885	L1185	L1284	L1445	L1546		ALA			C
		T980	E885	L1186	L1284	L1445	L1546		ALA			C
		T981	E885	L1187	L1284	L1445	L1546		ALA			C
		T982	E885	L1188	L1284	L1445	L1546		ALA			C
		T983	E885	L1189	L1284	L1445	L1546		ALA			C
		T984	E885	L1190	L1284	L1445	L1546		ALA			C
		T985	E885	L1191	L1284	L1445	L1546		ALA			C
		T986	E885	L1192	L1284	L1445	L1546		ALA			C
		T987	E885	L1193	L1284	L1445	L1546		ALA			C
		T988	E885	L1194	L1284	L1445	L1546		ALA			C
		T989	E885	L1195	L1284	L1445	L1546		ALA			C
		T990	E885	L1196	L1284	L1445	L1546		ALA			C
		T991	E885	L1197	L1284	L1445	L1546		ALA			C
		T992	E885	L1198	L1284	L1445	L1546		ALA			C
		T993	E885	L1199	L1284	L1445	L1546		ALA			C
		T994	E885	L1200	L1284	L1445	L1546		ALA			C
		T995	E885	L1201	L1284	L1445	L1546		ALA			C
		T996	E885	L1202	L1284	L1445	L1546		ALA			C
		T997	E885	L1203	L1284	L1445	L1546		ALA			C
		T998	E885	L1204	L1284	L1445	L1546		ALA			C
		T999	E885	L1205	L1284	L1445	L1546		ALA			C
		T1000	E885	L1206	L1284	L1445	L1546		ALA			C
		T1001	E885	L1207	L1284	L1445	L1546		ALA			C
		T1002	E885	L1208	L1284	L1445	L1546		ALA			C
		T1003	E885	L1209	L1284	L1445	L1546		ALA			C
		T1004	E885	L1210	L1284	L1445	L1546		ALA			C
		T1005	E885	L1211	L1284	L1445	L1546		ALA			C
		T1006	E885	L1212	L1284	L1445	L1546		ALA			C
		T1007	E885	L1213	L1284	L1445	L1546		ALA			C
		T1008	E885	L1214	L1284	L1445	L1546		ALA			C
		T1009	E885	L1215	L1284	L1445	L1546		ALA			C
		T1010	E885	L1216	L1284	L1445	L1546		ALA			C
		T1011	E885	L1217	L1284	L1445	L1546		ALA			C
		T1012	E885	L1218	L1284	L1445	L1546		ALA			C
		T1013	E885	L1219	L1284	L1445	L1546		ALA			C
		T1014	E885	L1220	L1284	L1445	L1546		ALA			C
		T1015	E885	L1221	L1284	L1445	L1546		ALA			C
		T1016	E885	L1222	L1284	L1445	L1546		ALA			C
		T1017	E885	L1223	L1284	L1445	L1546		ALA			C
		T1018	E885	L1224	L1284	L1445	L1546		ALA			C
		T1019	E885	L1225	L1284	L1445	L1546		ALA			C
		T1020	E885	L1226	L1284	L1445	L1546		ALA			C
		T1021	E885	L1227	L1284	L1445	L1546		ALA			C
		T1022	E885	L1228	L1284	L1445	L1546		ALA			C
		T1023	E885	L1229	L1284	L1445	L1546		ALA			C
		T1024	E885	L1230	L1284	L1445	L1546		ALA			C
		T1025	E885	L1231	L1284	L1445	L1546		ALA			C
		T1026	E885	L1232	L1284	L1445	L1546		ALA			C
		T1027	E885	L1233	L1284	L1445	L1546		ALA			C
		T1028	E885	L1234	L1284	L1445	L1546		ALA			C
		T1029	E885	L1235	L1284	L1445	L1546		ALA			C
		T1030	E885	L1236	L1284	L1445	L1546		ALA			C
		T1031	E885	L1237	L1284	L1445	L1546		ALA			C
		T1032	E885	L1238	L1284	L1445	L1546		ALA			C
		T1033	E885	L1239	L1284	L1445	L1546		ALA			C
		T1034	E885	L1240	L1284	L1445	L1546		ALA			C
		T1035	E885	L1241	L1284	L1445	L1546		ALA			C
		T1036	E885	L1242	L1284	L1445	L1546		ALA			C
</												






## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	140155	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	81000	Depositor
Image detector	Not provided	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	k	0.42	0/640	0.66	0/860
10	V	0.33	0/1350	0.77	0/2097
11	A	0.48	0/2064	0.67	0/2801
2	l	0.44	0/725	0.68	0/980
3	m	0.44	0/749	0.64	0/1009
4	n	0.37	0/634	0.57	0/859
5	p	0.48	0/590	0.61	0/802
6	q	0.42	0/585	0.63	0/791
7	r	0.38	0/529	0.57	0/711
8	E	0.41	0/1751	0.53	0/2411
9	B	0.46	0/13989	0.72	1/18966 (0.0%)
All	All	0.45	0/23606	0.69	1/32287 (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	k	0	1
9	B	0	5
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	643	ARG	NE-CZ-NH1	5.31	122.96	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	B	1200	PRO	Peptide
9	B	1484	TYR	Peptide
9	B	790	ASP	Peptide
9	B	791	PRO	Peptide
1	k	84	LEU	Peptide

## 5.2 Too-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 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	k	635	0	681	0	0
2	l	720	0	772	0	0
3	m	737	0	767	0	0
4	n	625	0	647	0	0
5	p	580	0	602	0	0
6	q	573	0	572	0	0
7	r	526	0	555	0	0
8	E	1763	0	1764	3	0
9	B	13690	0	13704	234	0
10	V	1209	0	612	15	0
11	A	2015	0	1970	28	0
All	All	23073	0	22646	267	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 7.

The worst 5 of 267 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)
9:B:1700:ILE:HD11	9:B:1740:LEU:HD13	1.37	1.06
9:B:1208:ALA:HB2	9:B:1218:PHE:CD2	2.23	0.74
9:B:1220:ILE:HD13	9:B:1241:LEU:HD11	1.71	0.72
9:B:1183:ILE:CD1	9:B:1192:VAL:HG11	2.19	0.71
9:B:1224:ALA:HB3	9:B:1264:VAL:HA	1.72	0.71

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 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	
1	k	76/196 (39%)	67 (88%)	8 (10%)	1 (1%)	15	60
2	l	87/146 (60%)	74 (85%)	12 (14%)	1 (1%)	17	64
3	m	92/110 (84%)	80 (87%)	10 (11%)	2 (2%)	8	51
4	n	80/101 (79%)	70 (88%)	10 (12%)	0	100	100
5	p	72/94 (77%)	64 (89%)	8 (11%)	0	100	100
6	q	70/86 (81%)	60 (86%)	10 (14%)	0	100	100
7	r	65/77 (84%)	58 (89%)	6 (9%)	1 (2%)	13	57
8	E	308/338 (91%)	266 (86%)	38 (12%)	4 (1%)	15	60
9	B	1707/2163 (79%)	1499 (88%)	174 (10%)	34 (2%)	9	53
11	A	253/267 (95%)	213 (84%)	34 (13%)	6 (2%)	7	49
All	All	2810/3578 (78%)	2451 (87%)	310 (11%)	49 (2%)	16	55

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	B	448	LEU
9	B	771	THR
9	B	792	SER
9	B	985	GLU
9	B	1370	SER

### 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 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	
1	k	71/176 (40%)	69 (97%)	2 (3%)	51	82
2	l	85/129 (66%)	82 (96%)	3 (4%)	43	79
3	m	78/103 (76%)	74 (95%)	4 (5%)	29	70
4	n	69/89 (78%)	67 (97%)	2 (3%)	50	82
5	p	65/83 (78%)	60 (92%)	5 (8%)	16	56
6	q	63/77 (82%)	62 (98%)	1 (2%)	70	90
7	r	57/66 (86%)	55 (96%)	2 (4%)	43	79
8	E	20/20 (100%)	18 (90%)	2 (10%)	9	43
9	B	1536/1955 (79%)	1428 (93%)	108 (7%)	19	60
11	A	220/236 (93%)	206 (94%)	14 (6%)	22	63
All	All	2264/2934 (77%)	2121 (94%)	143 (6%)	27	64

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	B	1057	LEU
9	B	1253	TYR
11	A	2170	TYR
9	B	1085	SER
9	B	1137	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
9	B	804	HIS
9	B	1280	ASN
11	A	2237	GLN
9	B	739	GLN
9	B	2069	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	V	55/96 (57%)	34 (61%)	5 (9%)

5 of 34 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	V	74	U
10	V	75	U
10	V	78	A
10	V	80	A
10	V	81	C

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	V	80	A
10	V	83	A
10	V	88	G
10	V	143	A
10	V	150	G

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

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

#### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	E	14

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	132:ALA	C	150:ALA	N	37.33
1	E	170:ALA	C	180:ALA	N	34.57
1	E	102:ALA	C	120:ALA	N	31.59
1	E	299:ALA	C	310:ALA	N	27.52
1	E	226:ALA	C	240:ALA	N	26.36