



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Nov 22, 2016 – 03:02 PM EST

PDB ID : 5LZY
EMDB ID: : EMD-4136
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l assembled on a polyadenylated mRNA.
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.99 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
EM map analysis : **NOT EXECUTED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

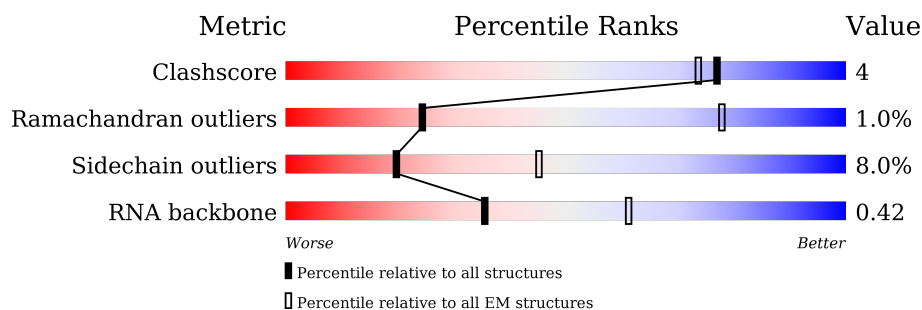
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.99 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.
















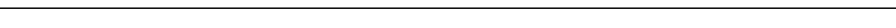




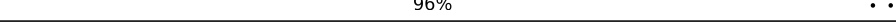






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	257	75% 19% . .
2	B	403	79% 18% ..
3	C	425	64% 19% . 15%
4	D	297	88% 10% ..
5	E	291	65% 8% . 26%
6	F	247	73% 16% . 9%
7	G	319	63% 9% 27%
8	H	192	83% 15% ..





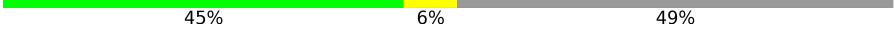


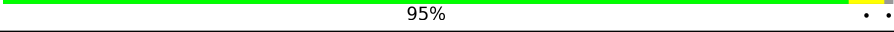



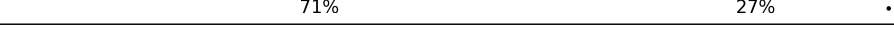







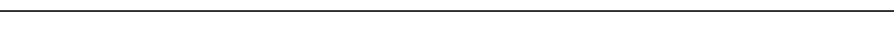

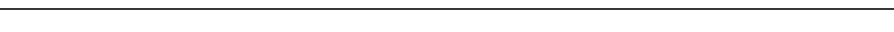
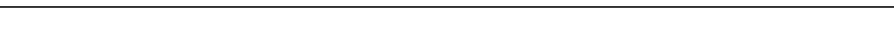


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	214	 79% 17% .
10	J	178	 81% 13% . .
11	L	211	 86% 12% .
12	M	218	 48% 15% 37%
13	N	204	 78% 20% .
14	O	203	 74% 23% . .
15	P	184	 67% 13% . 17%
16	Q	188	 80% 16% . .
17	R	196	 81% 10% . 8%
18	S	176	 82% 16% .
19	T	160	 83% 17% .
20	U	128	 67% 9% . 23%
21	V	140	 69% 22% . . 6%
22	W	157	 62% 6% 32%
23	X	156	 67% 8% 24%
24	Y	145	 81% 10% . 8%
25	Z	136	 88% 12% .
26	a	148	 96% . .
27	b	245	 40% . 58%
28	c	115	 80% 5% 15%
29	d	125	 77% 9% 14%
30	e	135	 87% 8% 5%
31	f	110	 89% 9% . .
32	g	117	 87% 10% .
33	h	123	 95% . .



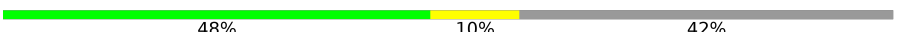









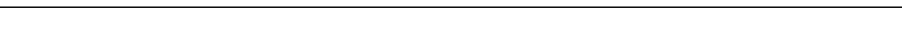

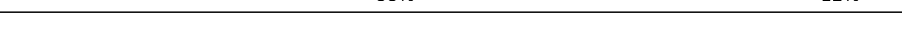

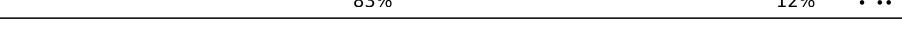








Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	i	105	 94% . .
35	j	97	 78% 9% . 11%
36	k	70	 91% 7% .
37	l	51	 90% 6% . .
38	m	102	 45% 6% 49%
39	n	25	 92% 8%
40	o	106	 92% 7% .
41	p	92	 95% . .
42	r	137	 80% 10% 9%
43	s	318	 59% . 38%
44	t	165	 90% . 7%
45	2	75	 71% 27% .
45	3	75	 68% 29% .
46	5	3543	 62% 31% 7%
47	7	120	 75% 24% .
48	8	156	 57% 35% . .
49	9	1869	 56% 30% 5% 9%
50	AA	295	 61% 12% . 26%
51	BB	264	 69% 12% 19%
52	CC	293	 61% 13% . 25%
53	DD	243	 84% 9% . 6%
54	EE	263	 84% 15%
55	FF	204	 75% 14% . 9%
56	GG	249	 82% 12% . 5%
57	HH	194	 78% 16% . 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
58	II	208	
59	JJ	194	
60	KK	165	
61	LL	158	
62	MM	132	
63	NN	151	
64	OO	168	
65	PP	145	
66	QQ	146	
67	RR	135	
68	SS	152	
69	TT	145	
70	UU	119	
71	VV	83	
72	WW	130	
73	XX	143	
74	YY	130	
75	ZZ	125	
76	aa	115	
77	bb	84	
78	cc	69	
79	dd	56	
80	ee	133	
81	ff	156	
82	gg	317	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
83	hh	8	<div><div></div><div>50%</div><div></div><div>50%</div></div>
84	ii	403	<div><div></div><div>88%</div><div></div><div>•</div><div>8%</div></div>
85	jj	710	<div><div></div><div>56%</div><div></div><div>•</div><div>40%</div></div>

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 221912 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	GLN	conflict	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		
45	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 46 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 50 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 52 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 53 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 54 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 57 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 58 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 61 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 63 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	PP	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 66 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 70 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 72 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 74 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 75 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 80 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 81 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is a RNA chain called mRNA (polyadenylated).

Mol	Chain	Residues	Atoms					AltConf	Trace
83	hh	8	Total	C	N	O	P	0	0
			176	80	40	48	8		

- Molecule 84 is a protein called Protein pelota homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	ii	372	Total	C	N	O	S	0	0
			2947	1844	528	559	16		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	221	MET	LEU	variant	UNP Q9BRX2
ii	386	GLY	-	expression tag	UNP Q9BRX2
ii	387	SER	-	expression tag	UNP Q9BRX2
ii	388	GLU	-	expression tag	UNP Q9BRX2
ii	389	ASN	-	expression tag	UNP Q9BRX2
ii	390	LEU	-	expression tag	UNP Q9BRX2
ii	391	TYR	-	expression tag	UNP Q9BRX2
ii	392	PHE	-	expression tag	UNP Q9BRX2
ii	393	GLN	-	expression tag	UNP Q9BRX2
ii	394	GLY	-	expression tag	UNP Q9BRX2
ii	395	ALA	-	expression tag	UNP Q9BRX2
ii	396	HIS	-	expression tag	UNP Q9BRX2
ii	397	HIS	-	expression tag	UNP Q9BRX2
ii	398	HIS	-	expression tag	UNP Q9BRX2
ii	399	HIS	-	expression tag	UNP Q9BRX2
ii	400	HIS	-	expression tag	UNP Q9BRX2
ii	401	HIS	-	expression tag	UNP Q9BRX2
ii	402	SER	-	expression tag	UNP Q9BRX2
ii	403	THR	-	expression tag	UNP Q9BRX2

- Molecule 85 is a protein called HBS1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	jj	425	Total	C	N	O	S	0	0
			3292	2100	565	609	18		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-25	MET	-	initiating methionine	UNP Q9Y450
jj	-24	ASP	-	expression tag	UNP Q9Y450
jj	-23	TYR	-	expression tag	UNP Q9Y450
jj	-22	LYS	-	expression tag	UNP Q9Y450
jj	-21	ASP	-	expression tag	UNP Q9Y450
jj	-20	HIS	-	expression tag	UNP Q9Y450
jj	-19	ASP	-	expression tag	UNP Q9Y450
jj	-18	GLY	-	expression tag	UNP Q9Y450
jj	-17	ASP	-	expression tag	UNP Q9Y450
jj	-16	TYR	-	expression tag	UNP Q9Y450
jj	-15	LYS	-	expression tag	UNP Q9Y450
jj	-14	ASP	-	expression tag	UNP Q9Y450
jj	-13	HIS	-	expression tag	UNP Q9Y450
jj	-12	ASP	-	expression tag	UNP Q9Y450

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-11	ILE	-	expression tag	UNP Q9Y450
jj	-10	ASP	-	expression tag	UNP Q9Y450
jj	-9	TYR	-	expression tag	UNP Q9Y450
jj	-8	LYS	-	expression tag	UNP Q9Y450
jj	-7	ASP	-	expression tag	UNP Q9Y450
jj	-6	ASP	-	expression tag	UNP Q9Y450
jj	-5	ASP	-	expression tag	UNP Q9Y450
jj	-4	ASP	-	expression tag	UNP Q9Y450
jj	-3	LYS	-	expression tag	UNP Q9Y450
jj	-2	ALA	-	expression tag	UNP Q9Y450
jj	-1	GLY	-	expression tag	UNP Q9Y450
jj	0	SER	-	expression tag	UNP Q9Y450

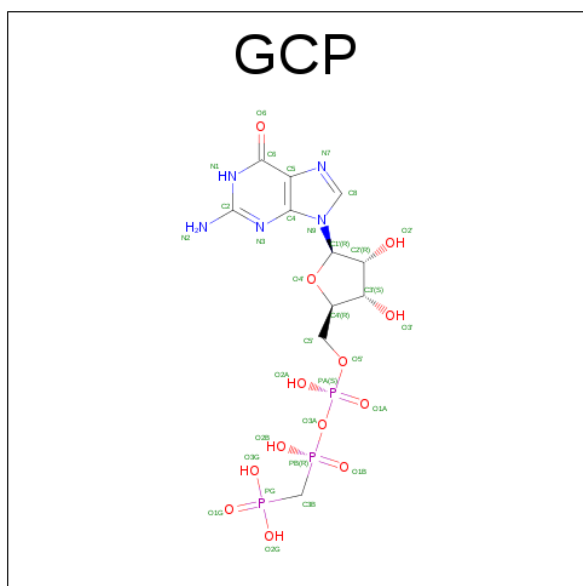
- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
86	P	1	Total Mg 1 1	0
86	TT	1	Total Mg 1 1	0
86	jj	1	Total Mg 1 1	0
86	I	1	Total Mg 1 1	0
86	V	1	Total Mg 1 1	0
86	7	5	Total Mg 5 5	0
86	a	1	Total Mg 1 1	0
86	5	164	Total Mg 164 164	0
86	8	3	Total Mg 3 3	0
86	9	56	Total Mg 56 56	0
86	L	1	Total Mg 1 1	0
86	hh	1	Total Mg 1 1	0

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	p	1	Total	Zn	0
			1	1	
87	g	1	Total	Zn	0
			1	1	
87	j	1	Total	Zn	0
			1	1	
87	dd	1	Total	Zn	0
			1	1	
87	ff	1	Total	Zn	0
			1	1	
87	aa	1	Total	Zn	0
			1	1	
87	o	1	Total	Zn	0
			1	1	
87	m	1	Total	Zn	0
			1	1	

- Molecule 88 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

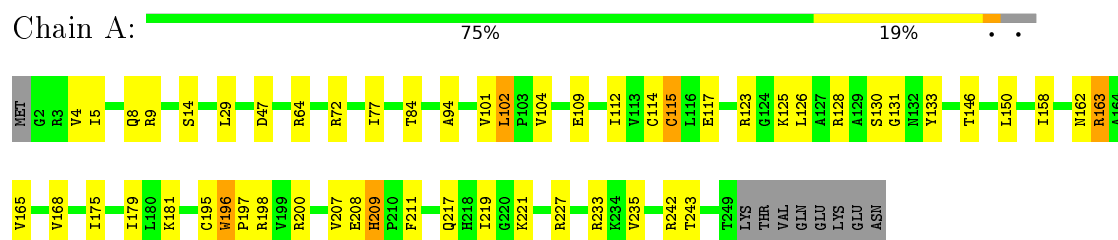


Mol	Chain	Residues	Atoms					AltConf
88	jj	1	Total	C	N	O	P	0
			32	11	5	13	3	

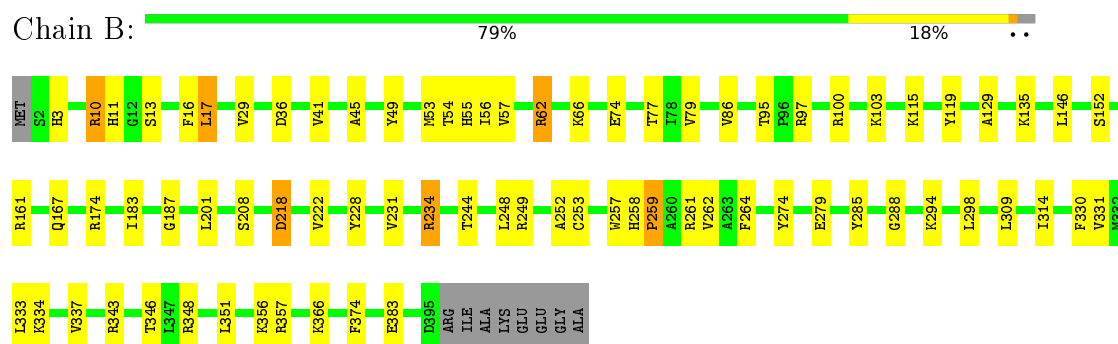
3 Residue-property plots

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

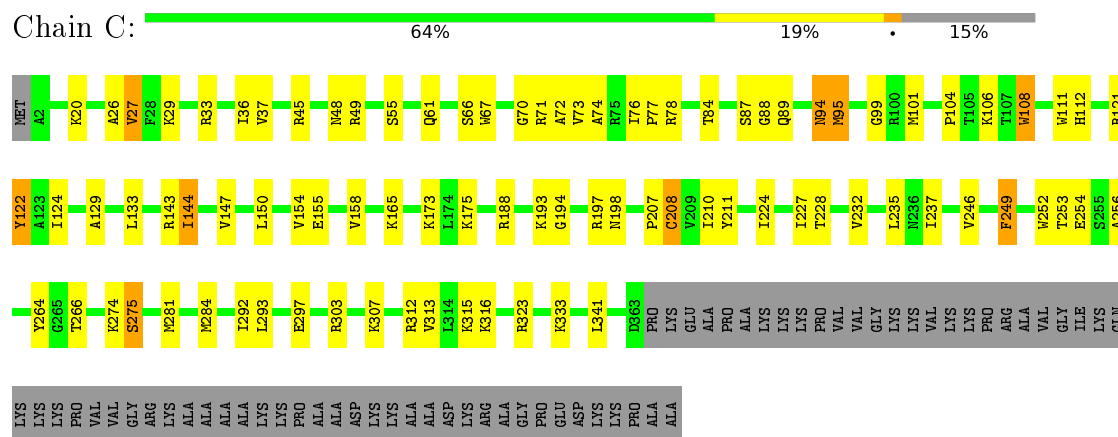
• Molecule 1: uL2



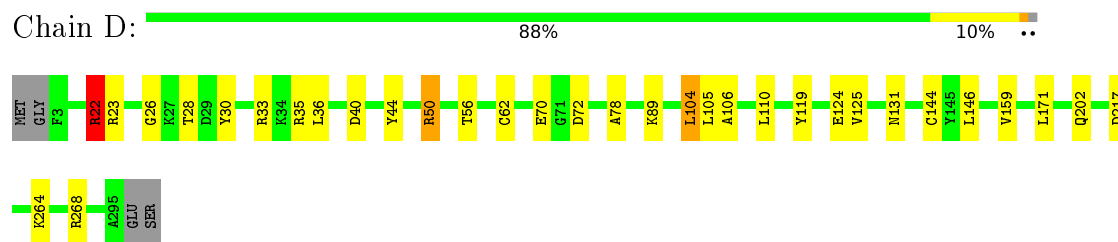
• Molecule 2: uL3



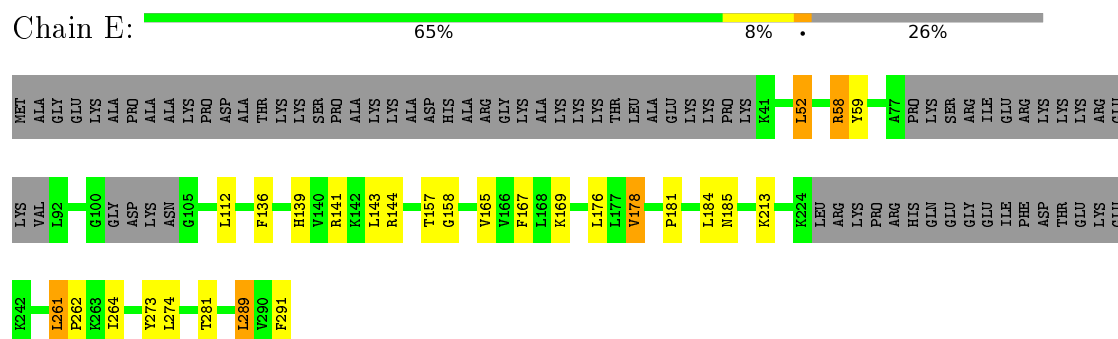
• Molecule 3: uL4



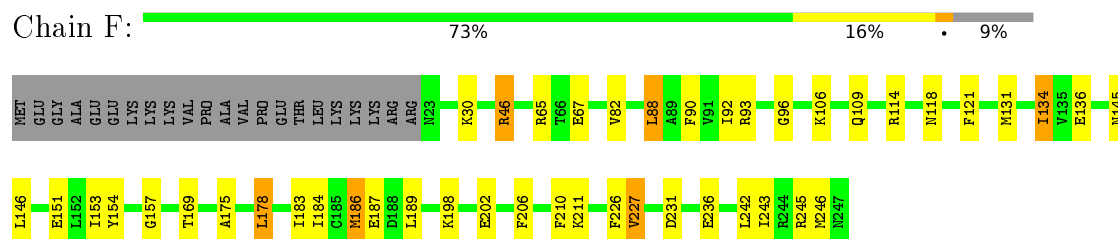
• Molecule 4: 60S ribosomal protein L5



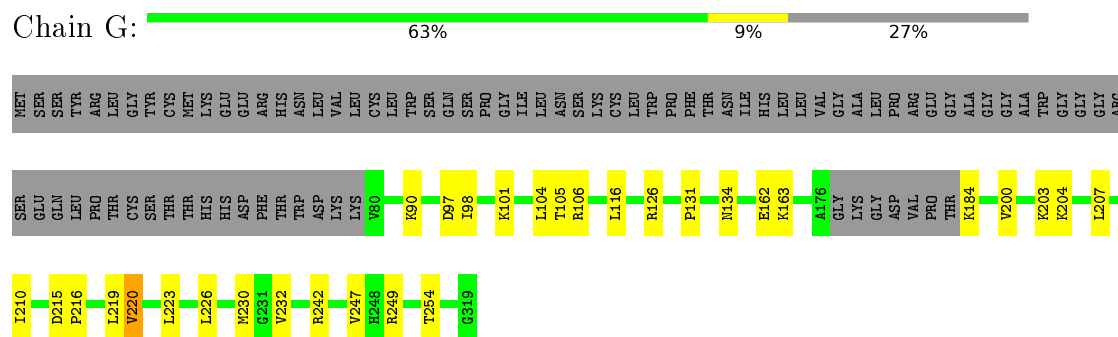
- Molecule 5: 60S ribosomal protein L6



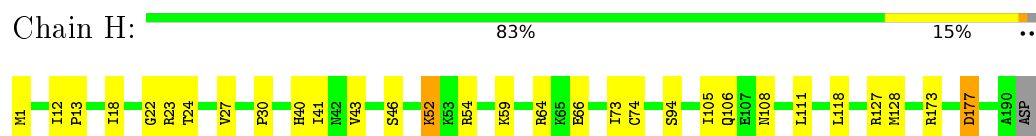
- Molecule 6: uL30



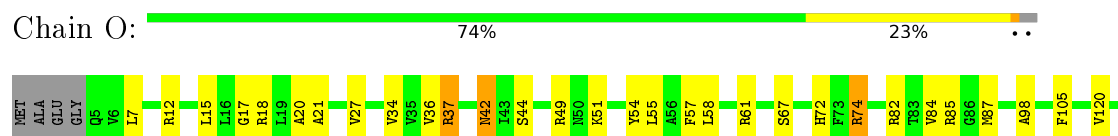
- Molecule 7: eL8



- Molecule 8: uL6



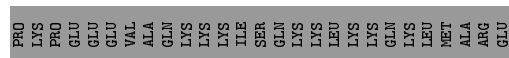
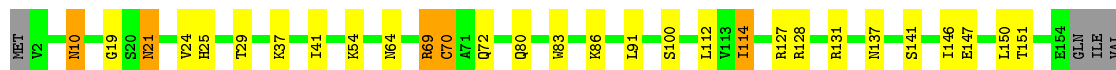
- Molecule 9: Ribosomal protein L10 (Predicted)





• Molecule 15: uL22

Chain P: 67% 13% 17%



• Molecule 16: eL18

Chain Q: 80% 16% 2%



• Molecule 17: eL19

Chain R: 81% 10% 8%



• Molecule 18: eL20

Chain S: 82% 16% 2%



• Molecule 19: eL21

Chain T: 83% 17% 0%



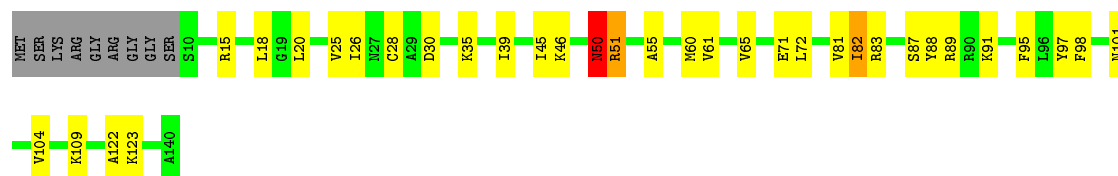
• Molecule 20: eL22

Chain U: 67% 9% 23%



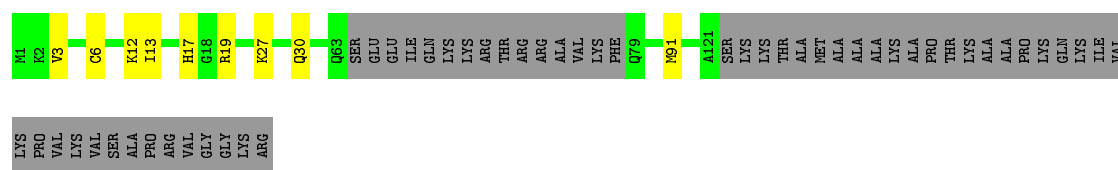
• Molecule 21: eL14

Chain V: 



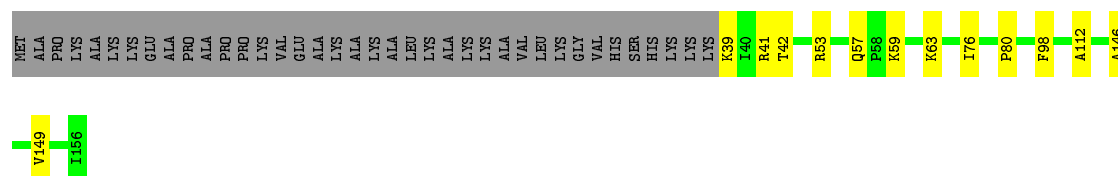
- Molecule 22: eL24

Chain W: 




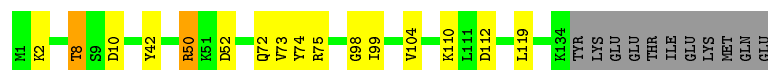
- Molecule 23: eL23

Chain X: 



- Molecule 24: uL24

Chain Y: 



- Molecule 25: 60S ribosomal protein L27

Chain Z: 



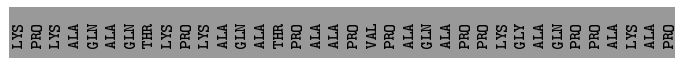
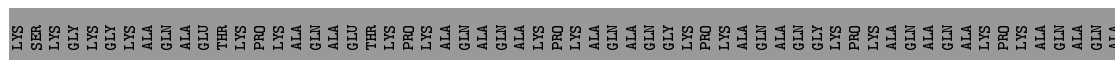
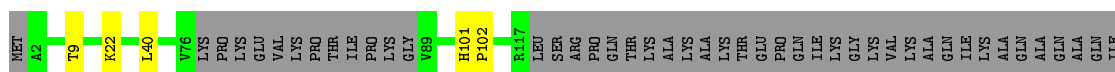
- Molecule 26: uL15

Chain a: 

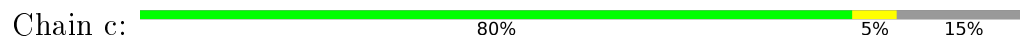


- Molecule 27: eL29

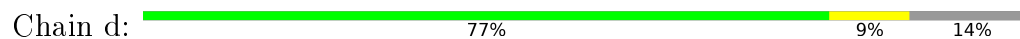
Chain b: 



• Molecule 28: eL30



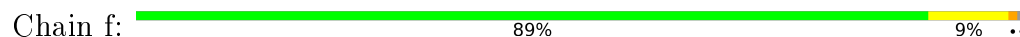
• Molecule 29: eL31



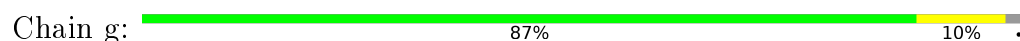
• Molecule 30: eL32



• Molecule 31: eL33



• Molecule 32: eL34



• Molecule 33: uL29




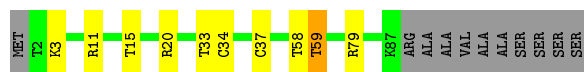
• Molecule 34: 60S ribosomal protein L36

Chain i:  94% . .



- Molecule 35: eL37

Chain j:  78% 9% . 11%




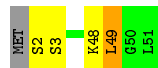
- Molecule 36: eL38

Chain k:  91% 7% .



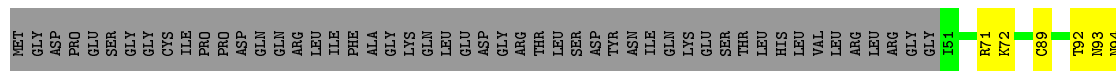
- Molecule 37: eL39

Chain l:  90% 6% . .



- Molecule 38: eL40

Chain m:  45% 6% 49%



- Molecule 39: eL41

Chain n:  92% 8%



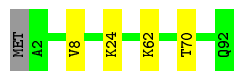
- Molecule 40: eL42

Chain o:  92% 7% .




- Molecule 41: eL43

Chain p:  95%



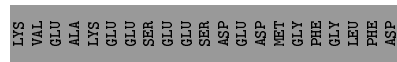
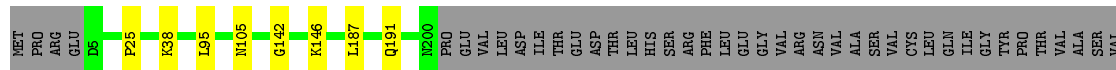
- Molecule 42: eL28

Chain r:  80% 10% 9%



- Molecule 43: uL10

Chain s:  59% 38%



- Molecule 44: uL11

Chain t:  90% 7%



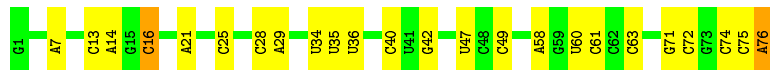
- Molecule 45: tRNA

Chain 2:  71% 27%



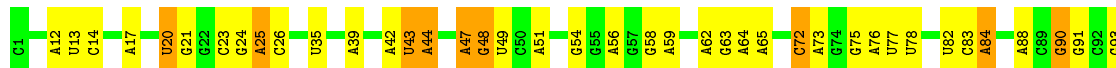
- Molecule 45: tRNA

Chain 3:  68% 29%



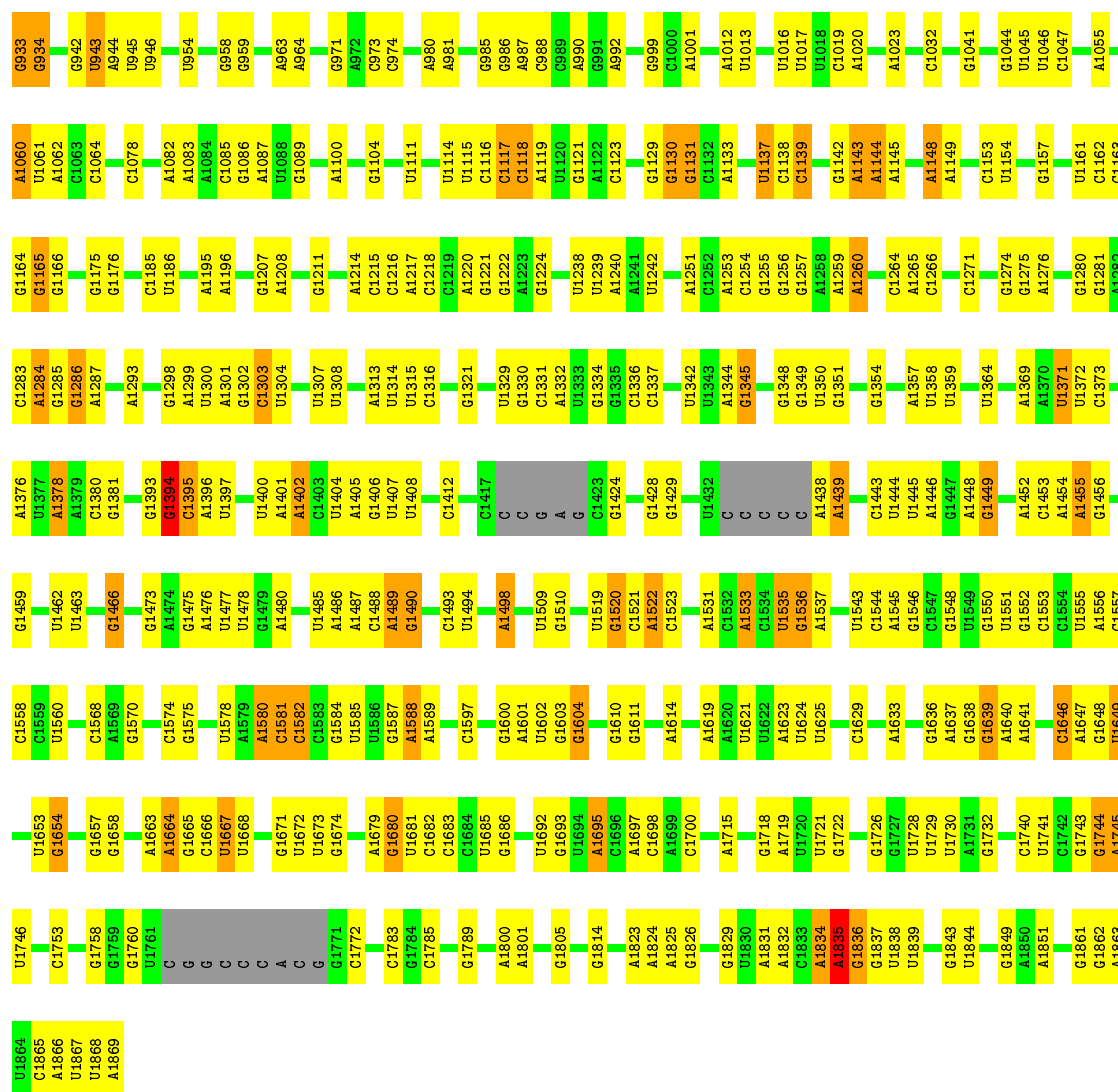
- Molecule 46: 28S ribosomal RNA

Chain 5:  62% 31% 7%



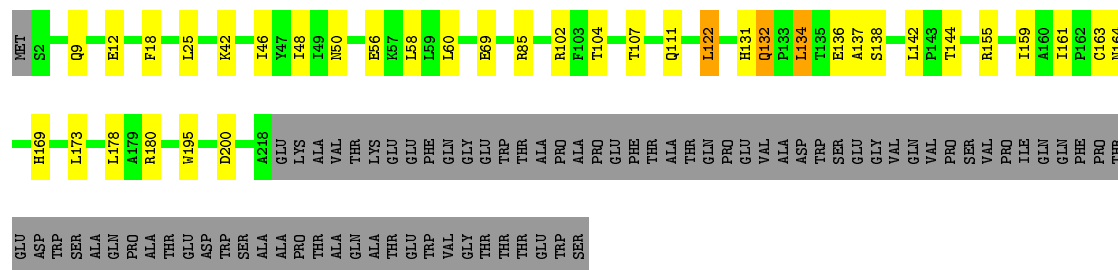
G2065	G1961	G1854	G1750	U1639	G1529	U1428	G1328	G1195	C934	C696	C446	C339	G219
G2066	A1962	G1855	A1751	C1640	G1532	C1429	G1329	G1205	A935	C697	C446	C340	A99
G2068	A1962	C1856	G1752	G1855	G1532	C1429	A1330	G1205	A935A	C696	C446	C341	C220
A2069	A1967	G1857	G1753	C1643	A1533	G1432	A1331	C1206	C936	C449	C449	C342	C221
		A1858	C1755	C1645	A1534	G1433	A1332		U937	C704	C450	A347	C222
C2077	G1976	A1867	C1756	A1646	C1535	G1434	G1336	U1209	C938	C705	C451	G348	A106
C2078	C1977	A1868	U1757	U1647	A1547	G1435	U1339	G1210	C939	G708	A452	A349	G107
G2079	C1978	G1869	U1757	C1648	A1547	C1340	U1339	G1211	C940		A453	C350	A108
		G1869	G1761	G1648	A1554	U1437	U1338	G1212	C941		U454	A227	C110
C2083	U1980	G1869	G1761	U1649	A1554	U1438	G1353	G1213		A711		A355	
U2085	G1981	G1872	C1763	A1650	A1563	U1440	A1354	C1214	A944	C712	A457	G356	A113
	G1982	U1876	G1763	A1651	A1564	C1441	A1354	C1215	U945			U357	G114
G2314	A1983	G1877	G1768	G1653	A1564	C1442	G1358			G725	A463	C358	G116
A2332	A1984	A1877	C1768	A1654	U1445	U1446	G1359	G1234	G955	U728	A466	C361	C117
G2333	G1985	G1887	U1772	C1655	U1567	C1446	G1360	G1235	A956	G729	U467	A362	G118
U2350	U1986	U1882	U1772	U1656	C1568		G1361	G1236	G957	G730	U468	A363	G119
	C1987		U1773	A1667		G1453	U1364	G1237	G958	G731	C469	G364	C243
G2343		A1888		C1661	G1576	G1453	U1364	A1238	G959			U365	G246
U2344	A1990	A1776		G1670	G1577	G1454	G1370	C1239	A960	C738	G481	C125	
G2348	A1991	A1891	A1786	U1671	U1578	C1456	A1371	G1272	G961	C738A	C481A	U370	C126
A2349	U1992	A1892	A1787	U1672	U1578	C1457	A1372	G1273	G962	G739	G482	A371	
G2350	C1993	C1893	U1781	C1666	G1586	C1458	A1373	A1274	G963		G483	A372	G134
A297			U1782	A1667			G1374	G1275	G965	G742	U484		G135
G2351	U1997	A1897	C1783		C1590	G1465	C1375	C1276	A966	G743	C485	U381	C285
U2352		G1898		U1671	U1591	C1468	G1376	G1280	C967	G744	C486	C382	G137
U2353	A2001	G1899	A1786	U1671	U1591	C1468	G1377	G1281	C968	G745		A383	G267
A2360	A2002	A1892	A1787	U1672	U1596	C1469	C1378	G1282	C969	A746	U492	A384	G143
	G2003	G1908	A1788	U1673	G1597	C1469	C1379	G1283		G747	G493	A385	C275
A2103	U2004	G1909	C1789	G1598	C1598	G1475	G1380	G1283	G971A	G748	C494	A386	C276
A2104	G2005	G1910		G1599	G1599	C1476	U1381	G1284		G749	C495	A387	C277
G2364	A2105	G1911	A1794	U1677	A1600	C1477	G1382		G972	U750	G496	A388	G278
A2366	U2008	G1912	G1799	C1678	U1601	C1478	G1383	G1287	G973	G751	C497	G387	
		C1913		A1679	A1602	C1478	C1384	G1288		G752	C498	G388	G151
A2370	C2011	G1916	G1799	G1680	U1602	C1481	G1385		G976	G753	C499	A400	U152
U2371	A1802	G1917	A1802	U1609	U1609	C1482	G1386	G1291	C977	C753	G500	G399	U157
G2372	G1803	A1917	G1803	C1610	C1610	C1483	C1386	G1292	C978		G500	G401	
	A2017	U1918	A1804	C1611	C1611	C1484	A1388	C1293	G979	G758	G504	A402	A158
		G1919	A1805	G1689	G1612	C1485	G1391	A1294	U980		G505	G403	C159
G2259	G2024	C1920	A1805	G1690	A1613	C1486	U1395	U1295	C983	U911	U510	C406	G160
G2260	A2025	G1921	C1812	G1691	A1613	C1486	U1395	G1296		G912	U510	A407	
G2261	A2026	G1922		G1691	G1617	A1497	G1396	U1297	C990	U914	G647	A306	C172
G2262		A1923	G1818	C1694	U1617	G1498	A1397			G915	G648	A307	C173
	U2044	U1929	G1819	C1694	U1622	G1498	A1398	C1301	G1070	C916	G649	G408	
G2265	G2046	C1928	A1820	G1724	A1623	G1502	U1398	U1302	G1071	A917	G649	G409	G177
U2267	G2046	A1929	G1821	A1503	G1624	A1503	C1401	A1303	C1072	G918	G654	G410	G308
A2268	A2047	U1930	U1822	G1504	G1625	G1504		C1304	G1073			G411	G309
C2269	U2048	C1931			G1626		G1411		G1074			G412	G178
							G1411					G413	G179
G2270			C1828	G1733	G1627	U1513	G1411A	C1308	G1075	C922A	C658	C414	A197
U2408	G2052	G1933		G1734	C1628	U1514	C1411C	C1309	C922B		G666	G417	U300
C2271	C2053	C1938	G1833	U1735	G1629	A1515	C1411C	C1309	C923	G923A	G667	A418	U200
G2273	U2054	G1938	A1834	A1736	A1630	G1516		C1318	C1077	C924	A667	C201	C201
C2274	G2055	C1938	G1835	A1736	A1631	G1517	G1412	U1319	A1078	C925	C668	A419	C202
G2275	G2056	A1941	G1836	G1739	A1632	A1518	G1416	C1319	C1079			C422	C205
A2276	A2057		A1837	G1740	G1633	A1518	G1416			G926	C672	A328	
C2277	G2058	U1947		G1741	A1634	A1523	G1419	A1322	C1082			G431	U209
G2278	G2058	G1948	G1842	A1742	C1635	A1524	A1420	A1323	A929	C883		A334	
G2421	C2062	U1949	G1842	A1742	U1636	A1525	G1421	A1324	G1174	G684	G685	A433	C216
G2280	G2063		G1846	U1748	A1637	A1525	G1422	A1326	U1179	C885	A686	A433	C217
U2381	C2064	A1956	C1847	A1749	A1638			C4326		A932	U837	C218	A212

U4965	C4880	U4682	G4578	A4396	U4302	G4197	A3943	U8331	A3717	G3603	A2795	G2693	U2530	U2425
A4966	U4881	G4690	U4579	A4397	C4303	G4201	U4067	G3839	A3718	G3604	A2798	G2694	U2537	U2426
A4967	U4882	G4694	U4580	U4398	A4304	U4202	U4068	U3840	G3722	C3605	G2799	A2695	U2538	G2427
U4976	C4883	G4694	C4583	U4399	A4305	A4203	U4069	A3845	A3723	U3606	G2800	A2696	C2539	A2428
U4977	C4884	G4694	A4584	G4400	A4306	A4204	A4070	A3856	A3724	U3613	A2806	A2697	G2546	G2433
U4978	U4885	G4694	U4585	G4401	A4307	A4205	A4071	G3857	G3725	G3614	A2807	C2698	C2547	C2432
U4985	C4886	G4694	U4586	A4415	A4311	A4206	A4072	G3858	G3726	G3615	G2808	C2699	C2548	G2435
U4988	U4887	G4694	A4510	A4416	A4312	A4207	A4073	G3859	G3727	G3616	G2809	C2704	G2549	G2436
U4989	G4694	G4694	A4511	G4417	C4313	A4212	A4074	A3860	G3728	C3617	C2814	U2707	U2550	U2439
C4990	U4888	G4694	U4512	U4418	A4314	A4213	A4075	A3861	U3729	G3618	G2815	U2708	U2440	U2441
U4991	G4694	G4694	A4513	U4419	C4315	A4214	G4076	A3862	U3730	G3619	G2816	C2709	U2554	G2442
G4994	C4889	G4694	U4514	U4420	A4316	U4215	A4077	A3863	G3731	G3620	G2817	C2710	G2555	G2443
U4995	U4890	G4694	G4515	A4421	C4317	A4216	A4078	A3864	A3747	A3621	C2818	G2711	G2556	U2447
C4996	C4891	G4694	U4516	A4422	A4318	A4217	A4079	A3865	A3748	C3622	G2819	G2712	G2557	
U4999	U4892	G4694	A4517	U4423	C4319	A4218	A4080	A3866	A3749	G3623	C2820	C2713	U2575	G2450
G5000	C4893	G4694	C4518	U4424	A4320	A4219	A4081	A3867	G3750	G3624	U2821	G2714	U2576	
U5001	U4894	G4694	A4519	A4425	A4321	A4220	A4082	A3868	G3751	G3625	G2822	G2715	G2577	A2453
U5002	C4895	G4694	C4520	U4426	A4322	A4221	A4083	A3869	G3752	A3635	U2823	C2716	C2583	
A5007	U4896	G4694	U4521	U4427	C4323	A4222	A4084	A3870	G3753	A3636	G2824	C2717	C2584	
C5008	C4897	G4694	G4522	U4428	A4324	A4223	A4085	A3871	A3754	A3637	U2825	C2718	C2585	
G5009	U4898	G4694	U4523	U4429	A4325	A4224	A4086	A3872	A3755	A3638	G2826	C2719	C2586	
C5013	C4899	G4694	A4524	U4430	A4326	A4225	A4087	A3873	A3756	A3639	U2827	C2720	A2587	
A5014	U4900	G4694	U4525	U4431	A4327	A4226	A4088	A3874	C3761	A3640	U2828	G2721	C2588	
G5015	C4901	G4694	G4526	U4432	A4328	A4227	A4089	A3875	G3762	U3641	U2829	G2722	A2601	
A5016	U4902	G4694	U4527	U4433	A4329	A4228	A4090	A3876	G3763	A3642	U2830	G2723	C2602	
G5017	C4903	G4694	G4528	U4434	A4330	A4229	A4091	A3877	A3764	A3643	U2831	G2724	U2467	
A5034	U4904	G4694	U4529	U4435	A4331	A4230	A4092	A3878	A3765	A3644	U2832	G2725	U2468	
U5035	C4905	G4694	G4530	U4436	A4332	A4231	A4093	A3879	U3773	A3645	U2833	G2726	C2469	
U5040	U4906	G4694	U4531	U4437	A4333	A4232	A4094	A3880	A3774	A3646	U2834	G2727	C2470	
G5041	C4907	G4694	A4532	U4438	A4334	A4233	A4095	A3881	A3775	A3647	U2835	G2728	C2471	
C5047	U4908	G4694	U4533	U4439	A4335	A4234	A4096	A3882	G3776	A3648	U2836	G2729	G2612	
U5050	C4909	G4694	G4534	U4440	A4336	A4235	A4097	A3883	G3777	A3649	U2837	G2730	C2613	
A5051	U4910	G4694	U4535	U4441	A4337	A4236	A4098	A3884	A3778	A3650	U2838	G2731	U2470	
G5052	C4911	G4694	C4536	U4442	A4338	A4237	A4099	A3885	A3779	A3651	U2839	G2732	C2491	
C5053	U4912	G4694	U4537	U4443	A4339	A4238	A4100	A3886	A3780	A3652	U2840	G2733	A2473	
A5054	C4913	G4694	G4538	U4444	A4340	A4239	A4101	A3887	A3781	A3653	U2841	G2734	C2474	
U5055	U4914	G4694	U4539	U4445	A4341	A4240	A4102	A3888	A3782	A3654	U2842	G2735	G2622	
C5056	C4915	G4694	A4540	U4446	A4342	A4241	A4103	A3889	A3783	A3655	U2843	G2736	C2627	
G5057	U4916	G4694	G4541	U4447	A4343	A4242	A4104	A3890	A3784	A3656	U2844	G2737	U2661	
U5058	C4917	G4694	U4542	U4448	A4344	A4243	A4105	A3891	A3785	A3657	U2845	G2738	G2663	
A5059	U4918	G4694	G4543	U4449	A4345	A4244	A4106	A3892	A3786	A3658	U2846	G2739	C2640	
C5060	C4919	G4694	U4544	U4450	A4346	A4245	A4107	A3893	U3798	A3659	U2847	G2740	A2647	
U5063	U4920	G4694	A4545	U4451	A4347	A4246	A4108	A3894	A3799	A3660	U2848	G2741	U2490	
G5064	C4921	G4694	G4546	U4452	A4348	A4247	A4109	A3895	A3800	A3661	U2849	G2742	C2491	
A5065	U4922	G4694	U4547	U4453	A4349	A4248	A4110	A3896	U3801	A3662	U2850	G2743	U2660	
C5066	C4923	G4694	G4548	U4454	A4350	A4249	A4111	A3897	A3802	A3663	U2851	G2744	G2661	
U5067	U4924	G4694	U4549	U4455	A4351	A4250	A4112	A3898	A3803	A3664	U2852	G2745	U2662	
G5068	C4925	G4694	A4550	U4456	A4352	A4251	A4113	A3899	A3804	A3665	U2853	G2746	C2663	
U5069	U4926	G4694	G4551	U4457	A4353	A4252	A4114	A3900	U3798	A3666	U2854	G2747	G2664	
	C4927	G4694	U4552	U4458	A4354	A4253	A4115	A3901	A3805	A3667	U2855	G2748	U2665	
	U4928	G4694	G4553	U4459	A4355	A4254	A4116	A3902	A3806	A3668	U2856	G2749	C2665	
	C4929	G4694	U4554	U4460	A4356	A4255	A4117	A3903	A3807	A3669	U2857	G2750	A2647	
	U4930	G4694	A4555	U4461	A4357	A4256	A4118	A3904	U3798	A3670	U2858	G2751	U2490	
	C4931	G4694	G4556	U4462	A4358	A4257	A4119	A3905	A3808	A3671	U2859	G2752	C2491	
	U4932	G4694	U4557	U4463	A4359	A4258	A4120	A3906	A3809	A3672	U2860	G2753	U2660	
	C4933	G4694	G4558	U4464	A4360	A4259	A4121	A3907	A3810	A3673	U2861	G2754	G2661	
	U4934	G4694	U4559	U4465	A4361	A4260	A4122	A3908	A3811	A3674	U2862	G2755	C2662	
	C4935	G4694	A4560	U4466	A4362	A4261	A4123	A3909	A3812	A3675	U2863	G2756	U2663	
	U4936	G4694	G4561	U4467	A4363	A4262	A4124	A3910	A3813	A3676	U2864	G2757	A2647	
	C4937	G4694	U4562	U4468	A4364	A4263	A4125	A3911	A3814	A3677	U2865	G2758	U2664	
	U4938	G4694	G4563	U4469	A4365	A4264	A4126	A3912	A3815	A3678	U2866	G2759	C2665	
	C4939	G4694	U4564	U4470	A4366	A4265	A4127	A3913	A3816	A3679	U2867	G2760	U2666	
	U4940	G4694	A4565	U4471	A4367	A4266	A4128	A3914	A3817	A3680	U2868	G2761	A2647	
	C4941	G4694	G4566	U4472	A4368	A4267	A4129	A3915	A3818	A3681	U2869	G2762	U2667	
	U4942	G4694	U4567	U4473	A4369	A4268	A4130	A3916	A3819	A3682	U2870	G2763	U2668	
	C4943	G4694	G4568	U4474	A4370	A4269	A4131	A3917	A3820	A3683	U2871	G2764	C2669	
	U4944	G4694	U4569	U4475	A4371	A4270	A4132	A3918	A3821	A3684	U2872	G2765	C2670	
	C4945	G4694	A4570	U4476	A4372	A4271	A4133	A3919	A3822	A3685	U2873	G2766	U2669	
	U4946	G4694	G4571	U4477	A4373	A4272	A4134	A3920	A3823	A3686	U2874	G2767	C2671	
	C4947	G4694	U4572	U4478	A4374	A4273	A4135	A3921	A3824	A3687	U2875	G2768	U2670	
	U4948	G4694	G4573	U4479	A4375	A4274	A4136	A3922	A3825	A3688	U2876	G2769	A2647	
	C4949	G4694	U4574	U4480	A4376	A4275	A4137	A3923	A3826	A3689	U2877	G2770	U2671	
	U4950	G4694	A4575	U4481	A4377	A4276	A4138	A3924	A3827	A3690	U2878	G2771	C2672	
	C4951	G4694	G4576	U4482	A4378	A4277	A4139	A3925	A3828	A3691	U2879	G2772	U2673	
	U4952	G4694	U4577	U4483	A4379	A4278	A4140	A3926	A3829	A3692	U2880	G2773	C2674	
	C4953	G4694	A4578	U4484	A4380	A4279	A4141	A3927	A3830	A3693	U2881	G2774	U2675	
	U4954	G4694	G4579	U4485	A4381	A4280	A4142	A3928	A3831	A3694	U2882	G2775	C2676	
	C4955	G4694	U4580	U4486	A4382	A4281	A4143	A3929	A3832	A3695	U2883	G2776	U2677	
	U4956	G4694	A4581	U4487	A4383	A4282	A4144	A3930	A3833	A3696	U2884	G2777	C2678	
	C4957	G4694	G4582	U4488	A4384	A4283	A4145	A3931	A3834	A3697	U2885	G2778	U2679	
	U4958	G4694	U4583	U4489	A4385	A4284	A4146	A3932	A3835	A3698	U2886	G2779	C2680	
	C4959	G4694	A4584	U4490	A4386	A4285	A4147	A3933	A3836	A3699	U2887	G2780	U2681	
	U4960	G4694	G4585	U4491	A4387	A4286	A4148	A3934	A3837	A3700	U2888	G2781	C2682	
	C4961	G4694	U4586	U4492	A4388	A4287	A4149	A3935	A3838	A3701	U2889	G2782	U2683	
	U4962	G4694	A4587	U4493	A4389	A4288	A4150	A3936	A3839	A3702	U2890	G2783	C2684	
	C4963	G4694	G4588	U4494	A4390	A4289	A4151	A3937	A3840	A3703	U2891	G2784	U2685	
	U4964	G4694	U4589	U4495	A4391	A4290	A4152	A3938	A3841	A3704	U2892	G2785	C2686	
	C4965	G4694	A4590	U4496	A4392	A4291	A4153	A3939	A3842	A3705	U2893	G2786	U2687	
	U4966	G4694	G4591	U4497	A4393	A4292	A4154	A3940	A3843	A3706	U2894	G2787	C2688	
	C4967	G4694	U4592	U4498	A4394	A4293	A4155	A3941	A3844	A3707	U2895	G2788	U2689	



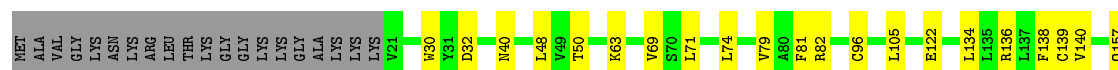
- Molecule 50: uS2

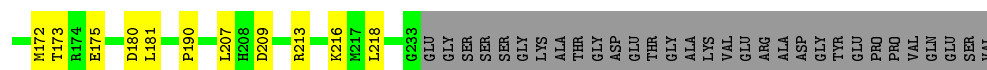
Chain AA: 61% 12% 26%



- Molecule 51: 40S ribosomal protein S3a

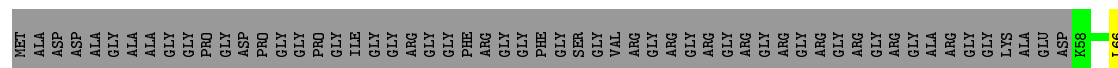
Chain BB: 69% 12% 19%





• Molecule 52: uS5

Chain CC: 61% 13% 25%



• Molecule 53: uS3

Chain DD: 84% 9% 6%



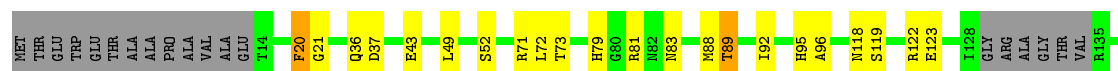
• Molecule 54: eS4

Chain EE: 84% 15% 1%



• Molecule 55: uS7

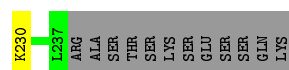
Chain FF: 75% 14% 9%



• Molecule 56: 40S ribosomal protein S6

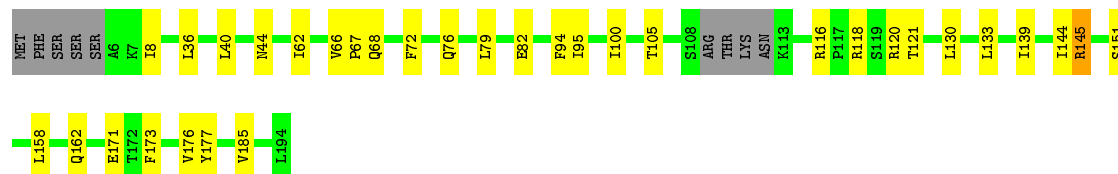
Chain GG: 82% 12% 5%





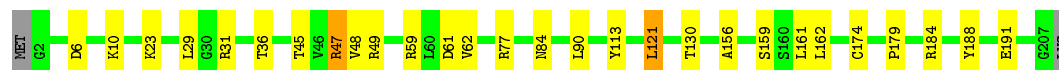
- Molecule 57: eS7

Chain HH: 78% 16% 5%



- Molecule 58: eS8

Chain II: 86% 13% ..



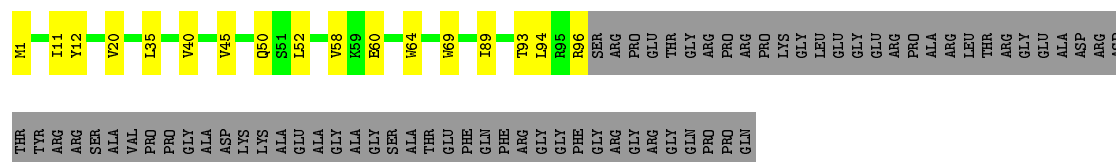
- Molecule 59: Ribosomal protein S9 (Predicted)

Chain JJ: 83% 12% 5%



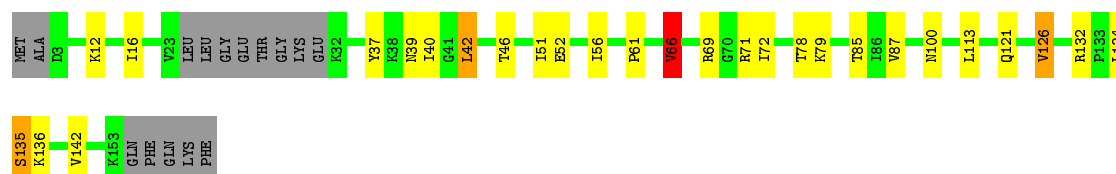
- Molecule 60: eS10

Chain KK: 48% 10% 42%



- Molecule 61: uS17

Chain LL: 73% 15% .. 9%



- Molecule 62: 40S ribosomal protein S12

Chain MM: 74% 14% 11%



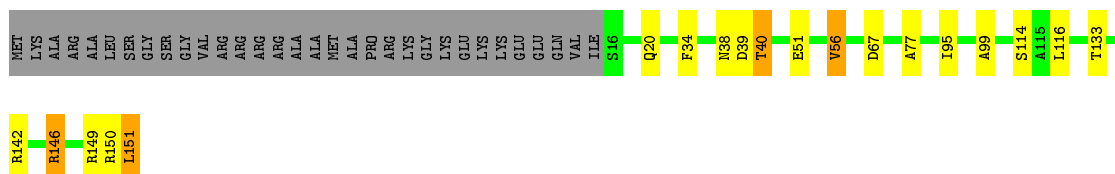
• Molecule 63: uS15

Chain NN: 81% 16% ..



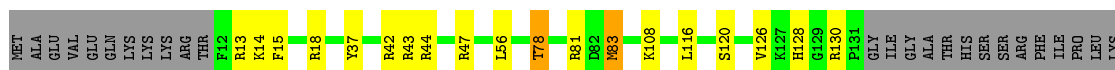
• Molecule 64: uS11

Chain OO: 70% 9% 19%



• Molecule 65: uS19

Chain PP: 70% 12% 17%



• Molecule 66: uS9

Chain QQ: 88% 9% .



• Molecule 67: eS17

Chain RR: 81% 16% ..



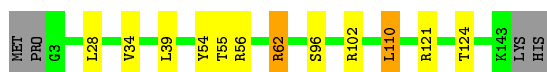
• Molecule 68: uS13

Chain SS: 78% 16% 5%



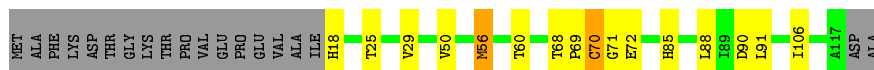
• Molecule 69: eS19

Chain TT: 89% 7% ..



- Molecule 70: uS10

Chain UU: 71% 12% 16%



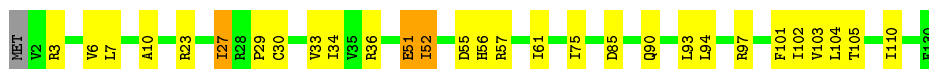
- Molecule 71: eS21

Chain VV: 88% 12%



- Molecule 72: uS8

Chain WW: 77% 20% ..



- Molecule 73: uS12

Chain XX: 83% 12% ..



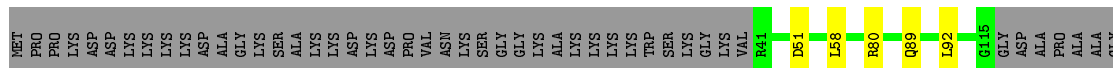
- Molecule 74: eS24

Chain YY: 78% 15% 5%



- Molecule 75: eS25

Chain ZZ: 56% 40%



- Molecule 76: eS26

Chain aa: 77% 11% 12%



- Molecule 77: 40S ribosomal protein S27

Chain bb: 89% 8% ..



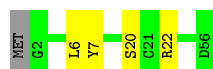
- Molecule 78: eS28

Chain cc: 80% 10% 10%



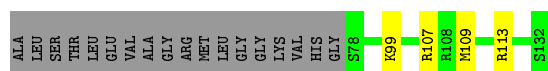
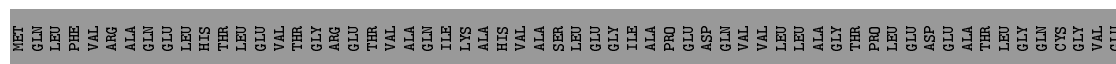
- Molecule 79: uS14

Chain dd: 91% 7% .



- Molecule 80: eS30

Chain ee: 38% . 59%



- Molecule 81: eS31

Chain ff: 38% 5% 56%



- Molecule 82: RACK1

Chain gg: 93% 5% .



- Molecule 83: mRNA (polyadenylated)

- Molecule 84: Protein pelota homolog

[illegible]

- Molecule 85: HBS1-like protein

[illegible]

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	20717	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)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	104478	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, ZN, 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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.44	0/1936	0.79	1/2596 (0.0%)
10	J	0.39	0/1385	0.68	0/1852
11	L	0.42	0/1733	0.77	1/2316 (0.0%)
12	M	0.45	0/1158	0.75	0/1547
13	N	0.44	0/1746	0.79	1/2338 (0.0%)
14	O	0.48	0/1662	0.77	0/2222
15	P	0.45	0/1268	0.71	0/1700
16	Q	0.47	0/1539	0.84	1/2054 (0.0%)
17	R	0.40	0/1524	0.74	0/2013
18	S	0.51	0/1501	0.80	0/2012
19	T	0.43	0/1326	0.73	0/1770
2	B	0.45	0/3240	0.77	2/4339 (0.0%)
20	U	0.39	0/823	0.63	0/1104
21	V	0.45	0/993	0.75	0/1332
22	W	0.44	0/873	0.61	0/1158
23	X	0.40	0/984	0.68	0/1323
24	Y	0.38	0/1132	0.69	0/1504
25	Z	0.42	0/1130	0.67	0/1507
26	a	0.46	0/1191	0.77	0/1590
27	b	0.40	0/861	0.68	0/1138
28	c	0.39	0/771	0.63	0/1034
29	d	0.43	0/903	0.75	0/1216
3	C	0.48	0/2937	0.79	0/3946
30	e	0.50	1/1071 (0.1%)	0.74	0/1429
31	f	0.48	0/895	0.80	0/1198
32	g	0.46	0/916	0.79	0/1220
33	h	0.38	0/1021	0.67	0/1348
34	i	0.38	0/841	0.68	0/1112
35	j	0.44	0/720	0.82	0/952
36	k	0.37	0/575	0.64	0/761
37	l	0.44	0/459	0.76	0/608
38	m	0.38	0/435	0.67	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n	0.38	0/240	0.71	0/305
4	D	0.40	0/2437	0.71	3/3264 (0.1%)
40	o	0.40	0/864	0.68	0/1140
41	p	0.44	0/718	0.68	0/953
42	r	0.42	0/1010	0.73	0/1354
43	s	0.37	0/1530	0.50	0/2064
44	t	0.37	0/1174	0.52	0/1582
45	2	0.23	0/1777	0.68	1/2763 (0.0%)
45	3	0.21	0/1777	0.66	0/2763
46	5	0.39	13/84961 (0.0%)	0.79	56/132460 (0.0%)
47	7	0.33	0/2858	0.67	0/4455
48	8	0.37	0/3581	0.73	0/5577
49	9	0.32	0/40524	0.73	12/63134 (0.0%)
5	E	0.39	0/1762	0.70	0/2362
50	AA	0.40	0/1747	0.68	0/2374
51	BB	0.36	0/1756	0.64	0/2350
52	CC	0.40	0/1753	0.71	0/2369
53	DD	0.38	0/1796	0.67	0/2417
54	EE	0.39	0/2118	0.68	0/2849
55	FF	0.39	0/1492	0.69	1/2005 (0.0%)
56	GG	0.37	0/1946	0.69	0/2590
57	HH	0.38	0/1510	0.64	0/2022
58	II	0.43	0/1715	0.75	0/2287
59	JJ	0.39	0/1550	0.76	0/2069
6	F	0.51	0/1911	0.78	0/2549
60	KK	0.39	0/834	0.60	0/1125
61	LL	0.41	0/1195	0.74	0/1597
62	MM	0.38	0/918	0.57	0/1233
63	NN	0.39	0/1226	0.72	0/1649
64	OO	0.40	0/1029	0.81	1/1380 (0.1%)
65	PP	0.40	0/1017	0.70	0/1358
66	QQ	0.37	0/1146	0.69	0/1534
67	RR	0.41	0/1082	0.64	0/1452
68	SS	0.40	0/1208	0.72	0/1618
69	TT	0.39	0/1115	0.68	1/1493 (0.1%)
7	G	0.37	0/1910	0.67	0/2569
70	UU	0.38	0/805	0.69	0/1081
71	VV	0.41	0/643	0.76	0/860
72	WW	0.41	0/1051	0.77	0/1406
73	XX	0.39	0/1116	0.72	0/1490
74	YY	0.37	0/1028	0.66	0/1366
75	ZZ	0.36	0/604	0.64	0/810
76	aa	0.40	0/828	0.83	1/1109 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
77	bb	0.39	0/665	0.66	0/891
78	cc	0.39	0/490	0.74	0/656
79	dd	0.43	0/470	0.71	0/623
8	H	0.41	0/1535	0.72	0/2063
80	ee	0.37	0/447	0.68	0/587
81	ff	0.38	0/567	0.55	0/753
82	gg	0.35	0/2493	0.58	0/3394
83	hh	0.27	0/199	0.76	0/308
84	ii	0.36	0/2996	0.58	0/4050
85	jj	0.36	0/3352	0.57	0/4523
9	I	0.42	0/1702	0.71	0/2272
All	All	0.39	14/237727 (0.0%)	0.74	82/348121 (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
11	L	0	1
2	B	0	3
31	f	0	1
37	l	0	1
4	D	0	1
46	5	0	2
72	WW	0	1
73	XX	0	1
All	All	0	11

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	5	935	A	C5-C6	-15.76	1.26	1.41
46	5	935	A	C6-N1	-11.91	1.27	1.35
46	5	935	A	C2-N3	10.06	1.42	1.33
46	5	481	G	N1-C2	-9.60	1.30	1.37
46	5	481	G	C2-N2	-9.49	1.25	1.34
46	5	481	G	C5-C6	8.75	1.51	1.42
46	5	935	A	N3-C4	7.09	1.39	1.34
46	5	922(A)	G	O3'-P	6.89	1.69	1.61
46	5	935	A	C6-N6	-6.64	1.28	1.33
46	5	481	G	C2-N3	-6.34	1.27	1.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	e	129	LEU	C-O	5.65	1.34	1.23
46	5	1411(B)	C	O3'-P	5.10	1.67	1.61
46	5	2273	G	O3'-P	-5.04	1.55	1.61
46	5	1517	G	O3'-P	-5.03	1.55	1.61

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	481	G	N1-C2-N2	-52.72	68.75	116.20
46	5	935	A	C5-C6-N6	-48.91	84.57	123.70
46	5	935	A	N1-C6-N6	-35.79	97.12	118.60
46	5	935	A	C6-N1-C2	-31.76	99.55	118.60
46	5	481	G	N3-C2-N2	-29.71	99.10	119.90
46	5	935	A	C4-C5-C6	-26.66	103.67	117.00
46	5	481	G	C6-N1-C2	-20.66	112.71	125.10
46	5	481	G	C2-N3-C4	-17.30	103.25	111.90
46	5	922	C	C2'-C3'-O3'	11.77	135.40	109.50
46	5	935	A	N3-C4-C5	-11.49	118.76	126.80
46	5	935	A	N1-C2-N3	-10.53	124.03	129.30
4	D	22	ARG	NE-CZ-NH1	9.56	125.08	120.30
46	5	90	G	C2'-C3'-O3'	8.10	127.32	109.50
46	5	922	C	O4'-C4'-C3'	-8.05	95.95	104.00
46	5	406	C	C2'-C3'-O3'	7.84	126.74	109.50
46	5	3697	U	C2'-C3'-O3'	7.81	126.69	109.50
49	9	1835	A	C2'-C3'-O3'	7.75	126.56	109.50
49	9	1394	G	C2'-C3'-O3'	7.63	126.29	109.50
46	5	922	C	N1-C1'-C2'	-7.58	103.66	112.00
49	9	110	U	C2'-C3'-O3'	7.51	126.03	109.50
46	5	3888	G	C2'-C3'-O3'	7.12	125.17	109.50
46	5	1211	G	C2'-C3'-O3'	6.80	124.58	113.70
46	5	1329	G	C2'-C3'-O3'	6.75	124.51	113.70
46	5	1834	U	C2'-C3'-O3'	6.61	124.28	113.70
46	5	481	G	N3-C4-C5	-6.59	125.30	128.60
46	5	1455	G	C2'-C3'-O3'	6.53	124.14	113.70
49	9	434	G	C2'-C3'-O3'	6.47	124.05	113.70
46	5	4884	G	C2'-C3'-O3'	6.41	123.95	113.70
49	9	1520	G	C4'-C3'-O3'	6.28	125.56	113.00
1	A	9	ARG	NE-CZ-NH1	6.26	123.43	120.30
46	5	125	C	C2'-C3'-O3'	6.00	123.31	113.70
46	5	2474	G	C2'-C3'-O3'	5.98	123.27	113.70
64	OO	146	ARG	NE-CZ-NH1	5.97	123.29	120.30
46	5	245	C	C2'-C3'-O3'	5.97	123.25	113.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	9	1535	U	N1-C1'-C2'	5.94	121.72	114.00
46	5	2068	C	C2'-C3'-O3'	5.92	123.18	113.70
46	5	930	G	C2'-C3'-O3'	5.91	123.16	113.70
46	5	3657	U	C2'-C3'-O3'	5.90	123.14	113.70
46	5	922	C	C4'-C3'-C2'	-5.90	96.70	102.60
45	2	71	G	C2'-C3'-O3'	5.89	123.13	113.70
46	5	971(A)	G	C4'-C3'-O3'	5.83	124.66	113.00
46	5	1818	G	C2'-C3'-O3'	5.81	123.00	113.70
46	5	3603	G	C2'-C3'-O3'	5.80	122.99	113.70
49	9	1646	C	C2'-C3'-O3'	5.78	122.95	113.70
13	N	202	ARG	NE-CZ-NH1	5.70	123.15	120.30
46	5	385	A	C4'-C3'-O3'	5.69	124.39	113.00
46	5	1683	U	C2'-C3'-O3'	5.66	122.75	113.70
46	5	481	G	C5-C6-N1	-5.63	108.69	111.50
4	D	22	ARG	CG-CD-NE	5.58	123.51	111.80
46	5	1477	C	C2'-C3'-O3'	5.58	122.62	113.70
46	5	4947	U	C2'-C3'-O3'	5.57	122.61	113.70
49	9	642	U	C2'-C3'-O3'	5.55	122.58	113.70
46	5	1411	C	C2'-C3'-O3'	-5.51	97.38	109.50
46	5	1236	C	C2'-C3'-O3'	5.50	122.50	113.70
46	5	1428	U	C2'-C3'-O3'	5.46	122.44	113.70
46	5	1908	A	C2'-C3'-O3'	5.46	122.43	113.70
2	B	161	ARG	NE-CZ-NH1	5.46	123.03	120.30
16	Q	104	ARG	NE-CZ-NH1	5.44	123.02	120.30
46	5	4446	U	O5'-P-OP1	-5.42	100.82	105.70
46	5	922	C	C5'-C4'-O4'	5.41	115.59	109.10
46	5	4448	G	C4'-C3'-O3'	5.39	123.77	113.00
49	9	1664	A	C4'-C3'-O3'	5.38	123.76	113.00
46	5	2807	A	C2'-C3'-O3'	5.36	122.28	113.70
46	5	1411(C)	C	C5'-C4'-O4'	5.33	115.50	109.10
46	5	48	G	C2'-C3'-O3'	5.32	122.21	113.70
76	aa	10	ARG	NE-CZ-NH2	5.31	122.96	120.30
46	5	1323	A	C2'-C3'-O3'	5.30	122.19	113.70
49	9	1060	A	N9-C1'-C2'	5.30	120.89	114.00
46	5	504	G	C2'-C3'-O3'	5.27	122.13	113.70
46	5	1445	U	C2'-C3'-O3'	5.27	122.12	113.70
69	TT	110	LEU	CA-CB-CG	5.26	127.40	115.30
46	5	1236	C	C4'-C3'-O3'	5.23	123.45	113.00
46	5	47	A	C4'-C3'-O3'	5.22	123.44	113.00
55	FF	145	ARG	NE-CZ-NH1	5.21	122.91	120.30
11	L	39	ARG	NE-CZ-NH1	5.21	122.91	120.30
4	D	22	ARG	NE-CZ-NH2	-5.20	117.70	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	2408	U	N1-C1'-C2'	5.19	120.75	114.00
46	5	922(A)	G	N9-C1'-C2'	5.15	120.70	114.00
46	5	3625	G	C2'-C3'-O3'	5.12	121.89	113.70
2	B	258	HIS	N-CA-C	5.10	124.76	111.00
49	9	1395	C	C4'-C3'-O3'	5.05	123.10	113.00
49	9	1130	G	C4'-C3'-O3'	5.02	123.05	113.00

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
46	5	481	G	Sidechain
46	5	935	A	Sidechain
2	B	16	PHE	Peptide
2	B	257	TRP	Peptide
2	B	259	PRO	Peptide
4	D	36	LEU	Peptide
11	L	46	ILE	Peptide
72	WW	27	ILE	Peptide
73	XX	61	GLN	Peptide
31	f	106	TYR	Peptide
37	l	48	LYS	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	A	1898	0	1993	23	0
2	B	3172	0	3310	31	0
3	C	2883	0	3053	50	0
4	D	2391	0	2424	13	0
5	E	1729	0	1887	15	0
6	F	1875	0	1995	23	0
7	G	1879	0	2027	12	0
8	H	1516	0	1597	13	0
9	I	1664	0	1712	15	0
10	J	1362	0	1399	14	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	L	1702	0	1820	11	0
12	M	1137	0	1211	18	0
13	N	1701	0	1749	24	0
14	O	1630	0	1778	29	0
15	P	1242	0	1274	14	0
16	Q	1515	0	1634	16	0
17	R	1508	0	1664	7	0
18	S	1462	0	1508	16	0
19	T	1298	0	1366	11	0
20	U	809	0	833	9	0
21	V	979	0	1039	13	0
22	W	860	0	903	3	0
23	X	967	0	1040	4	0
24	Y	1115	0	1205	6	0
25	Z	1107	0	1182	8	0
26	a	1162	0	1209	0	0
27	b	848	0	920	0	0
28	c	761	0	794	0	0
29	d	888	0	930	0	0
30	e	1053	0	1147	0	0
31	f	876	0	912	0	0
32	g	906	0	1001	0	0
33	h	1013	0	1147	0	0
34	i	830	0	916	0	0
35	j	705	0	738	0	0
36	k	569	0	637	0	0
37	l	447	0	480	0	0
38	m	429	0	466	0	0
39	n	239	0	289	0	0
40	o	851	0	920	0	0
41	p	708	0	758	0	0
42	r	994	0	1051	0	0
43	s	1507	0	1564	0	0
44	t	1160	0	1218	0	0
45	2	1593	0	811	4	0
45	3	1593	0	811	3	0
46	5	75972	0	38399	476	0
47	7	2558	0	1296	7	0
48	8	3208	0	1629	20	0
49	9	36249	0	18316	200	0
50	AA	1710	0	1708	12	0
51	BB	1729	0	1803	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	CC	1716	0	1806	14	0
53	DD	1768	0	1866	10	0
54	EE	2076	0	2177	13	0
55	FF	1471	0	1522	7	0
56	GG	1923	0	2089	14	0
57	HH	1488	0	1582	13	0
58	II	1686	0	1772	14	0
59	JJ	1525	0	1640	9	0
60	KK	810	0	836	6	0
61	LL	1175	0	1249	11	0
62	MM	908	0	939	11	0
63	NN	1202	0	1289	6	0
64	OO	1016	0	1039	7	0
65	PP	997	0	1045	7	0
66	QQ	1128	0	1195	5	0
67	RR	1068	0	1121	5	0
68	SS	1190	0	1249	9	0
69	TT	1097	0	1132	4	0
70	UU	795	0	862	5	0
71	VV	636	0	637	3	0
72	WW	1034	0	1080	13	0
73	XX	1098	0	1167	10	0
74	YY	1011	0	1083	7	0
75	ZZ	598	0	656	0	0
76	aa	814	0	864	0	0
77	bb	651	0	672	0	0
78	cc	488	0	514	0	0
79	dd	459	0	449	0	0
80	ee	443	0	492	0	0
81	ff	555	0	566	0	0
82	gg	2436	0	2393	0	0
83	hh	176	0	89	0	0
84	ii	2947	0	2957	0	0
85	jj	3292	0	3371	0	0
86	5	164	0	0	0	0
86	7	5	0	0	0	0
86	8	3	0	0	0	0
86	9	56	0	0	0	0
86	I	1	0	0	0	0
86	L	1	0	0	0	0
86	P	1	0	0	0	0
86	TT	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	hh	1	0	0	0	0
86	jj	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
88	jj	32	0	14	0	0
All	All	221912	0	166887	1173	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 4.

All (1173) 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)
46:5:3914:U:O4	46:5:4378:A:N1	1.60	1.32
49:9:830:A:N1	49:9:844:U:O4	1.71	1.20
46:5:1929:A:N1	46:5:2054:U:O4	1.73	1.20
46:5:77:U:O4	46:5:336:A:N1	1.70	1.20
46:5:922:C:C5'	46:5:922(A):G:H3'	1.74	1.17
46:5:922:C:H5'	46:5:922(A):G:H3'	1.22	1.16
46:5:2468:U:O4	46:5:2473:A:N1	1.83	1.10
49:9:1284:A:N1	62:MM:91:LEU:HD22	1.73	1.02
46:5:922:C:H5''	46:5:922(B):C:O5'	1.64	0.96
46:5:2409:U:C4	46:5:2783:A:N1	2.39	0.90
46:5:4699:U:N3	46:5:4701:A:N6	2.19	0.89
46:5:1411:C:H4'	46:5:1411(C):C:O4'	1.74	0.87
46:5:922:C:P	46:5:922(B):C:O5'	2.32	0.87
46:5:2409:U:O4	46:5:2783:A:N1	2.08	0.85
46:5:922:C:O2'	46:5:922(B):C:O2	1.95	0.83
49:9:1283:C:H41	62:MM:102:LYS:HE3	1.42	0.83
49:9:1283:C:N4	62:MM:102:LYS:HE3	1.94	0.82
54:EE:44:LEU:HD13	54:EE:72:ILE:HD11	1.61	0.82
8:H:41:ILE:HG21	8:H:73:ILE:HD11	1.59	0.82
60:KK:35:LEU:HD12	60:KK:40:VAL:HG21	1.62	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:12:ARG:O	18:S:171:ARG:NH2	2.14	0.80
46:5:4699:U:N3	46:5:4701:A:C6	2.50	0.79
46:5:4699:U:C4	46:5:4701:A:N6	2.51	0.78
46:5:922:C:O2'	46:5:922(B):C:C2	2.35	0.78
19:T:87:LYS:NZ	46:5:4301:U:OP2	2.17	0.77
46:5:922:C:H5'	46:5:922(A):G:C3'	2.11	0.76
16:Q:104:ARG:NH2	46:5:1353:G:N7	2.35	0.75
46:5:3914:U:C4	46:5:4378:A:N1	2.53	0.75
49:9:980:A:H2'	49:9:981:A:C8	2.21	0.75
53:DD:70:THR:HG22	53:DD:86:LEU:HD13	1.69	0.75
46:5:914:U:O4	46:5:918:G:N7	2.19	0.74
49:9:1284:A:C2	62:MM:91:LEU:HD22	2.21	0.74
46:5:1928:C:C4	46:5:2054:U:O2	2.41	0.74
46:5:2395:A:O2'	46:5:2806:A:H1'	1.89	0.73
46:5:1411:C:O3'	46:5:1411(C):C:C5'	2.37	0.73
46:5:1928:C:N4	46:5:2054:U:O2	2.21	0.73
3:C:101:MET:SD	3:C:104:PRO:HA	2.29	0.72
13:N:202:ARG:NH2	46:5:1372:A:OP1	2.23	0.71
46:5:922:C:C2'	46:5:922(B):C:C2	2.74	0.71
3:C:341:LEU:HD21	5:E:52:LEU:HD21	1.72	0.71
56:GG:5:ILE:HD12	56:GG:16:ILE:HD13	1.73	0.70
71:VV:20:SER:HB3	71:VV:59:ILE:HD11	1.73	0.70
3:C:84:THR:O	3:C:87:SER:OG	2.10	0.70
46:5:77:U:C4	46:5:336:A:N1	2.60	0.70
46:5:4396:A:OP1	46:5:4443:C:O2'	2.07	0.70
53:DD:21:LEU:HD21	53:DD:48:ILE:HD11	1.73	0.69
46:5:1670:G:C8	46:5:1855:G:C8	2.81	0.69
46:5:922:C:C5'	46:5:922(B):C:O5'	2.40	0.69
46:5:922:C:H2'	46:5:922(B):C:N3	2.08	0.69
46:5:3723:A:H2'	46:5:3724:A:C8	2.28	0.69
46:5:3914:U:O4	46:5:4378:A:C2	2.46	0.69
74:YY:34:THR:HG23	74:YY:69:THR:HG21	1.74	0.69
3:C:76:ILE:HG22	3:C:77:PRO:HD2	1.74	0.68
46:5:922:C:H5''	46:5:922(B):C:P	2.33	0.68
49:9:830:A:N1	49:9:844:U:C4	2.59	0.68
46:5:922:C:O3'	46:5:922(B):C:C6	2.47	0.68
4:D:62:CYS:HB3	4:D:105:LEU:HD22	1.75	0.68
46:5:922:C:O5'	46:5:922(A):G:H3'	1.94	0.67
46:5:77:U:H2'	46:5:77:U:O2	1.95	0.67
46:5:742:G:C2	46:5:922(A):G:C6	2.82	0.67
14:O:72:HIS:N	46:5:4586:G:OP1	2.27	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:3879:G:O2'	46:5:3881:G:OP2	2.12	0.67
6:F:114:ARG:NH1	16:Q:4:ASP:O	2.28	0.67
46:5:1370:G:O2'	46:5:1371:A:OP2	2.10	0.66
46:5:922:C:O5'	46:5:922(A):G:O5'	2.13	0.66
46:5:1929:A:C8	46:5:1932:A:H1'	2.30	0.66
49:9:830:A:N6	49:9:844:U:N3	2.43	0.66
49:9:1611:G:OP2	68:SS:121:ARG:NH1	2.27	0.66
61:LL:61:PRO:HA	61:LL:66:VAL:HG13	1.76	0.66
49:9:929:G:H2'	49:9:930:C:O4'	1.96	0.65
3:C:316:LYS:NZ	46:5:1281:G:OP1	2.28	0.65
17:R:98:ARG:NH2	46:5:2262:G:OP2	170.84	0.65
46:5:1411:C:C5'	46:5:1411(B):C:H2'	2.27	0.65
70:UU:50:VAL:HG23	70:UU:91:LEU:HD23	1.79	0.65
1:A:211:PHE:CD1	1:A:219:ILE:HG23	2.31	0.65
49:9:1284:A:C4	62:MM:91:LEU:HD13	2.31	0.65
49:9:293:C:O2'	49:9:294:U:H3'	1.97	0.65
46:5:1929:A:N1	46:5:2054:U:C4	2.61	0.64
46:5:1598:C:O2	46:5:2798:A:H2'	1.97	0.64
46:5:1854:G:N2	46:5:4394:A:O4'	2.30	0.64
72:WW:75:ILE:HD11	72:WW:93:LEU:HD11	1.78	0.64
49:9:1143:A:H2'	49:9:1144:A:C8	2.33	0.64
46:5:964:A:H2'	46:5:965:G:O4'	1.97	0.64
1:A:158:ILE:HG23	1:A:162:ASN:HD21	1.62	0.64
49:9:145:G:N7	56:GG:178:ARG:NH1	2.46	0.64
1:A:207:VAL:HG23	1:A:208:GLU:HG3	1.80	0.63
3:C:207:PRO:HB3	3:C:249:PHE:CD2	2.34	0.63
13:N:76:PRO:O	13:N:79:ALA:HB3	1.98	0.63
18:S:68:PHE:N	46:5:729:G:O6	2.28	0.63
46:5:4291:G:H5''	46:5:4291:G:N3	2.13	0.63
10:J:151:ILE:HD11	10:J:156:ARG:HG2	1.79	0.63
46:5:2416:G:O6	46:5:2426:U:OP2	2.17	0.63
46:5:3914:U:H3	46:5:4378:A:N6	1.95	0.63
49:9:1130:G:H2'	49:9:1130:G:N3	2.14	0.62
12:M:24:LEU:HD11	12:M:86:TRP:CG	2.34	0.62
49:9:1373:C:O2'	67:RR:10:LYS:NZ	2.32	0.62
52:CC:209:VAL:HG21	52:CC:233:LEU:HD13	1.81	0.62
48:8:19:C:H2'	48:8:20:A:C8	2.35	0.62
49:9:628:A:N6	49:9:1332:A:O4'	2.32	0.62
50:AA:69:GLU:HB3	52:CC:270:THR:HG21	1.82	0.62
46:5:738:C:O2'	46:5:738(A):C:O4'	2.16	0.62
46:5:1074:G:C2	46:5:1238:A:C2	2.88	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:1818:G:O2'	46:5:1819:G:OP1	2.12	0.61
7:G:215:ASP:HB3	7:G:216:PRO:HD3	1.81	0.61
49:9:1220:A:N6	49:9:1221:G:C6	2.68	0.61
46:5:3717:A:H2'	46:5:3718:A:C8	2.35	0.61
46:5:922:C:C6	46:5:922(A):G:C6	2.88	0.61
58:II:162:LEU:HD11	58:II:191:GLU:HG2	1.83	0.61
13:N:67:ARG:NH1	46:5:2458:C:OP1	2.33	0.61
2:B:249:ARG:NH1	46:5:2837:U:OP1	2.34	0.61
46:5:1528:U:H2'	46:5:1529:G:O4'	2.01	0.61
47:7:23:A:N3	47:7:118:C:O2'	2.31	0.61
49:9:1407:U:H2'	49:9:1408:U:C6	2.35	0.61
1:A:179:ILE:O	46:5:3653:A:O3'	2.19	0.60
10:J:43:LEU:HD11	10:J:82:ILE:HG23	1.83	0.60
46:5:1929:A:N3	46:5:1929:A:H3'	2.17	0.60
49:9:1351:G:O2'	49:9:1378:A:N1	2.32	0.59
46:5:5057:C:H2'	46:5:5058:A:C8	2.37	0.59
46:5:922:C:O5'	46:5:922(A):G:P	2.60	0.59
49:9:615:C:H2'	49:9:616:A:O4'	2.03	0.59
17:R:74:ARG:NH2	46:5:2891:U:OP2	2.36	0.59
59:JJ:130:ILE:HG12	59:JJ:135:ILE:HD11	1.85	0.59
46:5:113:A:H2'	46:5:114:G:O4'	2.02	0.58
4:D:23:ARG:NH2	46:5:4280:A:OP2	2.36	0.58
46:5:82:U:H2'	46:5:83:C:O4'	2.02	0.58
3:C:303:ARG:O	16:Q:38:ARG:NH1	2.36	0.58
46:5:2268:A:H4'	46:5:2269:C:H5'	1.84	0.58
46:5:4711:C:H2'	46:5:4712:C:O4'	2.04	0.58
46:5:2439:G:C6	46:5:2440:U:C4	2.92	0.58
46:5:2468:U:C4	46:5:2473:A:N1	2.68	0.58
46:5:3914:U:N3	46:5:4378:A:N6	2.49	0.58
46:5:747:A:H4'	46:5:748:G:OP1	2.04	0.58
49:9:183:G:O2'	49:9:184:G:O5'	2.22	0.58
5:E:52:LEU:HD23	5:E:58:ARG:HA	1.86	0.58
7:G:104:LEU:O	7:G:106:ARG:N	2.36	0.58
49:9:1284:A:C2	62:MM:91:LEU:CD2	2.85	0.58
50:AA:18:PHE:CD1	50:AA:173:LEU:HD11	2.39	0.58
49:9:1284:A:C6	62:MM:91:LEU:HD22	2.37	0.58
16:Q:14:ARG:NH2	46:5:2083:C:OP2	2.37	0.58
46:5:4320:G:H2'	46:5:4321:U:O4'	2.04	0.58
46:5:914:U:O4	46:5:918:G:C8	2.57	0.57
46:5:4723:A:H2'	46:5:4724:A:C8	2.38	0.57
52:CC:189:GLY:HA3	52:CC:235:ASN:OD1	2.04	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:HH:133:LEU:HD21	57:HH:176:VAL:HG11	1.85	0.57
13:N:49:ARG:HH12	46:5:152:U:P	2.27	0.57
2:B:77:THR:HG21	2:B:337:VAL:HG22	1.85	0.57
13:N:160:GLU:OE1	13:N:160:GLU:N	2.37	0.57
49:9:1286:G:O6	62:MM:34:GLY:HA3	2.04	0.57
46:5:2409:U:O4	46:5:2783:A:C6	2.57	0.57
9:I:54:SER:HB2	9:I:135:ILE:HD11	1.87	0.57
5:E:184:LEU:HD11	5:E:264:ILE:HD11	1.86	0.57
52:CC:196:ILE:HB	52:CC:223:TYR:HB2	1.87	0.57
59:JJ:130:ILE:CG1	59:JJ:135:ILE:HD11	2.34	0.57
46:5:922(B):C:N3	46:5:923:C:C5	2.73	0.57
13:N:89:VAL:HG11	46:5:3928:A:H5'	1.86	0.57
21:V:89:ARG:HD2	21:V:95:PHE:CZ	2.39	0.57
46:5:4273:A:H2'	46:5:4274:A:C8	2.40	0.56
46:5:77:U:O2	46:5:77:U:C2'	2.50	0.56
49:9:1667:U:H2'	49:9:1668:U:C6	2.40	0.56
11:L:47:ALA:HB3	11:L:48:PRO:HD3	1.87	0.56
15:P:70:CYS:SG	15:P:72:GLN:N	2.78	0.56
51:BB:136:ARG:HD2	51:BB:138:PHE:CZ	2.41	0.56
73:XX:61:GLN:HB3	73:XX:62:PRO:CD	2.34	0.56
46:5:2468:U:H3	46:5:2473:A:N6	2.03	0.56
45:3:16:C:O2	45:3:16:C:O4'	2.24	0.56
46:5:77:U:H3	46:5:336:A:N6	2.04	0.56
16:Q:85:THR:HG22	16:Q:104:ARG:HB2	1.87	0.56
46:5:2468:U:C2	46:5:2506:G:N7	2.73	0.56
49:9:1329:U:O2'	49:9:1332:A:OP2	2.11	0.56
49:9:928:G:H2'	49:9:929:G:C8	2.41	0.56
46:5:43:U:H2'	46:5:44:A:O5'	2.05	0.56
48:8:47:C:H1'	48:8:61:A:H2'	1.88	0.56
49:9:12:U:H2'	49:9:13:C:C6	2.40	0.56
46:5:4944:C:O4'	46:5:4944:C:O2	2.23	0.56
72:WW:104:LEU:HD12	72:WW:104:LEU:O	2.06	0.56
46:5:4871:C:O4'	46:5:4871:C:O2	2.24	0.55
46:5:923:C:C5	46:5:926:G:O4'	2.59	0.55
46:5:1337:A:C2	46:5:2349:A:C2	2.94	0.55
46:5:922:C:H3'	46:5:922:C:C6	2.41	0.55
49:9:1139:C:O4'	49:9:1139:C:O2	2.21	0.55
66:QQ:51:LEU:HD22	66:QQ:84:ILE:HG13	1.88	0.55
46:5:1600:A:C6	46:5:1638:A:C5	2.94	0.55
46:5:2292:C:H2'	46:5:2293:U:C6	2.41	0.55
46:5:4260:U:H2'	46:5:4261:C:C6	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:37:LYS:O	15:P:114:ILE:O	2.25	0.55
46:5:3829:G:C2	46:5:3830:A:C8	2.95	0.55
49:9:830:A:N6	49:9:844:U:H3	2.04	0.55
6:F:242:LEU:HD23	6:F:246:MET:HG3	1.89	0.55
60:KK:11:ILE:HD12	60:KK:45:VAL:HG22	1.87	0.55
46:5:1672:U:H2'	46:5:1673:U:C6	2.41	0.55
46:5:245:C:O2	46:5:245:C:O4'	2.25	0.55
46:5:2396:A:N6	46:5:2814:C:O2	2.40	0.55
46:5:4537:C:H2'	46:5:4538:G:C8	2.41	0.55
10:J:128:LEU:HD11	10:J:130:PHE:CE1	2.42	0.55
68:SS:121:ARG:HG3	68:SS:131:VAL:HG21	1.87	0.55
46:5:922:C:O3'	46:5:922:C:O5'	2.25	0.54
50:AA:18:PHE:CE1	50:AA:173:LEU:HD11	2.42	0.54
2:B:228:TYR:O	46:5:2835:A:O2'	2.16	0.54
46:5:4589:A:N1	46:5:4621:C:O2'	2.32	0.54
46:5:4942:C:H4'	46:5:4943:A:OP1	2.07	0.54
49:9:1624:U:O2	49:9:1624:U:O4'	2.23	0.54
2:B:56:ILE:HG22	2:B:74:GLU:HB3	1.89	0.54
13:N:115:VAL:HG22	13:N:134:LEU:HD21	1.90	0.54
45:2:16:C:O4'	45:2:16:C:O2	2.24	0.54
2:B:288:GLY:HA3	2:B:330:PHE:CE1	2.43	0.54
14:O:193:THR:HG23	14:O:202:LEU:HD23	1.89	0.54
67:RR:28:PHE:HA	67:RR:55:THR:HG21	1.88	0.54
46:5:1855:G:C6	46:5:1856:C:C4	2.95	0.54
46:5:2409:U:C4	46:5:2783:A:C2	2.95	0.54
15:P:127:ARG:NH2	46:5:2422:C:OP1	2.40	0.54
68:SS:13:LEU:HD11	68:SS:56:ALA:O	2.08	0.54
46:5:2627:C:O2	46:5:2627:C:O4'	2.25	0.54
9:I:3:ARG:NH2	46:5:4431:U:OP2	2.41	0.54
46:5:1872:G:O2'	46:5:4219:A:N3	2.32	0.54
49:9:1129:G:C6	49:9:1130:G:O6	2.60	0.54
7:G:219:LEU:HD21	13:N:45:PRO:HG2	1.89	0.54
10:J:141:ILE:HD11	47:7:55:A:N3	2.22	0.54
20:U:84:LYS:HG3	20:U:102:VAL:HG11	1.89	0.54
73:XX:51:VAL:HG13	73:XX:70:VAL:HG13	1.89	0.54
2:B:41:VAL:HA	2:B:187:GLY:HA3	1.90	0.54
3:C:27:VAL:HG22	3:C:264:TYR:HB2	1.90	0.54
5:E:184:LEU:O	46:5:4883:C:N4	2.41	0.54
20:U:33:ILE:HD12	20:U:96:LEU:HD22	1.89	0.54
25:Z:53:VAL:HG21	25:Z:62:ILE:HG23	1.90	0.54
46:5:3810:C:O4'	46:5:3810:C:O2	2.26	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:43:U:C2'	46:5:44:A:O5'	2.56	0.54
3:C:253:THR:O	3:C:256:ALA:N	2.41	0.54
73:XX:67:ARG:HG2	73:XX:115:ILE:HG23	1.89	0.54
46:5:1236:C:O2'	46:5:1238:A:OP1	2.25	0.53
48:8:94:G:H5'	48:8:94:G:C8	2.43	0.53
64:OO:95:ILE:HD13	64:OO:116:LEU:HG	1.90	0.53
46:5:2439:G:C5	46:5:2440:U:C5	2.96	0.53
46:5:3656:A:O4'	46:5:3747:A:C2	2.61	0.53
46:5:77:U:O4	46:5:336:A:C2	2.57	0.53
49:9:314:U:H2'	49:9:314:U:O2	2.08	0.53
49:9:1012:A:H2'	49:9:1013:U:O4'	2.08	0.53
54:EE:44:LEU:HD21	54:EE:70:ILE:HG21	1.90	0.53
46:5:1483:C:O4'	46:5:1483:C:O2	2.24	0.53
6:F:178:LEU:HB3	6:F:183:ILE:HB	1.91	0.53
49:9:371:A:OP2	58:II:10:LYS:HB2	2.08	0.53
49:9:501:C:H2'	49:9:501:C:O2	2.09	0.53
49:9:853:C:O2	49:9:853:C:O4'	2.27	0.53
51:BB:69:VAL:HG11	51:BB:74:LEU:HD13	1.89	0.53
46:5:2088:A:O2'	46:5:2089:G:P	2.67	0.53
46:5:2395:A:O2'	46:5:2806:A:N3	2.27	0.53
49:9:143:U:N3	49:9:314:U:OP1	2.42	0.53
49:9:1452:A:OP2	67:RR:32:LYS:NZ	2.41	0.53
46:5:2505:C:O4'	46:5:2505:C:O2	2.24	0.53
48:8:137:A:H2'	48:8:138:C:C6	2.43	0.53
49:9:1740:C:H2'	49:9:1741:U:C6	2.44	0.53
49:9:613:G:H2'	49:9:627:U:C6	2.44	0.53
56:GG:52:ILE:HD11	56:GG:109:LEU:CD1	2.39	0.53
50:AA:161:ILE:HG22	50:AA:163:CYS:SG	2.48	0.53
46:5:1411:C:O3'	46:5:1411(C):C:H5''	2.09	0.53
49:9:1315:U:O4'	49:9:1315:U:O2	2.26	0.53
14:O:7:LEU:O	14:O:34:VAL:N	2.40	0.53
11:L:74:ARG:NH2	46:5:109:G:OP2	2.42	0.52
46:5:2693:G:C6	46:5:2694:G:C6	2.97	0.52
46:5:3873:G:H2'	46:5:3874:G:C8	2.44	0.52
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.90	0.52
46:5:3891:A:H2'	46:5:3892:U:O4'	2.09	0.52
49:9:1406:G:O2'	49:9:1443:C:N3	2.42	0.52
46:5:224:U:O2	46:5:224:U:O4'	2.24	0.52
49:9:1629:C:OP1	68:SS:39:ARG:NE	2.34	0.52
8:H:18:ILE:HG22	8:H:27:VAL:HG22	1.90	0.52
9:I:9:TYR:CG	9:I:97:ILE:HG12	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:87:THR:HG23	20:U:102:VAL:HG21	1.91	0.52
46:5:1411:C:O3'	46:5:1411(C):C:O5'	2.27	0.52
13:N:4:TYR:OH	46:5:151:G:OP2	2.18	0.52
46:5:1929:A:C2	46:5:2054:U:O4	2.57	0.52
46:5:1667:A:H61	46:5:2280:G:H3'	1.74	0.52
49:9:1488:C:O2'	49:9:1490:G:OP2	2.26	0.52
4:D:106:ALA:HB1	4:D:171:LEU:HD13	1.91	0.52
6:F:88:LEU:HD11	6:F:121:PHE:CD1	2.44	0.52
8:H:41:ILE:CG2	8:H:73:ILE:HD11	2.36	0.52
63:NN:125:LEU:HD22	63:NN:129:TYR:CE2	2.44	0.52
46:5:2468:U:N3	46:5:2473:A:N6	2.57	0.52
49:9:846:G:OP2	54:EE:108:ARG:NH1	2.42	0.52
54:EE:126:VAL:HG22	54:EE:158:ASP:O	2.10	0.52
17:R:105:LEU:HD12	17:R:138:LEU:HD13	1.92	0.52
21:V:65:VAL:HG21	21:V:72:LEU:HB3	1.91	0.52
46:5:4579:U:H2'	46:5:4580:U:C6	2.45	0.52
46:5:84:A:N6	46:5:99:A:OP2	2.41	0.52
49:9:1334:G:C4	49:9:1498:A:C2	2.97	0.52
2:B:119:TYR:OH	2:B:129:ALA:N	2.43	0.52
53:DD:48:ILE:HG23	53:DD:86:LEU:HD12	1.92	0.52
12:M:118:MET:SD	46:5:4929:C:O4'	2.68	0.52
46:5:2094:C:O2	46:5:2094:C:O4'	2.27	0.52
46:5:4219:A:H2'	46:5:4220:A:C8	2.45	0.52
49:9:1284:A:C5	62:MM:91:LEU:HD13	2.45	0.52
49:9:1602:U:C4	49:9:1604:G:C8	2.97	0.52
12:M:66:HIS:CE1	12:M:67:SER:OG	2.62	0.52
4:D:35:ARG:HB2	46:5:4325:A:C2	2.45	0.52
3:C:45:ARG:O	3:C:48:ASN:OD1	2.27	0.52
64:OO:99:ALA:HB3	64:OO:133:THR:HG22	1.92	0.52
21:V:87:SER:HA	21:V:97:TYR:HB3	1.91	0.51
72:WW:6:VAL:HG12	72:WW:34:ILE:HD11	1.90	0.51
46:5:1961:G:O2'	46:5:2025:A:N6	2.43	0.51
46:5:307:A:C5	46:5:308:G:C6	2.98	0.51
46:5:922:C:C6	46:5:922(A):G:C5	2.99	0.51
46:5:922:C:O3'	46:5:922(B):C:C5	2.63	0.51
49:9:434:G:H2'	49:9:435:A:C8	2.44	0.51
49:9:501:C:O2	49:9:501:C:C2'	2.57	0.51
49:9:986:G:OP2	49:9:988:C:N4	2.44	0.51
68:SS:40:TYR:O	68:SS:44:VAL:HG23	2.10	0.51
46:5:3856:A:H2'	46:5:3857:G:O4'	2.10	0.51
61:LL:113:LEU:HD23	61:LL:142:VAL:HG21	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:1237:C:O2	46:5:1237:C:O4'	2.28	0.51
46:5:4269:G:C6	46:5:4270:C:C4	2.98	0.51
49:9:1546:G:H5'	66:QQ:18:THR:HG21	1.92	0.51
46:5:1411:C:H5'	46:5:1411(B):C:C2'	2.40	0.51
53:DD:72:VAL:HG23	60:KK:20:VAL:HG21	1.91	0.51
58:II:113:TYR:CE1	58:II:121:LEU:HD23	2.45	0.51
46:5:4658:G:C6	46:5:4659:G:C5	2.97	0.51
3:C:129:ALA:O	3:C:133:LEU:HD13	2.10	0.51
19:T:80:VAL:HG21	19:T:85:LEU:HD12	1.91	0.51
21:V:82:ILE:HG22	21:V:83:ARG:HG3	1.93	0.51
46:5:4989:U:O4'	46:5:4989:U:O2	2.27	0.51
49:9:1117:C:O2'	49:9:1118:C:O4'	2.28	0.51
71:VV:32:ILE:HD12	71:VV:60:ARG:HD2	1.91	0.51
46:5:1679:A:N1	46:5:4391:G:O2'	2.44	0.51
46:5:3723:A:C2	46:5:3724:A:C6	2.98	0.51
57:HH:116:ARG:NH2	57:HH:121:THR:OG1	2.44	0.51
46:5:1922:G:C2	46:5:1923:A:C8	2.99	0.51
46:5:4428:A:C5	46:5:4429:C:C5	2.99	0.51
49:9:1380:C:H2'	49:9:1381:G:O4'	2.11	0.51
46:5:1655:C:H2'	46:5:1656:U:H5''	1.93	0.50
46:5:2465:C:H2'	46:5:2466:G:O4'	2.10	0.50
46:5:4476:C:O2'	46:5:4478:G:OP2	2.28	0.50
2:B:174:ARG:NH1	46:5:4985:U:O2	2.44	0.50
49:9:628:A:H61	49:9:1332:A:C1'	2.24	0.50
18:S:78:PHE:O	18:S:96:GLU:HA	2.10	0.50
46:5:356:G:O2'	48:8:25:G:N3	2.45	0.50
1:A:207:VAL:HG12	46:5:3919:C:C5'	2.41	0.50
46:5:4583:C:O2'	46:5:4718:G:N2	2.44	0.50
49:9:1700:C:C2	49:9:1834:A:N6	2.79	0.50
1:A:126:LEU:HD13	1:A:150:LEU:HD21	1.93	0.50
2:B:29:VAL:HG23	2:B:346:THR:HG21	1.93	0.50
46:5:3685:C:H2'	46:5:3686:G:O4'	2.12	0.50
49:9:1401:A:H2'	49:9:1402:A:C8	2.46	0.50
61:LL:37:TYR:CE2	61:LL:51:ILE:HG23	2.46	0.50
46:5:932:A:H2'	46:5:939:G:O6	2.11	0.50
49:9:1444:U:H2'	49:9:1445:U:C6	2.46	0.50
49:9:363:A:N1	49:9:397:G:O2'	2.32	0.50
49:9:356:C:O2	49:9:356:C:C2'	2.59	0.50
22:W:3:VAL:HG21	22:W:12:LYS:HE2	1.92	0.50
49:9:1551:U:O2	49:9:1551:U:O4'	2.28	0.50
58:II:159:SER:HB3	58:II:162:LEU:HD12	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:7:GLN:N	17:R:7:GLN:OE1	2.45	0.50
45:2:18:U:O2'	45:2:57:A:C2	2.65	0.50
46:5:1381:U:O2	46:5:1381:U:H5''	2.12	0.50
46:5:1411:C:C4'	46:5:1411(C):C:O4'	2.55	0.50
46:5:1503:A:H4'	46:5:1504:G:H5'	1.92	0.50
49:9:944:A:C5	49:9:945:U:C5	2.99	0.50
6:F:145:ASN:OD1	6:F:146:LEU:N	2.45	0.50
14:O:55:LEU:HD23	14:O:58:LEU:HD12	1.93	0.50
46:5:1664:U:H2'	46:5:1665:C:C6	2.46	0.50
6:F:154:TYR:CE1	6:F:186:MET:HG2	2.46	0.50
16:Q:35:LEU:HB3	16:Q:44:ASN:ND2	2.27	0.50
18:S:35:PRO:HD2	18:S:39:VAL:HG21	1.92	0.50
46:5:106:A:H2'	46:5:107:G:O4'	2.12	0.50
2:B:13:SER:OG	46:5:1724:G:N2	75.59	0.50
49:9:1680:G:H2'	49:9:1681:U:C6	2.47	0.50
10:J:15:LEU:HD21	10:J:134:LEU:HD13	1.94	0.50
17:R:23:TRP:CH2	17:R:25:ASP:HA	2.46	0.50
46:5:2896:G:H5''	46:5:2897:G:OP2	2.12	0.49
49:9:1581:C:OP2	49:9:1582:C:N4	2.43	0.49
49:9:640:A:H2'	49:9:641:A:C8	2.46	0.49
49:9:823:U:O2	49:9:823:U:O4'	2.29	0.49
57:HH:133:LEU:HD22	57:HH:173:PHE:CD1	2.46	0.49
61:LL:12:LYS:HA	61:LL:56:ILE:HD13	1.94	0.49
13:N:48:ALA:HB1	13:N:53:TYR:HB3	1.94	0.49
46:5:1380:G:H4'	46:5:1381:U:H5''	1.95	0.49
2:B:259:PRO:HB3	46:5:2044:U:C2	2.48	0.49
46:5:2313:A:O2'	46:5:2314:G:OP1	2.20	0.49
46:5:2608:G:C2	46:5:2732:G:C2	3.00	0.49
46:5:4305:G:N3	46:5:4305:G:C2'	2.74	0.49
46:5:4633:G:N2	46:5:4664:A:OP2	2.40	0.49
48:8:128:C:C5	48:8:129:C:C5	3.00	0.49
61:LL:100:ASN:N	61:LL:100:ASN:HD22	2.10	0.49
12:M:17:PHE:CZ	12:M:54:CYS:HA	2.47	0.49
19:T:17:ARG:CD	19:T:47:THR:HG23	2.43	0.49
72:WW:90:GLN:HB3	72:WW:102:ILE:HD12	1.94	0.49
46:5:1322:A:C8	46:5:1326:A:C6	3.00	0.49
46:5:1888:A:N6	46:5:3873:G:O2'	2.46	0.49
9:I:191:ILE:HD12	9:I:200:ILE:HD11	1.93	0.49
73:XX:68:LYS:CG	73:XX:91:LEU:HD22	2.42	0.49
18:S:160:ARG:HB2	46:5:1921:C:O2	2.12	0.49
2:B:374:PHE:CE1	46:5:5050:C:H1'	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:41:PRO:HB3	12:M:70:GLN:HE21	1.77	0.49
16:Q:89:ASP:OD1	16:Q:91:ARG:N	2.45	0.49
49:9:1834:A:C2'	49:9:1834:A:N3	2.76	0.49
3:C:235:LEU:HD12	3:C:264:TYR:OH	2.13	0.49
10:J:151:ILE:HD11	10:J:156:ARG:CG	2.42	0.49
46:5:1411:C:H5'	46:5:1411(B):C:H2'	1.94	0.49
5:E:281:THR:OG1	46:5:4754:G:N7	2.46	0.49
49:9:1357:A:H5''	52:CC:112:VAL:HG11	1.93	0.49
49:9:1550:G:O2'	49:9:1558:C:O2	2.30	0.49
46:5:222:C:H2'	46:5:223:G:O4'	2.13	0.49
46:5:4551:U:H2'	46:5:4552:U:C6	2.48	0.49
49:9:183:G:C2'	49:9:183:G:N3	2.75	0.49
7:G:247:VAL:HG21	7:G:249:ARG:NH1	2.28	0.49
25:Z:75:TYR:CB	25:Z:80:LEU:HD21	2.43	0.49
46:5:2056:G:C8	46:5:2058:G:C8	3.01	0.49
46:5:5066:U:H2'	46:5:5067:U:C6	2.48	0.49
14:O:37:ARG:NH2	46:5:4761:G:OP2	2.46	0.49
19:T:57:TYR:CD1	19:T:76:VAL:HG21	2.48	0.49
46:5:1739:G:C6	46:5:1740:C:N4	2.81	0.48
46:5:2410:C:C2	46:5:2435:G:N2	2.81	0.48
46:5:3724:A:N6	46:5:3725:G:C6	2.81	0.48
15:P:64:ASN:O	15:P:80:GLN:NE2	2.45	0.48
46:5:275:C:H2'	46:5:276:C:C6	2.48	0.48
3:C:49:ARG:HD3	46:5:349:A:N7	2.27	0.48
46:5:4423:U:O2	46:5:4423:U:O4'	2.30	0.48
49:9:522:A:OP2	59:JJ:45:ARG:NH2	2.44	0.48
49:9:562:U:H2'	49:9:563:G:C8	2.47	0.48
46:5:1916:G:OP2	46:5:1917:A:OP2	2.31	0.48
46:5:384:A:C6	46:5:386:A:C6	3.01	0.48
1:A:77:ILE:HD12	1:A:115:CYS:SG	2.53	0.48
51:BB:134:LEU:HD22	51:BB:218:LEU:HD12	1.95	0.48
3:C:293:LEU:HD22	16:Q:34:PHE:CD2	2.48	0.48
3:C:76:ILE:HG22	3:C:77:PRO:CD	2.42	0.48
69:TT:39:LEU:HD21	69:TT:56:ARG:HE	1.78	0.48
22:W:6:CYS:HA	22:W:13:ILE:HD11	1.94	0.48
46:5:4966:A:C2	46:5:4967:A:C2	3.01	0.48
46:5:922:C:C2'	46:5:922(B):C:N3	2.76	0.48
15:P:10:ASN:N	15:P:10:ASN:OD1	2.47	0.48
46:5:1411:C:H1'	46:5:1411(C):C:C5	2.48	0.48
1:A:29:LEU:O	1:A:123:ARG:NH1	2.47	0.48
2:B:49:TYR:O	2:B:79:VAL:HA	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:12:ILE:HD12	8:H:13:PRO:O	2.13	0.48
20:U:82:TYR:CE2	20:U:86:LEU:HD11	2.49	0.48
46:5:2471:G:C6	46:5:2473:A:C6	3.02	0.48
1:A:4:VAL:HG12	1:A:8:GLN:HB2	1.95	0.48
50:AA:42:LYS:HG3	50:AA:48:ILE:HD11	1.96	0.48
9:I:96:VAL:HG22	9:I:125:THR:HG22	1.95	0.48
61:LL:71:ARG:C	61:LL:72:ILE:HD12	2.34	0.48
12:M:64:PHE:CE1	12:M:73:VAL:HG22	2.49	0.48
14:O:120:VAL:O	14:O:124:LEU:HD13	2.13	0.48
46:5:4489:G:N2	46:5:4592:C:OP1	2.47	0.48
49:9:183:G:O2'	49:9:184:G:O4'	2.31	0.48
3:C:210:ILE:HD12	3:C:210:ILE:N	2.29	0.48
6:F:82:VAL:HG22	18:S:62:VAL:HA	1.96	0.48
14:O:54:TYR:O	14:O:57:PHE:N	2.47	0.48
46:5:2816:G:C6	46:5:2817:C:C4	3.02	0.48
15:P:69:ARG:NH2	46:5:4568:A:N3	2.61	0.48
19:T:17:ARG:HD3	19:T:47:THR:HG23	1.96	0.48
46:5:100:C:O2	46:5:100:C:O4'	2.31	0.48
46:5:1748:U:C2	46:5:1783:C:C2	3.01	0.48
49:9:1336:C:H2'	49:9:1337:C:O4'	2.14	0.48
49:9:830:A:C2	49:9:844:U:O4	2.60	0.48
49:9:887:U:O4'	49:9:887:U:O2	2.32	0.48
53:DD:134:CYS:SG	53:DD:135:GLU:N	2.86	0.48
3:C:313:VAL:CG1	6:F:169:THR:HG21	2.44	0.48
48:8:125:C:O4'	48:8:125:C:O2	2.32	0.48
49:9:980:A:C2	49:9:981:A:C6	3.02	0.48
1:A:47:ASP:HA	1:A:84:THR:HG22	1.96	0.48
2:B:56:ILE:HG23	2:B:57:VAL:N	2.28	0.48
58:II:62:VAL:HG12	58:II:77:ARG:HA	1.96	0.48
18:S:13:VAL:HA	18:S:28:TYR:O	2.14	0.48
46:5:1835:G:O2'	46:5:1836:G:OP2	2.26	0.47
46:5:1929:A:N7	46:5:1932:A:H1'	2.28	0.47
46:5:3652:A:H2'	46:5:3653:A:C5	2.47	0.47
46:5:4389:C:H2'	46:5:4390:A:H8	1.78	0.47
46:5:979:C:C4	46:5:980:U:C4	3.02	0.47
4:D:22:ARG:NH1	4:D:28:THR:OG1	2.47	0.47
66:QQ:21:ALA:HB1	66:QQ:84:ILE:HG22	1.95	0.47
46:5:1804:A:N6	46:5:1833:G:O4'	2.46	0.47
46:5:2698:G:H2'	46:5:2699:C:O4'	2.14	0.47
46:5:1733:G:C4	46:5:4214:A:C2	3.02	0.47
49:9:1533:A:C2	49:9:1604:G:H4'	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:563:G:N7	59:JJ:172:ARG:NH2	2.63	0.47
46:5:1869:G:C4	46:5:3877:A:C2	3.02	0.47
49:9:146:G:O2'	49:9:147:A:O5'	2.30	0.47
3:C:33:ARG:HD2	3:C:36:ILE:HD12	1.95	0.47
8:H:106:GLN:N	8:H:106:GLN:OE1	2.47	0.47
19:T:143:THR:HG23	19:T:143:THR:O	2.14	0.47
49:9:29:G:H4'	73:XX:129:SER:HB2	1.95	0.47
46:5:2743:A:C2	46:5:2744:A:C4	3.02	0.47
46:5:922:C:P	46:5:922(B):C:C5'	3.01	0.47
57:HH:95:ILE:HD11	57:HH:133:LEU:HG	1.96	0.47
70:UU:70:CYS:SG	70:UU:72:GLU:N	2.87	0.47
2:B:234:ARG:NH2	46:5:4566:U:O3'	2.46	0.47
4:D:40:ASP:HB3	19:T:69:GLN:HA	1.96	0.47
1:A:131:GLY:HA3	46:5:3683:C:C4	2.50	0.47
49:9:1393:G:C6	49:9:1394:G:C6	3.02	0.47
49:9:1639:G:H2'	49:9:1640:A:C8	2.50	0.47
49:9:584:A:C6	49:9:585:C:C4	3.02	0.47
50:AA:104:THR:O	50:AA:107:THR:HG23	2.15	0.47
3:C:73:VAL:O	46:5:2350:U:C5	2.68	0.47
20:U:80:LYS:HD3	20:U:110:TYR:CE2	2.49	0.47
1:A:72:ARG:NH2	46:5:4084:G:N7	2.62	0.47
46:5:418:A:C2	46:5:419:A:C4	3.02	0.47
46:5:433:A:C2	46:5:3867:A:H4'	2.50	0.47
46:5:922:C:C5'	46:5:922(B):C:P	3.00	0.47
49:9:1364:U:O4'	49:9:1364:U:O2	2.31	0.47
49:9:1834:A:N3	49:9:1834:A:H2'	2.30	0.47
49:9:183:G:O2'	49:9:183:G:N3	2.47	0.47
14:O:44:SER:HB3	14:O:129:LEU:HD11	1.95	0.47
10:J:119:TYR:CD2	68:SS:12:ILE:HD12	2.50	0.47
25:Z:24:VAL:HG23	25:Z:130:PHE:CZ	2.50	0.47
25:Z:75:TYR:HB2	25:Z:80:LEU:HD21	1.97	0.47
46:5:1381:U:O2	46:5:1381:U:C5'	2.62	0.47
14:O:133:ARG:CZ	46:5:1928:C:C4	2.97	0.47
46:5:4635:A:C2	46:5:4664:A:C5	3.02	0.47
50:AA:122:LEU:HB3	50:AA:144:THR:HG23	1.97	0.47
2:B:252:ALA:HB3	46:5:4457:U:O2	2.15	0.47
58:II:61:ASP:OD2	58:II:62:VAL:HG13	2.14	0.47
14:O:84:VAL:O	14:O:85:ARG:C	2.53	0.47
16:Q:173:LYS:NZ	46:5:88:A:N7	2.63	0.47
49:9:1485:U:H2'	49:9:1486:A:O4'	2.15	0.47
49:9:1543:U:OP2	69:TT:62:ARG:NH1	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:DD:25:LEU:HD23	53:DD:50:ILE:HG12	1.97	0.47
55:FF:201:LYS:HA	55:FF:204:ARG:HG2	1.96	0.47
56:GG:52:ILE:HD11	56:GG:109:LEU:HD11	1.96	0.47
56:GG:52:ILE:O	56:GG:52:ILE:HG23	2.14	0.47
12:M:122:ILE:HG21	14:O:189:ILE:CG2	2.45	0.47
25:Z:24:VAL:HG23	25:Z:130:PHE:CE1	2.50	0.47
46:5:1374:G:C6	46:5:1375:C:C4	3.03	0.47
46:5:1411:C:H3'	46:5:1411(B):C:H3'	1.97	0.47
46:5:3652:A:H2'	46:5:3653:A:C4	2.50	0.47
46:5:3648:A:C4	46:5:3785:A:C6	3.03	0.47
49:9:1104:G:C2	49:9:1129:G:C2	3.03	0.47
49:9:1695:A:N1	49:9:1832:A:O2'	2.35	0.47
14:O:168:TYR:CE2	14:O:172:LYS:HD2	2.50	0.47
46:5:113:A:C2	46:5:278:G:C4	3.03	0.47
46:5:1468:C:H2'	46:5:1469:C:C6	2.50	0.47
46:5:2280:G:HO2'	46:5:2281:U:H6	1.61	0.47
46:5:2468:U:C5	46:5:2469:C:N4	2.83	0.47
46:5:4699:U:C2	46:5:4701:A:N6	2.83	0.47
1:A:209:HIS:CE1	1:A:235:VAL:HG11	2.50	0.47
3:C:208:CYS:HG	3:C:228:THR:HG1	1.59	0.47
9:I:135:ILE:HG22	9:I:136:MET:HG3	1.97	0.47
11:L:108:GLU:OE1	11:L:108:GLU:N	2.48	0.47
46:5:1609:U:H2'	46:5:1610:C:O4'	2.15	0.46
46:5:2408:U:O4'	46:5:2409:U:C5	2.67	0.46
49:9:92:A:C6	49:9:446:G:C6	3.03	0.46
49:9:845:G:H2'	49:9:846:G:O4'	2.15	0.46
49:9:943:U:OP2	51:BB:216:LYS:NZ	2.40	0.46
51:BB:139:CYS:SG	51:BB:140:VAL:N	2.87	0.46
6:F:93:ARG:NH2	6:F:96:GLY:O	2.48	0.46
8:H:118:LEU:HD21	8:H:177:ASP:HB2	1.97	0.46
70:UU:70:CYS:SG	70:UU:71:GLY:N	2.87	0.46
7:G:101:LYS:HB3	23:X:42:THR:HG23	1.98	0.46
8:H:12:ILE:HG21	8:H:18:ILE:HD13	1.97	0.46
46:5:2473:A:C2	46:5:2506:G:C2	3.03	0.46
46:5:4977:A:H2'	46:5:4978:G:O4'	2.15	0.46
46:5:51:A:N3	46:5:1528:U:O2'	2.46	0.46
3:C:74:ALA:HB2	46:5:2351:C:O5'	2.15	0.46
54:EE:55:ALA:HB1	54:EE:60:GLU:HB2	1.96	0.46
56:GG:2:LYS:HB3	56:GG:15:LEU:HD21	1.97	0.46
9:I:91:LEU:HD11	9:I:135:ILE:HG12	1.98	0.46
49:9:520:A:H5''	59:JJ:12:THR:HG23	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:9:GLU:HG3	18:S:33:PHE:CE1	2.51	0.46
46:5:1751:A:C2	46:5:1780:A:C2	3.02	0.46
46:5:4700:A:C4	46:5:4701:A:N7	2.82	0.46
49:9:415:A:H2'	49:9:416:U:O4'	2.14	0.46
5:E:136:PHE:HA	5:E:139:HIS:CE1	2.51	0.46
56:GG:5:ILE:CD1	56:GG:16:ILE:HD13	2.43	0.46
14:O:133:ARG:CZ	46:5:1928:C:N4	2.79	0.46
46:5:4522:G:O2'	46:5:4525:C:OP2	2.33	0.46
46:5:731:G:C6	46:5:932:A:C4	3.04	0.46
49:9:1137:U:C4	49:9:1148:A:N1	2.84	0.46
6:F:153:ILE:O	6:F:157:GLY:HA3	2.15	0.46
61:LL:135:SER:OG	61:LL:136:LYS:N	2.48	0.46
65:PP:81:ARG:NH1	65:PP:120:SER:OG	2.49	0.46
46:5:1308:C:H2'	46:5:1309:C:C6	2.50	0.46
19:T:54:HIS:CD2	46:5:4301:U:H4'	2.51	0.46
46:5:4508:C:N3	46:5:4512:U:C5	2.84	0.46
49:9:1743:G:C6	49:9:1744:G:N1	2.84	0.46
6:F:202:GLU:OE1	6:F:202:GLU:N	2.48	0.46
11:L:74:ARG:HB3	11:L:99:ASP:OD2	2.16	0.46
14:O:152:VAL:HG12	14:O:156:LEU:HD12	1.97	0.46
17:R:42:ARG:HA	17:R:45:ILE:HD12	1.97	0.46
74:YY:62:THR:HA	74:YY:69:THR:HG22	1.98	0.46
49:9:1303:C:O2	49:9:1303:C:O4'	2.32	0.46
49:9:1349:G:H2'	49:9:1350:U:C6	2.50	0.46
49:9:1401:A:C2	49:9:1402:A:C6	3.04	0.46
21:V:39:ILE:HG23	21:V:61:VAL:CG2	2.46	0.46
56:GG:16:ILE:N	56:GG:16:ILE:HD12	2.31	0.46
57:HH:62:ILE:HG21	57:HH:94:PHE:CE1	2.51	0.46
5:E:273:TYR:CE1	12:M:107:PHE:HA	2.50	0.46
13:N:184:ILE:O	13:N:194:ARG:NH1	2.49	0.46
24:Y:52:ASP:HB2	24:Y:110:LYS:HG3	1.97	0.46
74:YY:29:HIS:CE1	74:YY:34:THR:HA	2.51	0.46
46:5:2763:U:O2	46:5:2763:U:O4'	2.33	0.46
49:9:389:A:H2'	49:9:390:C:C6	2.51	0.46
3:C:313:VAL:HG11	6:F:169:THR:HG21	1.98	0.46
56:GG:59:GLN:OE1	56:GG:72:ARG:NH1	2.48	0.46
12:M:34:ASN:OD1	12:M:34:ASN:N	2.48	0.46
18:S:9:GLU:CG	18:S:33:PHE:CE1	2.99	0.46
46:5:1358:G:H4'	46:5:1359:G:OP1	2.15	0.45
46:5:1523:A:C8	46:5:1652:U:O4	2.69	0.45
46:5:2270:G:C6	46:5:2271:C:C4	3.04	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:961:G:C6	46:5:962:C:C4	3.04	0.45
47:7:113:G:H2'	47:7:114:U:C6	2.52	0.45
49:9:1438:A:H2'	49:9:1439:A:C8	2.50	0.45
1:A:104:VAL:CG1	1:A:146:THR:HG21	2.46	0.45
4:D:50:ARG:NH2	4:D:72:ASP:OD2	2.48	0.45
53:DD:162:ASP:N	53:DD:163:PRO:CD	2.79	0.45
5:E:184:LEU:HD11	5:E:264:ILE:CD1	2.46	0.45
12:M:122:ILE:HG21	14:O:189:ILE:HG23	1.98	0.45
72:WW:55:ASP:O	72:WW:57:ARG:N	2.49	0.45
46:5:3648:A:H1'	46:5:3785:A:N6	2.31	0.45
1:A:181:LYS:HB2	46:5:1577:G:C5	2.51	0.45
12:M:23:LYS:CE	46:5:935:A:H3'	2.46	0.45
19:T:108:ARG:HH12	46:5:1836:G:HO2'	1.63	0.45
72:WW:105:THR:HB	72:WW:110:ILE:HG12	1.97	0.45
46:5:1846:G:H2'	46:5:1847:C:H6	1.82	0.45
46:5:4510:A:O2'	46:5:4511:A:O4'	2.33	0.45
49:9:1144:A:H2'	49:9:1145:A:C8	2.51	0.45
49:9:1718:G:C6	49:9:1814:G:C6	3.05	0.45
4:D:26:GLY:O	10:J:146:ARG:O	2.35	0.45
46:5:5001:U:H2'	46:5:5002:U:O4'	2.15	0.45
2:B:86:VAL:HG12	2:B:201:LEU:HD12	1.99	0.45
3:C:224:ILE:CG2	3:C:227:ILE:HD13	2.47	0.45
55:FF:92:ILE:HD13	55:FF:169:ILE:HG21	1.98	0.45
13:N:119:TYR:CZ	13:N:131:GLU:HB2	2.52	0.45
21:V:26:ILE:HG22	21:V:101:ASN:HB3	1.98	0.45
46:5:2352:U:C2	46:5:2353:U:C5	3.04	0.45
46:5:2412:A:C2	46:5:2433:G:C2	3.05	0.45
19:T:2:THR:HG23	46:5:4220:A:OP2	2.17	0.45
46:5:4528:G:C2	46:5:4529:G:C8	3.05	0.45
1:A:208:GLU:HG2	46:5:1629:G:H1	1.82	0.45
6:F:106:LYS:O	6:F:109:GLN:HG2	2.17	0.45
63:NN:63:VAL:HG21	63:NN:71:ILE:HD11	1.99	0.45
14:O:21:ALA:HA	14:O:87:MET:SD	2.57	0.45
46:5:4699:U:C4	46:5:4702:G:C6	3.05	0.45
46:5:5008:C:H2'	46:5:5009:G:O4'	2.17	0.45
49:9:1345:G:N7	49:9:1371:U:H2'	2.31	0.45
49:9:1489:A:H4'	49:9:1490:G:OP2	2.17	0.45
50:AA:134:LEU:HD21	50:AA:144:THR:HG21	1.98	0.45
2:B:95:THR:HG21	2:B:100:ARG:HB2	1.99	0.45
9:I:135:ILE:HG21	9:I:159:PHE:CE2	2.51	0.45
49:9:291:G:N3	61:LL:42:LEU:HD13	2.32	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:17:PHE:CE2	12:M:54:CYS:HA	2.51	0.45
49:9:1286:G:C6	62:MM:34:GLY:HA3	2.52	0.45
65:PP:56:LEU:HD13	65:PP:78:THR:HG21	1.99	0.45
16:Q:18:PRO:HG3	16:Q:29:VAL:HG21	1.99	0.45
46:5:4564:A:C5	46:5:4565:C:C4	3.04	0.45
46:5:922(B):C:O2'	46:5:923:C:O5'	2.33	0.45
49:9:1597:C:H4'	49:9:1603:G:O6	2.16	0.45
55:FF:119:SER:OG	55:FF:189:ALA:HB1	2.17	0.45
3:C:292:ILE:HG23	16:Q:128:LEU:HD21	1.98	0.45
46:5:1736:A:C2	46:5:1794:A:C4	3.05	0.45
46:5:355:A:C6	46:5:356:G:C5	3.05	0.45
46:5:3675:G:C2	46:5:3676:G:C8	3.04	0.45
46:5:922(B):C:H1'	46:5:923:C:O5'	2.16	0.45
48:8:112:G:C6	48:8:113:C:C4	3.05	0.45
46:5:422:C:C2	48:8:13:G:C2	3.05	0.45
48:8:141:C:H2'	48:8:142:U:C6	2.52	0.45
7:G:200:VAL:HG13	7:G:232:VAL:HG21	1.98	0.45
8:H:52:LYS:NZ	48:8:62:A:OP1	160.72	0.45
15:P:131:ARG:CD	15:P:137:ASN:ND2	2.80	0.45
46:5:1532:G:C2	46:5:1643:A:C2	3.05	0.45
46:5:1655:C:O2'	46:5:4391:G:O2'	2.26	0.45
46:5:3777:G:N2	46:5:3815:G:H2'	2.31	0.45
13:N:108:ARG:NH2	46:5:54:G:O2'	2.41	0.45
49:9:1260:A:C6	49:9:1619:A:C6	3.05	0.45
51:BB:69:VAL:CG1	51:BB:74:LEU:HD13	2.46	0.45
52:CC:124:PHE:O	52:CC:143:CYS:HA	2.17	0.45
49:9:92:A:O4'	54:EE:3:ARG:NH1	2.50	0.45
11:L:56:ARG:O	11:L:116:ARG:NH2	2.50	0.45
13:N:172:ARG:NH1	46:5:62:A:OP1	2.50	0.45
13:N:184:ILE:HG23	13:N:194:ARG:HH12	1.81	0.45
63:NN:6:ALA:HB1	63:NN:7:PRO:HD2	1.99	0.45
46:5:2088:A:O2'	46:5:2089:G:OP2	2.33	0.45
46:5:2820:C:H2'	46:5:2821:U:H6	1.82	0.45
2:B:252:ALA:HB1	46:5:4524:G:C2	2.52	0.45
51:BB:79:VAL:HG21	51:BB:81:PHE:CZ	2.52	0.45
3:C:121:ARG:O	3:C:122:TYR:C	2.56	0.45
46:5:1634:A:C6	46:5:1635:C:C4	3.05	0.44
46:5:235:A:C2	46:5:238:C:C5	3.05	0.44
49:9:1445:U:O4	49:9:1446:A:N6	2.49	0.44
49:9:604:A:C6	49:9:605:A:N1	2.85	0.44
63:NN:60:VAL:HG23	63:NN:66:VAL:HG21	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:227:VAL:HA	18:S:39:VAL:HG12	1.98	0.44
46:5:1626:G:N2	46:5:1627:G:H1'	2.32	0.44
46:5:26:C:O2'	46:5:338:A:N3	2.48	0.44
49:9:1046:U:C4	49:9:1047:C:C4	3.05	0.44
49:9:443:U:O4	49:9:444:G:C6	2.71	0.44
4:D:78:ALA:HB1	4:D:104:LEU:HD13	2.00	0.44
53:DD:48:ILE:CG2	53:DD:86:LEU:HD12	2.48	0.44
57:HH:44:ASN:N	57:HH:68:GLN:OE1	2.51	0.44
60:KK:93:THR:HG23	60:KK:94:LEU:HD12	1.99	0.44
14:O:51:LYS:HE2	14:O:55:LEU:HD11	1.99	0.44
21:V:98:PHE:CZ	21:V:122:ALA:HB2	2.53	0.44
73:XX:46:HIS:HB3	73:XX:101:LEU:HD11	1.98	0.44
46:5:1318:C:H2'	46:5:1319:U:O4'	2.17	0.44
46:5:1525:A:C2	46:5:1651:G:N2	2.86	0.44
46:5:2809:G:O2'	46:5:4644:G:OP1	2.25	0.44
52:CC:66:LEU:HD12	52:CC:93:ILE:HD13	1.99	0.44
54:EE:80:ILE:HG13	54:EE:81:THR:HG23	1.98	0.44
14:O:27:VAL:HG12	14:O:98:ALA:HB1	1.99	0.44
15:P:29:THR:CG2	15:P:146:ILE:HD11	2.47	0.44
65:PP:83:MET:HB3	65:PP:116:LEU:HD12	1.99	0.44
46:5:2382:A:N1	46:5:2829:U:O2'	2.45	0.44
46:5:2443:G:N2	46:5:2780:C:C2	2.86	0.44
46:5:4515:G:C2	46:5:4516:G:C8	3.05	0.44
46:5:4583:C:O2	46:5:4719:G:O6	2.36	0.44
46:5:922:C:C3'	46:5:922:C:C6	2.99	0.44
49:9:1162:C:H2'	49:9:1163:C:O4'	2.17	0.44
49:9:1276:A:N6	49:9:1321:G:O2'	2.51	0.44
3:C:211:TYR:CD1	3:C:211:TYR:C	2.90	0.44
57:HH:133:LEU:HD21	57:HH:176:VAL:CG1	2.48	0.44
11:L:57:PRO:HG3	11:L:75:GLY:O	2.18	0.44
49:9:1614:A:OP2	65:PP:42:ARG:NH1	2.51	0.44
18:S:34:ALA:HB1	18:S:39:VAL:HG23	1.99	0.44
46:5:1622:U:O2'	46:5:1627:G:H4'	2.18	0.44
46:5:1786:A:H2'	46:5:1789:C:C5	2.52	0.44
46:5:20:U:O2'	48:8:37:A:N6	2.49	0.44
46:5:481(A):C:O4'	46:5:481(A):C:O2	2.35	0.44
46:5:686:A:N3	46:5:686:A:H2'	2.33	0.44
48:8:142:U:H2'	48:8:143:G:O4'	2.18	0.44
49:9:356:C:O2	49:9:356:C:H2'	2.18	0.44
49:9:362:C:C2	49:9:403:G:C2	3.05	0.44
3:C:133:LEU:HD12	3:C:133:LEU:N	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:144:CYS:SG	4:D:171:LEU:HD23	2.57	0.44
57:HH:130:LEU:HD23	57:HH:139:ILE:HD13	1.98	0.44
11:L:55:ILE:HG22	11:L:154:VAL:HG13	2.00	0.44
49:9:1546:G:C5'	66:QQ:18:THR:HG21	2.48	0.44
46:5:3798:U:C2	46:5:3801:U:C5	3.06	0.44
9:I:86:HIS:HB3	9:I:139:ARG:HG2	1.99	0.44
58:II:36:THR:HG21	58:II:179:PRO:HB2	1.99	0.44
21:V:50:ASN:O	21:V:51:ARG:HB2	2.17	0.44
46:5:3689:G:C5	46:5:3690:U:C5	3.06	0.44
46:5:4759:C:O2	46:5:4759:C:O4'	2.35	0.44
4:D:30:TYR:OH	47:7:8:G:OP2	2.20	0.44
49:9:1568:C:OP1	69:TT:96:SER:OG	2.30	0.44
1:A:117:GLU:HB2	1:A:162:ASN:HB2	2.00	0.44
50:AA:134:LEU:CD2	50:AA:144:THR:HG21	2.48	0.44
3:C:106:LYS:HG2	3:C:108:TRP:CZ2	2.52	0.44
52:CC:179:THR:OG1	52:CC:180:VAL:N	2.51	0.44
70:UU:56:MET:SD	70:UU:88:LEU:HD21	2.58	0.44
23:X:80:PRO:HA	23:X:98:PHE:HA	1.99	0.44
46:5:1296:G:C2	46:5:1297:U:C2	3.06	0.44
46:5:2514:G:C2	46:5:2515:G:C8	3.06	0.44
15:P:19:GLY:HA2	46:5:2874:U:O2	93.76	0.44
46:5:4303:C:O2'	46:5:4304:A:H2'	2.18	0.44
46:5:4348:A:C2	46:5:4350:C:C2	3.05	0.44
46:5:4371:G:O2'	46:5:4372:U:OP2	2.28	0.44
46:5:4564:A:H2'	46:5:4565:C:C6	2.53	0.44
46:5:4880:C:O4'	46:5:4880:C:O2	2.36	0.44
46:5:752:G:C6	46:5:753:C:C4	3.05	0.44
10:J:63:ARG:NH2	48:8:58:G:N7	130.18	0.44
49:9:1344:A:H4'	49:9:1345:G:H5'	1.99	0.44
49:9:1843:G:H2'	49:9:1844:U:O4'	2.18	0.44
2:B:79:VAL:HB	2:B:331:VAL:HG23	2.00	0.44
56:GG:57:ASP:OD1	56:GG:58:LYS:N	2.50	0.44
12:M:23:LYS:HE2	46:5:935:A:H3'	2.00	0.44
46:5:1876:U:H2'	46:5:1877:G:O4'	2.18	0.44
46:5:2002:A:N3	46:5:2002:A:H2'	2.33	0.44
46:5:384:A:C2	46:5:386:A:C4	3.06	0.44
46:5:5015:G:C2	46:5:5033:G:C2	3.05	0.44
49:9:1452:A:H4'	49:9:1453:C:O4'	2.18	0.44
49:9:1653:U:H2'	49:9:1654:G:C8	2.53	0.44
49:9:1692:U:H2'	49:9:1693:G:C8	2.52	0.44
46:5:1576:G:HO2'	46:5:1578:U:H6	1.62	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:1846:G:H2'	46:5:1847:C:C6	2.53	0.43
46:5:2079:G:N2	46:5:2278:G:C4	2.85	0.43
46:5:914:U:H6	46:5:914:U:H3'	1.83	0.43
49:9:1045:U:C4	49:9:1046:U:C4	3.06	0.43
49:9:1685:U:C4	49:9:1686:G:N7	2.86	0.43
49:9:1719:A:N6	49:9:1814:G:O2'	2.50	0.43
49:9:1835:A:HO2'	49:9:1836:G:P	2.41	0.43
3:C:323:ARG:NE	46:5:976:G:H21	2.16	0.43
54:EE:125:LYS:HB3	54:EE:142:HIS:HB3	2.00	0.43
9:I:191:ILE:HD11	9:I:212:LEU:HD11	1.99	0.43
14:O:36:VAL:HG23	14:O:105:PHE:HB2	2.00	0.43
46:5:1646:A:C6	46:5:1647:U:C4	3.06	0.43
49:9:1657:G:C6	49:9:1658:G:C5	3.06	0.43
49:9:398:A:H5'	49:9:398:A:C8	2.54	0.43
3:C:237:ILE:HD12	3:C:237:ILE:H	1.83	0.43
3:C:78:ARG:HB3	3:C:88:GLY:HA2	2.00	0.43
55:FF:96:ALA:CB	55:FF:173:LEU:HD12	2.48	0.43
9:I:189:ARG:O	9:I:200:ILE:N	2.50	0.43
24:Y:42:TYR:CG	24:Y:119:LEU:HD23	2.53	0.43
25:Z:75:TYR:CG	25:Z:80:LEU:HD21	2.53	0.43
46:5:3829:G:N3	46:5:3829:G:H2'	2.34	0.43
46:5:2818:C:OP1	46:5:4655:A:H4'	2.18	0.43
49:9:1221:G:H2'	49:9:1222:G:H8	1.83	0.43
2:B:54:THR:OG1	2:B:55:HIS:N	2.51	0.43
52:CC:74:LYS:HG2	52:CC:269:PHE:CE1	2.53	0.43
4:D:146:LEU:HD11	4:D:159:VAL:CG1	2.47	0.43
46:5:1676:C:N4	46:5:4378:A:C8	2.86	0.43
46:5:4928:C:O2	46:5:4928:C:O4'	2.36	0.43
49:9:1649:U:C5	49:9:1674:G:N2	2.86	0.43
49:9:507:G:O2'	49:9:508:A:OP1	2.30	0.43
50:AA:131:HIS:CG	50:AA:132:GLN:N	2.86	0.43
51:BB:136:ARG:HB2	51:BB:218:LEU:HD11	2.00	0.43
68:SS:65:GLU:O	68:SS:69:THR:HG23	2.17	0.43
72:WW:33:VAL:HG13	72:WW:110:ILE:HD13	2.00	0.43
25:Z:76:ASN:HB3	25:Z:78:ASN:OD1	2.19	0.43
9:I:22:PHE:CZ	46:5:1788:A:H2'	2.54	0.43
46:5:77:U:O2	46:5:78:U:O4'	2.37	0.43
49:9:1466:G:P	67:RR:10:LYS:HZ1	2.42	0.43
49:9:1745:A:N6	49:9:1789:G:O2'	2.51	0.43
49:9:445:A:H2'	49:9:446:G:C8	2.54	0.43
3:C:210:ILE:HG21	3:C:252:TRP:CZ3	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:70:GLY:O	3:C:72:ALA:N	2.50	0.43
53:DD:142:LEU:HD22	53:DD:150:MET:HG2	2.00	0.43
54:EE:11:ARG:HH22	54:EE:24:THR:HG1	1.67	0.43
13:N:181:HIS:O	13:N:184:ILE:HG22	2.18	0.43
67:RR:119:VAL:O	67:RR:119:VAL:HG13	2.19	0.43
46:5:4459:U:H2'	46:5:4460:U:C6	2.53	0.43
49:9:1164:G:C6	49:9:1165:G:O6	2.71	0.43
52:CC:88:ILE:HG21	52:CC:94:ILE:CD1	2.49	0.43
6:F:88:LEU:HD11	6:F:121:PHE:HD1	1.84	0.43
74:YY:20:ARG:NH2	74:YY:22:GLN:OE1	2.50	0.43
46:5:2517:A:N3	46:5:2539:C:O2'	2.50	0.43
46:5:384:A:N1	46:5:386:A:C4	2.87	0.43
46:5:4371:G:C5	46:5:4372:U:C4	3.07	0.43
46:5:4398:C:C4	46:5:4399:U:C5	3.07	0.43
49:9:1536:G:H2'	49:9:1537:A:C8	2.53	0.43
49:9:4:C:O2'	59:JJ:18:ARG:NH1	2.52	0.43
49:9:987:A:N6	51:BB:122:GLU:OE1	2.43	0.43
3:C:144:ILE:HD13	3:C:147:VAL:HB	2.00	0.43
55:FF:73:THR:O	55:FF:89:THR:HG21	2.19	0.43
21:V:82:ILE:HD12	21:V:104:VAL:HG13	2.00	0.43
24:Y:50:ARG:NH2	48:8:85:U:O4	2.52	0.43
46:5:1912:G:C6	46:5:1913:C:N4	2.87	0.43
46:5:1990:A:H3'	46:5:1991:A:H5''	2.01	0.43
46:5:2307:A:C8	46:5:2332:A:C6	3.06	0.43
46:5:1633:G:OP2	46:5:4535:A:OP1	2.36	0.43
46:5:492:U:O2'	46:5:493:G:P	2.76	0.43
49:9:1522:A:C2	65:PP:128:HIS:CE1	3.06	0.43
49:9:1444:U:O2'	49:9:1580:A:N1	2.52	0.43
49:9:26:U:H2'	49:9:27:A:O4'	2.19	0.43
49:9:344:U:H2'	49:9:345:U:C6	2.54	0.43
49:9:933:G:H1'	49:9:1001:A:O4'	2.19	0.43
3:C:154:VAL:HG11	3:C:158:VAL:HG21	2.00	0.43
3:C:297:GLU:OE2	3:C:297:GLU:N	2.45	0.43
8:H:40:HIS:ND1	46:5:4701:A:O2'	2.29	0.43
3:C:323:ARG:NH1	46:5:1281:G:C8	2.86	0.43
19:T:9:ARG:NH2	46:5:4218:U:OP2	2.50	0.43
46:5:492:U:HO2'	46:5:493:G:P	2.41	0.43
49:9:1400:U:C4	49:9:1401:A:N7	2.87	0.43
49:9:584:A:N6	49:9:585:C:N4	2.67	0.43
16:Q:188:ASN:N	16:Q:188:ASN:HD22	2.16	0.43
18:S:3:ALA:O	18:S:111:ARG:NH1	2.45	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:973:C:C5	49:9:974:C:C5	3.07	0.43
2:B:285:TYR:CE1	2:B:334:LYS:HB2	2.54	0.43
9:I:38:ARG:HG2	9:I:41:ALA:HB2	2.00	0.43
61:LL:78:THR:HG22	61:LL:87:VAL:O	2.18	0.43
13:N:159:ARG:NH2	13:N:165:THR:HG22	2.34	0.43
15:P:41:ILE:HD12	15:P:150:LEU:CD1	2.49	0.43
16:Q:43:PHE:CD2	16:Q:133:GLY:HA3	2.54	0.43
69:TT:28:LEU:HD12	69:TT:54:TYR:CE1	2.54	0.43
46:5:1667:A:N1	46:5:2281:U:OP2	2.51	0.42
46:5:1802:A:O2'	46:5:1837:A:OP1	2.37	0.42
46:5:2097:A:OP1	46:5:2107:A:N6	2.52	0.42
46:5:4352:U:C2	46:5:4363:A:C2	3.07	0.42
49:9:612:U:H2'	49:9:613:G:O4'	2.19	0.42
57:HH:177:TYR:CD2	57:HH:185:VAL:HG21	2.54	0.42
10:J:151:ILE:HD12	10:J:155:HIS:HB3	2.01	0.42
3:C:112:HIS:HB2	13:N:202:ARG:O	2.19	0.42
14:O:15:LEU:HA	14:O:42:ASN:O	2.19	0.42
14:O:185:VAL:HG12	14:O:185:VAL:O	2.19	0.42
14:O:20:ALA:HB1	14:O:84:VAL:HG22	2.00	0.42
74:YY:110:ARG:NH2	74:YY:114:MET:SD	2.92	0.42
46:5:115:C:O2	46:5:115:C:O4'	2.37	0.42
46:5:1667:A:N1	46:5:2280:G:H2'	2.34	0.42
46:5:2410:C:C6	46:5:2410:C:O5'	2.72	0.42
7:G:98:ILE:HG21	46:5:4125:C:H4'	2.00	0.42
50:AA:25:LEU:O	50:AA:164:ASN:HB2	2.19	0.42
2:B:218:ASP:N	2:B:218:ASP:OD1	2.51	0.42
52:CC:233:LEU:O	52:CC:233:LEU:HD12	2.18	0.42
61:LL:126:VAL:HG22	61:LL:142:VAL:HG13	2.02	0.42
46:5:1328:G:O2'	46:5:2349:A:OP1	2.32	0.42
46:5:3620:G:OP1	46:5:3622:C:N4	2.50	0.42
46:5:388:A:H1'	46:5:403:G:N2	2.33	0.42
49:9:1438:A:C2	49:9:1439:A:C6	3.06	0.42
49:9:942:G:H2'	49:9:943:U:C6	2.54	0.42
3:C:67:TRP:HE3	3:C:73:VAL:HG21	1.83	0.42
5:E:167:PHE:CE1	5:E:176:LEU:HD22	2.55	0.42
54:EE:126:VAL:HG23	54:EE:156:VAL:O	2.19	0.42
8:H:111:LEU:HD12	8:H:127:ARG:NH2	2.34	0.42
58:II:174:CYS:HB3	58:II:188:TYR:CE1	2.54	0.42
49:9:1610:G:OP1	68:SS:121:ARG:NE	2.53	0.42
20:U:84:LYS:HA	20:U:87:THR:HG22	2.01	0.42
46:5:1411:C:C3'	46:5:1411(C):C:O5'	2.67	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:4187:G:H2'	46:5:4188:U:O4'	2.18	0.42
46:5:4303:C:O2	46:5:4303:C:O5'	2.36	0.42
46:5:4631:G:H2'	46:5:4632:U:O4'	2.20	0.42
46:5:4690:G:O6	46:5:4698:C:H5''	2.19	0.42
46:5:922:C:P	46:5:922(B):C:P	3.17	0.42
49:9:1611:G:N2	49:9:1629:C:C2	2.88	0.42
2:B:95:THR:C	14:O:152:VAL:HG11	2.39	0.42
6:F:92:ILE:HA	6:F:118:ASN:O	2.19	0.42
49:9:821:G:C5	59:JJ:150:ARG:HD2	2.54	0.42
21:V:28:CYS:SG	21:V:30:ASP:OD1	2.78	0.42
46:5:2085:G:N2	46:5:2273:G:C4	2.88	0.42
46:5:2787:A:C2'	46:5:2787:A:N3	2.81	0.42
46:5:498:C:O2	46:5:498:C:O4'	2.37	0.42
49:9:1588:A:H2'	49:9:1589:A:C8	2.55	0.42
6:F:92:ILE:HD13	6:F:242:LEU:HD22	2.02	0.42
56:GG:132:ARG:HB3	56:GG:133:LEU:HD12	2.01	0.42
14:O:44:SER:HB3	14:O:129:LEU:HD21	2.01	0.42
64:OO:67:ASP:OD1	64:OO:67:ASP:N	2.52	0.42
45:2:18:U:O4'	45:2:58:A:C2	2.73	0.42
46:5:1411:C:C5	46:5:1411(B):C:C5	3.07	0.42
46:5:1411:C:C5'	46:5:1411(B):C:C2'	2.97	0.42
46:5:1411:C:H4'	46:5:1411(C):C:C1'	2.48	0.42
46:5:1929:A:N6	46:5:2054:U:N3	2.62	0.42
46:5:3896:C:O2	46:5:4564:A:N1	2.53	0.42
46:5:750:U:H2'	46:5:751:G:O4'	2.19	0.42
49:9:816:A:C6	49:9:817:G:C4	3.08	0.42
52:CC:180:VAL:HG11	52:CC:184:VAL:HG22	2.01	0.42
7:G:210:ILE:HG12	7:G:254:THR:HG22	2.01	0.42
8:H:43:VAL:HA	46:5:4764:A:C2	2.55	0.42
12:M:56:GLN:HB2	46:5:4870:G:C5	2.55	0.42
13:N:35:ALA:HB2	13:N:65:ARG:CZ	2.50	0.42
65:PP:43:ARG:NH1	65:PP:47:ARG:HD2	2.35	0.42
20:U:80:LYS:HE2	20:U:110:TYR:CZ	2.54	0.42
45:3:75:C:H2'	45:3:76:A:H4'	2.00	0.42
46:5:1205:G:C6	46:5:1206:C:C4	3.08	0.42
46:5:1411:C:O2'	46:5:1411(C):C:C6	2.60	0.42
46:5:1632:A:H2'	46:5:1632:A:N3	2.35	0.42
46:5:749:G:C2	46:5:912:G:C4	3.08	0.42
49:9:1358:U:H2'	49:9:1359:U:O4'	2.20	0.42
49:9:1834:A:H2	49:9:1837:G:N1	2.18	0.42
1:A:207:VAL:HG12	46:5:3919:C:H5''	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:EE:87:MET:N	54:EE:101:LEU:O	2.49	0.42
7:G:210:ILE:HG23	7:G:220:VAL:HG11	2.01	0.42
63:NN:105:ASN:N	63:NN:105:ASN:HD22	2.17	0.42
25:Z:73:LYS:HG2	25:Z:75:TYR:CZ	2.54	0.42
46:5:1664:U:H2'	46:5:1665:C:H6	1.85	0.42
46:5:25:A:C8	46:5:341:G:C8	3.08	0.42
46:5:3874:G:C6	46:5:3875:G:C5	3.08	0.42
46:5:4220:A:H2'	46:5:4222:G:O5'	2.19	0.42
46:5:711:A:H2'	46:5:712:C:C6	2.54	0.42
49:9:144:U:OP2	56:GG:178:ARG:HG2	2.19	0.42
49:9:15:U:H2'	49:9:16:G:O4'	2.20	0.42
49:9:945:U:H2'	49:9:946:U:C6	2.55	0.42
3:C:108:TRP:O	13:N:204:ARG:NH2	2.52	0.42
3:C:49:ARG:NH1	3:C:111:TRP:O	2.47	0.42
5:E:261:LEU:N	5:E:262:PRO:HD2	2.35	0.42
7:G:131:PRO:HA	7:G:134:ASN:HB3	2.02	0.42
10:J:105:PHE:O	10:J:132:VAL:N	2.53	0.42
49:9:521:A:OP1	59:JJ:45:ARG:NH1	2.53	0.42
21:V:20:LEU:HD12	21:V:81:VAL:HG21	2.01	0.42
57:HH:144:ILE:HD12	72:WW:52:ILE:HD11	2.01	0.42
74:YY:9:THR:HG22	74:YY:23:MET:HG3	2.00	0.42
45:3:71:G:N3	46:5:3715:U:O2'	2.49	0.42
46:5:1677:U:H4'	46:5:1680:G:N1	2.35	0.42
46:5:2265:G:O2'	46:5:2266:C:OP1	2.27	0.42
46:5:2408:U:C1'	46:5:2409:U:C5	3.02	0.42
46:5:382:G:N2	46:5:384:A:H3'	2.34	0.42
46:5:4664:A:H2'	46:5:4665:A:O4'	2.20	0.42
49:9:1142:G:N2	49:9:1145:A:OP2	2.48	0.42
49:9:963:A:C2	49:9:964:A:C4	3.08	0.42
6:F:175:ALA:HB2	6:F:184:ILE:HA	2.02	0.42
57:HH:145:ARG:HA	72:WW:51:GLU:HB2	2.02	0.42
59:JJ:35:TYR:CD2	59:JJ:106:LEU:HD23	2.55	0.42
13:N:118:SER:HB3	13:N:132:VAL:HG22	2.02	0.42
16:Q:106:THR:HG21	46:5:1353:G:H3'	2.01	0.42
24:Y:98:GLY:O	24:Y:99:ILE:HD13	2.20	0.42
46:5:106:A:H1'	46:5:336:A:N3	2.35	0.42
46:5:2693:G:C6	46:5:2694:G:N1	2.88	0.42
46:5:3867:A:H2'	46:5:3868:G:O4'	2.20	0.42
46:5:4439:U:H2'	46:5:4440:G:O4'	2.20	0.42
46:5:4524:G:OP2	46:5:4524:G:H4'	2.19	0.42
49:9:1185:C:C4	49:9:1186:U:C5	3.08	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:ILE:HG23	1:A:133:TYR:CD2	2.55	0.42
3:C:274:LYS:O	3:C:275:SER:C	2.58	0.42
56:GG:98:ARG:HG3	56:GG:99:GLY:N	2.35	0.42
13:N:65:ARG:HD3	13:N:127:TYR:CD1	2.54	0.42
7:G:219:LEU:HD23	13:N:7:ILE:HD11	2.02	0.42
16:Q:81:VAL:HG22	16:Q:101:CYS:SG	2.60	0.42
66:QQ:85:ARG:HG2	66:QQ:119:LEU:HD13	2.02	0.42
72:WW:30:CYS:SG	72:WW:61:ILE:HD11	2.60	0.42
24:Y:73:VAL:HG12	24:Y:75:ARG:HG2	2.01	0.42
46:5:1381:U:O4'	46:5:1381:U:O2	2.38	0.41
46:5:2839:U:C4	46:5:2840:A:N7	2.88	0.41
46:5:355:A:C4	46:5:356:G:C8	3.08	0.41
46:5:4944:C:H3'	46:5:4945:G:C5'	2.50	0.41
46:5:4995:U:C4	46:5:4996:C:C5	3.08	0.41
46:5:976:G:C2	46:5:977:C:C5	3.08	0.41
49:9:1045:U:H2'	49:9:1046:U:O4'	2.20	0.41
49:9:1217:A:H2'	49:9:1218:C:C6	2.54	0.41
51:BB:30:TRP:CH2	51:BB:48:LEU:HD23	2.55	0.41
3:C:95:MET:N	3:C:95:MET:SD	2.93	0.41
6:F:178:LEU:HD11	6:F:206:PHE:HB2	2.02	0.41
55:FF:72:LEU:HD11	55:FF:154:LEU:HD11	2.02	0.41
60:KK:12:TYR:CZ	60:KK:52:LEU:HD21	2.54	0.41
17:R:99:MET:SD	17:R:99:MET:N	2.93	0.41
46:5:1576:G:C2	46:5:1578:U:C2	3.08	0.41
46:5:1612:G:C2'	46:5:1612:G:N3	2.82	0.41
46:5:2857:A:N6	46:5:2858:A:C6	2.88	0.41
49:9:1284:A:C8	62:MM:104:VAL:HG21	2.55	0.41
49:9:1672:U:H2'	49:9:1673:U:C6	2.55	0.41
49:9:495:U:H2'	49:9:496:C:O4'	2.20	0.41
56:GG:64:LYS:HB3	56:GG:67:VAL:HG11	2.02	0.41
58:II:31:ARG:NH2	58:II:48:VAL:HG12	2.35	0.41
15:P:137:ASN:ND2	46:5:3861:A:H4'	2.35	0.41
15:P:54:LYS:HA	15:P:83:TRP:CD1	2.55	0.41
18:S:157:ARG:O	18:S:158:VAL:C	2.58	0.41
46:5:1394:G:H2'	46:5:1395:U:O4'	2.21	0.41
46:5:1899:G:N7	46:5:2278:G:C6	2.89	0.41
46:5:3613:U:H2'	46:5:3614:G:C8	2.55	0.41
46:5:4183:G:N3	46:5:4183:G:H2'	2.36	0.41
46:5:742:G:N1	46:5:743:G:C5	2.87	0.41
46:5:76:A:C6	46:5:77:U:C5	3.08	0.41
6:F:46:ARG:NH1	46:5:976:G:O3'	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:107:A:H2'	49:9:108:G:C8	2.55	0.41
49:9:27:A:H2'	49:9:28:U:O4'	2.20	0.41
49:9:290:U:O2'	49:9:292:A:N7	2.50	0.41
52:CC:231:ALA:O	52:CC:233:LEU:N	2.53	0.41
57:HH:66:VAL:N	57:HH:67:PRO:CD	2.84	0.41
9:I:68:ALA:O	9:I:69:ARG:C	2.59	0.41
58:II:113:TYR:OH	58:II:156:ALA:O	2.25	0.41
74:YY:27:VAL:HG22	74:YY:40:ILE:HD11	2.02	0.41
20:U:81:ARG:NH2	46:5:2622:G:O6	2.53	0.41
46:5:2844:A:N1	46:5:3845:A:C6	2.89	0.41
3:C:61:GLN:NE2	46:5:358:C:OP1	2.53	0.41
11:L:60:ARG:NH2	46:5:72:C:N3	2.67	0.41
49:9:1129:G:C6	49:9:1130:G:C6	3.09	0.41
49:9:1175:G:C6	49:9:1176:G:C5	3.08	0.41
49:9:1448:A:H2'	49:9:1449:G:O4'	2.21	0.41
3:C:26:ALA:O	3:C:27:VAL:C	2.59	0.41
64:OO:56:VAL:HG13	64:OO:77:ALA:HB1	2.02	0.41
15:P:112:LEU:HA	15:P:151:THR:O	2.21	0.41
71:VV:30:ALA:HB3	71:VV:57:GLY:HA3	2.03	0.41
72:WW:94:LEU:HD21	72:WW:101:PHE:O	2.20	0.41
45:2:19:G:C4	45:2:57:A:C2	3.09	0.41
46:5:1360:G:C6	46:5:1361:G:C5	3.08	0.41
46:5:2758:G:O2'	46:5:2765:A:N3	2.45	0.41
46:5:4432:C:H2'	46:5:4433:G:O4'	2.21	0.41
46:5:4461:C:O2	46:5:4516:G:C2	2.74	0.41
46:5:4538:G:C6	46:5:4539:U:C4	3.08	0.41
46:5:77:U:C2	46:5:78:U:C6	3.08	0.41
49:9:448:A:N6	58:II:29:LEU:HD13	2.35	0.41
50:AA:180:ARG:HG2	50:AA:195:TRP:CE3	2.56	0.41
2:B:10:ARG:HD3	2:B:11:HIS:N	2.35	0.41
2:B:222:VAL:HG11	2:B:274:TYR:CE1	2.56	0.41
3:C:36:ILE:O	3:C:37:VAL:C	2.57	0.41
5:E:157:THR:HG23	5:E:158:GLY:N	2.35	0.41
8:H:64:ARG:NH1	46:5:1949:U:OP1	2.53	0.41
11:L:91:ALA:HB1	11:L:96:ILE:HB	2.02	0.41
14:O:42:ASN:N	14:O:42:ASN:OD1	2.52	0.41
15:P:29:THR:HG21	15:P:146:ILE:HD11	2.03	0.41
46:5:1354:A:N1	46:5:1385:G:O2'	2.42	0.41
46:5:370:U:C6	46:5:1637:A:C2	3.08	0.41
46:5:1867:A:H2'	46:5:1868:A:C8	2.56	0.41
46:5:1932:A:H2'	46:5:1933:G:C8	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:2065:G:C5	46:5:2066:C:C5	3.08	0.41
7:G:90:LYS:NZ	46:5:4126:C:OP1	2.53	0.41
2:B:62:ARG:NH1	46:5:4617:G:OP1	2.53	0.41
46:5:4627:U:H2'	46:5:4628:U:O4'	2.21	0.41
11:L:31:ARG:HD2	46:5:337:U:OP1	2.20	0.41
14:O:74:ARG:HG3	14:O:145:VAL:HG12	2.03	0.41
20:U:82:TYR:CZ	20:U:86:LEU:HD11	2.56	0.41
16:Q:2:GLY:HA3	46:5:1897:A:O5'	2.21	0.41
13:N:169:ARG:NH1	46:5:63:G:OP2	2.49	0.41
46:5:976:G:N2	46:5:977:C:C4	2.89	0.41
49:9:1238:U:H2'	49:9:1239:U:O4'	2.20	0.41
55:FF:20:PHE:C	55:FF:20:PHE:CD1	2.92	0.41
73:XX:61:GLN:O	73:XX:63:ASN:N	2.54	0.41
73:XX:52:LEU:HD23	73:XX:73:GLN:HB2	2.02	0.41
46:5:372:A:C2	46:5:1645:C:O4'	2.73	0.41
46:5:4274:A:H2'	46:5:4275:G:C8	2.56	0.41
46:5:4538:G:C5	46:5:4539:U:C4	3.09	0.41
47:7:25:G:C5	47:7:26:C:C5	3.08	0.41
49:9:1666:C:O5'	49:9:1666:C:H6	2.04	0.41
49:9:297:A:H4'	54:EE:132:GLY:O	2.21	0.41
2:B:29:VAL:HG13	2:B:348:ARG:HD3	2.02	0.41
3:C:67:TRP:CE3	3:C:73:VAL:HG21	2.56	0.41
54:EE:181:CYS:SG	54:EE:225:ILE:HG23	2.61	0.41
57:HH:118:ARG:O	57:HH:121:THR:HG22	2.21	0.41
10:J:103:GLY:O	10:J:134:LEU:HD12	2.21	0.41
60:KK:58:VAL:HG21	60:KK:69:TRP:HB3	2.02	0.41
64:OO:39:ASP:OD1	64:OO:40:THR:N	2.54	0.41
70:UU:29:VAL:HG22	70:UU:85:HIS:NE2	2.35	0.41
2:B:55:HIS:HE1	22:W:17:HIS:CE1	2.38	0.41
73:XX:85:VAL:HG21	73:XX:91:LEU:CD1	2.51	0.41
46:5:1325:C:O5'	46:5:1325:C:O2	2.39	0.41
46:5:1513:U:H2'	46:5:1514:U:O4'	2.21	0.41
46:5:1929:A:N3	46:5:1929:A:C2'	2.83	0.41
46:5:4966:A:H2'	46:5:4967:A:C8	2.55	0.41
48:8:13:G:C6	48:8:14:U:C4	3.08	0.41
49:9:1130:G:O2'	49:9:1131:G:O5'	2.39	0.41
3:C:194:GLY:O	3:C:197:ARG:N	2.50	0.41
3:C:94:ASN:OD1	3:C:94:ASN:N	2.53	0.41
4:D:22:ARG:HH11	4:D:22:ARG:HG3	1.86	0.41
5:E:165:VAL:HG12	5:E:178:VAL:HG22	2.03	0.41
5:E:185:ASN:ND2	5:E:274:LEU:O	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:16:PRO:HA	9:I:95:HIS:CD2	2.56	0.41
11:L:75:GLY:O	11:L:99:ASP:OD1	2.39	0.41
12:M:64:PHE:CZ	12:M:73:VAL:HG22	2.56	0.41
23:X:146:ALA:HA	23:X:149:VAL:HG12	2.03	0.41
46:5:1622:U:O2'	46:5:1627:G:O3'	2.29	0.41
46:5:3642:A:OP1	46:5:3644:U:OP1	2.39	0.41
46:5:4368:G:C6	46:5:4369:A:C5	3.09	0.41
14:O:74:ARG:NH2	46:5:4712:C:OP1	2.54	0.41
47:7:27:G:C2	47:7:28:C:C2	3.09	0.41
48:8:40:A:H2'	48:8:41:A:O4'	2.21	0.41
49:9:1019:C:H2'	49:9:1020:A:O4'	2.21	0.41
49:9:932:G:H2'	49:9:934:G:OP2	2.20	0.41
1:A:94:ALA:HB3	1:A:102:LEU:HB3	2.03	0.41
1:A:101:VAL:HG22	1:A:163:ARG:HB3	2.03	0.41
2:B:222:VAL:HB	2:B:343:ARG:HD3	2.02	0.41
72:WW:10:ALA:HB1	72:WW:27:ILE:HD12	2.02	0.41
73:XX:68:LYS:HG2	73:XX:91:LEU:HD22	2.03	0.41
46:5:957:G:C2	46:5:1283:G:H2'	2.56	0.41
46:5:1590:C:H3'	46:5:1591:U:H4'	2.03	0.41
46:5:23:C:H2'	46:5:24:G:O4'	2.21	0.41
46:5:4418:G:H2'	46:5:4475:G:N2	2.36	0.41
6:F:131:MET:HA	6:F:134:ILE:HG22	2.03	0.41
5:E:289:LEU:HD12	12:M:109:ARG:CZ	2.51	0.41
63:NN:67:THR:OG1	63:NN:69:ASN:O	2.38	0.41
64:OO:151:LEU:N	64:OO:151:LEU:HD13	2.36	0.41
72:WW:75:ILE:HD11	72:WW:93:LEU:CD1	2.50	0.41
46:5:1612:G:H2'	46:5:1612:G:N3	2.37	0.40
46:5:1857:C:H2'	46:5:1858:A:C8	2.55	0.40
46:5:2863:G:C6	46:5:2864:A:C5	3.09	0.40
46:5:4190:U:O2	46:5:4381:A:C8	2.74	0.40
46:5:4277:G:O2'	46:5:4282:A:N1	2.45	0.40
49:9:46:A:C6	49:9:473:A:C2	3.09	0.40
49:9:92:A:H4'	49:9:93:U:OP2	2.20	0.40
1:A:196:TRP:HB3	1:A:197:PRO:HD3	2.03	0.40
2:B:45:ALA:HB3	2:B:183:ILE:HG23	2.03	0.40
18:S:7:LEU:HD12	18:S:35:PRO:HD3	2.02	0.40
68:SS:121:ARG:HG3	68:SS:131:VAL:CG2	2.50	0.40
21:V:89:ARG:HB2	21:V:95:PHE:CE1	2.56	0.40
46:5:1590:C:H4'	46:5:2857:A:H5'	2.04	0.40
46:5:288:G:C6	46:5:289:C:C4	3.09	0.40
46:5:4523:A:H1'	46:5:4558:U:C4	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:4523:A:H5''	46:5:4524:G:H5'	2.03	0.40
18:S:68:PHE:CD2	46:5:729:G:C6	3.09	0.40
49:9:1064:C:O2'	64:OO:149:ARG:NH2	2.55	0.40
49:9:191:A:C2'	49:9:192:C:OP1	2.69	0.40
49:9:636:C:C4	49:9:637:U:C4	3.09	0.40
49:9:958:G:C6	49:9:959:G:C6	3.09	0.40
6:F:90:PHE:CD2	6:F:243:ILE:HD11	2.56	0.40
58:II:84:ASN:OD1	58:II:90:LEU:HD12	2.21	0.40
10:J:74:VAL:HG11	10:J:82:ILE:HD12	2.04	0.40
61:LL:79:LYS:HB2	61:LL:87:VAL:HB	2.02	0.40
46:5:1301:C:O2	46:5:1301:C:O4'	2.37	0.40
46:5:1383:G:C5	46:5:1384:C:C4	3.10	0.40
46:5:3723:A:C2	46:5:3730:U:N3	2.88	0.40
46:5:417:G:HO2'	46:5:418:A:P	2.43	0.40
46:5:4508:C:N3	46:5:4512:U:H5	2.19	0.40
46:5:922:C:H6	46:5:922:C:H3'	1.81	0.40
48:8:70:G:O2'	48:8:87:G:N2	2.54	0.40
1:A:133:TYR:CD1	1:A:168:VAL:HG12	2.56	0.40
6:F:153:ILE:HD13	6:F:210:PHE:HZ	1.87	0.40
12:M:36:ALA:HB2	12:M:52:PHE:CZ	2.57	0.40
23:X:76:ILE:HG21	23:X:112:ALA:HB2	2.03	0.40
46:5:1353:G:N2	46:5:1504:G:C5	2.90	0.40
46:5:1689:G:H2'	46:5:1690:C:O4'	2.22	0.40
46:5:2553:A:C2	46:5:2764:A:C6	3.10	0.40
46:5:3871:A:H2'	46:5:3872:A:O4'	2.21	0.40
46:5:3890:A:N6	46:5:4570:G:O2'	2.54	0.40
49:9:1455:A:C2	49:9:1456:G:C8	3.08	0.40
49:9:620:G:C8	49:9:621:C:C5	3.10	0.40
3:C:101:MET:CE	46:5:2343:G:C4	3.04	0.40
52:CC:253:PRO:HA	52:CC:256:TRP:CD1	2.56	0.40
53:DD:179:GLN:HE21	53:DD:179:GLN:HA	1.86	0.40
8:H:41:ILE:HG12	8:H:73:ILE:HD11	2.04	0.40
12:M:7:VAL:HG13	12:M:27:ILE:HD13	2.02	0.40
21:V:20:LEU:O	21:V:55:ALA:N	2.53	0.40
46:5:1339:U:H2'	46:5:1340:C:C6	2.55	0.40
14:O:17:GLY:HA3	46:5:2052:G:O3'	2.21	0.40
46:5:4640:C:H2'	46:5:4641:U:O4'	2.21	0.40
47:7:56:G:C8	47:7:57:C:C5	3.09	0.40
48:8:15:G:C6	48:8:16:G:N1	2.89	0.40
48:8:7:U:H2'	48:8:8:U:C6	2.56	0.40
49:9:1238:U:O2'	65:PP:126:VAL:HG12	2.22	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:58:ARG:HB3	5:E:59:TYR:CD1	2.56	0.40
49:9:219:U:O4'	58:II:184:ARG:NH1	2.55	0.40
49:9:446:G:OP2	58:II:47:ARG:NH1	2.55	0.40
18:S:154:LEU:HB3	18:S:157:ARG:HD3	2.03	0.40
24:Y:8:THR:HG23	24:Y:10:ASP:HB2	2.03	0.40

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	
1	A	246/257 (96%)	217 (88%)	25 (10%)	4 (2%)	12	57
2	B	392/403 (97%)	343 (88%)	47 (12%)	2 (0%)	34	76
3	C	360/425 (85%)	319 (89%)	32 (9%)	9 (2%)	7	49
4	D	291/297 (98%)	270 (93%)	18 (6%)	3 (1%)	19	65
5	E	208/291 (72%)	182 (88%)	25 (12%)	1 (0%)	34	76
6	F	223/247 (90%)	199 (89%)	20 (9%)	4 (2%)	11	55
7	G	229/319 (72%)	212 (93%)	16 (7%)	1 (0%)	39	79
8	H	188/192 (98%)	168 (89%)	18 (10%)	2 (1%)	17	64
9	I	201/214 (94%)	178 (89%)	23 (11%)	0	100	100
10	J	168/178 (94%)	156 (93%)	10 (6%)	2 (1%)	16	62
11	L	208/211 (99%)	185 (89%)	21 (10%)	2 (1%)	19	65
12	M	136/218 (62%)	126 (93%)	7 (5%)	3 (2%)	8	52
13	N	201/204 (98%)	180 (90%)	17 (8%)	4 (2%)	9	54
14	O	197/203 (97%)	176 (89%)	21 (11%)	0	100	100
15	P	151/184 (82%)	138 (91%)	11 (7%)	2 (1%)	15	60
16	Q	185/188 (98%)	163 (88%)	20 (11%)	2 (1%)	17	64

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
18	S	174/176 (99%)	161 (92%)	11 (6%)	2 (1%)	17	64
19	T	157/160 (98%)	141 (90%)	16 (10%)	0	100	100
20	U	97/128 (76%)	86 (89%)	9 (9%)	2 (2%)	9	53
21	V	129/140 (92%)	117 (91%)	10 (8%)	2 (2%)	12	57
22	W	102/157 (65%)	91 (89%)	10 (10%)	1 (1%)	19	65
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	5 (4%)	2 (2%)	13	58
26	a	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
27	b	100/245 (41%)	89 (89%)	10 (10%)	1 (1%)	19	65
28	c	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d	105/125 (84%)	87 (83%)	16 (15%)	2 (2%)	10	54
30	e	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	24	69
31	f	107/110 (97%)	96 (90%)	8 (8%)	3 (3%)	6	47
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	11	55
33	h	120/123 (98%)	112 (93%)	7 (6%)	1 (1%)	24	69
34	i	100/105 (95%)	91 (91%)	9 (9%)	0	100	100
35	j	84/97 (87%)	72 (86%)	11 (13%)	1 (1%)	16	62
36	k	67/70 (96%)	61 (91%)	5 (8%)	1 (2%)	13	58
37	l	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	9	53
38	m	50/102 (49%)	46 (92%)	3 (6%)	1 (2%)	9	54
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	89 (87%)	11 (11%)	2 (2%)	9	54
41	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
42	r	122/137 (89%)	103 (84%)	16 (13%)	3 (2%)	7	49
43	s	194/318 (61%)	173 (89%)	19 (10%)	2 (1%)	19	65
44	t	151/165 (92%)	135 (89%)	14 (9%)	2 (1%)	15	60
50	AA	215/295 (73%)	189 (88%)	23 (11%)	3 (1%)	14	59
51	BB	211/264 (80%)	194 (92%)	17 (8%)	0	100	100
52	CC	219/293 (75%)	202 (92%)	14 (6%)	3 (1%)	14	59

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	DD	226/243 (93%)	207 (92%)	18 (8%)	1 (0%)	39	79
54	EE	260/263 (99%)	245 (94%)	13 (5%)	2 (1%)	24	69
55	FF	181/204 (89%)	164 (91%)	14 (8%)	3 (2%)	11	56
56	GG	235/249 (94%)	221 (94%)	13 (6%)	1 (0%)	39	79
57	HH	181/194 (93%)	170 (94%)	11 (6%)	0	100	100
58	II	204/208 (98%)	187 (92%)	17 (8%)	0	100	100
59	JJ	183/194 (94%)	172 (94%)	10 (6%)	1 (0%)	34	76
60	KK	94/165 (57%)	85 (90%)	8 (8%)	1 (1%)	17	64
61	LL	139/158 (88%)	119 (86%)	19 (14%)	1 (1%)	26	71
62	MM	115/132 (87%)	97 (84%)	18 (16%)	0	100	100
63	NN	147/151 (97%)	131 (89%)	16 (11%)	0	100	100
64	OO	134/168 (80%)	116 (87%)	17 (13%)	1 (1%)	26	71
65	PP	118/145 (81%)	103 (87%)	15 (13%)	0	100	100
66	QQ	140/146 (96%)	131 (94%)	8 (6%)	1 (1%)	26	71
67	RR	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	24	69
68	SS	142/152 (93%)	134 (94%)	6 (4%)	2 (1%)	14	59
69	TT	139/145 (96%)	130 (94%)	8 (6%)	1 (1%)	26	71
70	UU	98/119 (82%)	90 (92%)	7 (7%)	1 (1%)	19	65
71	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
72	WW	127/130 (98%)	112 (88%)	12 (9%)	3 (2%)	7	50
73	XX	139/143 (97%)	126 (91%)	10 (7%)	3 (2%)	8	52
74	YY	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
75	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
76	aa	99/115 (86%)	84 (85%)	13 (13%)	2 (2%)	9	54
77	bb	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	16	62
78	cc	60/69 (87%)	55 (92%)	4 (7%)	1 (2%)	11	56
79	dd	53/56 (95%)	44 (83%)	8 (15%)	1 (2%)	10	54
80	ee	53/133 (40%)	48 (91%)	5 (9%)	0	100	100
81	ff	66/156 (42%)	60 (91%)	4 (6%)	2 (3%)	5	45
82	gg	311/317 (98%)	281 (90%)	27 (9%)	3 (1%)	19	65
84	ii	370/403 (92%)	342 (92%)	28 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
85	jj	423/710 (60%)	383 (90%)	35 (8%)	5 (1%)	16	62
All	All	12312/14488 (85%)	11148 (90%)	1047 (8%)	117 (1%)	24	65

All (117) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
3	C	254	GLU
7	G	105	THR
18	S	155	PRO
29	d	58	GLY
31	f	107	PRO
42	r	11	ARG
42	r	68	SER
73	XX	62	PRO
85	jj	605	GLN
1	A	14	SER
3	C	71	ARG
3	C	99	GLY
3	C	275	SER
6	F	236	GLU
11	L	63	THR
12	M	9	VAL
13	N	79	ALA
13	N	89	VAL
13	N	160	GLU
20	U	24	ASP
20	U	62	SER
21	V	50	ASN
22	W	27	LYS
32	g	69	LYS
33	h	89	ARG
35	j	59	THR
43	s	142	GLY
44	t	125	LEU
52	CC	232	THR
61	LL	66	VAL
64	OO	20	GLN
68	SS	78	LYS
69	TT	34	VAL
73	XX	86	PRO
4	D	44	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	J	141	ILE
12	M	61	ILE
16	Q	14	ARG
18	S	165	PRO
25	Z	91	LEU
31	f	106	TYR
37	l	49	LEU
38	m	94	ASN
54	EE	68	ARG
55	FF	43	GLU
55	FF	79	HIS
59	JJ	147	PHE
60	KK	64	TRP
72	WW	29	PRO
76	aa	47	ALA
1	A	195	CYS
1	A	217	GLN
2	B	208	SER
4	D	119	TYR
11	L	28	GLN
12	M	104	MET
21	V	51	ARG
29	d	30	HIS
36	k	20	ALA
40	o	96	ASP
42	r	34	ALA
50	AA	137	ALA
56	GG	105	ASN
66	QQ	17	LYS
68	SS	118	ARG
72	WW	3	ARG
76	aa	26	CYS
77	bb	81	ARG
79	dd	7	TYR
85	jj	618	SER
2	B	17	LEU
3	C	108	TRP
3	C	155	GLU
3	C	315	LYS
5	E	181	PRO
6	F	226	PHE
15	P	21	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	Z	90	PRO
30	e	125	PRO
50	AA	159	ILE
52	CC	99	GLY
73	XX	61	GLN
81	ff	128	ALA
85	jj	271	ALA
85	jj	596	LYS
3	C	27	VAL
3	C	94	ASN
6	F	227	VAL
43	s	25	PRO
44	t	54	LYS
50	AA	102	ARG
53	DD	44	THR
54	EE	73	ASP
72	WW	56	HIS
85	jj	269	VAL
15	P	114	ILE
82	gg	224	GLY
10	J	68	ILE
16	Q	92	VAL
32	g	48	VAL
67	RR	119	VAL
70	UU	69	PRO
78	cc	25	GLY
4	D	125	VAL
6	F	136	GLU
8	H	22	GLY
27	b	102	PRO
31	f	82	GLY
40	o	50	GLY
82	gg	61	GLY
8	H	30	PRO
13	N	88	GLY
52	CC	253	PRO
55	FF	21	GLY
81	ff	122	PRO
82	gg	13	GLY

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	A	190/199 (96%)	170 (90%)	20 (10%)	8	40
2	B	342/348 (98%)	308 (90%)	34 (10%)	10	43
3	C	302/347 (87%)	275 (91%)	27 (9%)	12	48
4	D	247/250 (99%)	233 (94%)	14 (6%)	25	65
5	E	190/251 (76%)	178 (94%)	12 (6%)	22	61
6	F	196/215 (91%)	181 (92%)	15 (8%)	16	55
7	G	200/272 (74%)	186 (93%)	14 (7%)	19	58
8	H	169/171 (99%)	154 (91%)	15 (9%)	12	48
9	I	175/181 (97%)	161 (92%)	14 (8%)	15	53
10	J	143/149 (96%)	136 (95%)	7 (5%)	31	69
11	L	175/176 (99%)	164 (94%)	11 (6%)	22	61
12	M	117/161 (73%)	107 (92%)	10 (8%)	13	51
13	N	171/172 (99%)	158 (92%)	13 (8%)	16	55
14	O	171/173 (99%)	156 (91%)	15 (9%)	12	48
15	P	134/163 (82%)	122 (91%)	12 (9%)	12	47
16	Q	164/165 (99%)	147 (90%)	17 (10%)	9	40
17	R	159/175 (91%)	145 (91%)	14 (9%)	12	48
18	S	157/157 (100%)	145 (92%)	12 (8%)	16	55
19	T	139/140 (99%)	125 (90%)	14 (10%)	9	41
20	U	89/114 (78%)	87 (98%)	2 (2%)	60	84
21	V	101/107 (94%)	87 (86%)	14 (14%)	4	29
22	W	86/126 (68%)	83 (96%)	3 (4%)	43	76
23	X	106/134 (79%)	100 (94%)	6 (6%)	25	65
24	Y	124/135 (92%)	117 (94%)	7 (6%)	26	65
25	Z	117/118 (99%)	112 (96%)	5 (4%)	35	72
26	a	119/120 (99%)	114 (96%)	5 (4%)	36	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	b	84/184 (46%)	80 (95%)	4 (5%)	31	69
28	c	84/98 (86%)	78 (93%)	6 (7%)	18	58
29	d	98/110 (89%)	89 (91%)	9 (9%)	11	46
30	e	114/121 (94%)	105 (92%)	9 (8%)	15	54
31	f	88/89 (99%)	80 (91%)	8 (9%)	12	47
32	g	98/100 (98%)	88 (90%)	10 (10%)	9	41
33	h	109/110 (99%)	105 (96%)	4 (4%)	41	75
34	i	86/89 (97%)	83 (96%)	3 (4%)	43	76
35	j	73/80 (91%)	63 (86%)	10 (14%)	4	29
36	k	64/65 (98%)	60 (94%)	4 (6%)	22	61
37	l	47/48 (98%)	44 (94%)	3 (6%)	22	61
38	m	48/90 (53%)	43 (90%)	5 (10%)	9	40
39	n	24/24 (100%)	22 (92%)	2 (8%)	14	51
40	o	92/94 (98%)	87 (95%)	5 (5%)	27	67
41	p	74/75 (99%)	70 (95%)	4 (5%)	27	67
42	r	108/121 (89%)	97 (90%)	11 (10%)	9	41
43	s	164/258 (64%)	158 (96%)	6 (4%)	41	75
44	t	126/137 (92%)	123 (98%)	3 (2%)	57	82
50	AA	180/245 (74%)	161 (89%)	19 (11%)	8	39
51	BB	194/231 (84%)	176 (91%)	18 (9%)	11	46
52	CC	187/225 (83%)	168 (90%)	19 (10%)	9	41
53	DD	190/202 (94%)	178 (94%)	12 (6%)	22	61
54	EE	224/225 (100%)	205 (92%)	19 (8%)	13	51
55	FF	158/170 (93%)	140 (89%)	18 (11%)	7	36
56	GG	207/218 (95%)	187 (90%)	20 (10%)	10	43
57	HH	165/174 (95%)	150 (91%)	15 (9%)	12	47
58	II	178/180 (99%)	169 (95%)	9 (5%)	29	68
59	JJ	161/168 (96%)	146 (91%)	15 (9%)	11	46
60	KK	87/136 (64%)	82 (94%)	5 (6%)	25	65
61	LL	130/142 (92%)	116 (89%)	14 (11%)	8	39
62	MM	99/108 (92%)	84 (85%)	15 (15%)	3	25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	NN	130/131 (99%)	113 (87%)	17 (13%)	5	30
64	OO	106/130 (82%)	96 (91%)	10 (9%)	11	45
65	PP	109/130 (84%)	99 (91%)	10 (9%)	11	46
66	QQ	117/121 (97%)	111 (95%)	6 (5%)	29	68
67	RR	119/121 (98%)	102 (86%)	17 (14%)	4	28
68	SS	125/132 (95%)	110 (88%)	15 (12%)	6	33
69	TT	111/115 (96%)	105 (95%)	6 (5%)	27	67
70	UU	92/107 (86%)	84 (91%)	8 (9%)	13	48
71	VV	67/67 (100%)	63 (94%)	4 (6%)	24	63
72	WW	112/113 (99%)	104 (93%)	8 (7%)	18	58
73	XX	113/115 (98%)	103 (91%)	10 (9%)	12	48
74	YY	107/112 (96%)	92 (86%)	15 (14%)	4	29
75	ZZ	66/103 (64%)	61 (92%)	5 (8%)	16	55
76	aa	88/98 (90%)	78 (89%)	10 (11%)	7	36
77	bb	75/76 (99%)	67 (89%)	8 (11%)	8	39
78	cc	55/62 (89%)	49 (89%)	6 (11%)	8	38
79	dd	48/49 (98%)	45 (94%)	3 (6%)	22	61
80	ee	46/106 (43%)	42 (91%)	4 (9%)	13	48
81	ff	61/140 (44%)	55 (90%)	6 (10%)	10	43
82	gg	272/275 (99%)	258 (95%)	14 (5%)	29	68
84	ii	326/353 (92%)	310 (95%)	16 (5%)	31	69
85	jj	358/608 (59%)	332 (93%)	26 (7%)	17	57
All	All	10727/12300 (87%)	9867 (92%)	860 (8%)	20	53

All (860) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	64	ARG
1	A	102	LEU
1	A	109	GLU
1	A	114	CYS
1	A	115	CYS
1	A	125	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	128	ARG
1	A	130	SER
1	A	163	ARG
1	A	165	VAL
1	A	175	ILE
1	A	198	ARG
1	A	200	ARG
1	A	209	HIS
1	A	221	LYS
1	A	227	ARG
1	A	233	ARG
1	A	242	ARG
1	A	243	THR
2	B	3	HIS
2	B	10	ARG
2	B	17	LEU
2	B	36	ASP
2	B	53	MET
2	B	62	ARG
2	B	66	LYS
2	B	97	ARG
2	B	103	LYS
2	B	115	LYS
2	B	135	LYS
2	B	146	LEU
2	B	152	SER
2	B	167	GLN
2	B	218	ASP
2	B	231	VAL
2	B	234	ARG
2	B	244	THR
2	B	248	LEU
2	B	253	CYS
2	B	261	ARG
2	B	262	VAL
2	B	264	PHE
2	B	279	GLU
2	B	294	LYS
2	B	298	LEU
2	B	309	LEU
2	B	314	ILE
2	B	333	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	351	LEU
2	B	356	LYS
2	B	357	ARG
2	B	366	LYS
2	B	383	GLU
3	C	20	LYS
3	C	29	LYS
3	C	55	SER
3	C	66	SER
3	C	89	GLN
3	C	95	MET
3	C	122	TYR
3	C	124	ILE
3	C	143	ARG
3	C	144	ILE
3	C	150	LEU
3	C	165	LYS
3	C	173	LYS
3	C	175	LYS
3	C	188	ARG
3	C	193	LYS
3	C	198	ASN
3	C	208	CYS
3	C	232	VAL
3	C	246	VAL
3	C	249	PHE
3	C	266	THR
3	C	281	MET
3	C	284	MET
3	C	307	LYS
3	C	312	ARG
3	C	333	LYS
4	D	22	ARG
4	D	33	ARG
4	D	50	ARG
4	D	56	THR
4	D	70	GLU
4	D	89	LYS
4	D	104	LEU
4	D	110	LEU
4	D	124	GLU
4	D	131	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	D	202	GLN
4	D	217	ASP
4	D	264	LYS
4	D	268	ARG
5	E	52	LEU
5	E	58	ARG
5	E	112	LEU
5	E	141	ARG
5	E	143	LEU
5	E	144	ARG
5	E	169	LYS
5	E	178	VAL
5	E	213	LYS
5	E	261	LEU
5	E	289	LEU
5	E	291	PHE
6	F	30	LYS
6	F	46	ARG
6	F	65	ARG
6	F	67	GLU
6	F	88	LEU
6	F	134	ILE
6	F	151	GLU
6	F	178	LEU
6	F	186	MET
6	F	187	GLU
6	F	189	LEU
6	F	198	LYS
6	F	211	LYS
6	F	231	ASP
6	F	245	ARG
7	G	97	ASP
7	G	116	LEU
7	G	126	ARG
7	G	162	GLU
7	G	163	LYS
7	G	184	LYS
7	G	203	LYS
7	G	204	LYS
7	G	207	LEU
7	G	220	VAL
7	G	223	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	G	226	LEU
7	G	230	MET
7	G	242	ARG
8	H	1	MET
8	H	23	ARG
8	H	24	THR
8	H	46	SER
8	H	52	LYS
8	H	54	ARG
8	H	59	LYS
8	H	66	GLU
8	H	74	CYS
8	H	94	SER
8	H	105	ILE
8	H	108	ASN
8	H	128	MET
8	H	173	ARG
8	H	177	ASP
9	I	13	LYS
9	I	24	ARG
9	I	36	LEU
9	I	39	LYS
9	I	76	MET
9	I	116	ARG
9	I	123	GLN
9	I	142	LEU
9	I	153	ARG
9	I	163	GLN
9	I	164	LYS
9	I	183	ASP
9	I	195	CYS
9	I	208	LYS
10	J	16	ARG
10	J	28	GLU
10	J	33	LEU
10	J	72	CYS
10	J	81	GLU
10	J	113	ILE
10	J	175	LEU
11	L	10	LEU
11	L	61	CYS
11	L	63	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	L	67	HIS
11	L	74	ARG
11	L	104	ASN
11	L	106	SER
11	L	129	ARG
11	L	162	LYS
11	L	186	ARG
11	L	195	ARG
12	M	2	VAL
12	M	5	ARG
12	M	32	ASP
12	M	37	LEU
12	M	57	LEU
12	M	61	ILE
12	M	62	LEU
12	M	96	GLU
12	M	105	THR
12	M	119	ARG
13	N	9	GLU
13	N	26	ARG
13	N	32	GLN
13	N	44	ARG
13	N	64	ILE
13	N	72	LYS
13	N	75	VAL
13	N	77	LYS
13	N	87	HIS
13	N	104	GLU
13	N	146	PRO
13	N	162	ARG
13	N	182	HIS
14	O	18	ARG
14	O	37	ARG
14	O	42	ASN
14	O	49	ARG
14	O	61	ARG
14	O	67	SER
14	O	74	ARG
14	O	82	ARG
14	O	128	ARG
14	O	130	LYS
14	O	140	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	O	175	MET
14	O	179	LYS
14	O	188	LYS
14	O	196	LEU
15	P	10	ASN
15	P	21	ASN
15	P	24	VAL
15	P	25	HIS
15	P	69	ARG
15	P	70	CYS
15	P	86	LYS
15	P	91	LEU
15	P	100	SER
15	P	128	ARG
15	P	141	SER
15	P	147	GLU
16	Q	3	VAL
16	Q	5	ILE
16	Q	13	VAL
16	Q	31	LEU
16	Q	42	THR
16	Q	63	LEU
16	Q	75	ARG
16	Q	91	ARG
16	Q	95	VAL
16	Q	97	LYS
16	Q	101	CYS
16	Q	112	ARG
16	Q	138	LEU
16	Q	143	ARG
16	Q	168	ARG
16	Q	169	SER
16	Q	188	ASN
17	R	8	LYS
17	R	34	ASN
17	R	36	ASN
17	R	40	GLN
17	R	50	ILE
17	R	89	MET
17	R	99	MET
17	R	106	LEU
17	R	113	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	R	130	ASN
17	R	133	LYS
17	R	138	LEU
17	R	176	ARG
17	R	178	GLN
18	S	7	LEU
18	S	8	ARG
18	S	9	GLU
18	S	17	LEU
18	S	43	ARG
18	S	70	LYS
18	S	83	ARG
18	S	92	ASN
18	S	102	THR
18	S	149	LYS
18	S	159	LEU
18	S	174	THR
19	T	5	LYS
19	T	33	ILE
19	T	35	LYS
19	T	52	MET
19	T	60	LYS
19	T	96	ILE
19	T	113	ASP
19	T	117	LYS
19	T	135	PRO
19	T	142	ARG
19	T	144	ASN
19	T	146	LYS
19	T	157	GLU
19	T	159	MET
20	U	33	ILE
20	U	83	LEU
21	V	15	ARG
21	V	18	LEU
21	V	25	VAL
21	V	35	LYS
21	V	45	ILE
21	V	46	LYS
21	V	50	ASN
21	V	60	MET
21	V	71	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	V	82	ILE
21	V	88	TYR
21	V	91	LYS
21	V	109	LYS
21	V	123	LYS
22	W	19	ARG
22	W	30	GLN
22	W	91	MET
23	X	39	LYS
23	X	41	ARG
23	X	53	ARG
23	X	57	GLN
23	X	59	LYS
23	X	63	LYS
24	Y	2	LYS
24	Y	8	THR
24	Y	50	ARG
24	Y	72	GLN
24	Y	74	TYR
24	Y	104	VAL
24	Y	112	ASP
25	Z	11	VAL
25	Z	31	ASP
25	Z	83	THR
25	Z	84	ARG
25	Z	112	ARG
26	a	16	SER
26	a	56	VAL
26	a	84	GLU
26	a	122	VAL
26	a	132	ARG
27	b	9	THR
27	b	22	LYS
27	b	40	LEU
27	b	101	HIS
28	c	37	MET
28	c	50	ASN
28	c	78	ASN
28	c	81	LEU
28	c	83	THR
28	c	92	CYS
29	d	23	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	d	26	THR
29	d	44	ARG
29	d	48	GLU
29	d	56	GLU
29	d	78	ARG
29	d	79	ASN
29	d	85	ARG
29	d	98	SER
30	e	21	ILE
30	e	22	ARG
30	e	48	ARG
30	e	64	LYS
30	e	78	LEU
30	e	86	GLU
30	e	89	LEU
30	e	106	LYS
30	e	128	ARG
31	f	7	CYS
31	f	16	ARG
31	f	23	GLU
31	f	33	VAL
31	f	52	LYS
31	f	73	LYS
31	f	76	ARG
31	f	101	ILE
32	g	6	THR
32	g	14	ASN
32	g	21	ARG
32	g	22	LEU
32	g	32	TYR
32	g	54	ARG
32	g	60	ARG
32	g	66	ARG
32	g	90	ARG
32	g	114	GLN
33	h	15	GLU
33	h	28	LEU
33	h	67	GLU
33	h	77	LYS
34	i	34	THR
34	i	86	LYS
34	i	89	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	j	3	LYS
35	j	11	ARG
35	j	15	THR
35	j	20	ARG
35	j	33	THR
35	j	34	CYS
35	j	37	CYS
35	j	58	THR
35	j	59	THR
35	j	79	ARG
36	k	30	ASP
36	k	37	ARG
36	k	69	LEU
36	k	70	LYS
37	l	2	SER
37	l	3	SER
37	l	49	LEU
38	m	71	ARG
38	m	72	LYS
38	m	89	CYS
38	m	92	THR
38	m	93	ASN
39	n	1	MET
39	n	13	LEU
40	o	17	LYS
40	o	24	THR
40	o	31	ASP
40	o	61	LYS
40	o	82	MET
41	p	8	VAL
41	p	24	LYS
41	p	62	LYS
41	p	70	THR
42	r	2	SER
42	r	8	MET
42	r	20	ARG
42	r	26	SER
42	r	32	LEU
42	r	35	ARG
42	r	39	ARG
42	r	67	ARG
42	r	90	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
42	r	106	LEU
42	r	121	GLN
43	s	38	LYS
43	s	95	LEU
43	s	105	ASN
43	s	146	LYS
43	s	187	LEU
43	s	191	GLN
44	t	37	LEU
44	t	98	ILE
44	t	133	LEU
50	AA	9	GLN
50	AA	12	GLU
50	AA	46	ILE
50	AA	50	ASN
50	AA	56	GLU
50	AA	58	LEU
50	AA	60	LEU
50	AA	85	ARG
50	AA	111	GLN
50	AA	122	LEU
50	AA	132	GLN
50	AA	134	LEU
50	AA	136	GLU
50	AA	138	SER
50	AA	142	LEU
50	AA	155	ARG
50	AA	169	HIS
50	AA	178	LEU
50	AA	200	ASP
51	BB	32	ASP
51	BB	40	ASN
51	BB	50	THR
51	BB	63	LYS
51	BB	71	LEU
51	BB	82	ARG
51	BB	96	CYS
51	BB	105	LEU
51	BB	157	GLN
51	BB	172	MET
51	BB	173	THR
51	BB	175	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	BB	180	ASP
51	BB	181	LEU
51	BB	190	PRO
51	BB	207	LEU
51	BB	209	ASP
51	BB	213	ARG
52	CC	78	LEU
52	CC	114	LYS
52	CC	115	GLN
52	CC	117	ARG
52	CC	121	ARG
52	CC	132	ASP
52	CC	137	VAL
52	CC	167	ARG
52	CC	192	LEU
52	CC	227	ARG
52	CC	230	THR
52	CC	233	LEU
52	CC	235	ASN
52	CC	236	PHE
52	CC	244	ILE
52	CC	250	TYR
52	CC	251	LEU
52	CC	254	ASP
52	CC	255	LEU
53	DD	22	ASN
53	DD	31	GLU
53	DD	45	ARG
53	DD	65	ARG
53	DD	76	ARG
53	DD	127	MET
53	DD	134	CYS
53	DD	146	ARG
53	DD	179	GLN
53	DD	190	LEU
53	DD	218	LEU
53	DD	227	LYS
54	EE	6	LYS
54	EE	17	HIS
54	EE	41	CYS
54	EE	42	LEU
54	EE	51	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	EE	66	MET
54	EE	67	GLN
54	EE	77	ARG
54	EE	88	ASP
54	EE	105	THR
54	EE	115	THR
54	EE	145	ARG
54	EE	171	ASP
54	EE	205	PHE
54	EE	225	ILE
54	EE	232	ASN
54	EE	240	ARG
54	EE	246	LEU
54	EE	247	THR
55	FF	20	PHE
55	FF	36	GLN
55	FF	37	ASP
55	FF	49	LEU
55	FF	52	SER
55	FF	71	ARG
55	FF	81	ARG
55	FF	83	ASN
55	FF	88	MET
55	FF	89	THR
55	FF	95	HIS
55	FF	118	ASN
55	FF	122	ARG
55	FF	123	GLU
55	FF	140	ASP
55	FF	146	ARG
55	FF	168	THR
55	FF	204	ARG
56	GG	41	LEU
56	GG	59	GLN
56	GG	63	MET
56	GG	67	VAL
56	GG	76	LEU
56	GG	78	SER
56	GG	88	ARG
56	GG	92	ARG
56	GG	95	LYS
56	GG	98	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
56	GG	100	CYS
56	GG	116	LYS
56	GG	140	ARG
56	GG	159	ARG
56	GG	171	THR
56	GG	178	ARG
56	GG	181	THR
56	GG	190	ARG
56	GG	216	ARG
56	GG	230	LYS
57	HH	8	ILE
57	HH	36	LEU
57	HH	40	LEU
57	HH	72	PHE
57	HH	76	GLN
57	HH	79	LEU
57	HH	82	GLU
57	HH	100	ILE
57	HH	105	THR
57	HH	120	ARG
57	HH	145	ARG
57	HH	151	SER
57	HH	158	LEU
57	HH	162	GLN
57	HH	171	GLU
58	II	6	ASP
58	II	23	LYS
58	II	45	THR
58	II	47	ARG
58	II	49	ARG
58	II	59	ARG
58	II	121	LEU
58	II	130	THR
58	II	161	LEU
59	JJ	29	LEU
59	JJ	38	ARG
59	JJ	45	ARG
59	JJ	50	LEU
59	JJ	61	LEU
59	JJ	69	ARG
59	JJ	70	ARG
59	JJ	79	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
59	JJ	80	ARG
59	JJ	89	GLU
59	JJ	116	LYS
59	JJ	131	ARG
59	JJ	133	ARG
59	JJ	152	ASP
59	JJ	176	LYS
60	KK	1	MET
60	KK	50	GLN
60	KK	60	GLU
60	KK	89	ILE
60	KK	96	ARG
61	LL	16	ILE
61	LL	39	ASN
61	LL	40	ILE
61	LL	42	LEU
61	LL	46	THR
61	LL	52	GLU
61	LL	66	VAL
61	LL	69	ARG
61	LL	85	THR
61	LL	121	GLN
61	LL	126	VAL
61	LL	132	ARG
61	LL	134	LEU
61	LL	135	SER
62	MM	16	THR
62	MM	19	GLN
62	MM	31	LEU
62	MM	33	ARG
62	MM	40	LYS
62	MM	45	ARG
62	MM	55	ASN
62	MM	56	CYS
62	MM	76	LEU
62	MM	80	ASP
62	MM	83	LYS
62	MM	85	LEU
62	MM	96	ARG
62	MM	99	LYS
62	MM	101	ARG
63	NN	12	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
63	NN	20	ARG
63	NN	27	LYS
63	NN	39	LYS
63	NN	55	ARG
63	NN	60	VAL
63	NN	75	LEU
63	NN	78	LYS
63	NN	83	ASP
63	NN	84	LEU
63	NN	86	GLU
63	NN	94	LYS
63	NN	107	LYS
63	NN	110	ASP
63	NN	125	LEU
63	NN	132	LYS
63	NN	142	GLU
64	OO	34	PHE
64	OO	38	ASN
64	OO	40	THR
64	OO	51	GLU
64	OO	56	VAL
64	OO	114	SER
64	OO	142	ARG
64	OO	146	ARG
64	OO	150	ARG
64	OO	151	LEU
65	PP	13	ARG
65	PP	14	LYS
65	PP	15	PHE
65	PP	18	ARG
65	PP	37	TYR
65	PP	44	ARG
65	PP	78	THR
65	PP	83	MET
65	PP	108	LYS
65	PP	130	ARG
66	QQ	7	LEU
66	QQ	31	LEU
66	QQ	41	MET
66	QQ	46	THR
66	QQ	126	ARG
66	QQ	140	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
67	RR	7	LYS
67	RR	22	THR
67	RR	30	THR
67	RR	31	ASN
67	RR	33	ARG
67	RR	44	LYS
67	RR	49	LYS
67	RR	62	GLN
67	RR	70	SER
67	RR	78	ARG
67	RR	89	SER
67	RR	98	VAL
67	RR	99	ASP
67	RR	105	MET
67	RR	109	LEU
67	RR	123	THR
67	RR	132	ARG
68	SS	7	GLU
68	SS	21	ASP
68	SS	23	ARG
68	SS	49	ASP
68	SS	52	LEU
68	SS	59	LEU
68	SS	60	THR
68	SS	75	ARG
68	SS	76	GLN
68	SS	81	ASP
68	SS	83	PHE
68	SS	86	ARG
68	SS	115	LYS
68	SS	118	ARG
68	SS	132	ARG
69	TT	55	THR
69	TT	62	ARG
69	TT	102	ARG
69	TT	110	LEU
69	TT	121	ARG
69	TT	124	THR
70	UU	18	HIS
70	UU	25	THR
70	UU	56	MET
70	UU	60	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
70	UU	68	THR
70	UU	70	CYS
70	UU	90	ASP
70	UU	106	ILE
71	VV	2	GLN
71	VV	10	ASP
71	VV	12	TYR
71	VV	66	ASP
72	WW	7	LEU
72	WW	23	ARG
72	WW	36	ARG
72	WW	51	GLU
72	WW	52	ILE
72	WW	85	ASP
72	WW	97	ARG
72	WW	103	VAL
73	XX	8	ARG
73	XX	19	ASP
73	XX	61	GLN
73	XX	67	ARG
73	XX	98	ASP
73	XX	105	PHE
73	XX	115	ILE
73	XX	127	ASN
73	XX	129	SER
73	XX	130	LEU
74	YY	9	THR
74	YY	16	ARG
74	YY	17	LEU
74	YY	20	ARG
74	YY	40	ILE
74	YY	47	MET
74	YY	53	ASP
74	YY	61	ARG
74	YY	63	HIS
74	YY	74	MET
74	YY	80	ASP
74	YY	88	LYS
74	YY	101	LYS
74	YY	114	MET
74	YY	115	LYS
75	ZZ	51	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
75	ZZ	58	LEU
75	ZZ	80	ARG
75	ZZ	89	GLN
75	ZZ	92	LEU
76	aa	6	ARG
76	aa	18	VAL
76	aa	19	GLN
76	aa	33	ASP
76	aa	41	ILE
76	aa	42	ARG
76	aa	44	ILE
76	aa	55	GLU
76	aa	96	THR
76	aa	100	ARG
77	bb	17	ARG
77	bb	34	ASP
77	bb	37	CYS
77	bb	42	LYS
77	bb	48	SER
77	bb	64	CYS
77	bb	80	ARG
77	bb	81	ARG
78	cc	20	ARG
78	cc	31	ARG
78	cc	36	ASP
78	cc	40	ARG
78	cc	44	ARG
78	cc	51	ARG
79	dd	6	LEU
79	dd	20	SER
79	dd	22	ARG
80	ee	99	LYS
80	ee	107	ARG
80	ee	109	MET
80	ee	113	ARG
81	ff	83	LYS
81	ff	92	LYS
81	ff	99	LYS
81	ff	132	MET
81	ff	138	ARG
81	ff	140	TYR
82	gg	17	TRP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	gg	20	GLN
82	gg	36	ARG
82	gg	38	LYS
82	gg	113	PHE
82	gg	119	GLN
82	gg	133	ASN
82	gg	198	VAL
82	gg	207	CYS
82	gg	273	GLU
82	gg	287	THR
82	gg	289	LEU
82	gg	298	LEU
82	gg	306	LEU
84	ii	37	ASP
84	ii	40	ARG
84	ii	90	GLU
84	ii	107	ASN
84	ii	112	LEU
84	ii	149	ILE
84	ii	156	MET
84	ii	170	LYS
84	ii	198	HIS
84	ii	243	VAL
84	ii	280	ASP
84	ii	297	LYS
84	ii	311	LEU
84	ii	313	ILE
84	ii	319	ARG
84	ii	349	LEU
85	jj	269	VAL
85	jj	297	GLN
85	jj	298	GLU
85	jj	304	LYS
85	jj	311	TRP
85	jj	313	LEU
85	jj	327	ASP
85	jj	330	MET
85	jj	361	GLN
85	jj	369	VAL
85	jj	385	GLN
85	jj	389	HIS
85	jj	408	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
85	jj	425	LEU
85	jj	434	PHE
85	jj	436	GLU
85	jj	482	ARG
85	jj	489	ARG
85	jj	499	GLN
85	jj	505	ILE
85	jj	585	ILE
85	jj	613	ILE
85	jj	616	LEU
85	jj	640	ASN
85	jj	653	LEU
85	jj	664	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
2	B	167	GLN
2	B	175	GLN
2	B	245	HIS
2	B	354	GLN
3	C	50	GLN
4	D	191	ASN
5	E	131	HIS
5	E	214	HIS
6	F	130	ASN
6	F	191	HIS
6	F	247	ASN
7	G	134	ASN
7	G	135	GLN
9	I	95	HIS
12	M	66	HIS
12	M	70	GLN
13	N	201	HIS
15	P	56	GLN
15	P	97	ASN
15	P	137	ASN
16	Q	44	ASN
17	R	130	ASN
18	S	50	GLN
18	S	125	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	S	163	HIS
19	T	98	HIS
19	T	131	GLN
22	W	17	HIS
22	W	30	GLN
23	X	57	GLN
28	c	78	ASN
29	d	34	HIS
32	g	14	ASN
35	j	76	HIS
40	o	19	GLN
43	s	34	ASN
50	AA	9	GLN
50	AA	132	GLN
51	BB	163	GLN
52	CC	115	GLN
53	DD	22	ASN
53	DD	179	GLN
55	FF	83	ASN
55	FF	118	ASN
56	GG	177	GLN
56	GG	187	HIS
57	HH	126	HIS
58	II	99	ASN
61	LL	100	ASN
63	NN	105	ASN
66	QQ	48	GLN
66	QQ	142	GLN
68	SS	10	GLN
73	XX	77	ASN
77	bb	49	HIS
79	dd	3	HIS
81	ff	93	HIS
82	gg	14	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	72/75 (96%)	17 (23%)	1 (1%)
45	3	72/75 (96%)	21 (29%)	1 (1%)
46	5	3506/3543 (98%)	921 (26%)	179 (5%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	7	119/120 (99%)	19 (15%)	3 (2%)
48	8	149/156 (95%)	39 (26%)	6 (4%)
49	9	1679/1869 (89%)	452 (26%)	88 (5%)
83	hh	7/8 (87%)	4 (57%)	0
All	All	5604/5846 (95%)	1473 (26%)	278 (4%)

All (1473) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	7	A
45	2	13	C
45	2	16	C
45	2	21	A
45	2	25	C
45	2	34	U
45	2	35	U
45	2	36	U
45	2	40	C
45	2	42	G
45	2	47	U
45	2	49	C
45	2	61	C
45	2	63	C
45	2	72	C
45	2	75	C
45	2	76	A
45	3	7	A
45	3	13	C
45	3	14	A
45	3	16	C
45	3	21	A
45	3	25	C
45	3	28	C
45	3	29	A
45	3	34	U
45	3	35	U
45	3	36	U
45	3	40	C
45	3	42	G
45	3	47	U
45	3	49	C
45	3	58	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
45	3	60	U
45	3	61	C
45	3	63	C
45	3	72	C
45	3	76	A
46	5	12	A
46	5	13	U
46	5	14	C
46	5	17	A
46	5	21	G
46	5	25	A
46	5	35	U
46	5	39	A
46	5	42	A
46	5	43	U
46	5	44	A
46	5	48	G
46	5	49	U
46	5	56	A
46	5	58	G
46	5	59	A
46	5	64	A
46	5	65	A
46	5	72	C
46	5	73	A
46	5	75	G
46	5	84	A
46	5	91	G
46	5	93	G
46	5	108	A
46	5	109	G
46	5	110	C
46	5	116	G
46	5	118	C
46	5	119	G
46	5	120	A
46	5	126	C
46	5	134	G
46	5	135	G
46	5	136	C
46	5	137	G
46	5	143	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	144	G
46	5	146	G
46	5	157	U
46	5	159	C
46	5	160	G
46	5	172	C
46	5	173	C
46	5	177	G
46	5	179	G
46	5	197	A
46	5	200	U
46	5	201	C
46	5	202	C
46	5	205	C
46	5	209	U
46	5	216	C
46	5	217	C
46	5	218	A
46	5	220	C
46	5	221	C
46	5	224	U
46	5	226	G
46	5	227	A
46	5	233	U
46	5	234	G
46	5	245	C
46	5	246	G
46	5	253	G
46	5	262	G
46	5	265	C
46	5	266	C
46	5	267	G
46	5	276	C
46	5	279	A
46	5	280	G
46	5	281	U
46	5	297	U
46	5	306	A
46	5	309	C
46	5	310	G
46	5	315	G
46	5	316	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	321	U
46	5	322	C
46	5	328	A
46	5	334	A
46	5	340	C
46	5	347	A
46	5	349	A
46	5	350	C
46	5	357	U
46	5	361	C
46	5	363	A
46	5	365	U
46	5	381	U
46	5	386	A
46	5	387	G
46	5	399	G
46	5	401	G
46	5	406	C
46	5	407	A
46	5	409	G
46	5	410	A
46	5	412	G
46	5	413	G
46	5	414	C
46	5	431	G
46	5	432	U
46	5	433	A
46	5	440	U
46	5	446	C
46	5	449	C
46	5	450	G
46	5	452	A
46	5	453	G
46	5	454	U
46	5	457	G
46	5	463	A
46	5	466	A
46	5	467	U
46	5	468	U
46	5	469	C
46	5	482	G
46	5	483	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	484	U
46	5	485	C
46	5	486	C
46	5	492	U
46	5	493	G
46	5	495	C
46	5	497	G
46	5	498	C
46	5	499	G
46	5	505	G
46	5	510	U
46	5	647	G
46	5	649	A
46	5	654	C
46	5	658	C
46	5	666	G
46	5	667	A
46	5	668	C
46	5	672	C
46	5	683	C
46	5	685	C
46	5	687	U
46	5	696	C
46	5	697	G
46	5	704	C
46	5	705	G
46	5	708	G
46	5	729	G
46	5	730	G
46	5	731	G
46	5	739	G
46	5	742	G
46	5	744	G
46	5	747	A
46	5	748	G
46	5	749	G
46	5	750	U
46	5	758	G
46	5	911	U
46	5	913	U
46	5	914	U
46	5	917	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	918	G
46	5	922(A)	G
46	5	922(B)	C
46	5	923	C
46	5	924	C
46	5	925	C
46	5	926	G
46	5	929	A
46	5	931	C
46	5	932	A
46	5	933	G
46	5	934	C
46	5	936	C
46	5	938	C
46	5	939	G
46	5	941	C
46	5	944	A
46	5	945	U
46	5	956	A
46	5	959	G
46	5	960	A
46	5	961	G
46	5	962	C
46	5	965	G
46	5	966	A
46	5	967	C
46	5	968	C
46	5	969	C
46	5	972	C
46	5	973	G
46	5	979	C
46	5	983	C
46	5	990	C
46	5	1070	G
46	5	1072	C
46	5	1073	G
46	5	1075	G
46	5	1076	C
46	5	1078	A
46	5	1079	C
46	5	1082	C
46	5	1174	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	1179	U
46	5	1195	G
46	5	1209	U
46	5	1210	C
46	5	1211	G
46	5	1212	G
46	5	1214	C
46	5	1215	C
46	5	1234	G
46	5	1235	G
46	5	1236	C
46	5	1237	C
46	5	1238	A
46	5	1239	C
46	5	1272	C
46	5	1273	G
46	5	1274	A
46	5	1275	G
46	5	1276	C
46	5	1280	C
46	5	1284	G
46	5	1287	G
46	5	1288	G
46	5	1291	G
46	5	1292	C
46	5	1293	G
46	5	1295	U
46	5	1296	G
46	5	1301	C
46	5	1303	A
46	5	1304	C
46	5	1326	A
46	5	1329	G
46	5	1330	A
46	5	1337	A
46	5	1354	A
46	5	1359	G
46	5	1364	U
46	5	1370	G
46	5	1371	A
46	5	1377	G
46	5	1378	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	1380	G
46	5	1381	U
46	5	1387	A
46	5	1388	A
46	5	1394	G
46	5	1397	A
46	5	1398	A
46	5	1401	C
46	5	1411(B)	C
46	5	1411(C)	C
46	5	1412	G
46	5	1416	G
46	5	1419	G
46	5	1420	A
46	5	1421	G
46	5	1422	G
46	5	1429	C
46	5	1433	A
46	5	1435	G
46	5	1436	C
46	5	1437	C
46	5	1438	U
46	5	1441	C
46	5	1442	C
46	5	1445	U
46	5	1446	C
46	5	1453	G
46	5	1455	G
46	5	1456	C
46	5	1457	G
46	5	1458	C
46	5	1465	G
46	5	1475	G
46	5	1478	C
46	5	1482	G
46	5	1483	C
46	5	1484	G
46	5	1485	C
46	5	1486	C
46	5	1497	A
46	5	1498	G
46	5	1502	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	1503	A
46	5	1504	G
46	5	1514	U
46	5	1516	G
46	5	1518	A
46	5	1523	A
46	5	1525	A
46	5	1534	A
46	5	1535	C
46	5	1547	A
46	5	1554	A
46	5	1563	A
46	5	1564	A
46	5	1566	C
46	5	1568	C
46	5	1578	U
46	5	1586	G
46	5	1591	U
46	5	1596	U
46	5	1602	U
46	5	1612	G
46	5	1613	A
46	5	1617	G
46	5	1624	G
46	5	1625	G
46	5	1628	C
46	5	1631	A
46	5	1633	G
46	5	1634	A
46	5	1640	C
46	5	1645	C
46	5	1649	U
46	5	1650	A
46	5	1652	U
46	5	1654	G
46	5	1656	U
46	5	1661	C
46	5	1670	G
46	5	1676	C
46	5	1677	U
46	5	1678	C
46	5	1679	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	1683	U
46	5	1691	G
46	5	1694	C
46	5	1724	G
46	5	1729	A
46	5	1733	G
46	5	1734	G
46	5	1740	C
46	5	1741	G
46	5	1742	A
46	5	1750	G
46	5	1753	G
46	5	1755	C
46	5	1756	U
46	5	1757	U
46	5	1761	G
46	5	1763	C
46	5	1764	G
46	5	1768	C
46	5	1772	C
46	5	1773	U
46	5	1776	A
46	5	1781	U
46	5	1787	A
46	5	1799	G
46	5	1803	G
46	5	1804	A
46	5	1805	A
46	5	1812	C
46	5	1819	G
46	5	1821	G
46	5	1822	U
46	5	1828	C
46	5	1833	G
46	5	1834	U
46	5	1835	G
46	5	1836	G
46	5	1837	A
46	5	1842	G
46	5	1855	G
46	5	1867	A
46	5	1869	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	1882	U
46	5	1891	A
46	5	1892	A
46	5	1893	C
46	5	1897	A
46	5	1899	G
46	5	1910	G
46	5	1918	U
46	5	1920	C
46	5	1921	C
46	5	1922	G
46	5	1923	A
46	5	1931	C
46	5	1938	C
46	5	1941	A
46	5	1947	U
46	5	1948	G
46	5	1956	A
46	5	1961	G
46	5	1962	A
46	5	1967	A
46	5	1976	G
46	5	1977	C
46	5	1978	C
46	5	1980	U
46	5	1982	G
46	5	1983	A
46	5	1984	A
46	5	1986	U
46	5	1987	C
46	5	1991	A
46	5	1992	U
46	5	1993	C
46	5	1997	U
46	5	2001	G
46	5	2002	A
46	5	2003	G
46	5	2005	G
46	5	2008	U
46	5	2011	C
46	5	2016	C
46	5	2017	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	2024	G
46	5	2025	A
46	5	2026	A
46	5	2046	G
46	5	2047	A
46	5	2048	U
46	5	2052	G
46	5	2055	G
46	5	2056	G
46	5	2062	C
46	5	2064	G
46	5	2068	C
46	5	2069	A
46	5	2077	C
46	5	2084	U
46	5	2085	G
46	5	2089	G
46	5	2090	U
46	5	2092	G
46	5	2093	G
46	5	2094	C
46	5	2095	A
46	5	2097	A
46	5	2098	G
46	5	2100	G
46	5	2101	A
46	5	2102	G
46	5	2104	A
46	5	2105	A
46	5	2106	G
46	5	2107	A
46	5	2108	G
46	5	2110	G
46	5	2259	G
46	5	2260	C
46	5	2262	G
46	5	2266	C
46	5	2267	U
46	5	2268	A
46	5	2269	C
46	5	2270	G
46	5	2274	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	2275	G
46	5	2277	C
46	5	2279	A
46	5	2288	G
46	5	2289	C
46	5	2300	A
46	5	2301	G
46	5	2313	A
46	5	2314	G
46	5	2333	G
46	5	2344	U
46	5	2348	G
46	5	2351	C
46	5	2352	U
46	5	2360	A
46	5	2364	G
46	5	2366	A
46	5	2370	A
46	5	2372	U
46	5	2395	A
46	5	2396	A
46	5	2399	G
46	5	2402	G
46	5	2416	G
46	5	2417	A
46	5	2421	G
46	5	2422	C
46	5	2425	U
46	5	2433	G
46	5	2441	C
46	5	2447	U
46	5	2450	G
46	5	2453	A
46	5	2467	U
46	5	2468	U
46	5	2470	C
46	5	2471	G
46	5	2475	G
46	5	2483	G
46	5	2485	U
46	5	2488	C
46	5	2489	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	2490	U
46	5	2491	C
46	5	2495	U
46	5	2503	G
46	5	2504	C
46	5	2505	C
46	5	2506	G
46	5	2513	A
46	5	2521	G
46	5	2530	U
46	5	2537	A
46	5	2546	G
46	5	2547	G
46	5	2549	G
46	5	2553	A
46	5	2554	U
46	5	2555	G
46	5	2566	G
46	5	2575	U
46	5	2583	C
46	5	2586	G
46	5	2587	A
46	5	2601	A
46	5	2611	A
46	5	2612	G
46	5	2620	G
46	5	2627	C
46	5	2638	G
46	5	2639	U
46	5	2640	G
46	5	2647	A
46	5	2660	A
46	5	2661	U
46	5	2662	G
46	5	2663	G
46	5	2669	C
46	5	2670	C
46	5	2676	A
46	5	2679	G
46	5	2681	G
46	5	2686	G
46	5	2687	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	2695	A
46	5	2696	A
46	5	2704	C
46	5	2707	U
46	5	2708	U
46	5	2709	C
46	5	2710	C
46	5	2711	G
46	5	2712	G
46	5	2714	G
46	5	2716	C
46	5	2719	C
46	5	2721	G
46	5	2724	G
46	5	2725	A
46	5	2726	G
46	5	2740	U
46	5	2743	A
46	5	2744	A
46	5	2754	G
46	5	2760	G
46	5	2761	U
46	5	2763	U
46	5	2764	A
46	5	2769	U
46	5	2772	C
46	5	2787	A
46	5	2788	U
46	5	2789	A
46	5	2790	U
46	5	2795	A
46	5	2798	A
46	5	2799	G
46	5	2806	A
46	5	2807	A
46	5	2808	G
46	5	2814	C
46	5	2826	U
46	5	2827	G
46	5	2828	U
46	5	2829	U
46	5	2835	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	2838	G
46	5	2842	G
46	5	2844	A
46	5	2846	G
46	5	2855	G
46	5	2869	U
46	5	2879	A
46	5	2884	G
46	5	2896	G
46	5	2897	G
46	5	3598	C
46	5	3599	A
46	5	3604	A
46	5	3605	C
46	5	3606	U
46	5	3615	G
46	5	3618	C
46	5	3620	G
46	5	3621	A
46	5	3625	G
46	5	3626	G
46	5	3635	A
46	5	3644	U
46	5	3653	A
46	5	3662	A
46	5	3673	C
46	5	3674	G
46	5	3692	A
46	5	3696	C
46	5	3698	G
46	5	3711	A
46	5	3712	A
46	5	3722	G
46	5	3729	U
46	5	3740	G
46	5	3747	A
46	5	3748	A
46	5	3750	G
46	5	3753	G
46	5	3759	A
46	5	3760	A
46	5	3761	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	3765	G
46	5	3773	U
46	5	3774	A
46	5	3776	G
46	5	3777	G
46	5	3778	U
46	5	3780	G
46	5	3784	A
46	5	3786	U
46	5	3798	U
46	5	3799	A
46	5	3809	G
46	5	3810	C
46	5	3811	G
46	5	3813	A
46	5	3814	U
46	5	3817	A
46	5	3819	G
46	5	3822	U
46	5	3831	U
46	5	3839	G
46	5	3840	U
46	5	3859	G
46	5	3867	A
46	5	3876	A
46	5	3877	A
46	5	3878	C
46	5	3879	G
46	5	3880	G
46	5	3888	G
46	5	3889	G
46	5	3892	U
46	5	3897	G
46	5	3901	A
46	5	3905	A
46	5	3906	A
46	5	3907	G
46	5	3914	U
46	5	3915	U
46	5	3916	G
46	5	3917	A
46	5	3923	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	3926	C
46	5	3927	U
46	5	3939	G
46	5	3943	A
46	5	4067	U
46	5	4069	U
46	5	4073	A
46	5	4076	G
46	5	4084	G
46	5	4085	A
46	5	4086	G
46	5	4088	C
46	5	4092	G
46	5	4099	G
46	5	4100	C
46	5	4116	C
46	5	4117	U
46	5	4118	U
46	5	4119	C
46	5	4120	U
46	5	4121	G
46	5	4122	G
46	5	4125	C
46	5	4127	A
46	5	4136	G
46	5	4138	C
46	5	4161	G
46	5	4162	C
46	5	4163	U
46	5	4164	C
46	5	4165	C
46	5	4166	G
46	5	4171	C
46	5	4183	G
46	5	4184	G
46	5	4191	G
46	5	4197	G
46	5	4201	G
46	5	4203	A
46	5	4205	A
46	5	4212	A
46	5	4213	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	4214	A
46	5	4218	U
46	5	4219	A
46	5	4221	C
46	5	4222	G
46	5	4225	G
46	5	4229	U
46	5	4232	U
46	5	4233	A
46	5	4237	C
46	5	4251	A
46	5	4255	A
46	5	4257	A
46	5	4258	C
46	5	4266	G
46	5	4267	G
46	5	4268	A
46	5	4271	A
46	5	4273	A
46	5	4281	A
46	5	4291	G
46	5	4297	G
46	5	4304	A
46	5	4305	G
46	5	4306	U
46	5	4307	A
46	5	4311	A
46	5	4314	C
46	5	4317	A
46	5	4319	C
46	5	4329	G
46	5	4330	G
46	5	4331	G
46	5	4335	C
46	5	4336	A
46	5	4349	C
46	5	4350	C
46	5	4354	U
46	5	4355	G
46	5	4368	G
46	5	4373	G
46	5	4376	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	4377	G
46	5	4378	A
46	5	4379	A
46	5	4380	A
46	5	4382	G
46	5	4387	C
46	5	4391	G
46	5	4394	A
46	5	4395	U
46	5	4396	A
46	5	4398	C
46	5	4401	G
46	5	4415	A
46	5	4419	U
46	5	4421	C
46	5	4422	A
46	5	4433	G
46	5	4437	U
46	5	4438	U
46	5	4440	G
46	5	4444	C
46	5	4447	C
46	5	4448	G
46	5	4449	A
46	5	4450	U
46	5	4453	C
46	5	4463	U
46	5	4464	A
46	5	4466	C
46	5	4471	U
46	5	4475	G
46	5	4476	C
46	5	4487	A
46	5	4488	A
46	5	4489	G
46	5	4495	G
46	5	4500	U
46	5	4511	A
46	5	4512	U
46	5	4513	A
46	5	4515	G
46	5	4518	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	4519	C
46	5	4520	G
46	5	4524	G
46	5	4531	U
46	5	4532	U
46	5	4548	A
46	5	4549	G
46	5	4560	C
46	5	4567	G
46	5	4572	U
46	5	4573	G
46	5	4575	G
46	5	4578	G
46	5	4584	A
46	5	4585	U
46	5	4586	G
46	5	4589	A
46	5	4590	A
46	5	4599	A
46	5	4606	G
46	5	4635	A
46	5	4636	U
46	5	4637	G
46	5	4652	G
46	5	4656	A
46	5	4661	G
46	5	4668	U
46	5	4670	C
46	5	4672	A
46	5	4677	U
46	5	4678	G
46	5	4682	U
46	5	4694	G
46	5	4699	U
46	5	4700	A
46	5	4701	A
46	5	4709	U
46	5	4719	G
46	5	4720	C
46	5	4721	G
46	5	4728	U
46	5	4729	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	4736	C
46	5	4737	G
46	5	4745	G
46	5	4751	G
46	5	4754	G
46	5	4755	G
46	5	4756	C
46	5	4757	C
46	5	4759	C
46	5	4761	G
46	5	4764	A
46	5	4765	G
46	5	4771	C
46	5	4772	C
46	5	4868	G
46	5	4870	G
46	5	4871	C
46	5	4872	G
46	5	4873	G
46	5	4874	A
46	5	4875	G
46	5	4876	A
46	5	4877	G
46	5	4881	U
46	5	4882	U
46	5	4883	C
46	5	4885	U
46	5	4887	C
46	5	4891	G
46	5	4895	C
46	5	4897	G
46	5	4910	A
46	5	4911	A
46	5	4913	G
46	5	4914	G
46	5	4915	G
46	5	4919	G
46	5	4921	C
46	5	4922	C
46	5	4924	C
46	5	4926	C
46	5	4927	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	4928	C
46	5	4931	G
46	5	4935	C
46	5	4937	C
46	5	4938	A
46	5	4940	C
46	5	4943	A
46	5	4944	C
46	5	4945	G
46	5	4948	C
46	5	4949	G
46	5	4950	U
46	5	4951	G
46	5	4956	A
46	5	4957	C
46	5	4958	C
46	5	4964	C
46	5	4965	U
46	5	4966	A
46	5	4967	A
46	5	4976	U
46	5	4985	U
46	5	4988	U
46	5	4989	U
46	5	4990	C
46	5	4991	U
46	5	4994	G
46	5	4997	G
46	5	4999	G
46	5	5007	A
46	5	5013	C
46	5	5014	A
46	5	5017	G
46	5	5035	U
46	5	5040	U
46	5	5041	G
46	5	5047	C
46	5	5050	C
46	5	5053	U
46	5	5054	C
46	5	5056	A
46	5	5061	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	5062	G
46	5	5066	U
47	7	7	G
47	7	10	C
47	7	22	A
47	7	25	G
47	7	33	U
47	7	38	U
47	7	41	G
47	7	42	A
47	7	53	U
47	7	54	A
47	7	64	G
47	7	76	U
47	7	97	G
47	7	99	G
47	7	100	A
47	7	109	U
47	7	110	G
47	7	111	C
47	7	120	U
48	8	2	G
48	8	3	A
48	8	22	U
48	8	23	C
48	8	32	C
48	8	34	U
48	8	35	C
48	8	49	G
48	8	51	U
48	8	52	A
48	8	57	C
48	8	59	A
48	8	62	A
48	8	63	U
48	8	75	G
48	8	79	G
48	8	86	U
48	8	87	G
48	8	94	G
48	8	95	A
48	8	99	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	8	101	C
48	8	103	A
48	8	104	A
48	8	105	C
48	8	109	C
48	8	110	U
48	8	111	U
48	8	112	G
48	8	114	G
48	8	121	G
48	8	123	U
48	8	124	U
48	8	125	C
48	8	126	C
48	8	127	U
48	8	137	A
48	8	143	G
48	8	156	U
49	9	2	A
49	9	3	C
49	9	4	C
49	9	17	C
49	9	25	A
49	9	26	U
49	9	33	G
49	9	37	C
49	9	41	G
49	9	44	U
49	9	45	A
49	9	46	A
49	9	56	G
49	9	58	C
49	9	60	A
49	9	63	U
49	9	65	C
49	9	67	C
49	9	68	A
49	9	70	G
49	9	71	G
49	9	73	C
49	9	74	G
49	9	75	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	77	A
49	9	79	A
49	9	99	A
49	9	100	U
49	9	103	A
49	9	104	A
49	9	110	U
49	9	111	A
49	9	113	G
49	9	115	U
49	9	116	U
49	9	124	U
49	9	126	G
49	9	127	C
49	9	128	U
49	9	129	C
49	9	130	G
49	9	141	A
49	9	142	C
49	9	143	U
49	9	147	A
49	9	155	G
49	9	158	A
49	9	161	U
49	9	162	C
49	9	163	U
49	9	167	G
49	9	168	C
49	9	173	A
49	9	175	A
49	9	182	C
49	9	183	G
49	9	184	G
49	9	188	C
49	9	189	U
49	9	191	A
49	9	192	C
49	9	200	G
49	9	202	G
49	9	206	G
49	9	213	G
49	9	215	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	292	A
49	9	302	A
49	9	304	C
49	9	307	G
49	9	308	G
49	9	309	G
49	9	312	G
49	9	314	U
49	9	317	C
49	9	318	A
49	9	319	C
49	9	322	C
49	9	331	C
49	9	332	G
49	9	340	C
49	9	347	G
49	9	351	G
49	9	360	A
49	9	362	C
49	9	363	A
49	9	364	A
49	9	368	U
49	9	370	G
49	9	371	A
49	9	372	U
49	9	379	C
49	9	381	C
49	9	382	C
49	9	383	G
49	9	384	U
49	9	385	G
49	9	386	C
49	9	398	A
49	9	400	C
49	9	407	G
49	9	409	C
49	9	417	C
49	9	418	A
49	9	434	G
49	9	435	A
49	9	438	G
49	9	441	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	448	A
49	9	449	A
49	9	450	C
49	9	452	G
49	9	459	C
49	9	460	A
49	9	462	C
49	9	463	C
49	9	464	A
49	9	465	A
49	9	466	G
49	9	472	C
49	9	473	A
49	9	474	G
49	9	476	A
49	9	482	G
49	9	485	A
49	9	487	U
49	9	492	C
49	9	496	C
49	9	501	C
49	9	508	A
49	9	523	A
49	9	525	A
49	9	531	A
49	9	532	C
49	9	533	A
49	9	544	G
49	9	545	A
49	9	546	G
49	9	548	C
49	9	549	C
49	9	550	C
49	9	551	U
49	9	554	A
49	9	555	A
49	9	556	U
49	9	559	G
49	9	560	A
49	9	562	U
49	9	563	G
49	9	564	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	568	C
49	9	576	A
49	9	583	A
49	9	587	A
49	9	588	G
49	9	589	G
49	9	590	A
49	9	591	U
49	9	592	C
49	9	594	A
49	9	595	U
49	9	597	G
49	9	604	A
49	9	606	G
49	9	607	U
49	9	608	C
49	9	613	G
49	9	614	C
49	9	615	C
49	9	616	A
49	9	617	G
49	9	620	G
49	9	626	G
49	9	627	U
49	9	628	A
49	9	629	A
49	9	631	U
49	9	632	C
49	9	643	A
49	9	644	G
49	9	646	G
49	9	659	G
49	9	660	C
49	9	663	C
49	9	664	A
49	9	668	A
49	9	669	A
49	9	670	A
49	9	671	A
49	9	672	A
49	9	678	U
49	9	684	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	688	U
49	9	689	U
49	9	696	G
49	9	733	C
49	9	752	G
49	9	753	C
49	9	754	G
49	9	798	G
49	9	811	A
49	9	812	A
49	9	821	G
49	9	822	U
49	9	827	A
49	9	830	A
49	9	834	C
49	9	844	U
49	9	847	A
49	9	869	A
49	9	870	A
49	9	871	U
49	9	872	A
49	9	873	G
49	9	874	G
49	9	875	A
49	9	876	C
49	9	877	C
49	9	878	G
49	9	885	U
49	9	887	U
49	9	890	U
49	9	892	U
49	9	913	A
49	9	914	U
49	9	919	A
49	9	920	A
49	9	921	G
49	9	922	A
49	9	930	C
49	9	933	G
49	9	934	G
49	9	943	U
49	9	954	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	971	G
49	9	985	G
49	9	990	A
49	9	992	A
49	9	999	G
49	9	1016	U
49	9	1017	U
49	9	1023	A
49	9	1032	C
49	9	1041	G
49	9	1044	G
49	9	1055	A
49	9	1060	A
49	9	1061	U
49	9	1062	A
49	9	1078	C
49	9	1082	A
49	9	1083	A
49	9	1085	C
49	9	1086	G
49	9	1089	G
49	9	1100	A
49	9	1111	U
49	9	1115	U
49	9	1116	C
49	9	1117	C
49	9	1118	C
49	9	1119	A
49	9	1121	G
49	9	1123	C
49	9	1131	G
49	9	1133	A
49	9	1138	C
49	9	1139	C
49	9	1143	A
49	9	1144	A
49	9	1148	A
49	9	1149	A
49	9	1153	C
49	9	1154	U
49	9	1157	G
49	9	1161	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	1165	G
49	9	1166	G
49	9	1195	A
49	9	1196	A
49	9	1207	G
49	9	1208	A
49	9	1211	G
49	9	1214	A
49	9	1215	C
49	9	1216	C
49	9	1224	G
49	9	1240	A
49	9	1242	U
49	9	1251	A
49	9	1253	A
49	9	1254	C
49	9	1255	G
49	9	1256	G
49	9	1257	G
49	9	1259	A
49	9	1260	A
49	9	1265	A
49	9	1266	C
49	9	1271	C
49	9	1274	G
49	9	1275	G
49	9	1280	G
49	9	1281	G
49	9	1284	A
49	9	1285	G
49	9	1286	G
49	9	1287	A
49	9	1293	A
49	9	1298	G
49	9	1299	A
49	9	1300	U
49	9	1301	A
49	9	1302	G
49	9	1303	C
49	9	1304	U
49	9	1307	U
49	9	1308	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	1313	A
49	9	1314	U
49	9	1316	C
49	9	1330	G
49	9	1331	C
49	9	1342	U
49	9	1345	G
49	9	1348	G
49	9	1354	G
49	9	1369	A
49	9	1371	U
49	9	1372	U
49	9	1376	A
49	9	1378	A
49	9	1395	C
49	9	1396	A
49	9	1397	U
49	9	1402	A
49	9	1404	U
49	9	1405	A
49	9	1412	C
49	9	1424	G
49	9	1428	G
49	9	1429	G
49	9	1439	A
49	9	1449	G
49	9	1454	A
49	9	1455	A
49	9	1459	G
49	9	1462	U
49	9	1463	U
49	9	1466	G
49	9	1473	G
49	9	1475	G
49	9	1476	A
49	9	1477	U
49	9	1478	U
49	9	1480	A
49	9	1487	A
49	9	1490	G
49	9	1494	U
49	9	1498	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	1509	U
49	9	1510	G
49	9	1519	U
49	9	1520	G
49	9	1521	C
49	9	1522	A
49	9	1523	C
49	9	1531	A
49	9	1533	A
49	9	1536	G
49	9	1544	C
49	9	1545	A
49	9	1548	G
49	9	1552	G
49	9	1553	C
49	9	1555	U
49	9	1556	A
49	9	1557	C
49	9	1560	U
49	9	1570	G
49	9	1574	C
49	9	1575	G
49	9	1580	A
49	9	1581	C
49	9	1582	C
49	9	1585	U
49	9	1587	G
49	9	1588	A
49	9	1600	G
49	9	1601	A
49	9	1604	G
49	9	1621	U
49	9	1623	A
49	9	1625	U
49	9	1633	A
49	9	1637	A
49	9	1638	G
49	9	1639	G
49	9	1641	A
49	9	1647	A
49	9	1648	G
49	9	1649	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	1654	G
49	9	1663	A
49	9	1664	A
49	9	1665	G
49	9	1667	U
49	9	1671	G
49	9	1680	G
49	9	1683	C
49	9	1695	A
49	9	1698	C
49	9	1715	A
49	9	1721	U
49	9	1722	G
49	9	1726	G
49	9	1728	U
49	9	1729	U
49	9	1730	U
49	9	1732	G
49	9	1744	G
49	9	1745	A
49	9	1746	U
49	9	1753	C
49	9	1758	G
49	9	1760	G
49	9	1772	C
49	9	1783	C
49	9	1785	C
49	9	1800	A
49	9	1801	A
49	9	1805	G
49	9	1823	A
49	9	1824	A
49	9	1825	A
49	9	1826	G
49	9	1829	G
49	9	1831	A
49	9	1834	A
49	9	1835	A
49	9	1836	G
49	9	1838	U
49	9	1839	U
49	9	1849	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	1851	A
49	9	1861	G
49	9	1862	G
49	9	1863	A
49	9	1865	C
49	9	1866	A
49	9	1867	U
49	9	1869	A
83	hh	42	A
83	hh	43	A
83	hh	45	A
83	hh	46	A

All (278) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	2	71	G
45	3	74	C
46	5	12	A
46	5	20	U
46	5	47	A
46	5	48	G
46	5	64	A
46	5	90	G
46	5	119	G
46	5	125	C
46	5	134	G
46	5	143	C
46	5	159	C
46	5	217	C
46	5	224	U
46	5	226	G
46	5	232	G
46	5	245	C
46	5	265	C
46	5	275	C
46	5	278	G
46	5	308	G
46	5	315	G
46	5	385	A
46	5	406	C
46	5	409	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	417	G
46	5	449	C
46	5	453	G
46	5	484	U
46	5	485	C
46	5	492	U
46	5	497	G
46	5	498	C
46	5	504	G
46	5	696	C
46	5	725	G
46	5	728	U
46	5	729	G
46	5	738(A)	C
46	5	746	A
46	5	747	A
46	5	916	C
46	5	922	C
46	5	922(B)	C
46	5	930	G
46	5	935(A)	G
46	5	936	C
46	5	955	G
46	5	956	A
46	5	959	G
46	5	966	A
46	5	968	C
46	5	969	C
46	5	971(A)	G
46	5	978	G
46	5	1072	C
46	5	1209	U
46	5	1211	G
46	5	1214	C
46	5	1236	C
46	5	1238	A
46	5	1287	G
46	5	1291	G
46	5	1295	U
46	5	1324	A
46	5	1329	G
46	5	1358	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	1370	G
46	5	1378	C
46	5	1432	G
46	5	1440	U
46	5	1445	U
46	5	1455	G
46	5	1477	C
46	5	1481	C
46	5	1484	G
46	5	1485	C
46	5	1497	A
46	5	1502	G
46	5	1625	G
46	5	1633	G
46	5	1654	G
46	5	1678	C
46	5	1724	G
46	5	1733	G
46	5	1740	C
46	5	1804	A
46	5	1818	G
46	5	1833	G
46	5	1834	U
46	5	1835	G
46	5	1892	A
46	5	1908	A
46	5	1921	C
46	5	1947	U
46	5	1983	A
46	5	1986	U
46	5	2046	G
46	5	2054	U
46	5	2068	C
46	5	2088	A
46	5	2089	G
46	5	2090	U
46	5	2100	G
46	5	2103	A
46	5	2265	G
46	5	2266	C
46	5	2278	G
46	5	2313	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	2396	A
46	5	2398	U
46	5	2425	U
46	5	2428	A
46	5	2467	U
46	5	2474	G
46	5	2475	G
46	5	2490	U
46	5	2502	A
46	5	2530	U
46	5	2546	G
46	5	2553	A
46	5	2661	U
46	5	2695	A
46	5	2696	A
46	5	2724	G
46	5	2754	G
46	5	2769	U
46	5	2789	A
46	5	2806	A
46	5	3603	G
46	5	3625	G
46	5	3673	C
46	5	3697	U
46	5	3710	G
46	5	3759	A
46	5	3760	A
46	5	3765	G
46	5	3809	G
46	5	3876	A
46	5	3888	G
46	5	3904	G
46	5	4075	U
46	5	4076	G
46	5	4084	G
46	5	4116	C
46	5	4119	C
46	5	4121	G
46	5	4124	G
46	5	4157	A
46	5	4162	C
46	5	4170	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5	4204	C
46	5	4221	C
46	5	4232	U
46	5	4254	G
46	5	4266	G
46	5	4291	G
46	5	4331	G
46	5	4378	A
46	5	4379	A
46	5	4395	U
46	5	4448	G
46	5	4449	A
46	5	4463	U
46	5	4475	G
46	5	4527	G
46	5	4583	C
46	5	4635	A
46	5	4671	C
46	5	4699	U
46	5	4718	G
46	5	4719	G
46	5	4873	G
46	5	4884	G
46	5	4925	U
46	5	4936	G
46	5	4942	C
46	5	4947	U
46	5	4965	U
46	5	5013	C
47	7	10	C
47	7	41	G
47	7	109	U
48	8	23	C
48	8	51	U
48	8	86	U
48	8	94	G
48	8	110	U
48	8	124	U
49	9	2	A
49	9	3	C
49	9	25	A
49	9	72	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	87	U
49	9	98	C
49	9	110	U
49	9	126	G
49	9	127	C
49	9	128	U
49	9	142	C
49	9	160	U
49	9	182	C
49	9	191	A
49	9	214	U
49	9	293	C
49	9	312	G
49	9	314	U
49	9	360	A
49	9	363	A
49	9	369	C
49	9	434	G
49	9	448	A
49	9	465	A
49	9	516	A
49	9	532	C
49	9	553	U
49	9	555	A
49	9	559	G
49	9	563	G
49	9	587	A
49	9	591	U
49	9	594	A
49	9	613	G
49	9	626	G
49	9	627	U
49	9	628	A
49	9	642	U
49	9	670	A
49	9	688	U
49	9	752	G
49	9	821	G
49	9	869	A
49	9	870	A
49	9	872	A
49	9	875	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	9	1016	U
49	9	1087	A
49	9	1114	U
49	9	1137	U
49	9	1165	G
49	9	1253	A
49	9	1259	A
49	9	1264	C
49	9	1274	G
49	9	1284	A
49	9	1285	G
49	9	1313	A
49	9	1330	G
49	9	1394	G
49	9	1395	C
49	9	1396	A
49	9	1454	A
49	9	1476	A
49	9	1489	A
49	9	1493	C
49	9	1519	U
49	9	1520	G
49	9	1535	U
49	9	1578	U
49	9	1581	C
49	9	1584	G
49	9	1621	U
49	9	1636	G
49	9	1637	A
49	9	1646	C
49	9	1663	A
49	9	1664	A
49	9	1679	A
49	9	1682	C
49	9	1697	A
49	9	1721	U
49	9	1744	G
49	9	1824	A
49	9	1825	A
49	9	1835	A
49	9	1867	U
49	9	1868	U

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 245 ligands modelled in this entry, 244 are 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	$\# Z > 2$
88	GCP	jj	700	86	29,34,34	2.50	8 (27%)	31,54,54	1.07	2 (6%)

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
88	GCP	jj	700	86	-	0/18/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	jj	700	GCP	C4-N9	-10.26	1.34	1.47
88	jj	700	GCP	C8-N9	-3.77	1.35	1.47
88	jj	700	GCP	C5-C6	-2.10	1.49	1.53
88	jj	700	GCP	PB-C3B	2.03	1.82	1.80
88	jj	700	GCP	PB-O2B	2.07	1.61	1.56
88	jj	700	GCP	PG-O3G	2.56	1.61	1.54
88	jj	700	GCP	PG-O2G	2.63	1.61	1.54
88	jj	700	GCP	C1'-N9	3.99	1.49	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	jj	700	GCP	C4-C5-N7	2.32	106.29	102.67
88	jj	700	GCP	C8-N9-C4	3.06	108.27	104.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	5	42
49	9	7
45	2	2
45	3	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.66
1	5	1252:C	O3'	1271:G	P	36.39
1	5	1405:C	O3'	1406:G	P	23.89
1	5	1219:G	O3'	1233:G	P	22.08
1	5	1406:G	O3'	1406(A):G	P	20.74
1	5	3948:C	O3'	4065:G	P	19.58
1	5	523:C	O3'	638:G	P	18.11
1	5	4138:C	O3'	4146:G	P	17.87
1	5	990:C	O3'	1064:G	P	17.71
1	5	4101:C	O3'	4107:G	P	17.24
1	5	4777:C	O3'	4859:C	P	16.45
1	5	5022:U	O3'	5028:G	P	15.42
1	5	760:G	O3'	904:C	P	15.08

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1696:C	O3'	1720:C	P	14.92
1	5	1364:U	O3'	1368:A	P	14.40
1	5	182:G	O3'	189:G	P	13.89
1	5	2901:G	O3'	3597:G	P	13.20
1	5	1406(C):G	O3'	1411:C	P	13.13
1	5	1411:C	O3'	1411(A):G	P	12.97
1	5	481:G	O3'	481(A):C	P	12.34
1	5	921:C	O3'	922:C	P	12.33
1	5	934:C	O3'	935:A	P	10.70
1	5	970:G	O3'	971:U	P	10.66
1	5	737:C	O3'	738:C	P	10.59
1	5	971:U	O3'	971(A):G	P	9.97
1	5	512:U	O3'	515:C	P	9.68
1	5	4729:A	O3'	4735:G	P	9.50
1	5	1180:C	O3'	1183:C	P	9.31
1	5	500:G	O3'	504:G	P	7.18
1	5	1100:U	O3'	1168:G	P	6.11
1	3	19:G	O3'	20:U	P	5.51
1	2	19:G	O3'	20:U	P	5.30
1	5	4740:G	O3'	4743:G	P	5.20
1	2	16:C	O3'	18:U	P	5.18
1	5	480:C	O3'	481:G	P	5.17
1	9	322:C	O3'	323:C	P	5.05
1	3	16:C	O3'	18:U	P	4.93
1	9	304:C	O3'	305:U	P	4.29
1	9	798:G	O3'	799:U	P	4.28
1	9	309:G	O3'	310:C	P	4.21
1	5	1239:C	O3'	1244:G	P	4.20
1	5	935:A	O3'	935(A):G	P	4.08
1	5	170:C	O3'	171:U	P	3.84
1	5	1438:U	O3'	1440:U	P	3.64
1	5	4899:G	O3'	4902:C	P	3.41
1	9	902:G	O3'	903:A	P	3.38
1	5	738:C	O3'	738(A):C	P	3.34
1	9	903:A	O3'	904:A	P	3.30
1	9	1295:A	O3'	1296:U	P	3.19
1	5	267:G	O3'	268:G	P	3.10
1	5	5020:G	O3'	5021:C	P	3.05
1	5	751:G	O3'	752:G	P	3.02
1	5	2031:C	O3'	2032:U	P	2.80