



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 02:10 AM UTC

PDB ID : 3JBP / pdb_00003jbp
EMDB ID : EMD-6454
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to E-tRNA
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.
Deposited on : 2015-09-16
Resolution : 6.70 Å (reported)
Based on initial models : 3J7A, 3J79

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

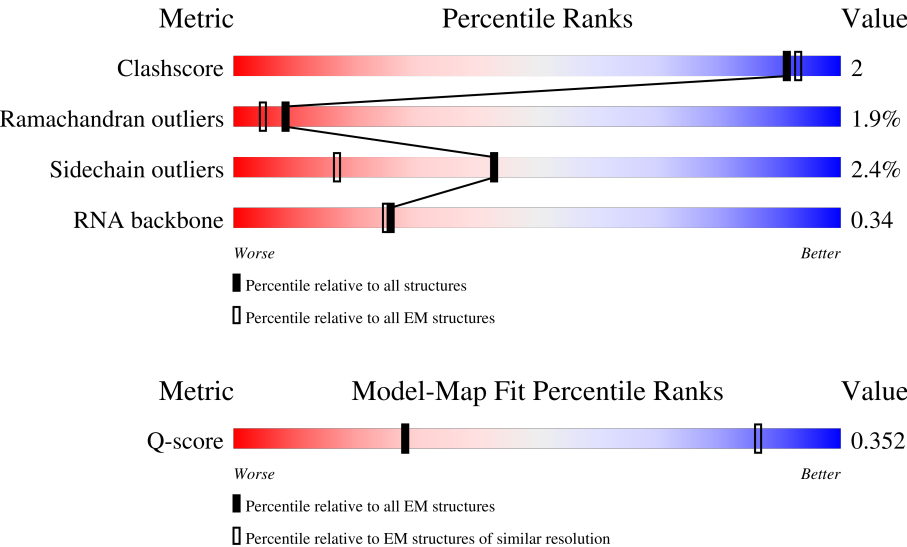
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 6.70 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.



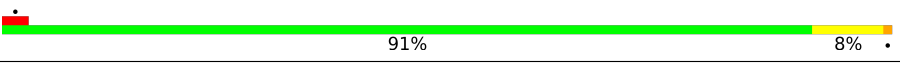
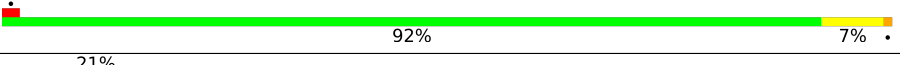
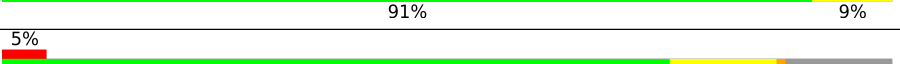
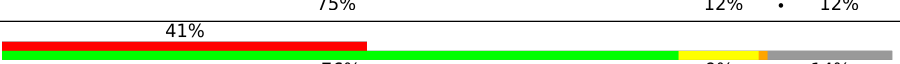
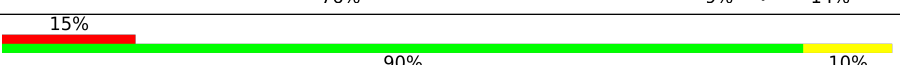
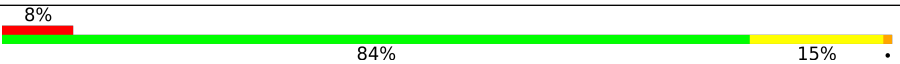
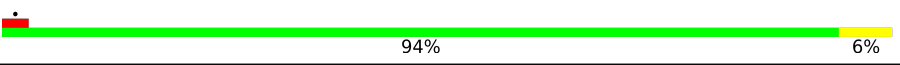
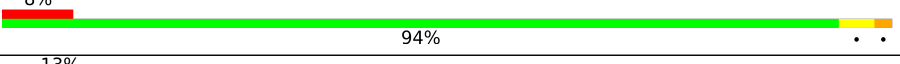
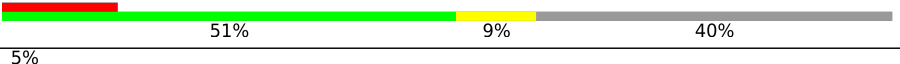
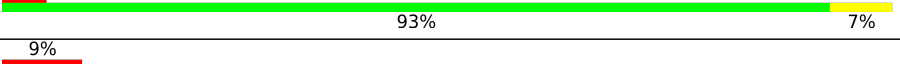
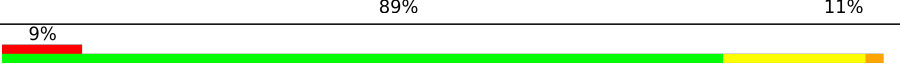
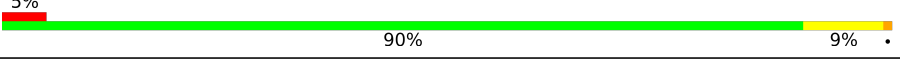
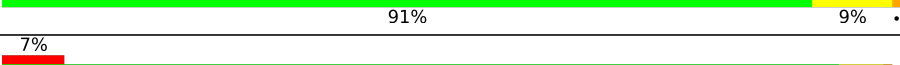
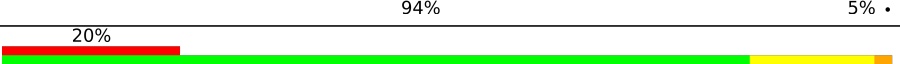
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1608	51% 35% 12% •
2	7	74	22% 32% 42% 19% 7%
3	D	209	9% 71% • 25%

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Mol	Chain	Length	Quality of chain
4	E	185	
5	G	224	
6	I	189	
7	K	129	
8	M	138	
9	W	108	
10	R	114	
11	O	79	
12	Y	154	
13	Z	72	
14	1	120	
15	2	68	
16	3	95	
17	4	76	
18	5	65	
19	6	43	
20	B	210	
21	F	257	
22	H	214	
23	J	188	
24	L	214	
25	N	98	
26	P	127	
27	Q	144	
28	S	128	

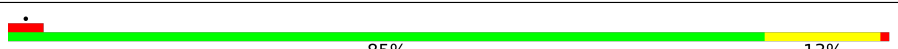
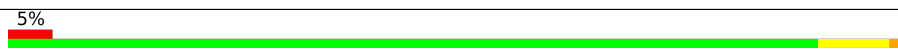
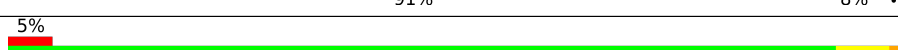
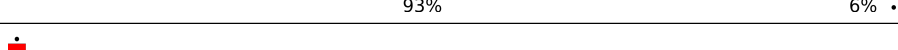
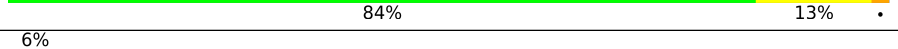
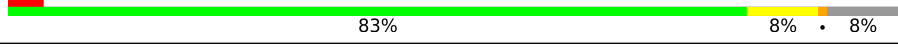
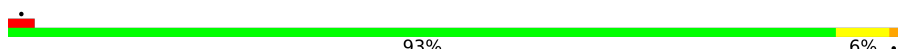
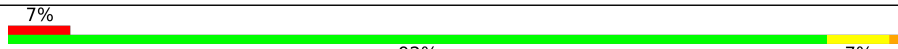
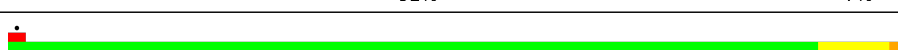
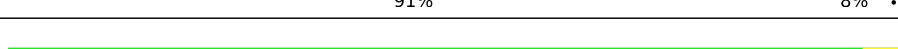
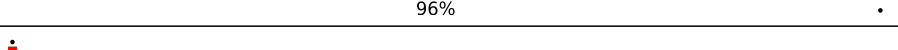
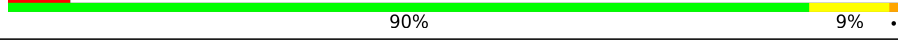
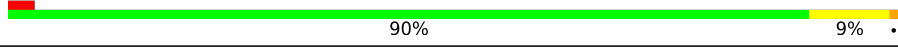
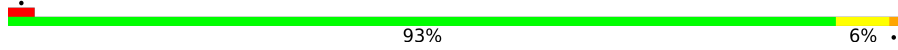
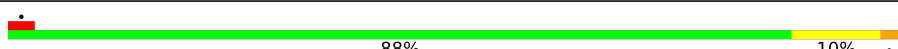
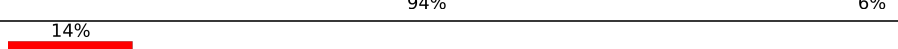
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Mol	Chain	Length	Quality of chain
29	T	48	
30	U	149	
31	V	156	
32	X	103	
33	C	195	
34	AA	3193	
35	AC	151	
36	AB	118	
37	AL	211	
38	A1	145	
39	A2	118	
40	A4	66	
41	A6	98	
42	A7	102	
43	AN	146	
44	A8	125	
45	A9	103	
46	Aa	106	
47	Ab	105	
48	Ad	76	
49	Ae	50	
50	Af	51	
51	AP	204	
52	Ah	85	
53	Ai	95	

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Mol	Chain	Length	Quality of chain
54	AI	213	
55	AJ	244	
56	Ac	89	
57	AK	201	
58	AM	132	
59	AS	186	
60	AO	147	
61	AQ	205	
62	AR	289	
63	AW	170	
64	AY	101	
65	AT	181	
66	AZ	121	
67	A3	119	
68	A5	223	
69	AD	247	
70	AE	380	
71	AF	390	
72	AG	159	
73	AU	180	
74	AH	185	
75	AV	155	
76	Ag	37	
77	AX	97	
78	A0	62	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193012 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1608	Total	C	N	O	P	0	0
			34207	15346	6106	11169	1586		

- Molecule 2 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 3 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	157	Total	C	N	O	S	0	0
			1229	782	225	215	7		

- Molecule 4 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	185	Total	C	N	O	S	0	0
			1515	962	290	261	2		

- Molecule 5 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	224	Total	C	N	O	S	0	0
			1758	1132	307	310	9		

- Molecule 6 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 7 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 8 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	138	Total	C	N	O	S	0	0
			1099	704	200	194	1		

- Molecule 9 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	95	Total	C	N	O	S	0	0
			786	498	149	136	3		

- Molecule 10 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	98	Total	C	N	O	S	0	0
			747	474	123	146	4		

- Molecule 11 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	79	Total	C	N	O	S	0	0
			687	450	116	119	2		

- Molecule 12 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Y	154	Total	C	N	O	S	0	0
			1267	811	239	215	2		

- Molecule 13 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Z	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 14 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1	120	Total	C	N	O	S	0	0
			986	632	189	163	2		

- Molecule 15 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2	41	Total	C	N	O		0	0
			321	208	56	57			

- Molecule 16 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 17 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 18 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	58	Total	C	N	O		0	0
			458	285	93	80			

- Molecule 19 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	6	43	Total	C	N	O		0	0
			346	213	75	58			

- Molecule 20 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	B	210	Total	C	N	O	S	0	0
			1714	1097	301	304	12		

- Molecule 21 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	F	257	Total	C	N	O	S	0	0
			2062	1320	377	357	8		

- Molecule 22 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H	204	Total	C	N	O	S	0	0
			1648	1045	313	284	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	158	ILE	-	insertion	UNP Q8IDR9
H	195	ASP	GLU	conflict	UNP Q8IDR9

- Molecule 23 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J	188	Total	C	N	O	S	0	0
			1529	982	264	279	4		

- Molecule 24 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 25 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	N	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 26 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 27 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 28 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	128	Total	C	N	O	S	0	0
			1047	657	205	181	4		

- Molecule 29 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 30 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 31 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 32 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	96	Total	C	N	O	S	0	0
			777	497	137	139	4		

- Molecule 33 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	195	Total	C	N	O	S	0	0
			1539	990	266	274	9		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12054	22223	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2522	1128	461	816	117		

- Molecule 37 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1757	1116	346	291	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL	19	HIS	ARG	conflict	UNP Q8IAX6
AL	20	ARG	HIS	conflict	UNP Q8IAX6
AL	201	CYS	ARG	conflict	UNP Q8IAX6

- Molecule 38 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	104	Total	C	N	O	S	0	0
			831	529	151	148	3		

- Molecule 40 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	98	Total	C	N	O	S	0	0
			741	462	132	140	7		

- Molecule 42 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total	C	N	O	S	0	0
			794	508	151	130	5		

- Molecule 43 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	146	Total	C	N	O	S	0	0
			1202	781	210	205	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	LYS	deletion	UNP Q8ILE8

- Molecule 44 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	125	Total	C	N	O	S	0	0
			1037	660	206	164	7		

- Molecule 45 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	103	Total	C	N	O	S	0	0
			845	543	163	136	3		

- Molecule 46 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	106	Total	C	N	O	S	0	0
			859	530	184	139	6		

- Molecule 47 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ab	95	Total	C	N	O	S	0	0
			757	477	150	130			

- Molecule 48 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total	C	N	O	S	0	0
			604	395	107	100	2		

- Molecule 49 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			414	255	87	67	5		

- Molecule 51 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 52 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	85	Total	C	N	O	S	0	0
			659	417	127	108	7		

- Molecule 53 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	95	Total	C	N	O	S	0	0
			779	490	152	128	9		

- Molecule 54 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			710	441	150	114	5		

- Molecule 57 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1660	1064	311	277	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	109	ALA	TYR	conflict	UNP Q8IJZ7

- Molecule 58 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 60 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1545	984	291	262	8		

- Molecule 62 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2050	1300	385	359	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	?	-	LYS	deletion	UNP Q8ILL3

- Molecule 63 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			797	502	144	145	6		

- Molecule 65 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1001	626	206	166	3		

- Molecule 67 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			995	635	194	164	2		

- Molecule 68 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1867	1166	374	318	9		

- Molecule 70 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3062	1948	575	522	17		

- Molecule 71 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3095	1962	594	528	11		

- Molecule 72 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1011	636	197	172	6		

- Molecule 73 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1476	950	264	256	6		

- Molecule 75 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1276	814	241	215	6		

- Molecule 76 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			825	548	135	140	2		

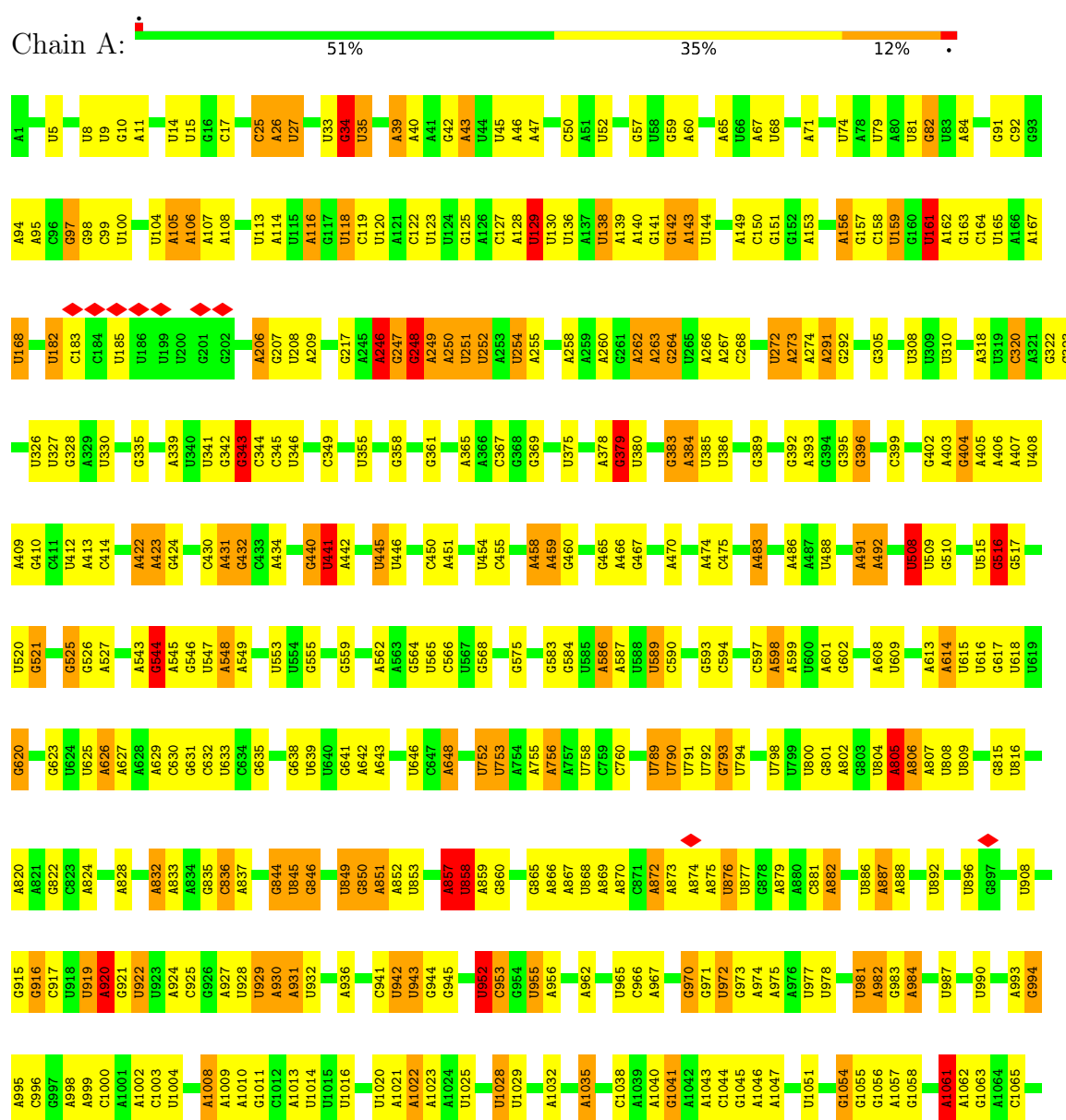
- Molecule 78 is a protein called 60S ribosomal protein eL24.

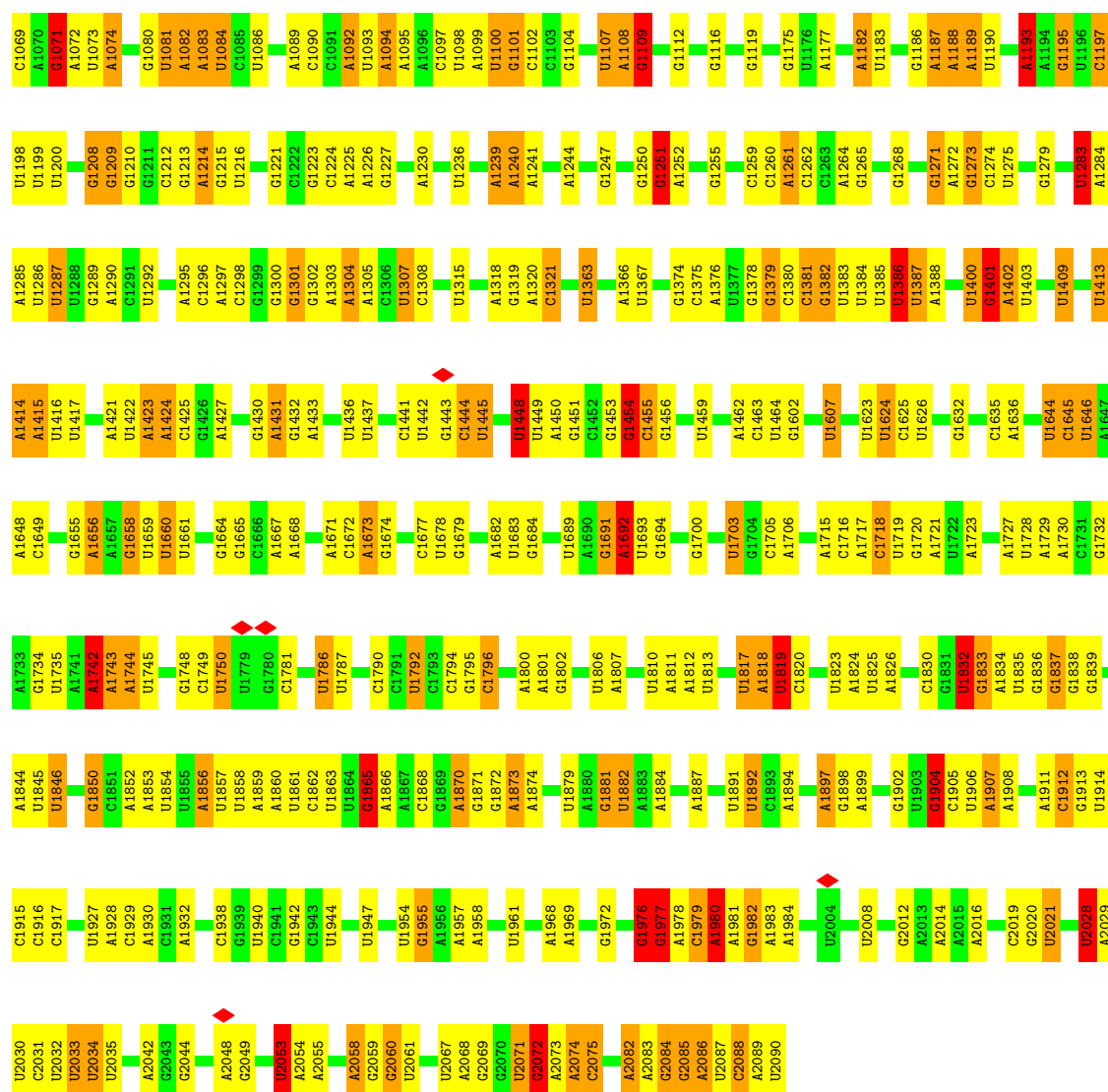
Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			522	336	97	88	1		

3 Residue-property plots

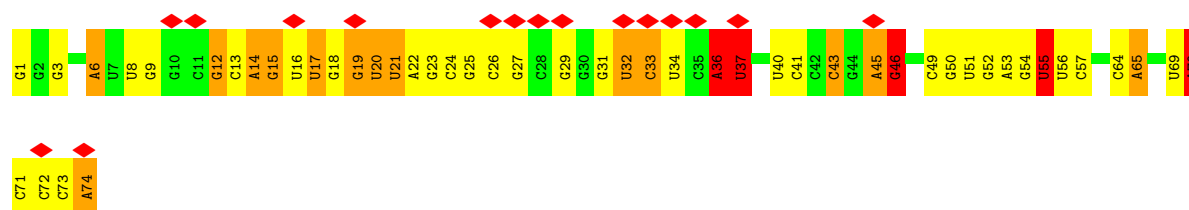
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 18S ribosomal RNA

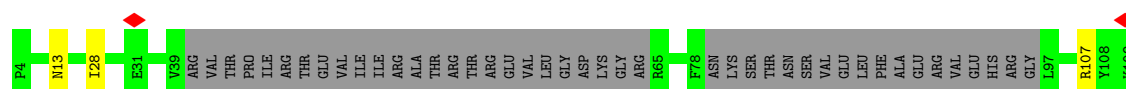


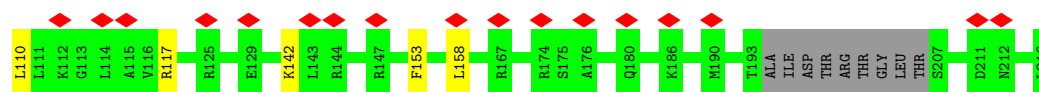


• Molecule 2: E-tRNA

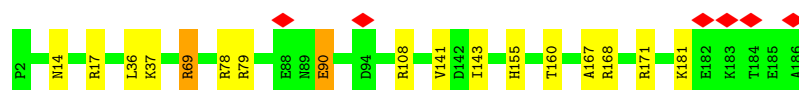


• Molecule 3: 40S ribosomal protein uS3

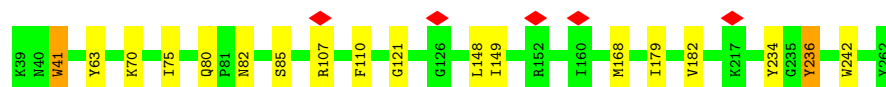




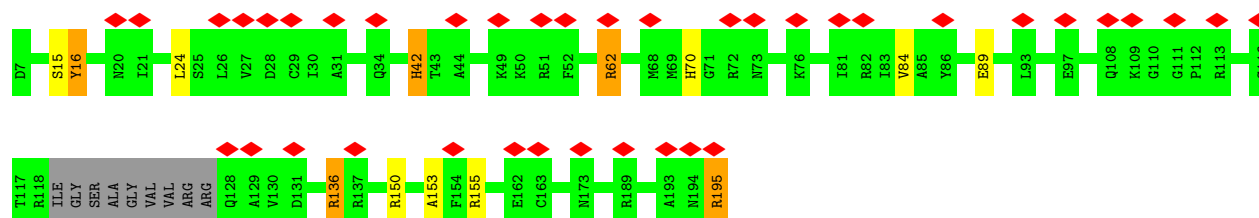
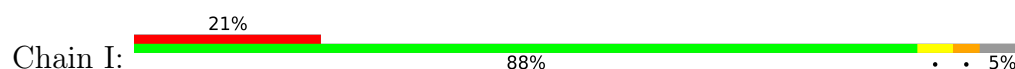
- Molecule 4: 40S ribosomal protein uS4



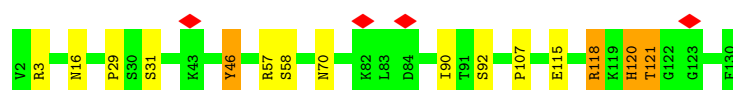
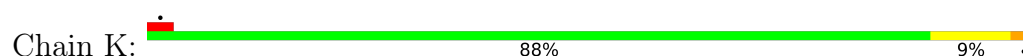
- Molecule 5: 40S ribosomal protein uS5



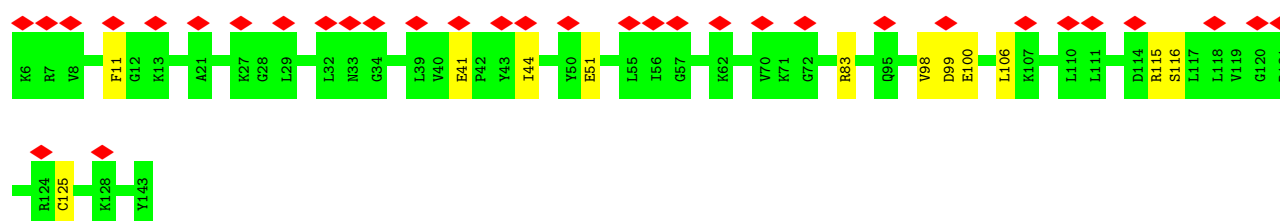
- Molecule 6: 40S ribosomal protein uS7



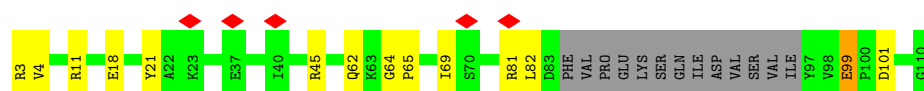
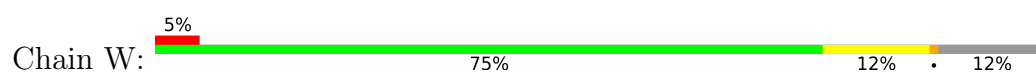
- Molecule 7: 40S ribosomal protein uS8



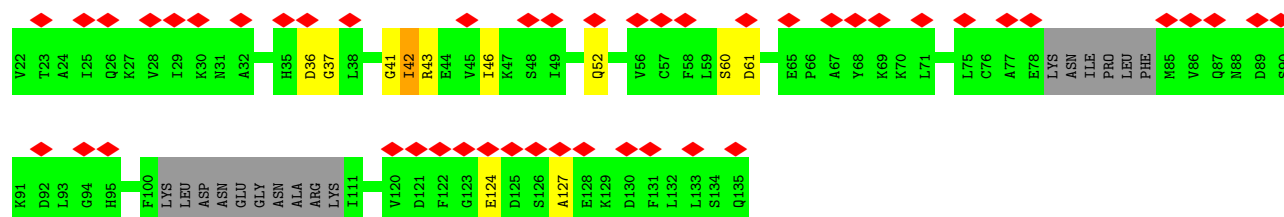
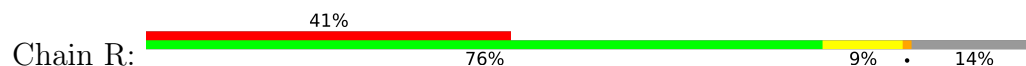
- Molecule 8: 40S ribosomal protein uS9



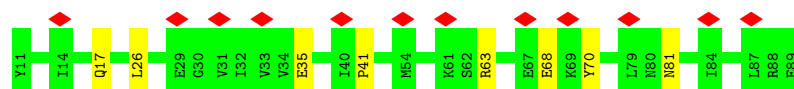
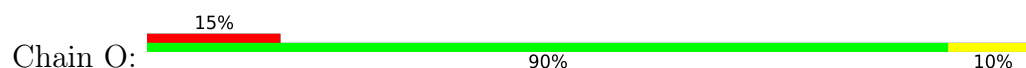
- Molecule 9: 40S ribosomal protein eS17



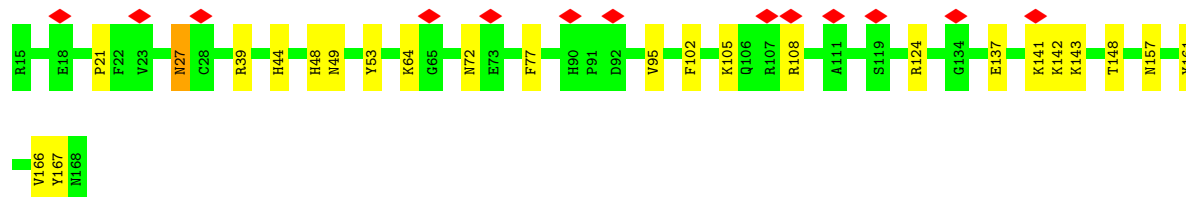
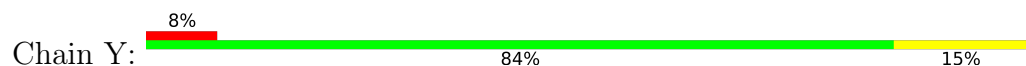
- Molecule 10: 40S ribosomal protein eS12



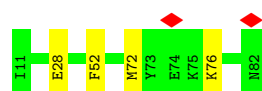
- Molecule 11: 40S ribosomal protein eS10



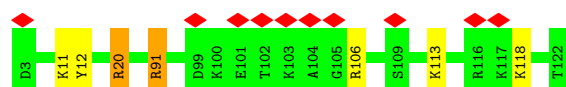
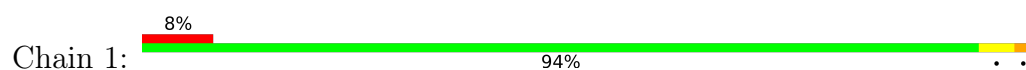
- Molecule 12: 40S ribosomal protein eS19



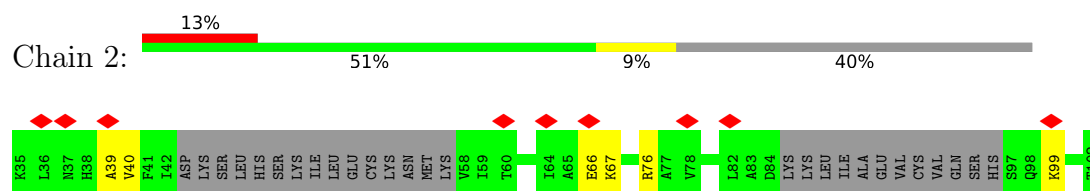
- Molecule 13: 40S ribosomal protein eS21



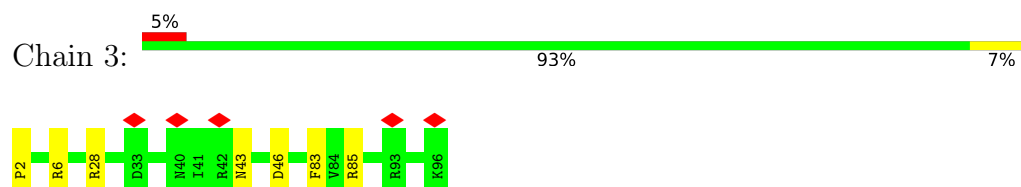
- Molecule 14: 40S ribosomal protein eS24



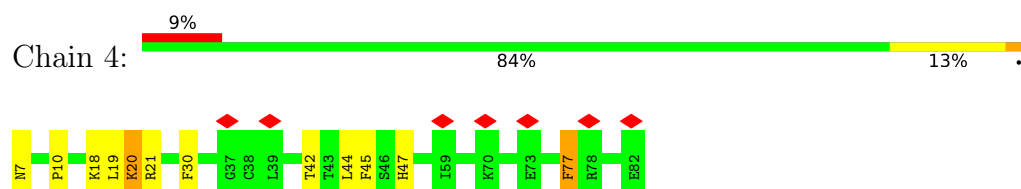
- Molecule 15: 40S ribosomal protein eS25



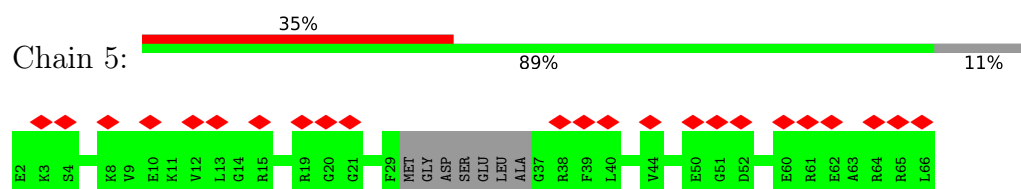
- Molecule 16: 40S ribosomal protein eS26



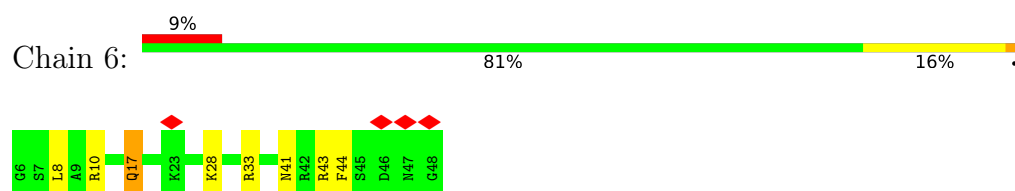
- Molecule 17: 40S ribosomal protein eS27



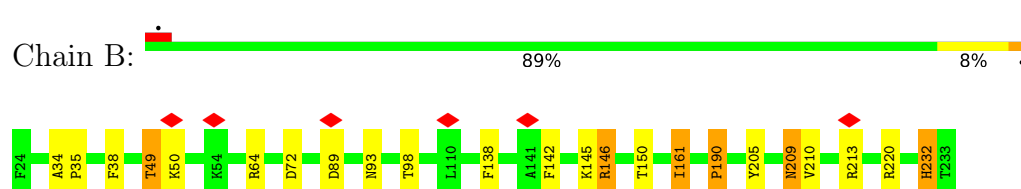
- Molecule 18: 40S ribosomal protein eS28



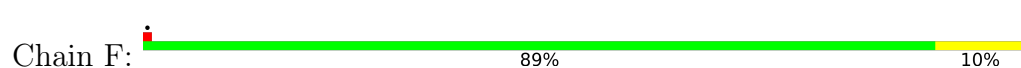
- Molecule 19: 40S ribosomal protein eS30

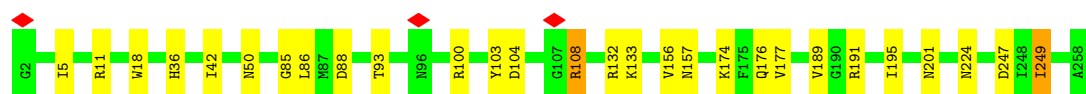


- Molecule 20: 40S ribosomal protein eS1

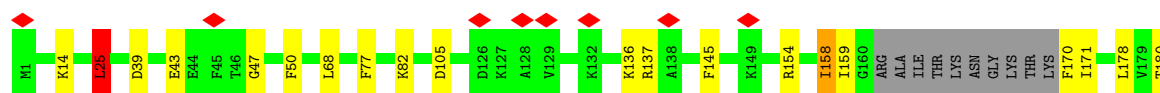
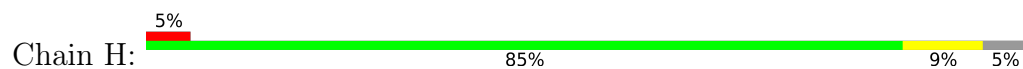


- Molecule 21: 40S ribosomal protein eS4

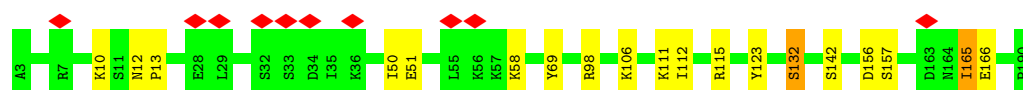
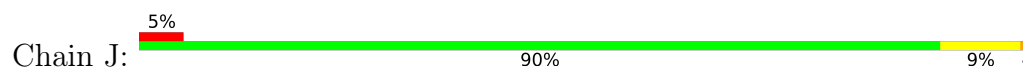




- Molecule 22: 40S ribosomal protein eS6



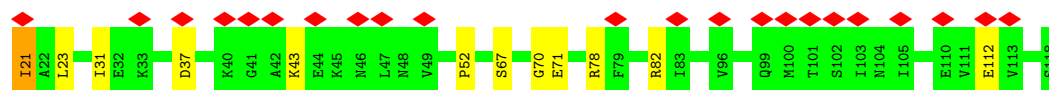
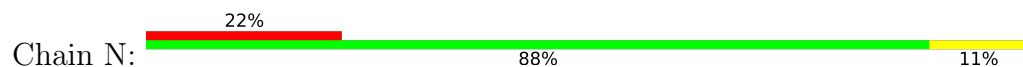
- Molecule 23: 40S ribosomal protein eS7



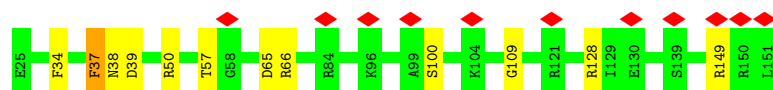
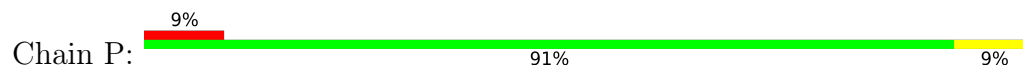
- Molecule 24: 40S ribosomal protein eS8



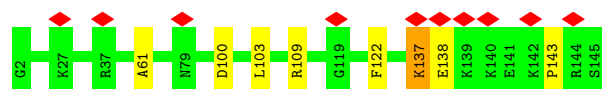
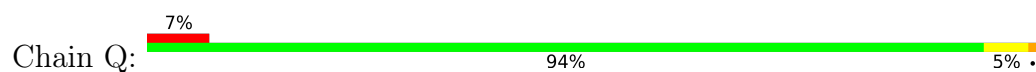
- Molecule 25: 40S ribosomal protein uS10



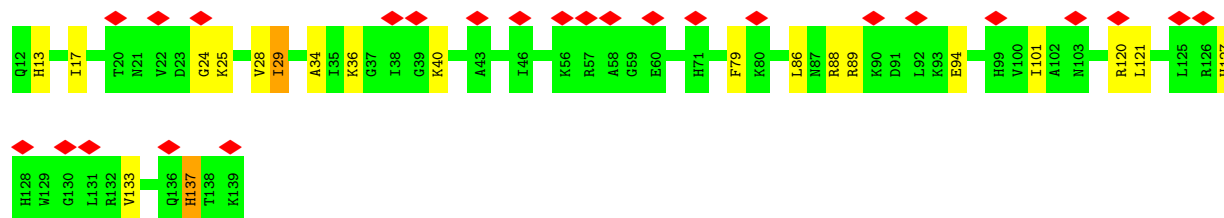
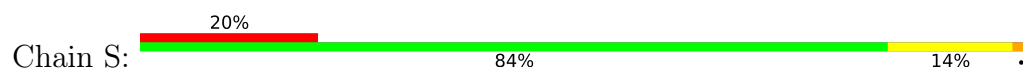
- Molecule 26: 40S ribosomal protein uS11



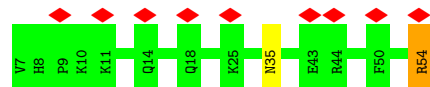
- Molecule 27: 40S ribosomal protein uS12



- Molecule 28: 40S ribosomal protein uS13



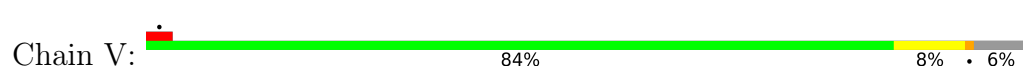
- Molecule 29: 40S ribosomal protein uS14



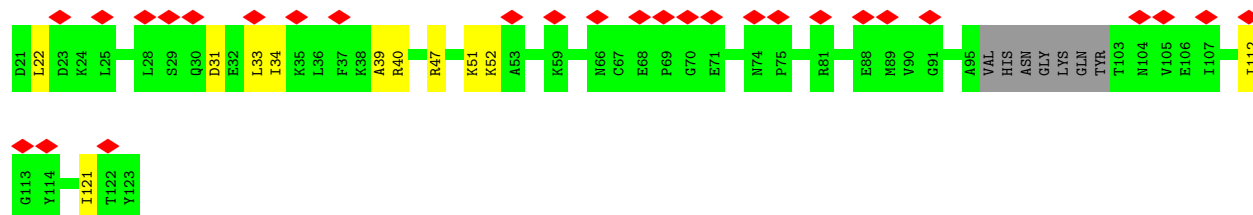
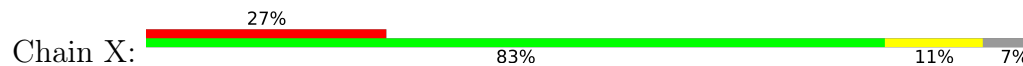
- Molecule 30: 40S ribosomal protein uS15



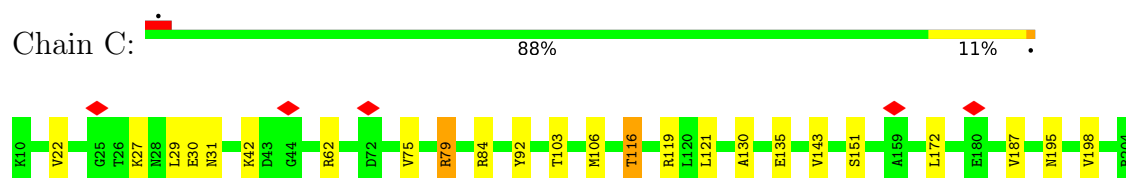
- Molecule 31: 40S ribosomal protein uS17



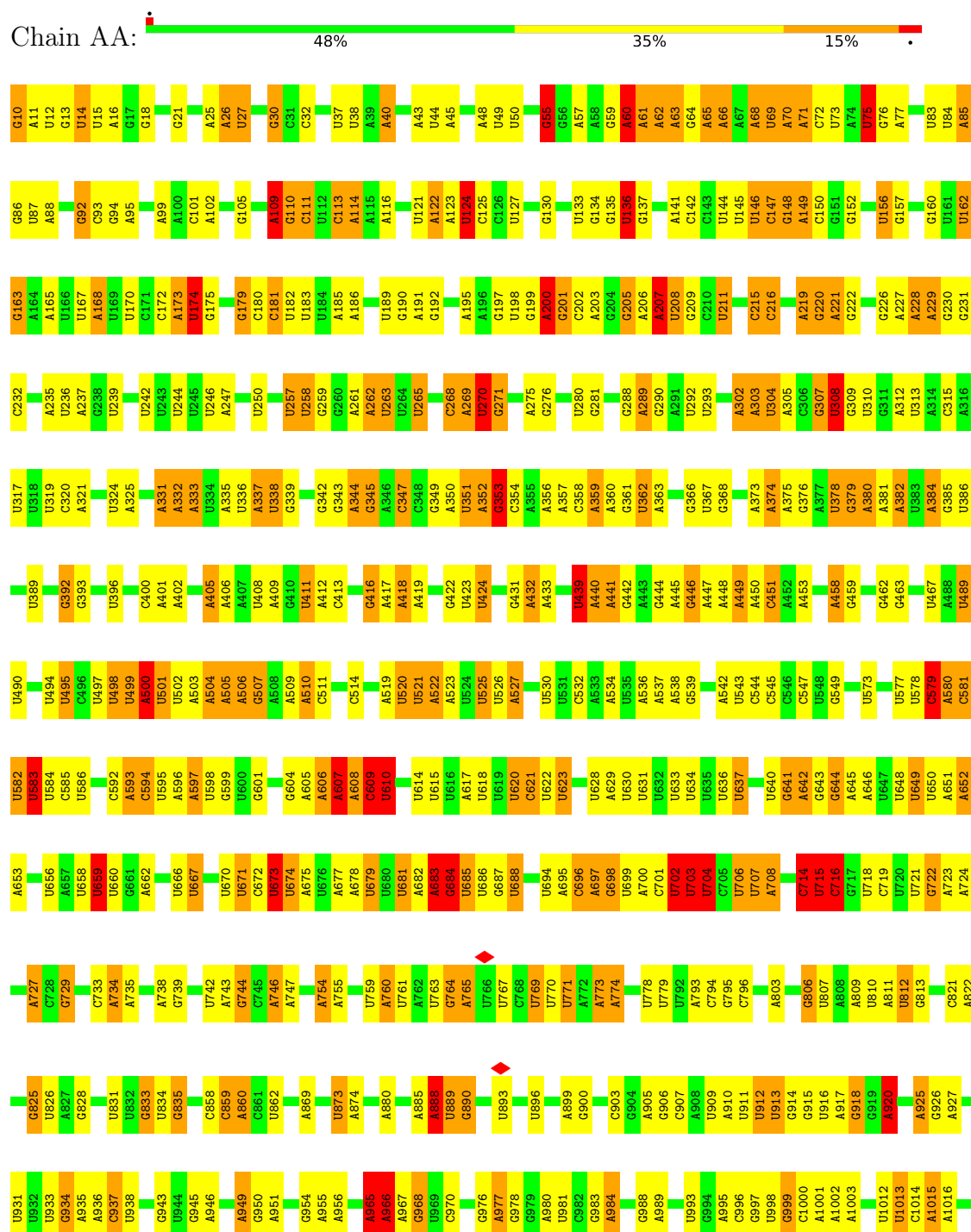
- Molecule 32: 40S ribosomal protein uS19



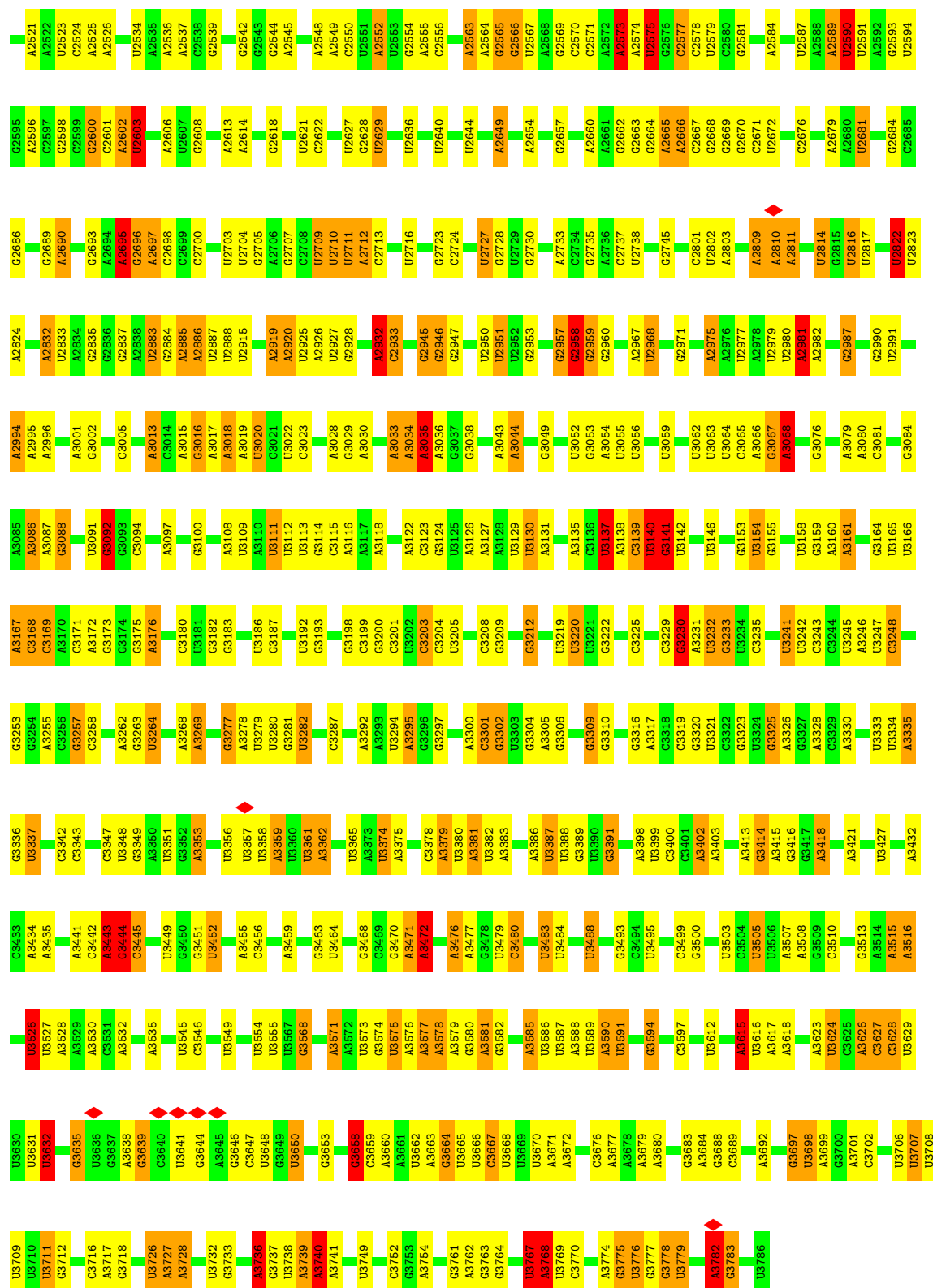
• Molecule 33: 40S ribosomal protein uS2



• Molecule 34: 28S ribosomal RNA



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A2437	U2180	A2094	A1970	G1844	G1756	G1688	C1586	U1497	G1334	A1258	A1189	A1092	U1023
A2438	G2182	U2095	A1971	C1845	G1757	U1671	U1587	U1498	G1335	G1259	G1193	G1093	U1024
C2439	G2183	G2096	A1972	C1846	G1758	U1672	U1588	U1499	U1336	A1194	A1194	U1094	A1025
A2440	U2184	A2097	G1973	C1847	G1759	C1675	G1589	U1500	G1337	A1263	A1195	U1099	G1026
U2441	C2185	A2102	U1974	U1849	G1760	C1676	G1592	A1501	G1340	A1264	A1196	A1100	A1027
A2442	C2186	C2103	A1975	U1850	U1766	C1677	G1595	G1502	G1341	U1266	U1197	A1101	G1027
G2443	C2104	A2105	U1976	A1851	U1767	C1681	A1595	A1504	C1344	U1272	A1198	U1102	G1031
A2451	A2106	A2106	U1978	C1852	U1768	U1682	U1596	U1505	C1345	G1273	A1199	A1103	A1032
A2452	C2107	C1978	U1769	U1853	U1769	U1683	U1597	U1506	U1346	U1274	A1200	A1033	A1034
A2453	U2108	U1856	G1770	A1684	G1771	A1684	A1598	U1507	U1416	C1202	C1203	G1035	A1036
C2457	A1857	A1857	A1771	G1685	U1774	G1685	C1600	U1510	U1415	A1204	A1204	A1106	C1037
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A2461	A1872	A1872	G1780	U1691	G1781	U1691	A1602	U1512	U1418	G1280	U1206	U1110	A1040
C2462	U1873	U1873	U1781	G1692	U1782	G1692	A1605	U1513	U1419	C1281	U1207	U1111	U1041
U2463	C1874	C1874	U1782	U1693	G1783	U1693	U1606	G1516	C1420	U1282	U1208	C1113	U1042
G2464	A1875	A1875	G1783	U1694	U1784	U1694	U1613	U1517	U1421	C1283	U1209	A1114	G1043
G2465	U1876	U1876	U1785	G1695	U1785	U1695	G1613	A1518	U1422	U1284	U1210	G1116	A1047
A2473	U1877	U1877	U1786	A1696	U1786	A1696	A1617	U1524	U1423	U1285	U1211	U1117	C1050
C2474	U1878	U1878	A1787	A1697	U1787	A1697	C1618	U1525	A1429	A1286	U1212	U1118	U1063
U2477	G1881	G1881	C1788	U1698	U1788	U1698	U1619	G1531	A1430	C1288	C1214	G1119	U1064
G2480	U1882	U1882	U1793	G1699	U1794	U1699	G1625	U1534	A1432	U1291	C1216	G1120	U1065
A2481	A1886	A1886	U1794	U1701	G1701	U1701	A1626	U1535	U1433	A1295	U1217	A1122	U1066
A2482	C1887	C1887	U1795	U1702	U1702	U1702	C1627	U1536	U1434	U1296	C1218	U1123	A1055
U2483	A1889	A1889	U1796	U1703	U1703	U1703	U1628	U1537	U1435	A1297	A1219	A1124	G1056
U2484	U1894	U1894	A1797	U1704	U1704	U1704	G1629	U1538	U1436	U1298	U1220	G1132	C1057
C2485	U1799	U1799	A1705	A1630	U1705	A1630	U1631	U1539	U1441	G1299	U1222	G1135	U1058
U2486	U1800	U1800	G1632	A1631	U1706	A1631	A1542	U1540	A1444	U1300	U1223	A1136	G1060
C2489	U1898	U1898	U1801	U1707	U1707	U1707	G1635	A1541	A1445	U1301	A1224	U1062	U1061
C2490	U1899	U1899	U1805	G1721	U1805	G1721	A1636	U1549	A1446	G1141	A1226	G1141	A1063
A2404	A1901	A1901	C1806	U1725	U1806	U1725	G1637	A1550	U1447	G1142	A1229	G1142	U1064
A2405	C1902	C1902	C1812	C1726	U1807	C1726	G1642	G1552	G1450	A1306	A1230	U1066	U1065
G2409	U1904	U1904	U1813	A1730	U1808	A1730	U1643	G1553	U1451	A1307	A1231	U1067	U1066
A2410	C1905	C1905	U1814	A1731	U1809	A1731	U1644	G1554	U1452	U1308	U1232	G1068	G1069
C2411	A1906	A1906	G1816	U1732	U1810	U1732	C1645	U1555	U1453	A1310	A1233	U1157	G1069
A2149	C1910	C1910	G1817	G1733	U1811	G1733	U1646	G1556	U1454	C1313	A1234	G1158	A1070
A2153	A1913	A1913	U1820	G1734	U1812	G1734	U1647	G1565	U1457	G1314	U1235	U1164	A1071
A2154	A1914	A1914	U1821	G1735	U1813	G1735	U1648	G1566	U1458	U1237	U1236	A1072	A1072
U2158	U1915	U1915	U1822	U1736	U1814	U1736	U1649	A1566	U1459	A1318	C1237	G1073	G1073
A2159	U1956	U1956	A1822	U1737	U1815	U1737	U1650	G1567	A1460	U1319	A1239	A1167	A1074
G2160	U1957	U1957	G1829	U1738	U1816	U1738	C1651	U1568	A1473	G1320	A1240	A1169	U1075
G2165	U1958	U1958	G1830	U1739	U1817	U1739	U1655	A1569	U1476	A1321	A1244	A1170	C1078
G2166	U1959	U1959	G1831	U1740	U1818	U1740	G1656	U1572	A1477	U1324	G1245	A1171	C1079
G2173	U1960	U1960	U1832	U1741	U1819	U1741	U1657	C1573	A1478	C1325	G1246	C1172	C1080
G2174	U1961	U1961	U1833	G1745	U1820	G1745	U1659	C1574	A1479	C1326	C1247	U1173	A1081
C2175	U1962	U1962	G1835	U1746	U1821	U1746	U1660	C1575	A1481	C1327	U1248	C1174	G1082
A2176	U1963	U1963	U1836	U1747	U1822	U1747	U1661	U1576	A1486	A1328	U1249	A1177	G1083
A2177	U1964	U1964	U1841	U1748	U1823	U1748	U1662	G1578	U1487	U1329	A1250	U1184	U1084
A2178	U1965	U1965	U1842	U1749	U1824	U1749	A1663	G1583	U1493	A1330	U1251	A1185	C1086
G2092	A1966	A1966	U1842	C1751	U1842	C1751	A1664	A1584	U1493	A1332	U1256	A1187	G1087



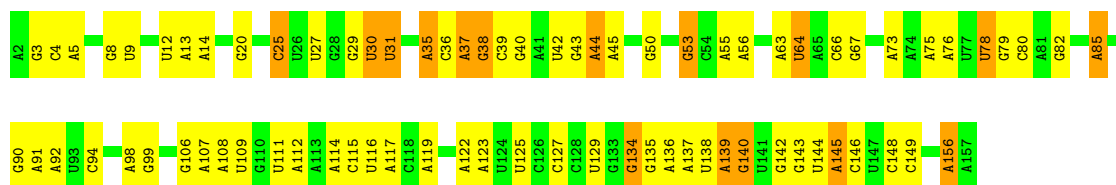
• Molecule 35: 5.8S ribosomal RNA

Chain AC:

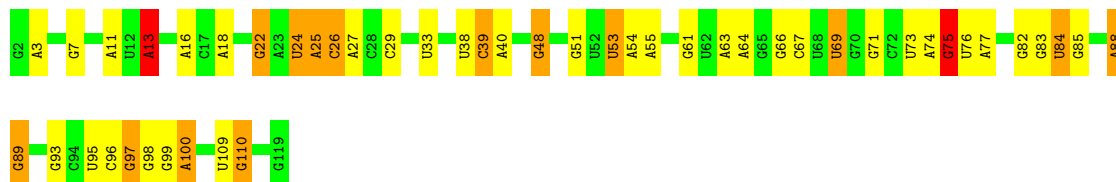
49%

40%

11%



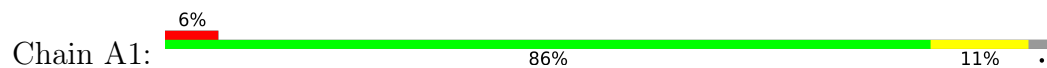
• Molecule 36: 5S ribosomal RNA



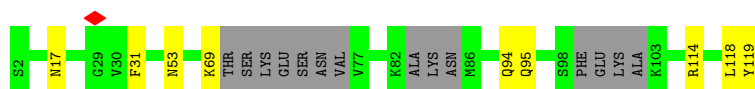
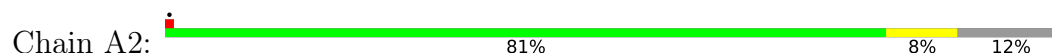
• Molecule 37: 60S ribosomal protein eL13



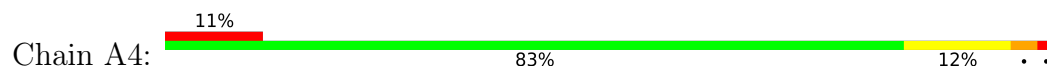
• Molecule 38: 60S ribosomal protein eL27



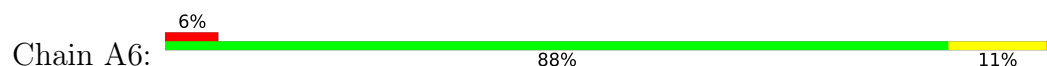
• Molecule 39: 60S ribosomal protein eL28



• Molecule 40: 60S ribosomal protein eL29

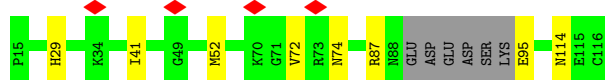
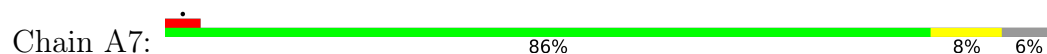


• Molecule 41: 60S ribosomal protein eL30

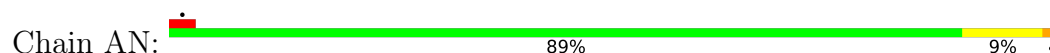




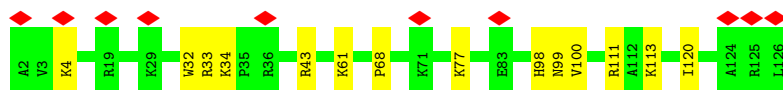
- Molecule 42: 60S ribosomal protein eL31



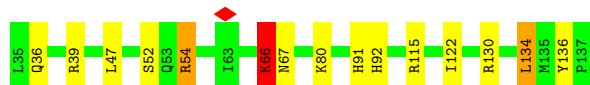
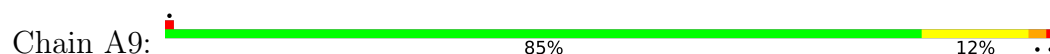
- Molecule 43: 60S ribosomal protein eL14



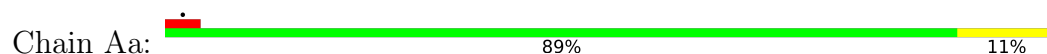
- Molecule 44: 60S ribosomal protein eL32



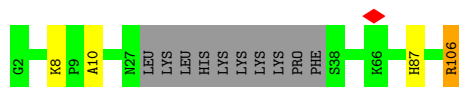
- Molecule 45: 60S ribosomal protein eL33



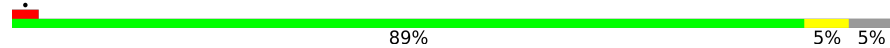
- Molecule 46: 60S ribosomal protein eL34

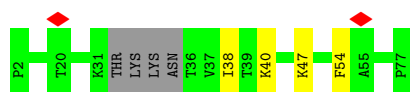


- Molecule 47: 60S ribosomal protein eL36



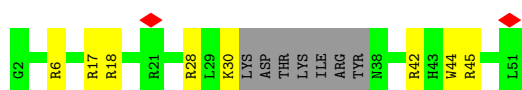
- Molecule 48: 60S ribosomal protein eL38

Chain Ad:  89% 5% 5%

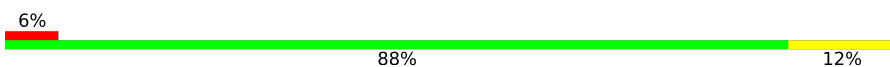


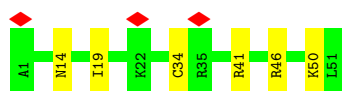
- Molecule 49: 60S ribosomal protein eL39

Chain Ae:  70% 16% 14%



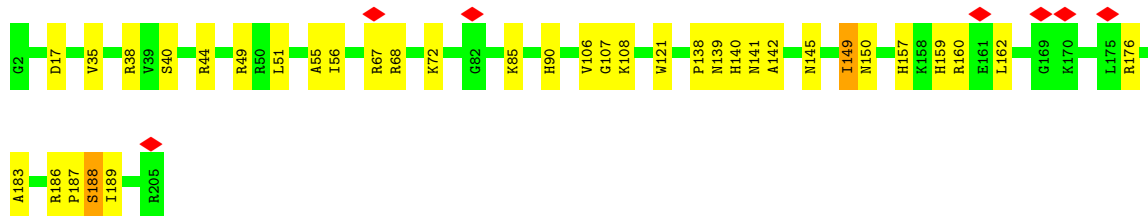
- Molecule 50: 60S ribosomal protein eL40

Chain Af:  6% 88% 12%

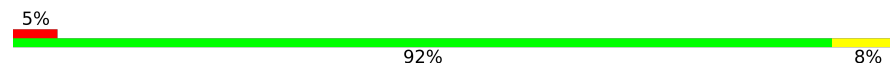


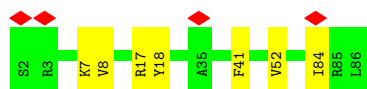
- Molecule 51: 60S ribosomal protein eL15

Chain AP:  82% 17% .



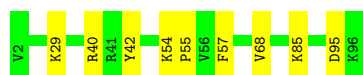
- Molecule 52: 60S ribosomal protein eL43

Chain Ah:  5% 92% 8%



- Molecule 53: 60S ribosomal protein eL44

Chain Ai:  91% 9%



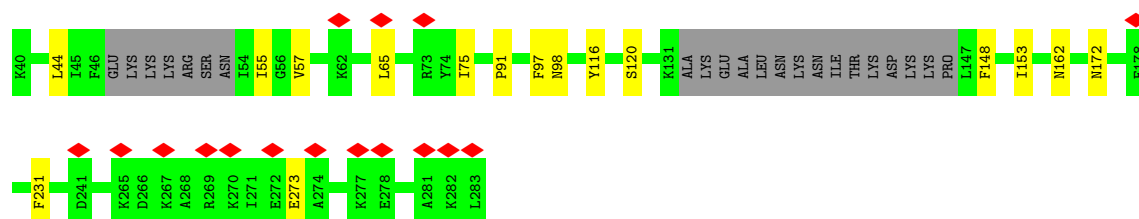
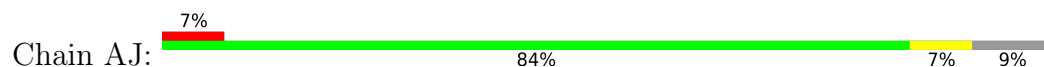
- Molecule 54: 60S ribosomal protein eL6

Chain AI:  88% 8% ..

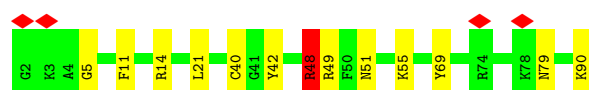
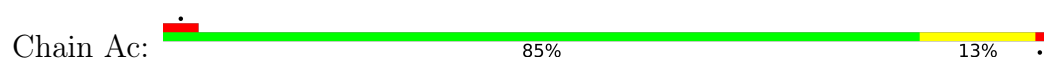




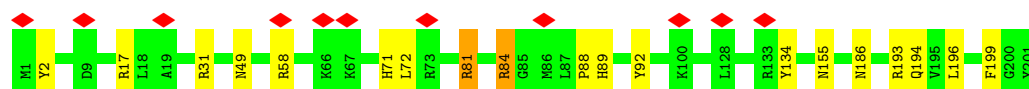
- Molecule 55: 60S ribosomal protein eL8



- Molecule 56: 60S ribosomal protein eL37



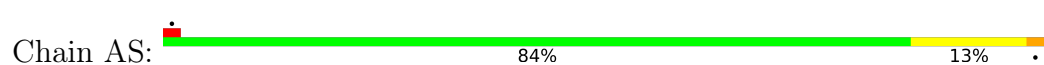
- Molecule 57: 60S ribosomal protein uL13



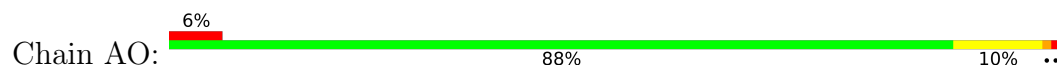
- Molecule 58: 60S ribosomal protein uL14

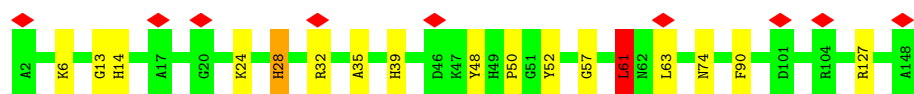


- Molecule 59: 60S ribosomal protein eL18



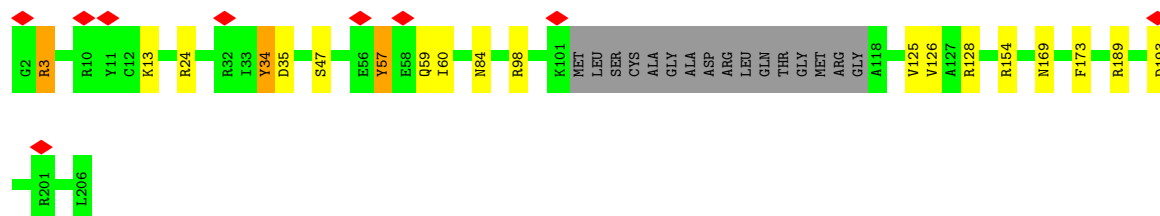
- Molecule 60: 60S ribosomal protein uL15





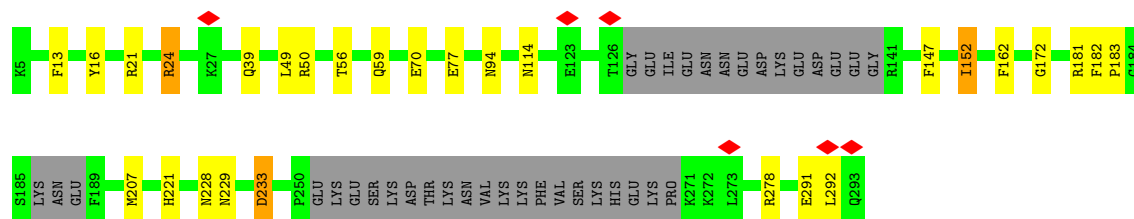
- Molecule 61: 60S ribosomal protein uL16

Chain AQ: 83% 8% 8%



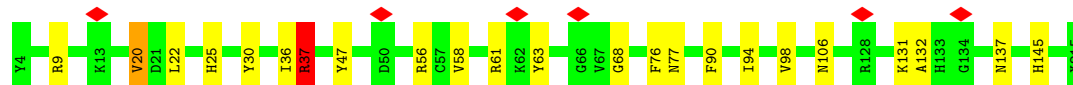
- Molecule 62: 60S ribosomal protein uL18

Chain AR: 78% 9% 13%



- Molecule 63: 60S ribosomal protein uL22

Chain AW: 86% 12% 2%



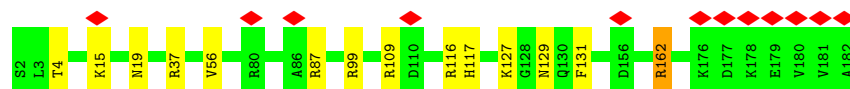
- Molecule 64: 60S ribosomal protein uL23

Chain AY: 93% 6% 1%



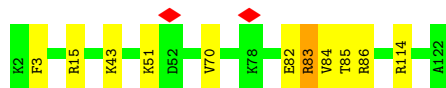
- Molecule 65: 60S ribosomal protein eL19

Chain AT: 7% 92% 7%

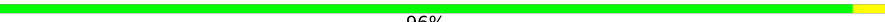


- Molecule 66: 60S ribosomal protein uL24

Chain AZ:  91% 8% .



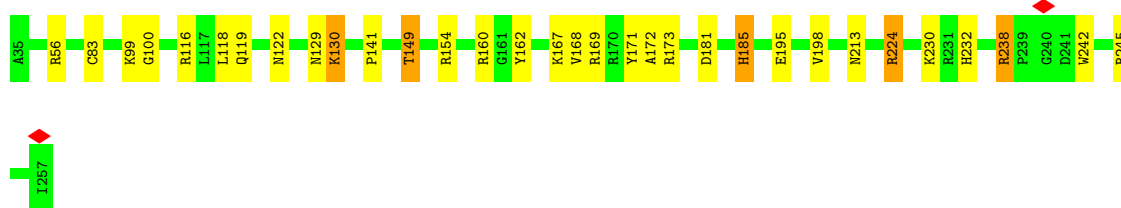
- Molecule 67: 60S ribosomal protein uL29

Chain A3:  96% .



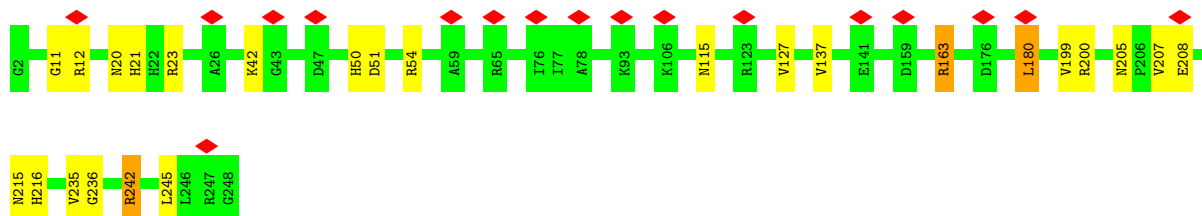
- Molecule 68: 60S ribosomal protein uL30

Chain A5:  86% 12% .



- Molecule 69: 60S ribosomal protein uL2

Chain AD:  7% 90% 9% .



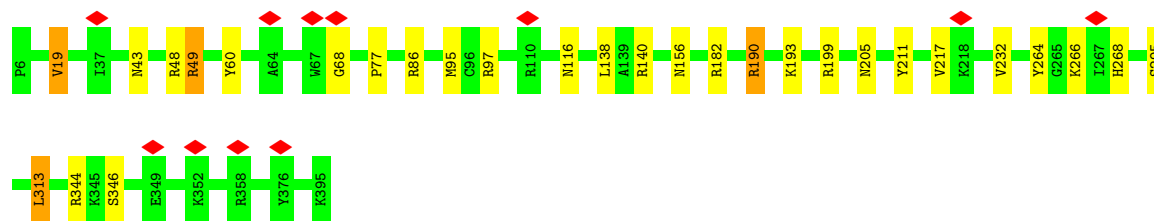
- Molecule 70: 60S ribosomal protein uL3

Chain AE:  90% 9% .

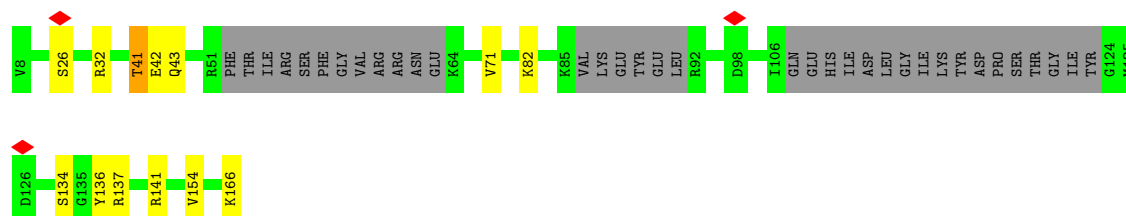


- Molecule 71: 60S ribosomal protein uL4

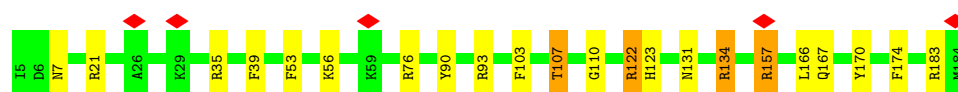
Chain AF:  93% 6% .



- Molecule 72: 60S ribosomal protein uL5



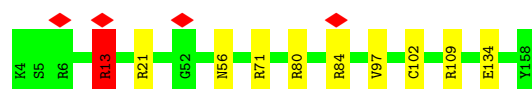
- Molecule 73: 60S ribosomal protein eL20



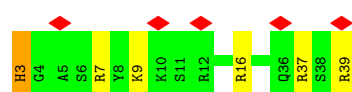
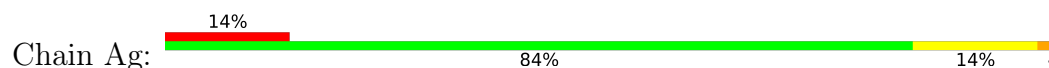
- Molecule 74: 60S ribosomal protein uL6



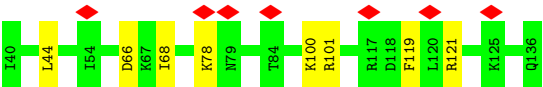
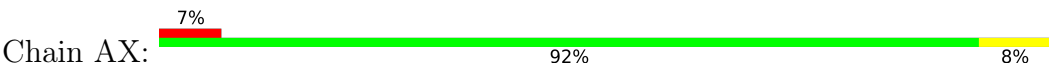
- Molecule 75: 60S ribosomal protein eL21



- Molecule 76: 60S ribosomal protein eL41



- Molecule 77: 60S ribosomal protein eL22



• Molecule 78: 60S ribosomal protein eL24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96732	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	30120	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.159	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	491.36, 491.36, 491.36	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.66, 1.66, 1.66	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.97	0/38275	1.17	153/59596 (0.3%)
2	7	1.00	1/1754 (0.1%)	1.36	21/2732 (0.8%)
3	D	0.89	0/1241	1.44	6/1652 (0.4%)
4	E	0.87	0/1539	1.47	4/2055 (0.2%)
5	G	0.86	0/1800	1.40	6/2429 (0.2%)
6	I	0.85	0/1443	1.63	10/1936 (0.5%)
7	K	0.92	0/1054	1.50	9/1411 (0.6%)
8	M	0.84	0/1114	1.48	7/1487 (0.5%)
9	W	0.88	0/793	1.62	5/1053 (0.5%)
10	R	0.92	0/755	1.68	6/1013 (0.6%)
11	O	0.85	0/706	1.50	1/950 (0.1%)
12	Y	0.86	0/1295	1.61	11/1742 (0.6%)
13	Z	0.87	0/565	1.48	3/758 (0.4%)
14	1	0.84	0/999	1.44	3/1321 (0.2%)
15	2	0.91	0/324	1.61	6/435 (1.4%)
16	3	0.91	0/794	1.47	3/1055 (0.3%)
17	4	0.89	0/597	1.55	6/801 (0.7%)
18	5	0.89	0/459	1.35	0/606
19	6	0.89	0/349	1.60	5/458 (1.1%)
20	B	0.83	0/1738	1.50	12/2321 (0.5%)
21	F	0.87	0/2098	1.46	7/2819 (0.2%)
22	H	0.81	0/1665	1.47	12/2210 (0.5%)
23	J	0.83	0/1545	1.41	2/2064 (0.1%)
24	L	0.88	0/1407	1.50	11/1879 (0.6%)
25	N	0.87	0/780	1.59	7/1053 (0.7%)
26	P	0.90	0/966	1.55	8/1295 (0.6%)
27	Q	0.86	0/1149	1.47	5/1532 (0.3%)
28	S	0.89	0/1063	1.68	10/1425 (0.7%)
29	T	0.88	0/412	1.44	2/544 (0.4%)
30	U	0.83	0/1223	1.48	7/1634 (0.4%)
31	V	0.87	0/1233	1.40	3/1645 (0.2%)
32	X	0.84	0/788	1.63	6/1050 (0.6%)
33	C	0.85	0/1570	1.48	12/2129 (0.6%)
34	AA	0.98	1/75947 (0.0%)	1.16	285/118255 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	0.98	0/3599	1.12	10/5603 (0.2%)
36	AB	0.98	0/2823	1.05	5/4400 (0.1%)
37	AL	0.85	0/1789	1.54	9/2381 (0.4%)
38	A1	0.84	0/1151	1.48	8/1531 (0.5%)
39	A2	0.86	0/840	1.43	2/1114 (0.2%)
40	A4	0.86	0/564	1.57	5/737 (0.7%)
41	A6	0.89	0/749	1.51	3/1001 (0.3%)
42	A7	0.94	0/806	1.47	2/1073 (0.2%)
43	AN	0.83	0/1218	1.46	6/1621 (0.4%)
44	A8	0.87	0/1054	1.56	5/1399 (0.4%)
45	A9	0.95	0/865	1.52	10/1160 (0.9%)
46	Aa	0.87	0/872	1.55	4/1161 (0.3%)
47	Ab	0.89	0/763	1.48	1/1008 (0.1%)
48	Ad	0.85	0/612	1.44	1/812 (0.1%)
49	Ae	0.96	0/396	1.56	1/521 (0.2%)
50	Af	0.84	0/419	1.50	3/556 (0.5%)
51	AP	0.90	0/1735	1.60	21/2320 (0.9%)
52	Ah	0.88	0/668	1.46	2/887 (0.2%)
53	Ai	0.83	0/789	1.41	2/1032 (0.2%)
54	AI	0.83	0/1708	1.53	14/2274 (0.6%)
55	AJ	0.85	0/1840	1.54	10/2456 (0.4%)
56	Ac	0.89	0/723	1.58	4/951 (0.4%)
57	AK	0.85	0/1690	1.46	11/2260 (0.5%)
58	AM	0.86	0/1012	1.45	2/1363 (0.1%)
59	AS	0.87	0/1531	1.51	15/2040 (0.7%)
60	AO	0.85	0/1199	1.52	10/1597 (0.6%)
61	AQ	0.89	0/1580	1.49	11/2113 (0.5%)
62	AR	0.85	0/2079	1.51	14/2777 (0.5%)
63	AW	0.90	0/1244	1.49	10/1663 (0.6%)
64	AY	0.85	0/806	1.43	5/1074 (0.5%)
65	AT	0.85	0/1525	1.51	6/2016 (0.3%)
66	AZ	0.88	0/1013	1.44	3/1339 (0.2%)
67	A3	0.80	0/1005	1.48	2/1329 (0.2%)
68	A5	0.88	0/1917	1.55	16/2562 (0.6%)
69	AD	0.90	0/1902	1.50	12/2544 (0.5%)
70	AE	0.87	0/3130	1.50	18/4195 (0.4%)
71	AF	0.87	0/3145	1.52	16/4205 (0.4%)
72	AG	0.88	0/1021	1.55	9/1349 (0.7%)
73	AU	0.88	0/1527	1.48	10/2043 (0.5%)
74	AH	0.89	0/1501	1.50	10/2025 (0.5%)
75	AV	0.86	0/1301	1.47	5/1732 (0.3%)
76	Ag	0.94	0/348	1.66	2/448 (0.4%)
77	AX	0.83	0/842	1.45	4/1125 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
78	A0	0.84	0/534	1.40	1/711 (0.1%)
All	All	0.93	2/207275 (0.0%)	1.30	974/303853 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	231
2	7	0	18
3	D	0	1
4	E	0	6
5	G	0	4
6	I	0	4
7	K	0	2
8	M	0	1
9	W	0	3
11	O	0	1
12	Y	0	6
14	1	0	2
15	2	0	1
16	3	0	2
17	4	0	3
19	6	0	2
20	B	0	4
21	F	0	5
22	H	0	3
23	J	0	5
24	L	0	3
25	N	0	1
26	P	0	3
27	Q	0	2
29	T	0	1
30	U	0	2
31	V	0	6
32	X	0	1
33	C	0	6
34	AA	1	546
35	AC	0	19
36	AB	0	14
37	AL	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
38	A1	0	1
39	A2	0	1
40	A4	0	2
41	A6	0	4
42	A7	0	1
43	AN	0	3
44	A8	0	2
45	A9	0	2
46	Aa	0	4
47	Ab	0	1
49	Ae	0	5
50	Af	0	2
51	AP	0	6
52	Ah	0	2
53	Ai	0	3
54	AI	0	2
55	AJ	0	2
56	Ac	0	3
57	AK	0	5
58	AM	0	5
59	AS	0	8
60	AO	0	3
61	AQ	0	4
62	AR	0	4
63	AW	0	6
64	AY	0	1
65	AT	0	6
66	AZ	0	4
67	A3	0	1
68	A5	0	7
69	AD	0	6
70	AE	0	4
71	AF	0	6
72	AG	0	3
73	AU	0	7
74	AH	0	3
75	AV	0	5
76	Ag	0	2
77	AX	0	1
78	A0	0	2
All	All	1	1052

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	275	A	O3'-P	-6.35	1.51	1.61
2	7	74	A	C4'-C3'	6.32	1.62	1.53

All (974) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	3632	U	P-O5'-C5'	20.99	152.39	120.90
34	AA	257	U	P-O3'-C3'	14.67	142.20	120.20
2	7	74	A	O4'-C4'-C3'	-13.00	93.10	106.10
2	7	74	A	C5'-C4'-C3'	12.76	134.34	115.20
34	AA	181	C	P-O3'-C3'	12.12	138.38	120.20
34	AA	3018	A	P-O3'-C3'	11.91	138.06	120.20
2	7	74	A	C5'-C4'-O4'	-11.88	91.28	109.10
1	A	981	U	P-O3'-C3'	11.47	137.41	120.20
34	AA	2219	A	C2'-C3'-O3'	11.43	126.64	109.50
34	AA	860	A	P-O5'-C5'	11.16	137.63	120.90
34	AA	859	C	P-O3'-C3'	10.88	136.52	120.20
1	A	1912	C	P-O3'-C3'	10.84	136.46	120.20
34	AA	2695	A	P-O5'-C5'	10.82	137.12	120.90
34	AA	621	C	P-O3'-C3'	10.13	135.40	120.20
34	AA	162	U	P-O3'-C3'	9.74	134.81	120.20
34	AA	1873	U	C2'-C3'-O3'	9.59	123.89	109.50
35	AC	37	A	P-O3'-C3'	9.44	134.36	120.20
34	AA	1205	U	P-O3'-C3'	9.39	134.29	120.20
1	A	1413	U	P-O3'-C3'	9.27	134.10	120.20
1	A	1448	U	P-O3'-C3'	9.23	134.05	120.20
1	A	250	A	P-O3'-C3'	9.22	134.03	120.20
1	A	1897	A	P-O3'-C3'	9.16	133.94	120.20
34	AA	289	A	P-O3'-C3'	9.12	133.87	120.20
34	AA	1574	C	P-O3'-C3'	9.12	133.87	120.20
34	AA	674	U	P-O3'-C3'	9.11	133.87	120.20
1	A	1386	U	C2'-C3'-O3'	9.06	123.10	109.50
34	AA	270	U	P-O3'-C3'	9.05	133.78	120.20
34	AA	2696	G	P-O3'-C3'	8.93	133.59	120.20
34	AA	1881	C	C2'-C3'-O3'	8.91	122.87	109.50
34	AA	1989	A	P-O3'-C3'	8.89	133.54	120.20
1	A	291	A	P-O3'-C3'	8.87	133.50	120.20
1	A	1109	G	P-O5'-C5'	8.75	134.02	120.90
1	A	2053	U	C2'-C3'-O3'	8.72	122.58	109.50
69	AD	215	ASN	CA-CB-CG	-8.69	103.91	112.60
34	AA	1705	A	C2'-C3'-O3'	8.67	122.50	109.50
34	AA	2180	U	P-O3'-C3'	8.59	133.08	120.20
34	AA	697	A	P-O3'-C3'	8.56	133.04	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	270	U	C2'-C3'-O3'	8.48	122.23	109.50
34	AA	2883	U	P-O3'-C3'	8.46	132.88	120.20
15	2	40	VAL	N-CA-C	8.44	119.23	110.62
34	AA	1435	G	P-O3'-C3'	8.44	132.86	120.20
34	AA	2822	U	P-O3'-C3'	8.43	132.84	120.20
34	AA	179	G	P-O3'-C3'	8.38	132.77	120.20
34	AA	2034	G	P-O5'-C5'	8.36	133.44	120.90
1	A	105	A	C2'-C3'-O3'	8.33	121.99	109.50
34	AA	411	U	P-O3'-C3'	8.32	132.68	120.20
55	AJ	162	ASN	CA-CB-CG	-8.32	104.28	112.60
34	AA	3302	G	P-O5'-C5'	8.28	133.31	120.90
34	AA	580	A	P-O3'-C3'	8.27	132.60	120.20
1	A	1865	G	P-O3'-C3'	8.26	132.60	120.20
1	A	156	A	P-O3'-C3'	8.21	132.51	120.20
1	A	1673	A	P-O3'-C3'	8.21	132.51	120.20
34	AA	889	U	C2'-C3'-O3'	8.20	121.79	109.50
1	A	251	U	C2'-C3'-O3'	8.15	121.72	109.50
1	A	1832	U	P-O3'-C3'	8.06	132.29	120.20
34	AA	146	U	C2'-C3'-O3'	8.06	121.59	109.50
34	AA	1780	G	P-O5'-C5'	8.06	132.99	120.90
1	A	1381	C	P-O3'-C3'	8.03	132.24	120.20
1	A	752	U	C2'-C3'-O3'	8.00	121.50	109.50
1	A	1645	C	P-O3'-C3'	8.00	132.19	120.20
34	AA	2919	A	P-O3'-C3'	7.91	132.07	120.20
67	A3	112	ASN	CA-CB-CG	-7.89	104.71	112.60
1	A	1071	G	P-O3'-C3'	7.88	132.02	120.20
57	AK	49	ASN	CA-CB-CG	-7.88	104.72	112.60
1	A	2044	G	O3'-P-O5'	-7.83	92.26	104.00
34	AA	3282	U	P-O5'-C5'	-7.80	109.20	120.90
34	AA	3631	U	O3'-P-O5'	-7.79	92.31	104.00
54	AI	114	PHE	CA-CB-CG	-7.79	106.01	113.80
43	AN	44	PHE	CA-CB-CG	-7.78	106.02	113.80
1	A	544	G	P-O3'-C3'	7.77	131.86	120.20
34	AA	1231	A	P-O5'-C5'	7.75	132.52	120.90
10	R	60	SER	CA-C-N	7.74	130.50	120.44
10	R	60	SER	C-N-CA	7.74	130.50	120.44
65	AT	127	LYS	CA-C-N	7.73	128.73	119.99
65	AT	127	LYS	C-N-CA	7.73	128.73	119.99
34	AA	577	U	P-O5'-C5'	7.73	132.50	120.90
7	K	121	THR	N-CA-CB	7.70	123.51	110.49
45	A9	39	ARG	N-CA-C	7.70	119.31	111.07
22	H	50	PHE	CA-CB-CG	-7.69	106.11	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	AT	131	PHE	CA-CB-CG	-7.68	106.12	113.80
32	X	112	ILE	N-CA-C	7.68	117.79	110.42
1	A	1980	A	C2'-C3'-O3'	7.66	121.00	109.50
65	AT	19	ASN	CA-CB-CG	-7.65	104.95	112.60
68	A5	171	TYR	N-CA-C	7.63	119.38	111.14
1	A	1414	A	P-O3'-C3'	7.60	131.60	120.20
34	AA	3667	C	C2'-C3'-O3'	7.58	120.87	109.50
34	AA	3013	A	P-O5'-C5'	7.56	132.24	120.90
1	A	248	G	P-O3'-C3'	7.55	131.53	120.20
34	AA	500	A	P-O3'-C3'	7.51	131.46	120.20
34	AA	579	C	P-O3'-C3'	7.48	131.41	120.20
37	AL	19	HIS	CA-CB-CG	7.46	121.26	113.80
34	AA	3230	G	P-O3'-C3'	7.46	131.40	120.20
37	AL	151	PHE	CA-CB-CG	-7.46	106.34	113.80
34	AA	1630	A	P-O3'-C3'	-7.45	109.03	120.20
34	AA	432	A	P-O3'-C3'	7.44	131.37	120.20
34	AA	3140	U	C2'-C3'-O3'	7.43	120.65	109.50
26	P	38	ASN	CA-CB-CG	-7.42	105.18	112.60
10	R	52	GLN	N-CA-C	7.41	120.97	110.23
34	AA	1538	U	C2'-C3'-O3'	7.41	120.61	109.50
59	AS	145	ARG	NE-CZ-NH2	7.37	125.83	119.20
12	Y	102	PHE	CA-CB-CG	-7.36	106.44	113.80
60	AO	52	TYR	N-CA-C	7.36	118.94	111.07
34	AA	607	A	P-O3'-C3'	7.33	131.20	120.20
7	K	16	ASN	CA-CB-CG	-7.32	105.28	112.60
1	A	1283	U	P-O3'-C3'	7.29	131.13	120.20
51	AP	55	ALA	N-CA-C	7.29	119.22	111.28
34	AA	581	C	P-O3'-C3'	7.29	131.13	120.20
34	AA	2394	C	P-O3'-C3'	7.28	131.12	120.20
34	AA	3476	A	C2'-C3'-O3'	7.27	120.41	109.50
45	A9	52	SER	N-CA-C	-7.27	98.13	108.96
1	A	789	U	P-O3'-C3'	7.24	131.06	120.20
1	A	1907	A	C4'-C3'-C2'	-7.24	95.36	102.60
53	Ai	57	PHE	CA-CB-CG	7.24	121.04	113.80
1	A	1455	C	P-O3'-C3'	7.23	131.05	120.20
21	F	157	ASN	CA-CB-CG	-7.20	105.40	112.60
35	AC	35	A	P-O3'-C3'	7.20	131.00	120.20
1	A	1182	A	P-O3'-C3'	7.18	130.98	120.20
37	AL	61	THR	CA-C-N	7.16	129.88	120.28
37	AL	61	THR	C-N-CA	7.16	129.88	120.28
1	A	1845	U	C5'-C4'-C3'	-7.14	105.29	116.00
34	AA	1805	U	P-O3'-C3'	7.13	130.90	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7	74	A	C4'-C3'-O3'	7.10	120.05	109.40
61	AQ	173	PHE	CA-CB-CG	-7.10	106.70	113.80
34	AA	504	A	P-O3'-C3'	7.08	130.83	120.20
34	AA	1537	G	C5'-C4'-C3'	-7.08	105.38	116.00
73	AU	123	HIS	CA-CB-CG	-7.06	106.74	113.80
34	AA	3361	U	C2'-C3'-O3'	7.05	120.08	109.50
34	AA	698	G	P-O3'-C3'	7.04	130.77	120.20
34	AA	3658	G	P-O3'-C3'	7.03	130.75	120.20
1	A	981	U	C2'-C3'-O3'	7.03	120.05	109.50
1	A	1796	C	C5'-C4'-C3'	-7.02	105.47	116.00
34	AA	888	A	P-O3'-C3'	7.02	130.73	120.20
55	AJ	148	PHE	CA-CB-CG	-7.01	106.79	113.80
2	7	74	A	C4'-C3'-C2'	-7.00	95.60	102.60
73	AU	39	PHE	CA-CB-CG	-6.99	106.81	113.80
34	AA	2885	A	P-O3'-C3'	6.99	130.68	120.20
12	Y	166	VAL	N-CA-C	6.99	117.13	110.42
34	AA	337	A	C2'-C3'-O3'	6.98	119.97	109.50
34	AA	521	U	C2'-C3'-O3'	6.97	119.96	109.50
77	AX	119	PHE	CA-CB-CG	-6.97	106.83	113.80
51	AP	121	TRP	N-CA-C	6.97	118.66	111.14
34	AA	833	G	P-O5'-C5'	6.95	131.32	120.90
28	S	127	HIS	CA-CB-CG	-6.95	106.85	113.80
51	AP	157	HIS	CA-CB-CG	-6.93	106.86	113.80
22	H	145	PHE	CA-CB-CG	-6.93	106.87	113.80
34	AA	1217	U	C2'-C3'-O3'	6.93	119.89	109.50
34	AA	3587	U	C5'-C4'-C3'	6.91	126.36	116.00
34	AA	3476	A	P-O3'-C3'	6.89	130.53	120.20
34	AA	3067	G	C2'-C3'-O3'	6.88	119.83	109.50
34	AA	1990	A	P-O3'-C3'	6.88	130.52	120.20
34	AA	1574	C	O4'-C1'-N1	6.87	118.81	108.50
71	AF	116	ASN	CA-CB-CG	-6.87	105.73	112.60
63	AW	90	PHE	CA-CB-CG	-6.86	106.94	113.80
1	A	1786	U	P-O3'-C3'	6.85	130.47	120.20
34	AA	2816	U	P-O3'-C3'	6.85	130.47	120.20
39	A2	31	PHE	CA-CB-CG	-6.82	106.98	113.80
19	6	44	PHE	CA-CB-CG	-6.81	106.99	113.80
1	A	972	U	P-O5'-C5'	-6.80	110.69	120.90
34	AA	3130	U	C2'-C3'-O3'	6.80	119.71	109.50
1	A	251	U	P-O3'-C3'	6.79	130.39	120.20
34	AA	2033	C	P-O3'-C3'	6.79	130.38	120.20
1	A	790	U	C2'-C3'-O3'	6.78	119.67	109.50
34	AA	3590	A	P-O3'-C3'	6.78	130.36	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	110	PHE	CA-CB-CG	-6.77	107.03	113.80
34	AA	1794	U	C1'-O4'-C4'	-6.75	102.95	109.70
1	A	129	U	C2'-C3'-O3'	6.74	119.62	109.50
54	AI	123	ASP	CA-CB-CG	-6.73	105.87	112.60
34	AA	859	C	P-O5'-C5'	6.73	130.99	120.90
28	S	88	ARG	NE-CZ-NH2	6.72	125.25	119.20
34	AA	3043	A	C2'-C3'-O3'	6.71	119.56	109.50
1	A	1976	G	P-O3'-C3'	6.70	130.25	120.20
1	A	1381	C	C2'-C3'-O3'	6.68	123.72	113.70
70	AE	130	PHE	CA-CB-CG	-6.68	107.12	113.80
34	AA	3590	A	C2'-C3'-O3'	6.67	119.51	109.50
34	AA	1481	A	P-O3'-C3'	6.66	130.19	120.20
56	Ac	11	PHE	CA-CB-CG	-6.64	107.16	113.80
20	B	232	HIS	N-CA-C	6.62	118.15	111.07
1	A	2029	A	C5'-C4'-C3'	6.62	125.92	116.00
6	I	62	ARG	NE-CZ-NH2	6.61	125.15	119.20
73	AU	122	ARG	NE-CZ-NH2	6.61	125.15	119.20
34	AA	1035	G	P-O3'-C3'	6.61	130.11	120.20
1	A	206	A	P-O3'-C3'	6.60	130.10	120.20
22	H	212	LEU	N-CA-C	6.59	118.12	111.07
1	A	1671	A	C5'-C4'-C3'	-6.59	106.12	116.00
1	A	1321	C	C5'-C4'-C3'	-6.58	106.13	116.00
1	A	753	U	C2'-C3'-O3'	6.57	119.35	109.50
2	7	51	U	C5'-C4'-C3'	6.57	125.85	116.00
62	AR	221	HIS	CA-CB-CG	-6.57	107.23	113.80
34	AA	1224	A	P-O3'-C3'	6.56	130.04	120.20
70	AE	136	VAL	N-CA-C	6.56	116.17	108.96
34	AA	3067	G	C1'-O4'-C4'	-6.56	103.14	109.70
31	V	115	SER	N-CA-C	-6.55	102.33	108.22
52	Ah	8	VAL	N-CA-C	6.55	117.30	110.62
59	AS	122	PHE	CA-CB-CG	-6.55	107.25	113.80
48	Ad	54	PHE	CA-CB-CG	-6.54	107.26	113.80
1	A	383	G	P-O3'-C3'	6.54	130.01	120.20
51	AP	35	VAL	N-CA-C	6.54	117.29	110.62
1	A	2071	U	P-O3'-C3'	6.52	129.97	120.20
64	AY	180	ALA	N-CA-C	6.51	119.21	111.33
34	AA	61	A	P-O3'-C3'	6.51	129.97	120.20
12	Y	157	ASN	CA-CB-CG	-6.50	106.10	112.60
34	AA	3679	A	O3'-P-O5'	-6.50	94.25	104.00
34	AA	3650	U	P-O5'-C5'	6.50	130.64	120.90
54	AI	48	ARG	N-CA-C	6.49	118.01	111.07
34	AA	1537	G	P-O3'-C3'	-6.48	110.48	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	AK	71	HIS	CA-CB-CG	-6.47	107.33	113.80
34	AA	101	C	O4'-C1'-N1	6.47	118.20	108.50
34	AA	1705	A	P-O3'-C3'	6.47	129.90	120.20
69	AD	21	HIS	N-CA-C	6.47	118.33	111.28
36	AB	39	C	P-O3'-C3'	6.46	129.89	120.20
70	AE	16	PHE	CA-CB-CG	-6.45	107.35	113.80
70	AE	206	PHE	CA-CB-CG	-6.45	107.36	113.80
24	L	21	HIS	N-CA-C	-6.44	99.85	108.74
34	AA	1913	A	P-O3'-C3'	6.43	129.85	120.20
47	Ab	87	HIS	CA-CB-CG	-6.42	107.38	113.80
70	AE	240	HIS	N-CA-C	6.41	118.06	111.14
30	U	123	HIS	CA-CB-CG	-6.41	107.39	113.80
29	T	54	ARG	NE-CZ-NH1	-6.39	115.11	121.50
69	AD	216	HIS	CA-CB-CG	-6.39	107.41	113.80
20	B	35	PRO	CA-C-N	6.39	129.13	120.38
20	B	35	PRO	C-N-CA	6.39	129.13	120.38
34	AA	10	G	P-O3'-C3'	6.39	129.78	120.20
17	4	30	PHE	CA-CB-CG	-6.38	107.42	113.80
35	AC	38	G	C4'-C3'-C2'	-6.38	96.22	102.60
1	A	1386	U	P-O3'-C3'	6.38	129.76	120.20
34	AA	1805	U	C2'-C3'-O3'	6.37	123.26	113.70
34	AA	2957	G	P-O5'-C5'	6.37	130.45	120.90
71	AF	217	VAL	N-CA-C	6.36	117.04	110.36
1	A	1750	U	P-O5'-C5'	6.35	130.43	120.90
69	AD	42	LYS	CA-C-N	6.35	128.12	122.47
69	AD	42	LYS	C-N-CA	6.35	128.12	122.47
75	AV	84	ARG	NE-CZ-NH1	-6.34	115.16	121.50
68	A5	122	ASN	CA-C-N	6.34	126.56	122.18
68	A5	122	ASN	C-N-CA	6.34	126.56	122.18
34	AA	1841	U	P-O3'-C3'	6.34	129.71	120.20
34	AA	62	A	P-O3'-C3'	6.33	129.70	120.20
34	AA	620	U	P-O3'-C3'	6.33	129.70	120.20
12	Y	124	ARG	NE-CZ-NH2	6.32	124.89	119.20
12	Y	143	LYS	N-CA-C	6.32	118.25	111.36
32	X	34	ILE	N-CA-CB	6.32	119.13	110.54
26	P	66	ARG	N-CA-C	-6.32	99.85	108.38
69	AD	115	ASN	CA-CB-CG	-6.32	106.28	112.60
72	AG	82	LYS	CA-C-N	6.32	127.13	119.99
72	AG	82	LYS	C-N-CA	6.32	127.13	119.99
34	AA	889	U	P-O3'-C3'	6.31	129.66	120.20
68	A5	213	ASN	CA-C-N	6.31	128.64	120.44
68	A5	213	ASN	C-N-CA	6.31	128.64	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	AI	130	ASP	N-CA-C	6.30	118.15	111.28
1	A	2084	G	P-O3'-C3'	6.29	129.64	120.20
34	AA	580	A	C5'-C4'-C3'	6.29	125.44	116.00
74	AH	165	LEU	N-CA-C	6.28	119.34	110.23
1	A	65	A	C2'-C3'-O3'	6.28	118.91	109.50
34	AA	1224	A	P-O5'-C5'	6.27	130.31	120.90
71	AF	205	ASN	CA-CB-CG	-6.27	106.33	112.60
19	6	17	GLN	N-CA-C	6.26	117.77	111.07
33	C	106	MET	N-CA-C	6.26	117.77	111.07
34	AA	858	C	P-O3'-C3'	6.26	129.59	120.20
68	A5	245	ARG	NE-CZ-NH2	6.25	124.83	119.20
34	AA	1101	A	P-O3'-C3'	6.25	129.58	120.20
71	AF	49	ARG	N-CA-C	6.25	119.10	110.35
24	L	70	PHE	CA-CB-CG	-6.25	107.56	113.80
44	A8	100	VAL	N-CA-C	6.24	117.36	108.93
45	A9	36	GLN	N-CA-C	6.24	118.84	110.35
34	AA	620	U	C2'-C3'-O3'	6.24	118.86	109.50
70	AE	121	ASN	CA-CB-CG	-6.24	106.36	112.60
1	A	492	A	P-O5'-C5'	6.24	130.25	120.90
34	AA	3381	A	C2'-C3'-O3'	6.23	118.85	109.50
1	A	508	U	O5'-C5'-C4'	6.23	120.85	111.50
34	AA	1996	C	P-O3'-C3'	6.22	129.54	120.20
63	AW	76	PHE	CA-CB-CG	-6.22	107.58	113.80
34	AA	1503	A	P-O3'-C3'	6.22	129.53	120.20
34	AA	2107	C	P-O3'-C3'	6.22	129.53	120.20
34	AA	2107	C	C2'-C3'-O3'	6.22	118.83	109.50
50	Af	34	CYS	N-CA-C	6.21	118.85	111.71
34	AA	1230	A	O4'-C1'-N9	6.21	117.51	108.20
1	A	2028	U	O3'-P-O5'	-6.20	94.71	104.00
34	AA	1233	A	P-O5'-C5'	6.20	130.19	120.90
35	AC	145	A	C2'-C3'-O3'	6.18	122.97	113.70
6	I	195	ARG	NE-CZ-NH1	6.17	127.67	121.50
9	W	82	LEU	N-CA-C	6.17	118.01	111.28
28	S	79	PHE	CA-CB-CG	-6.17	107.63	113.80
34	AA	2959	G	P-O3'-C3'	6.17	129.45	120.20
34	AA	1797	A	P-O5'-C5'	6.17	130.15	120.90
73	AU	122	ARG	NE-CZ-NH1	-6.17	115.33	121.50
55	AJ	75	ILE	N-CA-CB	6.16	121.40	111.23
62	AR	182	PHE	CA-CB-CG	-6.16	107.64	113.80
1	A	1942	G	C5'-C4'-C3'	-6.16	106.76	116.00
58	AM	117	THR	N-CA-C	6.16	118.07	111.36
62	AR	292	LEU	N-CA-C	6.16	117.66	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	2665	A	C2'-C3'-O3'	6.15	118.73	109.50
59	AS	173	PHE	CA-CB-CG	-6.15	107.65	113.80
21	F	50	ASN	CA-CB-CG	-6.15	106.45	112.60
34	AA	652	A	C2'-C3'-O3'	6.14	122.91	113.70
34	AA	1435	G	C2'-C3'-O3'	6.14	118.71	109.50
54	AI	16	LYS	N-CA-C	6.14	118.05	111.36
20	B	142	PHE	CA-CB-CG	-6.13	107.67	113.80
30	U	55	ARG	NE-CZ-NH1	-6.12	115.38	121.50
34	AA	1705	A	P-O5'-C5'	6.12	130.08	120.90
30	U	146	ALA	N-CA-C	6.12	117.62	111.07
51	AP	106	VAL	CA-C-N	6.12	127.84	120.13
51	AP	106	VAL	C-N-CA	6.12	127.84	120.13
71	AF	193	LYS	CA-C-N	6.12	126.88	120.03
71	AF	193	LYS	C-N-CA	6.12	126.88	120.03
28	S	25	LYS	CA-C-N	6.11	129.98	120.75
28	S	25	LYS	C-N-CA	6.11	129.98	120.75
53	Ai	29	LYS	N-CA-C	6.11	117.74	111.14
1	A	548	A	P-O3'-C3'	-6.11	111.03	120.20
1	A	844	G	P-O3'-C3'	6.11	129.36	120.20
1	A	1786	U	P-O5'-C5'	6.11	130.06	120.90
1	A	423	A	C2'-C3'-O3'	6.10	118.65	109.50
1	A	648	A	P-O5'-C5'	6.10	130.05	120.90
12	Y	167	TYR	N-CA-C	6.09	117.59	111.07
34	AA	1535	G	P-O5'-C5'	6.09	130.04	120.90
35	AC	140	G	P-O5'-C5'	6.09	130.03	120.90
30	U	135	LEU	O-C-N	-6.09	117.59	121.85
51	AP	38	ARG	NE-CZ-NH2	6.09	124.68	119.20
34	AA	500	A	C2'-C3'-O3'	6.08	118.63	109.50
24	L	217	ARG	NE-CZ-NH1	-6.08	115.42	121.50
74	AH	101	ASN	CA-CB-CG	-6.08	106.52	112.60
38	A1	135	LYS	CA-C-N	6.07	128.34	120.44
38	A1	135	LYS	C-N-CA	6.07	128.34	120.44
56	Ac	21	LEU	N-CA-C	6.07	117.90	111.28
1	A	1870	A	C2'-C3'-O3'	6.07	118.60	109.50
2	7	33	C	P-O3'-C3'	-6.06	111.11	120.20
59	AS	145	ARG	NE-CZ-NH1	-6.06	115.44	121.50
24	L	65	PHE	CA-CB-CG	-6.05	107.75	113.80
34	AA	3577	A	C2'-C3'-O3'	6.05	118.57	109.50
34	AA	2932	A	P-O3'-C3'	6.05	129.27	120.20
72	AG	41	THR	CA-C-N	6.05	128.38	120.28
72	AG	41	THR	C-N-CA	6.05	128.38	120.28
34	AA	1999	A	P-O3'-C3'	6.04	129.27	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	AI	202	HIS	CA-CB-CG	-6.04	107.75	113.80
35	AC	37	A	C2'-C3'-O3'	6.04	122.77	113.70
52	Ah	41	PHE	CA-CB-CG	-6.04	107.76	113.80
1	A	138	U	C2'-C3'-O3'	6.04	118.55	109.50
28	S	25	LYS	N-CA-C	-6.04	106.05	113.41
66	AZ	3	PHE	CA-CB-CG	-6.03	107.77	113.80
28	S	137	HIS	CA-CB-CG	-6.03	107.77	113.80
54	AI	18	LYS	N-CA-C	6.02	117.92	111.36
34	AA	215	C	C2'-C3'-O3'	6.01	122.72	113.70
24	L	164	LYS	N-CA-C	6.01	118.52	110.35
1	A	876	U	P-O3'-C3'	6.01	129.21	120.20
37	AL	99	ARG	N-CA-C	6.00	117.62	111.14
57	AK	199	PHE	CA-CB-CG	-6.00	107.80	113.80
34	AA	3639	G	O3'-P-O5'	6.00	112.99	104.00
2	7	36	A	P-O5'-C5'	5.99	129.89	120.90
40	A4	8	THR	N-CA-CB	5.99	120.61	110.49
34	AA	2832	A	C2'-C3'-O3'	5.99	118.48	109.50
38	A1	141	HIS	N-CA-C	5.99	117.48	111.07
1	A	516	G	C2'-C3'-O3'	5.99	118.48	109.50
56	Ac	51	ASN	CA-CB-CG	-5.98	106.62	112.60
34	AA	312	A	C5'-C4'-C3'	-5.98	106.23	115.20
34	AA	1705	A	C5'-C4'-C3'	5.98	124.17	115.20
34	AA	3154	U	C4'-C3'-C2'	5.98	108.58	102.60
34	AA	715	U	P-O3'-C3'	5.97	129.15	120.20
34	AA	3034	A	C2'-C3'-O3'	5.97	118.45	109.50
1	A	161	U	C5'-C4'-O4'	5.96	118.75	109.80
5	G	236	TYR	N-CA-C	5.96	117.58	111.14
63	AW	25	HIS	CA-CB-CG	-5.96	107.84	113.80
45	A9	80	LYS	CA-C-N	5.96	129.17	120.71
45	A9	80	LYS	C-N-CA	5.96	129.17	120.71
3	D	153	PHE	CA-CB-CG	-5.96	107.84	113.80
6	I	15	SER	N-CA-C	5.96	117.77	111.28
34	AA	1026	G	P-O3'-C3'	5.95	129.13	120.20
34	AA	2733	A	O3'-P-O5'	-5.95	95.08	104.00
63	AW	137	ASN	CA-CB-CG	-5.95	106.65	112.60
25	N	78	ARG	NE-CZ-NH2	5.95	124.55	119.20
55	AJ	91	PRO	N-CA-C	5.95	117.96	110.70
24	L	217	ARG	NE-CZ-NH2	5.94	124.55	119.20
34	AA	579	C	C2'-C3'-O3'	5.94	118.41	109.50
20	B	138	PHE	CA-CB-CG	-5.94	107.86	113.80
71	AF	156	ASN	CA-CB-CG	-5.94	106.66	112.60
26	P	128	ARG	NE-CZ-NH2	5.94	124.54	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	A	C2'-C3'-O3'	5.93	118.40	109.50
34	AA	207	A	O3'-P-O5'	-5.93	95.10	104.00
34	AA	2089	C	P-O3'-C3'	5.93	129.10	120.20
1	A	272	U	P-O5'-C5'	5.93	129.80	120.90
1	A	1800	A	P-O3'-C3'	5.93	129.09	120.20
34	AA	2437	A	C1'-O4'-C4'	-5.93	103.77	109.70
38	A1	98	SER	CA-C-N	5.93	128.54	120.54
38	A1	98	SER	C-N-CA	5.93	128.54	120.54
2	7	37	U	P-O5'-C5'	5.92	129.78	120.90
26	P	37	PHE	N-CA-CB	5.92	120.02	114.10
34	AA	1272	U	C2'-C3'-O3'	5.92	118.38	109.50
34	AA	1003	A	P-O3'-C3'	5.92	129.08	120.20
2	7	74	A	C2'-C3'-O3'	-5.92	100.63	109.50
1	A	82	G	C5'-C4'-C3'	5.91	124.86	116.00
2	7	17	U	P-O3'-C3'	5.91	129.07	120.20
34	AA	769	U	O4'-C1'-N1	5.91	117.36	108.50
19	6	33	ARG	NE-CZ-NH2	5.91	124.52	119.20
20	B	205	TYR	O-C-N	-5.91	117.72	121.85
45	A9	67	ASN	CA-CB-CG	-5.90	106.70	112.60
34	AA	1222	U	P-O3'-C3'	5.90	129.05	120.20
15	2	39	ALA	CA-C-N	5.90	128.54	120.46
15	2	39	ALA	C-N-CA	5.90	128.54	120.46
34	AA	3140	U	P-O3'-C3'	5.90	129.05	120.20
16	3	6	ARG	NE-CZ-NH2	5.90	124.51	119.20
59	AS	57	ARG	NE-CZ-NH1	-5.90	115.60	121.50
1	A	1856	A	C1'-O4'-C4'	-5.89	104.01	109.90
13	Z	52	PHE	CA-CB-CG	-5.89	107.91	113.80
34	AA	1000	C	O3'-P-O5'	5.88	112.82	104.00
1	A	1897	A	C4'-C3'-O3'	5.88	118.22	109.40
12	Y	137	GLU	N-CA-C	5.88	118.02	108.26
34	AA	268	C	C2'-C3'-O3'	5.88	118.32	109.50
35	AC	145	A	P-O3'-C3'	5.88	129.01	120.20
34	AA	888	A	C2'-C3'-O3'	5.87	118.31	109.50
2	7	40	U	C5'-C4'-C3'	5.87	124.80	116.00
34	AA	3575	U	C2'-C3'-O3'	5.86	118.30	109.50
59	AS	154	ALA	N-CA-C	5.86	117.08	109.64
1	A	1980	A	C4'-C3'-C2'	-5.86	96.74	102.60
21	F	156	VAL	N-CA-C	5.86	116.59	110.62
78	A0	65	ASN	CA-CB-CG	-5.86	106.75	112.60
1	A	1108	A	C2'-C3'-O3'	5.85	118.28	109.50
1	A	1819	U	C2'-C3'-O3'	5.85	118.27	109.50
68	A5	149	THR	N-CA-CB	5.85	120.38	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1818	A	C2'-C3'-O3'	5.85	118.27	109.50
73	AU	56	LYS	N-CA-C	5.85	117.65	111.28
34	AA	659	U	C5'-C4'-C3'	-5.84	107.25	116.00
20	B	72	ASP	CA-CB-CG	-5.83	106.77	112.60
1	A	1431	A	P-O3'-C3'	5.83	128.94	120.20
33	C	116	THR	N-CA-CB	5.83	120.34	110.49
34	AA	2696	G	C2'-C3'-O3'	5.83	118.24	109.50
1	A	614	A	C2'-C3'-O3'	5.82	118.23	109.50
6	I	155	ARG	NE-CZ-NH2	5.82	124.44	119.20
49	Ae	44	TRP	N-CA-C	5.82	117.71	111.36
24	L	212	MET	N-CA-C	5.82	117.62	111.28
34	AA	61	A	C2'-C3'-O3'	5.82	122.43	113.70
1	A	544	G	C4'-C3'-C2'	-5.82	96.78	102.60
28	S	133	VAL	N-CA-C	5.82	116.00	110.53
36	AB	75	G	C2'-C3'-O3'	5.82	118.23	109.50
37	AL	153	ASN	CA-CB-CG	-5.82	106.78	112.60
51	AP	139	ASN	CA-CB-CG	-5.81	106.79	112.60
51	AP	187	PRO	N-CA-C	-5.81	108.00	114.92
34	AA	353	G	C2'-C3'-O3'	5.81	122.41	113.70
40	A4	40	PHE	CA-CB-CG	-5.80	108.00	113.80
34	AA	803	A	O4'-C1'-N9	5.80	117.20	108.50
43	AN	107	ASN	CA-CB-CG	-5.80	106.80	112.60
1	A	1644	U	C2'-C3'-O3'	5.80	118.19	109.50
5	G	85	SER	N-CA-C	5.79	117.40	111.14
25	N	70	GLY	CA-C-N	5.79	129.34	120.82
25	N	70	GLY	C-N-CA	5.79	129.34	120.82
73	AU	53	PHE	CA-CB-CG	-5.79	108.00	113.80
34	AA	1685	G	P-O5'-C5'	5.79	129.59	120.90
55	AJ	153	ILE	N-CA-C	5.79	116.53	110.62
4	E	17	ARG	CA-C-N	5.79	125.26	119.24
4	E	17	ARG	C-N-CA	5.79	125.26	119.24
26	P	65	ASP	CA-C-N	5.79	131.70	122.10
26	P	65	ASP	C-N-CA	5.79	131.70	122.10
34	AA	807	U	C5'-C4'-C3'	5.79	124.68	116.00
21	F	88	ASP	CA-CB-CG	-5.78	106.82	112.60
35	AC	134	G	P-O3'-C3'	5.78	128.88	120.20
42	A7	114	ASN	CA-CB-CG	-5.78	106.82	112.60
67	A3	12	LEU	N-CA-C	5.78	118.21	110.35
34	AA	3767	U	C4'-C3'-O3'	5.78	118.07	109.40
63	AW	36	ILE	N-CA-C	5.78	115.97	110.42
38	A1	99	ASP	CA-C-N	5.77	128.59	120.28
38	A1	99	ASP	C-N-CA	5.77	128.59	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Ac	79	ASN	CA-CB-CG	-5.77	106.83	112.60
1	A	432	G	P-O5'-C5'	-5.77	112.25	120.90
25	N	78	ARG	NE-CZ-NH1	-5.76	115.74	121.50
34	AA	453	A	C5'-C4'-C3'	5.76	124.64	116.00
34	AA	697	A	C2'-C3'-O3'	5.76	118.14	109.50
62	AR	16	TYR	N-CA-C	5.76	118.83	110.42
8	M	11	PHE	CA-C-N	5.75	126.93	121.46
8	M	11	PHE	C-N-CA	5.75	126.93	121.46
1	A	525	G	P-O3'-C3'	5.75	128.83	120.20
21	F	247	ASP	CA-CB-CG	-5.75	106.85	112.60
68	A5	185	HIS	N-CA-C	5.75	117.55	111.28
3	D	13	ASN	CA-CB-CG	-5.75	106.85	112.60
66	AZ	51	LYS	N-CA-C	5.75	117.22	111.07
34	AA	3301	C	P-O3'-C3'	-5.75	111.58	120.20
34	AA	683	A	C4'-C3'-O3'	5.75	118.02	109.40
34	AA	1336	U	P-O3'-C3'	-5.75	111.58	120.20
34	AA	501	U	P-O3'-C3'	5.75	128.82	120.20
62	AR	291	GLU	N-CA-C	5.74	117.22	111.07
34	AA	1643	U	C5'-C4'-C3'	5.74	123.81	115.20
55	AJ	98	ASN	CA-CB-CG	-5.74	106.86	112.60
1	A	246	A	P-O3'-C3'	5.74	128.81	120.20
2	7	32	U	C2'-C3'-O3'	5.74	118.10	109.50
71	AF	19	VAL	CA-C-N	5.73	126.51	120.43
71	AF	19	VAL	C-N-CA	5.73	126.51	120.43
21	F	133	LYS	N-CA-C	5.73	118.78	110.42
23	J	132	SER	N-CA-C	5.73	122.46	109.81
34	AA	1501	A	O3'-P-O5'	-5.72	95.43	104.00
59	AS	55	PRO	CA-C-N	5.71	127.94	120.28
59	AS	55	PRO	C-N-CA	5.71	127.94	120.28
76	Ag	3	HIS	CA-CB-CG	5.71	119.51	113.80
34	AA	621	C	C4'-C3'-C2'	-5.71	96.89	102.60
34	AA	215	C	P-O3'-C3'	5.70	128.75	120.20
10	R	42	ILE	N-CA-C	5.70	121.20	109.34
43	AN	78	LYS	CA-C-N	5.70	128.94	120.90
43	AN	78	LYS	C-N-CA	5.70	128.94	120.90
77	AX	66	ASP	N-CA-C	5.70	117.17	111.07
3	D	28	ILE	N-CA-C	5.70	115.78	110.42
34	AA	1202	C	P-O5'-C5'	5.70	129.45	120.90
12	Y	95	VAL	CA-C-N	5.69	126.30	119.98
12	Y	95	VAL	C-N-CA	5.69	126.30	119.98
76	Ag	39	ARG	NE-CZ-NH2	5.69	124.32	119.20
4	E	155	HIS	CA-CB-CG	-5.69	108.11	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
75	AV	13	ARG	NE-CZ-NH2	5.69	124.32	119.20
34	AA	3664	G	P-O3'-C3'	5.69	128.73	120.20
72	AG	154	VAL	N-CA-C	5.68	115.88	110.42
1	A	2085	G	P-O3'-C3'	-5.68	111.68	120.20
30	U	55	ARG	NE-CZ-NH2	5.68	124.31	119.20
70	AE	32	PHE	CA-CB-CG	-5.68	108.12	113.80
54	AI	179	LEU	CA-C-N	5.68	127.89	120.28
54	AI	179	LEU	C-N-CA	5.68	127.89	120.28
46	Aa	69	ASN	CA-CB-CG	-5.67	106.93	112.60
62	AR	228	ASN	CA-CB-CG	-5.67	106.93	112.60
68	A5	130	LYS	N-CA-C	-5.67	105.14	112.68
27	Q	100	ASP	CA-C-N	5.67	130.21	122.84
27	Q	100	ASP	C-N-CA	5.67	130.21	122.84
36	AB	13	A	C4'-C3'-C2'	-5.67	96.93	102.60
40	A4	19	ASN	CA-CB-CG	-5.67	106.93	112.60
65	AT	117	HIS	CA-CB-CG	-5.67	108.13	113.80
4	E	79	ARG	NE-CZ-NH2	5.67	124.30	119.20
34	AA	236	U	P-O3'-C3'	5.67	128.70	120.20
34	AA	259	G	C5'-C4'-C3'	5.67	124.50	116.00
34	AA	1496	U	C5'-C4'-C3'	5.67	124.50	116.00
57	AK	186	ASN	CA-CB-CG	-5.67	106.93	112.60
1	A	1197	C	P-O5'-C5'	5.66	129.39	120.90
34	AA	1618	C	P-O3'-C3'	-5.66	111.70	120.20
34	AA	1996	C	C4'-C3'-O3'	5.66	117.89	109.40
51	AP	159	HIS	N-CA-C	5.66	119.39	111.74
34	AA	1534	U	C2'-C3'-O3'	5.66	117.99	109.50
1	A	849	U	P-O5'-C5'	5.66	129.39	120.90
6	I	153	ALA	N-CA-C	5.66	117.12	111.07
34	AA	3658	G	C4'-C3'-O3'	5.66	117.88	109.40
62	AR	13	PHE	CA-CB-CG	-5.66	108.14	113.80
16	3	43	ASN	CA-CB-CG	-5.65	106.95	112.60
46	Aa	33	HIS	CA-CB-CG	-5.65	108.15	113.80
1	A	1817	U	C2'-C3'-O3'	5.65	117.98	109.50
1	A	793	G	C4'-C3'-C2'	5.65	108.25	102.60
27	Q	61	ALA	N-CA-C	5.65	118.03	110.35
34	AA	833	G	P-O3'-C3'	5.65	128.67	120.20
1	A	1028	U	C2'-C3'-O3'	5.64	117.97	109.50
34	AA	521	U	C4'-C3'-C2'	-5.64	96.96	102.60
34	AA	581	C	C2'-C3'-O3'	5.64	122.17	113.70
1	A	1454	G	P-O5'-C5'	5.64	129.36	120.90
1	A	758	U	P-O5'-C5'	5.63	129.34	120.90
73	AU	131	ASN	CA-CB-CG	-5.63	106.97	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	1206	U	C2'-C3'-O3'	5.63	117.94	109.50
7	K	120	HIS	N-CA-CB	5.62	120.00	110.49
55	AJ	231	PHE	CA-CB-CG	-5.62	108.17	113.80
51	AP	145	ASN	CA-CB-CG	-5.62	106.98	112.60
69	AD	200	ARG	NE-CZ-NH2	5.62	124.26	119.20
71	AF	138	LEU	CA-C-N	5.62	127.75	120.44
71	AF	138	LEU	C-N-CA	5.62	127.75	120.44
1	A	379	G	C5'-C4'-C3'	-5.62	107.58	116.00
60	AO	28	HIS	O-C-N	-5.61	118.95	121.53
75	AV	84	ARG	NE-CZ-NH2	5.61	124.25	119.20
1	A	836	C	C2'-C3'-O3'	5.61	117.91	109.50
34	AA	1002	A	P-O3'-C3'	-5.61	111.79	120.20
34	AA	2095	U	P-O3'-C3'	5.61	128.61	120.20
59	AS	96	GLN	N-CA-C	5.61	119.08	111.17
1	A	844	G	C5'-C4'-C3'	5.61	124.41	116.00
34	AA	2485	C	C5'-C4'-C3'	-5.60	107.60	116.00
51	AP	67	ARG	NE-CZ-NH2	5.60	124.24	119.20
70	AE	331	ARG	N-CA-C	5.60	116.95	109.83
20	B	38	PHE	CA-CB-CG	-5.60	108.20	113.80
34	AA	1430	A	P-O3'-C3'	-5.60	111.80	120.20
1	A	143	A	C2'-C3'-O3'	5.60	117.90	109.50
22	H	170	PHE	CA-C-N	5.60	128.13	120.35
22	H	170	PHE	C-N-CA	5.60	128.13	120.35
1	A	1403	U	C5'-C4'-C3'	-5.59	107.62	116.00
22	H	43	GLU	CA-C-N	5.59	128.04	120.38
22	H	43	GLU	C-N-CA	5.59	128.04	120.38
34	AA	2958	G	P-O3'-C3'	5.59	128.59	120.20
34	AA	3740	A	C2'-C3'-O3'	5.59	117.89	109.50
70	AE	148	ILE	CA-C-N	5.59	127.70	120.44
70	AE	148	ILE	C-N-CA	5.59	127.70	120.44
34	AA	451	C	C4'-C3'-C2'	5.59	108.19	102.60
23	J	10	LYS	N-CA-C	5.58	117.36	111.28
34	AA	1873	U	P-O3'-C3'	5.58	128.57	120.20
27	Q	122	PHE	CA-CB-CG	-5.57	108.23	113.80
70	AE	253	HIS	CA-CB-CG	-5.57	108.23	113.80
1	A	39	A	C2'-C3'-O3'	5.56	117.84	109.50
1	A	1382	G	P-O5'-C5'	5.56	129.24	120.90
34	AA	2090	U	C5'-C4'-C3'	-5.56	107.66	116.00
7	K	92	SER	N-CA-C	5.56	117.02	111.07
34	AA	1042	C	C2'-C3'-O3'	5.56	117.84	109.50
34	AA	1643	U	O4'-C1'-C2'	-5.56	100.24	105.80
57	AK	193	ARG	NE-CZ-NH2	5.56	124.20	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	1217	U	P-O3'-C3'	5.55	128.53	120.20
34	AA	2146	A	C1'-O4'-C4'	-5.55	104.15	109.70
45	A9	122	ILE	N-CA-CB	5.55	115.71	109.99
34	AA	2994	A	P-O5'-C5'	-5.55	112.58	120.90
61	AQ	84	ASN	CA-CB-CG	-5.55	107.05	112.60
34	AA	1750	U	C2'-C3'-O3'	5.54	117.81	109.50
69	AD	163	ARG	NE-CZ-NH2	5.54	124.19	119.20
5	G	82	ASN	CA-CB-CG	-5.54	107.06	112.60
31	V	45	PHE	CA-CB-CG	-5.54	108.26	113.80
51	AP	149	ILE	CA-C-N	5.54	132.11	121.54
51	AP	149	ILE	C-N-CA	5.54	132.11	121.54
20	B	145	LYS	N-CA-C	5.53	117.39	111.36
34	AA	702	U	O4'-C1'-N1	5.53	116.80	108.50
68	A5	160	ARG	NE-CZ-NH2	5.53	124.18	119.20
44	A8	120	ILE	N-CA-C	5.53	117.03	111.00
1	A	1863	U	C5'-C4'-C3'	-5.53	107.71	116.00
19	6	8	LEU	N-CA-C	5.53	117.31	111.28
27	Q	138	GLU	N-CA-C	-5.53	102.28	110.46
7	K	3	ARG	N-CA-C	5.52	117.30	111.28
1	A	919	U	P-O5'-C5'	5.52	129.18	120.90
57	AK	196	LEU	CA-C-N	5.52	127.68	120.28
57	AK	196	LEU	C-N-CA	5.52	127.68	120.28
60	AO	90	PHE	CA-CB-CG	-5.52	108.28	113.80
60	AO	57	GLY	CA-C-N	5.51	128.54	120.71
60	AO	57	GLY	C-N-CA	5.51	128.54	120.71
70	AE	234	ARG	NE-CZ-NH2	5.51	124.16	119.20
60	AO	6	LYS	N-CA-C	5.51	117.84	110.35
34	AA	1431	A	C1'-O4'-C4'	-5.51	104.19	109.70
40	A4	38	ASN	N-CA-CB	5.51	119.80	110.49
51	AP	90	HIS	N-CA-C	5.50	117.36	111.36
34	AA	3768	A	P-O3'-C3'	-5.50	111.95	120.20
33	C	130	ALA	N-CA-C	5.50	117.98	111.33
68	A5	230	LYS	CA-C-N	5.50	128.20	120.28
68	A5	230	LYS	C-N-CA	5.50	128.20	120.28
14	1	91	ARG	NE-CZ-NH1	-5.50	116.00	121.50
34	AA	308	U	C2'-C3'-O3'	5.49	117.74	109.50
60	AO	74	ASN	CA-CB-CG	-5.49	107.11	112.60
1	A	1624	U	P-O3'-C3'	5.49	128.44	120.20
14	1	106	ARG	NE-CZ-NH2	5.49	124.14	119.20
74	AH	47	LEU	N-CA-CB	-5.49	101.67	110.46
1	A	952	U	P-O5'-C5'	5.49	129.13	120.90
39	A2	118	LEU	N-CA-C	5.48	117.81	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	2932	A	C4'-C3'-O3'	5.48	117.62	109.40
2	7	36	A	C5'-C4'-C3'	5.48	124.22	116.00
28	S	28	VAL	N-CA-C	5.48	116.11	110.36
34	AA	1550	A	C5'-C4'-C3'	-5.48	107.78	116.00
34	AA	1503	A	C2'-C3'-O3'	5.48	117.71	109.50
73	AU	7	ASN	CA-CB-CG	-5.48	107.12	112.60
61	AQ	169	ASN	CA-CB-CG	-5.47	107.13	112.60
34	AA	1026	G	O4'-C1'-C2'	-5.47	100.33	105.80
54	AI	87	GLY	CA-C-N	5.47	126.68	119.84
54	AI	87	GLY	C-N-CA	5.47	126.68	119.84
62	AR	21	ARG	N-CA-CB	5.47	117.94	110.01
24	L	109	PHE	CA-CB-CG	-5.46	108.33	113.80
34	AA	353	G	P-O3'-C3'	5.46	128.39	120.20
70	AE	365	GLY	N-CA-C	5.46	117.75	111.36
2	7	20	U	C2'-C3'-O3'	5.46	117.69	109.50
33	C	195	ASN	CA-CB-CG	-5.45	107.15	112.60
30	U	138	ASN	CA-CB-CG	-5.45	107.15	112.60
34	AA	1502	G	C5'-C4'-O4'	5.45	117.28	109.10
68	A5	181	ASP	CA-CB-CG	-5.45	107.15	112.60
61	AQ	128	ARG	N-CA-C	5.45	118.76	111.24
32	X	31	ASP	CA-CB-CG	-5.45	107.15	112.60
74	AH	98	PHE	CA-CB-CG	-5.45	108.36	113.80
34	AA	2697	A	C2'-C3'-O3'	5.44	117.66	109.50
6	I	42	HIS	N-CA-CB	5.44	119.68	110.49
62	AR	233	ASP	CA-CB-CG	-5.44	107.16	112.60
64	AY	173	ARG	NE-CZ-NH2	-5.43	114.31	119.20
34	AA	673	U	O4'-C1'-N1	5.43	116.35	108.20
1	A	1865	G	C4'-C3'-O3'	5.43	117.54	109.40
71	AF	295	SER	N-CA-C	5.43	117.95	110.35
19	6	41	ASN	CA-CB-CG	-5.42	107.18	112.60
34	AA	1631	A	C5'-C4'-O4'	5.42	117.24	109.10
51	AP	159	HIS	CA-CB-CG	-5.42	108.38	113.80
70	AE	326	ALA	N-CA-C	5.42	117.29	110.24
34	AA	537	A	C5'-C4'-C3'	-5.42	107.87	116.00
71	AF	190	ARG	NE-CZ-NH2	5.42	124.08	119.20
15	2	39	ALA	N-CA-C	5.42	115.70	108.38
1	A	586	A	C1'-O4'-C4'	-5.42	104.28	109.70
33	C	187	VAL	N-CA-C	5.42	115.62	110.42
63	AW	37	ARG	N-CA-C	5.42	122.34	110.80
1	A	1431	A	C4'-C3'-C2'	-5.42	97.18	102.60
26	P	109	GLY	CA-C-N	5.42	125.06	119.05
26	P	109	GLY	C-N-CA	5.42	125.06	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	U	124	ARG	NE-CZ-NH1	-5.42	116.08	121.50
34	AA	522	A	P-O5'-C5'	5.42	129.02	120.90
1	A	167	A	P-O3'-C3'	5.41	128.32	120.20
1	A	1387	U	C4'-C3'-C2'	-5.41	97.19	102.60
34	AA	3137	U	C2'-C3'-O3'	5.41	121.82	113.70
51	AP	107	GLY	N-CA-C	5.41	120.47	113.27
60	AO	61	LEU	N-CA-C	5.41	117.26	111.36
62	AR	24	ARG	CA-C-N	5.41	127.53	120.28
62	AR	24	ARG	C-N-CA	5.41	127.53	120.28
1	A	1742	A	C2'-C3'-O3'	5.41	121.81	113.70
1	A	431	A	P-O5'-C5'	5.40	129.00	120.90
14	1	20	ARG	NE-CZ-NH2	5.40	124.06	119.20
24	L	117	PHE	CA-CB-CG	-5.40	108.40	113.80
34	AA	3615	A	P-O3'-C3'	-5.40	112.10	120.20
34	AA	2180	U	C2'-C3'-O3'	5.40	121.80	113.70
34	AA	3639	G	C5'-C4'-C3'	-5.40	107.90	116.00
38	A1	27	ASN	CA-CB-CG	-5.40	107.20	112.60
1	A	1413	U	C2'-C3'-O3'	5.40	121.79	113.70
34	AA	597	A	P-O3'-C3'	5.40	128.29	120.20
60	AO	39	HIS	CA-CB-CG	-5.39	108.41	113.80
54	AI	32	LYS	N-CA-C	5.39	117.16	111.28
10	R	124	GLU	N-CA-C	5.39	117.68	110.35
34	AA	667	U	C2'-C3'-O3'	5.38	117.58	109.50
34	AA	1762	A	C2'-C3'-O3'	5.38	117.58	109.50
61	AQ	98	ARG	NE-CZ-NH1	-5.38	116.12	121.50
22	H	25	LEU	N-CA-C	5.38	121.70	109.81
34	AA	683	A	P-O3'-C3'	5.38	128.27	120.20
33	C	79	ARG	CA-C-N	5.38	124.83	119.24
33	C	79	ARG	C-N-CA	5.38	124.83	119.24
37	AL	50	ILE	CA-C-N	5.38	128.87	120.75
37	AL	50	ILE	C-N-CA	5.38	128.87	120.75
44	A8	68	PRO	CA-C-N	5.37	128.02	120.28
44	A8	68	PRO	C-N-CA	5.37	128.02	120.28
57	AK	92	TYR	N-CA-C	-5.37	106.41	113.12
62	AR	162	PHE	CA-CB-CG	-5.37	108.43	113.80
41	A6	103	ILE	N-CA-C	5.37	116.09	110.62
1	A	874	A	P-O3'-C3'	5.36	128.24	120.20
59	AS	73	ASN	CA-CB-CG	-5.36	107.24	112.60
1	A	1976	G	C5'-C4'-C3'	-5.35	107.97	116.00
34	AA	2095	U	C2'-C3'-O3'	5.35	117.53	109.50
35	AC	76	A	C4'-C3'-O3'	-5.35	104.98	113.00
43	AN	149	LYS	N-CA-C	5.34	117.10	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	984	A	P-O5'-C5'	5.34	128.91	120.90
1	A	635	G	P-O5'-C5'	5.34	128.91	120.90
1	A	1448	U	O4'-C1'-N1	5.34	116.51	108.50
34	AA	3139	C	C5'-C4'-O4'	5.34	117.11	109.10
1	A	1441	C	P-O5'-C5'	5.33	128.90	120.90
69	AD	180	LEU	N-CA-C	5.33	117.17	111.36
5	G	70	LYS	N-CA-C	5.33	117.09	111.28
34	AA	359	A	C2'-C3'-O3'	5.33	117.50	109.50
34	AA	489	U	P-O3'-C3'	5.33	128.19	120.20
63	AW	58	VAL	N-CA-CB	5.33	118.67	111.21
46	Aa	50	ALA	N-CA-C	5.33	117.75	110.24
1	A	1672	C	C2'-C3'-O3'	5.32	117.48	109.50
20	B	89	ASP	CA-CB-CG	-5.32	107.28	112.60
34	AA	2573	A	C2'-C3'-O3'	5.32	117.48	109.50
34	AA	703	U	C2'-C3'-O3'	5.32	121.67	113.70
34	AA	312	A	P-O3'-C3'	-5.31	112.23	120.20
2	7	21	U	P-O5'-C5'	5.31	128.86	120.90
34	AA	3129	U	C2'-C3'-O3'	5.31	117.47	109.50
71	AF	97	ARG	NE-CZ-NH2	5.30	123.97	119.20
13	Z	28	GLU	N-CA-C	5.30	116.74	111.07
22	H	180	THR	N-CA-C	5.30	117.37	110.43
34	AA	3379	A	P-O5'-C5'	5.30	128.85	120.90
57	AK	155	ASN	CA-CB-CG	-5.30	107.30	112.60
17	4	42	THR	CA-C-N	5.30	128.29	120.82
17	4	42	THR	C-N-CA	5.30	128.29	120.82
40	A4	62	LYS	N-CA-C	5.29	116.73	111.07
33	C	42	LYS	CA-C-N	5.29	127.63	120.38
33	C	42	LYS	C-N-CA	5.29	127.63	120.38
34	AA	1534	U	P-O5'-C5'	5.29	128.83	120.90
2	7	20	U	C5'-C4'-C3'	5.29	123.13	115.20
1	A	1689	U	C5'-C4'-C3'	5.28	123.92	116.00
34	AA	765	A	C2'-C3'-O3'	5.28	117.42	109.50
34	AA	1704	U	P-O3'-C3'	-5.28	112.28	120.20
34	AA	1779	A	C4'-C3'-O3'	5.28	117.32	109.40
1	A	1907	A	C2'-C3'-O3'	5.28	117.42	109.50
34	AA	1630	A	C5'-C4'-C3'	-5.28	107.28	115.20
36	AB	84	U	C2'-C3'-O3'	5.28	117.42	109.50
34	AA	500	A	C4'-C3'-O3'	5.28	117.31	109.40
51	AP	17	ASP	CA-CB-CG	-5.27	107.33	112.60
34	AA	179	G	P-O5'-C5'	-5.27	112.99	120.90
74	AH	138	ASN	CA-CB-CG	-5.27	107.33	112.60
15	2	66	GLU	N-CA-C	5.27	116.71	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	4	20	LYS	N-CA-CB	5.27	119.39	110.49
70	AE	108	ASN	CA-CB-CG	-5.27	107.33	112.60
74	AH	38	PHE	CA-CB-CG	-5.27	108.53	113.80
34	AA	683	A	C2'-C3'-O3'	5.26	117.39	109.50
69	AD	163	ARG	NE-CZ-NH1	-5.26	116.24	121.50
51	AP	40	SER	N-CA-C	5.26	116.69	111.07
34	AA	1730	A	P-O3'-C3'	-5.25	112.32	120.20
16	3	83	PHE	CA-CB-CG	-5.25	108.55	113.80
34	AA	806	G	P-O5'-C5'	5.25	128.78	120.90
34	AA	168	A	C5'-C4'-C3'	-5.25	108.13	116.00
34	AA	3568	G	C5'-C4'-C3'	-5.25	108.12	116.00
43	AN	123	ALA	N-CA-C	5.25	117.84	110.23
34	AA	3232	U	C2'-C3'-O3'	5.25	117.37	109.50
34	AA	3782	A	P-O3'-C3'	5.25	128.07	120.20
55	AJ	97	PHE	CA-CB-CG	-5.25	108.55	113.80
34	AA	439	U	P-O5'-C5'	5.25	128.77	120.90
45	A9	54	ARG	N-CA-C	5.25	118.83	111.90
34	AA	501	U	C4'-C3'-C2'	-5.24	97.36	102.60
2	7	49	C	C5'-C4'-C3'	-5.24	108.14	116.00
34	AA	714	C	C4'-C3'-C2'	-5.24	97.36	102.60
1	A	1069	C	O4'-C1'-N1	5.24	116.36	108.50
25	N	112	GLU	CA-C-N	5.24	127.59	120.63
25	N	112	GLU	C-N-CA	5.24	127.59	120.63
68	A5	198	VAL	CB-CA-C	-5.23	105.18	111.88
34	AA	3233	G	C5'-C4'-C3'	-5.23	108.15	116.00
1	A	185	U	P-O5'-C5'	-5.23	113.05	120.90
74	AH	69	ILE	CB-CA-C	-5.23	105.28	111.97
9	W	65	PRO	N-CA-C	5.23	119.42	111.11
34	AA	1910	C	C5'-C4'-C3'	5.23	123.84	116.00
35	AC	139	A	C2'-C3'-O3'	5.23	117.34	109.50
34	AA	610	U	C5'-C4'-C3'	5.23	123.84	116.00
63	AW	77	ASN	CA-CB-CG	-5.23	107.37	112.60
34	AA	2886	A	C2'-C3'-O3'	5.22	117.33	109.50
1	A	1781	C	P-O5'-C5'	5.22	128.73	120.90
55	AJ	273	GLU	CA-C-N	5.22	127.27	120.28
55	AJ	273	GLU	C-N-CA	5.22	127.27	120.28
32	X	33	LEU	N-CA-C	5.21	116.65	111.07
34	AA	3711	U	C2'-C3'-O3'	5.21	117.32	109.50
44	A8	32	TRP	N-CA-C	5.21	117.26	110.43
66	AZ	82	GLU	N-CA-C	5.21	119.92	111.37
34	AA	2480	G	C5'-C4'-O4'	5.21	116.92	109.10
8	M	106	LEU	CA-C-N	5.21	127.26	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	M	106	LEU	C-N-CA	5.21	127.26	120.28
72	AG	42	GLU	N-CA-C	5.21	116.96	111.28
34	AA	3169	C	C5'-C4'-C3'	-5.21	108.19	116.00
74	AH	164	VAL	N-CA-C	5.21	115.31	110.42
64	AY	162	ASN	CA-CB-CG	-5.21	107.39	112.60
1	A	142	G	C2'-C3'-O3'	5.20	117.31	109.50
1	A	920	A	C5'-C4'-C3'	5.20	123.81	116.00
1	A	1108	A	C4'-C3'-C2'	-5.20	97.40	102.60
1	A	1193	A	C2'-C3'-O3'	5.20	117.31	109.50
61	AQ	57	TYR	CA-C-N	5.20	128.61	120.75
61	AQ	57	TYR	C-N-CA	5.20	128.61	120.75
34	AA	1964	G	C2'-C3'-O3'	5.20	117.30	109.50
9	W	64	GLY	CA-C-N	5.20	125.19	119.89
9	W	64	GLY	C-N-CA	5.20	125.19	119.89
34	AA	3319	C	P-O5'-C5'	5.20	128.70	120.90
58	AM	50	ARG	NE-CZ-NH2	5.20	123.88	119.20
34	AA	1750	U	P-O5'-C5'	5.19	128.69	120.90
1	A	1658	G	P-O3'-C3'	-5.19	112.41	120.20
63	AW	98	VAL	CB-CA-C	-5.19	105.32	111.97
72	AG	136	TYR	CA-C-N	5.19	127.96	120.38
72	AG	136	TYR	C-N-CA	5.19	127.96	120.38
74	AH	4	ILE	N-CA-C	5.19	115.41	110.53
34	AA	156	U	P-O5'-C5'	-5.19	113.11	120.90
12	Y	77	PHE	CA-CB-CG	-5.19	108.61	113.80
34	AA	1500	U	O3'-P-O5'	-5.19	96.22	104.00
59	AS	77	ASP	CA-CB-CG	-5.19	107.41	112.60
29	T	54	ARG	NE-CZ-NH2	5.19	123.87	119.20
1	A	845	U	P-O3'-C3'	5.18	127.97	120.20
34	AA	1223	U	O3'-P-O5'	-5.18	96.23	104.00
34	AA	2603	U	P-O5'-C5'	5.18	128.68	120.90
34	AA	2146	A	C2'-C3'-O3'	5.18	117.27	109.50
34	AA	2154	A	C1'-O4'-C4'	-5.18	104.72	109.90
63	AW	68	GLY	N-CA-C	5.18	117.88	111.93
12	Y	27	ASN	CA-CB-CG	5.18	117.78	112.60
22	H	171	ILE	N-CA-C	5.18	117.96	109.78
34	AA	3381	A	P-O3'-C3'	5.18	127.96	120.20
34	AA	3628	C	P-O5'-C5'	5.18	128.66	120.90
72	AG	137	ARG	NE-CZ-NH2	5.18	123.86	119.20
13	Z	72	MET	CG-SD-CE	-5.17	89.52	100.90
17	4	19	LEU	CA-C-N	5.17	131.42	121.54
17	4	19	LEU	C-N-CA	5.17	131.42	121.54
34	AA	1234	A	C5'-C4'-C3'	-5.17	108.24	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	1661	U	P-O5'-C5'	5.17	128.66	120.90
1	A	1817	U	P-O3'-C3'	5.17	127.95	120.20
8	M	125	CYS	N-CA-C	5.17	117.72	110.23
34	AA	2004	U	O4'-C1'-N1	5.17	116.25	108.50
50	Af	14	ASN	CA-CB-CG	-5.17	107.44	112.60
31	V	63	PHE	CA-CB-CG	-5.16	108.64	113.80
34	AA	2093	U	C5'-C4'-C3'	-5.16	107.46	115.20
34	AA	1068	C	C5'-C4'-C3'	5.16	123.74	116.00
34	AA	1881	C	O4'-C1'-N1	5.16	115.94	108.20
34	AA	499	U	C4'-C3'-O3'	-5.16	105.26	113.00
34	AA	15	U	P-O5'-C5'	5.16	128.63	120.90
2	7	43	C	P-O5'-C5'	5.16	128.63	120.90
7	K	31	SER	CA-C-N	5.16	127.44	120.38
7	K	31	SER	C-N-CA	5.16	127.44	120.38
22	H	77	PHE	CA-CB-CG	-5.16	108.64	113.80
24	L	11	LEU	N-CA-C	5.15	117.36	110.35
1	A	2053	U	P-O3'-C3'	5.15	127.93	120.20
34	AA	812	U	C5'-C4'-C3'	-5.15	107.48	115.20
45	A9	66	LYS	N-CA-C	5.15	121.77	110.80
1	A	981	U	C5'-C4'-C3'	-5.15	107.48	115.20
34	AA	3154	U	P-O3'-C3'	-5.15	112.48	120.20
34	AA	3554	U	C4'-C3'-C2'	5.15	107.75	102.60
61	AQ	34	TYR	CA-CB-CG	-5.15	104.63	113.90
6	I	84	VAL	N-CA-CB	5.14	117.54	110.54
77	AX	121	ARG	NE-CZ-NH2	5.14	123.83	119.20
33	C	92	TYR	CA-CB-CG	-5.14	104.65	113.90
34	AA	949	A	O4'-C1'-N9	5.14	116.21	108.50
34	AA	2457	C	P-O3'-C3'	-5.13	112.50	120.20
45	A9	92	HIS	CA-CB-CG	-5.13	108.67	113.80
61	AQ	98	ARG	NE-CZ-NH2	5.13	123.82	119.20
68	A5	173	ARG	NE-CZ-NH2	5.13	123.82	119.20
70	AE	349	ALA	N-CA-C	5.13	117.33	110.35
21	F	201	ASN	CA-CB-CG	-5.13	107.47	112.60
3	D	110	LEU	CA-C-N	5.13	127.15	120.28
3	D	110	LEU	C-N-CA	5.13	127.15	120.28
28	S	89	ARG	NE-CZ-NH2	5.13	123.81	119.20
34	AA	759	U	P-O3'-C3'	-5.13	112.51	120.20
41	A6	36	ALA	N-CA-C	5.12	116.55	111.07
34	AA	1197	U	C2'-C3'-O3'	5.12	121.39	113.70
1	A	1215	G	C2'-C3'-O3'	5.12	117.18	109.50
24	L	119	THR	N-CA-CB	5.12	119.15	110.49
46	Aa	95	PHE	CA-CB-CG	-5.12	108.68	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	AK	81	ARG	NE-CZ-NH2	5.12	123.81	119.20
42	A7	72	VAL	N-CA-C	5.12	115.84	110.62
1	A	1844	A	O3'-P-O5'	-5.12	96.33	104.00
1	A	1856	A	P-O5'-C5'	5.11	128.57	120.90
68	A5	173	ARG	NE-CZ-NH1	-5.11	116.39	121.50
33	C	198	VAL	CA-C-N	5.11	127.84	120.38
33	C	198	VAL	C-N-CA	5.11	127.84	120.38
61	AQ	3	ARG	NE-CZ-NH1	-5.11	116.39	121.50
74	AH	87	PHE	CA-CB-CG	-5.11	108.69	113.80
6	I	16	TYR	N-CA-C	5.10	118.24	111.30
77	AX	100	LYS	N-CA-CB	-5.10	102.36	110.22
10	R	46	ILE	N-CA-CB	5.10	116.52	110.55
34	AA	3414	G	P-O3'-C3'	5.10	127.85	120.20
7	K	70	ASN	CA-CB-CG	-5.09	107.51	112.60
20	B	161	ILE	N-CA-CB	5.09	117.47	110.54
34	AA	2810	A	P-O3'-C3'	5.09	127.84	120.20
34	AA	873	U	P-O3'-C3'	5.09	127.83	120.20
61	AQ	3	ARG	NE-CZ-NH2	5.09	123.78	119.20
2	7	32	U	P-O3'-C3'	5.09	127.83	120.20
9	W	81	ARG	N-CA-C	5.09	116.82	111.28
1	A	343	G	C2'-C3'-O3'	5.08	117.12	109.50
1	A	789	U	C2'-C3'-O3'	5.08	121.33	113.70
3	D	142	LYS	N-CA-C	5.08	116.51	111.07
15	2	67	LYS	N-CA-C	5.08	116.51	111.07
34	AA	597	A	P-O5'-C5'	-5.08	113.27	120.90
51	AP	141	ASN	CA-CB-CG	-5.08	107.52	112.60
32	X	47	ARG	NE-CZ-NH2	5.08	123.77	119.20
34	AA	505	A	C2'-C3'-O3'	5.08	121.32	113.70
37	AL	111	ASN	CA-CB-CG	-5.08	107.52	112.60
69	AD	205	ASN	CA-CB-CG	-5.08	107.52	112.60
1	A	868	U	P-O3'-C3'	5.08	127.81	120.20
34	AA	3154	U	C1'-C2'-O2'	5.08	116.01	108.40
57	AK	194	GLN	N-CA-C	5.08	116.50	111.07
34	AA	858	C	O4'-C1'-N1	5.07	116.11	108.50
51	AP	188	SER	N-CA-CB	5.07	119.06	110.49
34	AA	3443	A	C4'-C3'-C2'	-5.07	97.53	102.60
70	AE	224	LYS	CA-C-N	5.07	124.92	120.10
70	AE	224	LYS	C-N-CA	5.07	124.92	120.10
22	H	158	ILE	N-CA-C	5.07	116.54	109.80
32	X	22	LEU	N-CA-C	5.07	117.19	111.11
25	N	37	ASP	N-CA-C	5.06	116.49	111.07
34	AA	2885	A	C2'-C3'-O3'	5.06	121.30	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1035	A	P-O5'-C5'	5.06	128.49	120.90
34	AA	3526	U	C2'-C3'-O3'	5.06	117.09	109.50
75	AV	102	CYS	CA-C-N	5.06	127.31	120.38
75	AV	102	CYS	C-N-CA	5.06	127.31	120.38
1	A	805	A	C5'-C4'-C3'	-5.06	108.41	116.00
2	7	45	A	P-O3'-C3'	5.06	127.79	120.20
6	I	24	LEU	CA-C-N	5.06	127.02	120.44
6	I	24	LEU	C-N-CA	5.06	127.02	120.44
1	A	510	G	P-O5'-C5'	-5.06	113.31	120.90
7	K	90	ILE	N-CA-CB	5.05	118.16	110.58
60	AO	35	ALA	N-CA-C	5.05	116.79	111.28
5	G	148	LEU	N-CA-C	5.05	118.12	110.64
62	AR	147	PHE	CA-CB-CG	-5.05	108.75	113.80
1	A	1853	A	C2'-C3'-O3'	5.05	117.08	109.50
65	AT	56	VAL	N-CA-C	5.05	116.90	109.63
1	A	1819	U	C5'-C4'-C3'	5.05	122.77	115.20
69	AD	245	LEU	N-CA-C	5.05	117.62	110.50
73	AU	174	PHE	CA-CB-CG	-5.05	108.75	113.80
1	A	874	A	C5'-C4'-C3'	-5.05	108.43	116.00
50	Af	50	LYS	CA-C-O	5.04	120.87	117.94
1	A	2088	C	C2'-C3'-O3'	5.04	117.06	109.50
1	A	1236	U	C5'-C4'-C3'	5.04	123.56	116.00
1	A	1301	G	O5'-C5'-C4'	-5.04	104.14	111.70
34	AA	109	A	P-O3'-C3'	5.04	127.76	120.20
36	AB	29	C	P-O5'-C5'	5.04	128.46	120.90
54	AI	212	ASN	CA-C-N	5.04	127.03	120.28
54	AI	212	ASN	C-N-CA	5.04	127.03	120.28
1	A	422	A	C2'-C3'-O3'	5.04	117.05	109.50
41	A6	50	ASN	CA-CB-CG	-5.04	107.56	112.60
1	A	25	C	P-O5'-C5'	-5.03	113.35	120.90
64	AY	152	GLY	CA-C-N	5.03	127.24	120.50
64	AY	152	GLY	C-N-CA	5.03	127.24	120.50
59	AS	186	LYS	CA-C-N	5.03	130.75	121.70
59	AS	186	LYS	C-N-CA	5.03	130.75	121.70
1	A	1298	C	P-O3'-C3'	-5.02	112.67	120.20
34	AA	1538	U	C5'-C4'-C3'	-5.02	107.67	115.20
59	AS	45	ASN	CA-CB-CG	-5.02	107.58	112.60
34	AA	3115	C	P-O5'-C5'	5.02	128.43	120.90
20	B	220	ARG	NE-CZ-NH2	5.02	123.72	119.20
34	AA	72	C	C5'-C4'-C3'	5.02	123.53	116.00
1	A	460	G	O4'-C1'-N9	5.02	115.72	108.20
59	AS	75	PRO	N-CA-C	-5.02	108.95	114.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	AU	103	PHE	CA-CB-CG	-5.02	108.78	113.80
11	O	81	ASN	CA-CB-CG	-5.01	107.58	112.60
34	AA	3167	A	O4'-C1'-N9	5.01	115.72	108.20
8	M	100	GLU	N-CA-C	5.01	116.74	111.28
71	AF	43	ASN	CA-CB-CG	-5.01	107.59	112.60
1	A	1862	C	C5'-C4'-C3'	5.01	123.51	116.00
1	A	525	G	C2'-C3'-O3'	5.01	121.21	113.70
62	AR	94	ASN	N-CA-C	5.01	117.16	110.35
71	AF	182	ARG	NE-CZ-NH2	-5.01	114.69	119.20
8	M	98	VAL	N-CA-C	5.00	115.29	110.74
1	A	1857	U	O4'-C1'-N1	5.00	116.00	108.50
1	A	127	C	C2'-C3'-O3'	5.00	117.00	109.50
34	AA	122	A	O4'-C1'-N9	5.00	115.70	108.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
34	AA	3018	A	C3'

All (1052) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	1	12	TYR	Sidechain
14	1	91	ARG	Sidechain
15	2	76	ARG	Sidechain
16	3	28	ARG	Sidechain
16	3	85	ARG	Sidechain
17	4	21	ARG	Sidechain
17	4	7	ASN	Peptide
17	4	77	PHE	Sidechain
19	6	10	ARG	Sidechain
19	6	43	ARG	Sidechain
2	7	1	G	Sidechain
2	7	12	G	Sidechain
2	7	14	A	Sidechain
2	7	15	G	Sidechain
2	7	27	G	Sidechain
2	7	29	G	Sidechain
2	7	3	G	Sidechain
2	7	31	G	Sidechain
2	7	36	A	Sidechain
2	7	37	U	Sidechain

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Mol	Chain	Res	Type	Group
2	7	46	G	Sidechain
2	7	52	G	Sidechain
2	7	55	U	Sidechain
2	7	6	A	Sidechain
2	7	64	C	Sidechain
2	7	65	A	Sidechain
2	7	70	A	Sidechain
2	7	9	G	Sidechain
1	A	100	U	Sidechain
1	A	1000	C	Sidechain
1	A	1008	A	Sidechain
1	A	1014	U	Sidechain
1	A	1016	U	Sidechain
1	A	1020	U	Sidechain
1	A	1022	A	Sidechain
1	A	1025	U	Sidechain
1	A	104	U	Sidechain
1	A	1041	G	Sidechain
1	A	1056	G	Sidechain
1	A	1058	G	Sidechain
1	A	106	A	Sidechain
1	A	1061	A	Sidechain
1	A	1063	G	Sidechain
1	A	1071	G	Sidechain
1	A	1074	A	Sidechain
1	A	1080	G	Sidechain
1	A	1081	U	Sidechain
1	A	1083	A	Sidechain
1	A	1084	U	Sidechain
1	A	1086	U	Sidechain
1	A	1094	A	Sidechain
1	A	1100	U	Sidechain
1	A	1104	G	Sidechain
1	A	1107	U	Sidechain
1	A	114	A	Sidechain
1	A	118	U	Sidechain
1	A	1186	G	Sidechain
1	A	1187	A	Sidechain
1	A	1188	A	Sidechain
1	A	1189	A	Sidechain
1	A	120	U	Sidechain
1	A	1200	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1208	G	Sidechain
1	A	1213	G	Sidechain
1	A	1214	A	Sidechain
1	A	1216	U	Sidechain
1	A	1221	G	Sidechain
1	A	1223	G	Sidechain
1	A	1224	C	Sidechain
1	A	1240	A	Sidechain
1	A	1241	A	Sidechain
1	A	1244	A	Sidechain
1	A	1250	G	Sidechain
1	A	1251	G	Sidechain
1	A	1264	A	Sidechain
1	A	1273	G	Sidechain
1	A	1275	U	Sidechain
1	A	1283	U	Sidechain
1	A	1287	U	Sidechain
1	A	1289	G	Sidechain
1	A	129	U	Sidechain
1	A	1290	A	Sidechain
1	A	1300	G	Sidechain
1	A	1307	U	Sidechain
1	A	1320	A	Sidechain
1	A	136	U	Sidechain
1	A	1363	U	Sidechain
1	A	1379	G	Sidechain
1	A	14	U	Sidechain
1	A	1401	G	Sidechain
1	A	1402	A	Sidechain
1	A	1409	U	Sidechain
1	A	141	G	Sidechain
1	A	1415	A	Sidechain
1	A	1423	A	Sidechain
1	A	1436	U	Sidechain
1	A	1442	U	Sidechain
1	A	1448	U	Sidechain
1	A	1454	G	Sidechain
1	A	15	U	Sidechain
1	A	153	A	Sidechain
1	A	159	U	Sidechain
1	A	1602	G	Sidechain
1	A	1607	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	161	U	Sidechain
1	A	1632	G	Sidechain
1	A	1646	U	Sidechain
1	A	1655	G	Sidechain
1	A	1656	A	Sidechain
1	A	1658	G	Sidechain
1	A	1660	U	Sidechain
1	A	1665	G	Sidechain
1	A	168	U	Sidechain
1	A	1683	U	Sidechain
1	A	1691	G	Sidechain
1	A	1692	A	Sidechain
1	A	1700	G	Sidechain
1	A	1718	C	Sidechain
1	A	1742	A	Sidechain
1	A	1743	A	Sidechain
1	A	1744	A	Sidechain
1	A	1745	U	Sidechain
1	A	1748	G	Sidechain
1	A	1792	U	Sidechain
1	A	1794	C	Sidechain
1	A	1807	A	Sidechain
1	A	1819	U	Sidechain
1	A	182	U	Sidechain
1	A	1823	U	Sidechain
1	A	1826	A	Sidechain
1	A	1832	U	Sidechain
1	A	1836	G	Sidechain
1	A	1839	G	Sidechain
1	A	1850	G	Sidechain
1	A	1858	U	Sidechain
1	A	1865	G	Sidechain
1	A	1872	G	Sidechain
1	A	1873	A	Sidechain
1	A	1879	U	Sidechain
1	A	1881	G	Sidechain
1	A	1882	U	Sidechain
1	A	1884	A	Sidechain
1	A	1891	U	Sidechain
1	A	1892	U	Sidechain
1	A	1904	G	Sidechain
1	A	1906	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1914	U	Sidechain
1	A	1917	C	Sidechain
1	A	1940	U	Sidechain
1	A	1947	U	Sidechain
1	A	1955	G	Sidechain
1	A	1972	G	Sidechain
1	A	1977	G	Sidechain
1	A	1979	C	Sidechain
1	A	1980	A	Sidechain
1	A	1984	A	Sidechain
1	A	2014	A	Sidechain
1	A	2021	U	Sidechain
1	A	2028	U	Sidechain
1	A	2030	U	Sidechain
1	A	2031	C	Sidechain
1	A	2032	U	Sidechain
1	A	2033	U	Sidechain
1	A	2053	U	Sidechain
1	A	2055	A	Sidechain
1	A	2059	G	Sidechain
1	A	2060	G	Sidechain
1	A	2067	U	Sidechain
1	A	2072	G	Sidechain
1	A	2074	A	Sidechain
1	A	2075	C	Sidechain
1	A	2082	A	Sidechain
1	A	248	G	Sidechain
1	A	252	U	Sidechain
1	A	254	U	Sidechain
1	A	263	A	Sidechain
1	A	264	G	Sidechain
1	A	273	A	Sidechain
1	A	310	U	Sidechain
1	A	327	U	Sidechain
1	A	328	G	Sidechain
1	A	33	U	Sidechain
1	A	34	G	Sidechain
1	A	341	U	Sidechain
1	A	343	G	Sidechain
1	A	346	U	Sidechain
1	A	355	U	Sidechain
1	A	369	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	389	G	Sidechain
1	A	395	G	Sidechain
1	A	396	G	Sidechain
1	A	402	G	Sidechain
1	A	404	G	Sidechain
1	A	412	U	Sidechain
1	A	440	G	Sidechain
1	A	441	U	Sidechain
1	A	445	U	Sidechain
1	A	455	C	Sidechain
1	A	46	A	Sidechain
1	A	465	G	Sidechain
1	A	483	A	Sidechain
1	A	486	A	Sidechain
1	A	491	A	Sidechain
1	A	5	U	Sidechain
1	A	508	U	Sidechain
1	A	516	G	Sidechain
1	A	517	G	Sidechain
1	A	544	G	Sidechain
1	A	553	U	Sidechain
1	A	555	G	Sidechain
1	A	559	G	Sidechain
1	A	583	G	Sidechain
1	A	589	U	Sidechain
1	A	598	A	Sidechain
1	A	620	G	Sidechain
1	A	623	G	Sidechain
1	A	625	U	Sidechain
1	A	626	A	Sidechain
1	A	74	U	Sidechain
1	A	798	U	Sidechain
1	A	8	U	Sidechain
1	A	802	A	Sidechain
1	A	805	A	Sidechain
1	A	820	A	Sidechain
1	A	822	G	Sidechain
1	A	832	A	Sidechain
1	A	835	G	Sidechain
1	A	836	C	Sidechain
1	A	846	G	Sidechain
1	A	850	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	857	A	Sidechain
1	A	858	U	Sidechain
1	A	859	A	Sidechain
1	A	860	G	Sidechain
1	A	872	A	Sidechain
1	A	882	A	Sidechain
1	A	892	U	Sidechain
1	A	9	U	Sidechain
1	A	916	G	Sidechain
1	A	920	A	Sidechain
1	A	922	U	Sidechain
1	A	931	A	Sidechain
1	A	932	U	Sidechain
1	A	936	A	Sidechain
1	A	94	A	Sidechain
1	A	942	U	Sidechain
1	A	943	U	Sidechain
1	A	952	U	Sidechain
1	A	953	C	Sidechain
1	A	955	U	Sidechain
1	A	97	G	Sidechain
1	A	970	G	Sidechain
1	A	972	U	Sidechain
1	A	977	U	Sidechain
1	A	978	U	Sidechain
1	A	982	A	Sidechain
1	A	987	U	Sidechain
1	A	994	G	Sidechain
1	A	998	A	Sidechain
78	A0	57	ARG	Sidechain
78	A0	64	ARG	Sidechain
38	A1	17	ARG	Sidechain
39	A2	114	ARG	Sidechain
67	A3	105	ARG	Sidechain
40	A4	14	ARG	Sidechain
40	A4	36	ASP	Peptide
68	A5	119	GLN	Peptide
68	A5	154	ARG	Sidechain
68	A5	162	TYR	Sidechain
68	A5	224	ARG	Sidechain
68	A5	238	ARG	Peptide,Sidechain
68	A5	56	ARG	Sidechain

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Mol	Chain	Res	Type	Group
41	A6	30	ARG	Sidechain
41	A6	56	ARG	Sidechain
41	A6	62	TYR	Sidechain
41	A6	89	ARG	Sidechain
42	A7	87	ARG	Sidechain
44	A8	33	ARG	Sidechain
44	A8	43	ARG	Sidechain
45	A9	115	ARG	Sidechain
45	A9	130	ARG	Sidechain
34	AA	1013	U	Sidechain
34	AA	1019	A	Sidechain
34	AA	102	A	Sidechain
34	AA	1023	U	Sidechain
34	AA	1033	A	Sidechain
34	AA	1047	A	Sidechain
34	AA	1050	C	Sidechain
34	AA	1053	U	Sidechain
34	AA	1055	A	Sidechain
34	AA	1056	G	Sidechain
34	AA	1058	U	Sidechain
34	AA	1064	U	Sidechain
34	AA	1065	U	Sidechain
34	AA	1067	U	Sidechain
34	AA	1073	G	Sidechain
34	AA	1075	U	Sidechain
34	AA	1079	U	Sidechain
34	AA	109	A	Sidechain
34	AA	1091	G	Sidechain
34	AA	1094	U	Sidechain
34	AA	1101	A	Sidechain
34	AA	1109	U	Sidechain
34	AA	1110	U	Sidechain
34	AA	1115	G	Sidechain
34	AA	1135	G	Sidechain
34	AA	114	A	Sidechain
34	AA	1142	G	Sidechain
34	AA	116	A	Sidechain
34	AA	1167	U	Sidechain
34	AA	1169	A	Sidechain
34	AA	1171	A	Sidechain
34	AA	1203	A	Sidechain
34	AA	1206	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	1209	U	Sidechain
34	AA	1211	U	Sidechain
34	AA	1213	U	Sidechain
34	AA	1217	U	Sidechain
34	AA	1220	U	Sidechain
34	AA	1222	U	Sidechain
34	AA	1223	U	Sidechain
34	AA	1224	A	Sidechain
34	AA	1231	A	Sidechain
34	AA	1232	U	Sidechain
34	AA	1239	A	Sidechain
34	AA	124	U	Sidechain
34	AA	1244	G	Sidechain
34	AA	1247	C	Sidechain
34	AA	1248	A	Sidechain
34	AA	1249	U	Sidechain
34	AA	1250	U	Sidechain
34	AA	1251	U	Sidechain
34	AA	1256	U	Sidechain
34	AA	1264	A	Sidechain
34	AA	1266	U	Sidechain
34	AA	127	U	Sidechain
34	AA	1273	G	Sidechain
34	AA	1276	G	Sidechain
34	AA	1280	G	Sidechain
34	AA	1297	A	Sidechain
34	AA	1318	A	Sidechain
34	AA	1321	A	Sidechain
34	AA	1327	C	Sidechain
34	AA	1329	U	Sidechain
34	AA	1330	A	Sidechain
34	AA	1331	A	Sidechain
34	AA	136	U	Sidechain
34	AA	14	U	Sidechain
34	AA	1416	U	Sidechain
34	AA	1417	G	Sidechain
34	AA	1423	G	Sidechain
34	AA	1429	A	Sidechain
34	AA	1434	G	Sidechain
34	AA	1445	A	Sidechain
34	AA	1447	G	Sidechain
34	AA	1453	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	1457	G	Sidechain
34	AA	1459	U	Sidechain
34	AA	146	U	Sidechain
34	AA	147	C	Sidechain
34	AA	1473	A	Sidechain
34	AA	1476	A	Sidechain
34	AA	148	G	Sidechain
34	AA	149	A	Sidechain
34	AA	1493	U	Sidechain
34	AA	1497	U	Sidechain
34	AA	1499	U	Sidechain
34	AA	1503	A	Sidechain
34	AA	1507	U	Sidechain
34	AA	1510	U	Sidechain
34	AA	1511	U	Sidechain
34	AA	1513	U	Sidechain
34	AA	1516	G	Sidechain
34	AA	1518	A	Sidechain
34	AA	1524	U	Sidechain
34	AA	1534	U	Sidechain
34	AA	1549	U	Sidechain
34	AA	1552	G	Sidechain
34	AA	1553	U	Sidechain
34	AA	1554	G	Sidechain
34	AA	156	U	Sidechain
34	AA	1572	U	Sidechain
34	AA	1574	C	Sidechain
34	AA	1583	G	Sidechain
34	AA	1585	U	Sidechain
34	AA	1588	U	Sidechain
34	AA	1595	A	Sidechain
34	AA	1597	U	Sidechain
34	AA	1598	A	Sidechain
34	AA	160	G	Sidechain
34	AA	1602	A	Sidechain
34	AA	1606	U	Sidechain
34	AA	1613	G	Sidechain
34	AA	1617	A	Sidechain
34	AA	1619	U	Sidechain
34	AA	1625	G	Sidechain
34	AA	1628	U	Sidechain
34	AA	1629	G	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	1635	G	Sidechain
34	AA	1643	U	Sidechain
34	AA	1644	U	Sidechain
34	AA	1645	U	Sidechain
34	AA	1647	U	Sidechain
34	AA	1650	U	Sidechain
34	AA	1655	U	Sidechain
34	AA	1658	G	Sidechain
34	AA	1671	U	Sidechain
34	AA	1695	A	Sidechain
34	AA	170	U	Sidechain
34	AA	1700	U	Sidechain
34	AA	1701	G	Sidechain
34	AA	1726	C	Sidechain
34	AA	1731	A	Sidechain
34	AA	1735	G	Sidechain
34	AA	1737	A	Sidechain
34	AA	174	U	Sidechain
34	AA	1740	A	Sidechain
34	AA	1745	G	Sidechain
34	AA	1747	U	Sidechain
34	AA	1755	U	Sidechain
34	AA	1763	G	Sidechain
34	AA	1784	G	Sidechain
34	AA	1785	U	Sidechain
34	AA	1786	A	Sidechain
34	AA	1787	A	Sidechain
34	AA	1797	A	Sidechain
34	AA	1798	A	Sidechain
34	AA	1805	U	Sidechain
34	AA	1815	A	Sidechain
34	AA	1820	U	Sidechain
34	AA	1821	U	Sidechain
34	AA	1829	G	Sidechain
34	AA	1830	G	Sidechain
34	AA	1832	U	Sidechain
34	AA	1835	G	Sidechain
34	AA	1836	U	Sidechain
34	AA	1841	U	Sidechain
34	AA	1842	U	Sidechain
34	AA	1844	G	Sidechain
34	AA	1846	A	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	1848	U	Sidechain
34	AA	1851	A	Sidechain
34	AA	1872	A	Sidechain
34	AA	1878	U	Sidechain
34	AA	1882	U	Sidechain
34	AA	1886	A	Sidechain
34	AA	1889	A	Sidechain
34	AA	1894	U	Sidechain
34	AA	1899	U	Sidechain
34	AA	1902	A	Sidechain
34	AA	1906	A	Sidechain
34	AA	1958	U	Sidechain
34	AA	1960	U	Sidechain
34	AA	1969	A	Sidechain
34	AA	1981	U	Sidechain
34	AA	1997	G	Sidechain
34	AA	200	A	Sidechain
34	AA	2000	G	Sidechain
34	AA	2001	U	Sidechain
34	AA	2004	U	Sidechain
34	AA	2018	G	Sidechain
34	AA	2019	A	Sidechain
34	AA	2030	G	Sidechain
34	AA	205	G	Sidechain
34	AA	207	A	Sidechain
34	AA	2072	U	Sidechain
34	AA	208	U	Sidechain
34	AA	2080	C	Sidechain
34	AA	2081	U	Sidechain
34	AA	2102	A	Sidechain
34	AA	2103	C	Sidechain
34	AA	2104	C	Sidechain
34	AA	2108	A	Sidechain
34	AA	2109	A	Sidechain
34	AA	211	U	Sidechain
34	AA	2112	G	Sidechain
34	AA	2117	A	Sidechain
34	AA	2127	G	Sidechain
34	AA	2137	C	Sidechain
34	AA	2138	U	Sidechain
34	AA	2141	G	Sidechain
34	AA	2148	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	216	C	Sidechain
34	AA	2161	G	Sidechain
34	AA	2165	G	Sidechain
34	AA	2173	G	Sidechain
34	AA	2176	A	Sidechain
34	AA	2178	A	Sidechain
34	AA	2180	U	Sidechain
34	AA	2184	U	Sidechain
34	AA	2194	C	Sidechain
34	AA	2198	A	Sidechain
34	AA	2214	A	Sidechain
34	AA	2393	A	Sidechain
34	AA	2396	C	Sidechain
34	AA	2409	G	Sidechain
34	AA	2411	C	Sidechain
34	AA	2412	A	Sidechain
34	AA	2423	G	Sidechain
34	AA	2424	A	Sidechain
34	AA	2429	U	Sidechain
34	AA	2432	A	Sidechain
34	AA	2433	U	Sidechain
34	AA	2434	U	Sidechain
34	AA	244	U	Sidechain
34	AA	2441	U	Sidechain
34	AA	2443	G	Sidechain
34	AA	2457	C	Sidechain
34	AA	2460	A	Sidechain
34	AA	2463	U	Sidechain
34	AA	2473	A	Sidechain
34	AA	2481	A	Sidechain
34	AA	2482	U	Sidechain
34	AA	2484	U	Sidechain
34	AA	2486	U	Sidechain
34	AA	2497	U	Sidechain
34	AA	2499	G	Sidechain
34	AA	2503	G	Sidechain
34	AA	2506	A	Sidechain
34	AA	2510	U	Sidechain
34	AA	2514	G	Sidechain
34	AA	2518	U	Sidechain
34	AA	2534	U	Sidechain
34	AA	2552	A	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	2554	G	Sidechain
34	AA	2563	A	Sidechain
34	AA	2565	G	Sidechain
34	AA	2566	G	Sidechain
34	AA	2567	U	Sidechain
34	AA	2573	A	Sidechain
34	AA	2575	U	Sidechain
34	AA	2577	C	Sidechain
34	AA	2579	U	Sidechain
34	AA	258	U	Sidechain
34	AA	2587	U	Sidechain
34	AA	2589	A	Sidechain
34	AA	2590	U	Sidechain
34	AA	2600	G	Sidechain
34	AA	2603	U	Sidechain
34	AA	262	A	Sidechain
34	AA	2629	U	Sidechain
34	AA	2636	U	Sidechain
34	AA	2644	U	Sidechain
34	AA	2649	A	Sidechain
34	AA	265	U	Sidechain
34	AA	2654	A	Sidechain
34	AA	2660	A	Sidechain
34	AA	2662	G	Sidechain
34	AA	2669	G	Sidechain
34	AA	2670	G	Sidechain
34	AA	2672	U	Sidechain
34	AA	2681	U	Sidechain
34	AA	2690	A	Sidechain
34	AA	2693	G	Sidechain
34	AA	27	U	Sidechain
34	AA	270	U	Sidechain
34	AA	2707	G	Sidechain
34	AA	2709	U	Sidechain
34	AA	271	G	Sidechain
34	AA	2711	U	Sidechain
34	AA	2716	U	Sidechain
34	AA	2727	U	Sidechain
34	AA	2809	A	Sidechain
34	AA	2811	A	Sidechain
34	AA	2814	U	Sidechain
34	AA	2822	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	288	G	Sidechain
34	AA	2915	U	Sidechain
34	AA	2920	A	Sidechain
34	AA	2925	U	Sidechain
34	AA	2951	U	Sidechain
34	AA	2957	G	Sidechain
34	AA	2968	U	Sidechain
34	AA	2971	G	Sidechain
34	AA	2975	A	Sidechain
34	AA	2977	U	Sidechain
34	AA	2979	U	Sidechain
34	AA	2981	A	Sidechain
34	AA	2987	G	Sidechain
34	AA	2994	A	Sidechain
34	AA	3016	G	Sidechain
34	AA	3020	U	Sidechain
34	AA	3033	A	Sidechain
34	AA	3035	A	Sidechain
34	AA	3038	G	Sidechain
34	AA	304	U	Sidechain
34	AA	3044	A	Sidechain
34	AA	3049	G	Sidechain
34	AA	3052	U	Sidechain
34	AA	3062	U	Sidechain
34	AA	3063	U	Sidechain
34	AA	3064	U	Sidechain
34	AA	3065	C	Sidechain
34	AA	3068	A	Sidechain
34	AA	308	U	Sidechain
34	AA	3080	A	Sidechain
34	AA	3084	G	Sidechain
34	AA	3088	G	Sidechain
34	AA	3092	G	Sidechain
34	AA	3097	A	Sidechain
34	AA	3109	U	Sidechain
34	AA	3111	U	Sidechain
34	AA	3114	G	Sidechain
34	AA	3122	A	Sidechain
34	AA	3137	U	Sidechain
34	AA	3141	G	Sidechain
34	AA	3142	U	Sidechain
34	AA	3182	G	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	3183	G	Sidechain
34	AA	3186	U	Sidechain
34	AA	3192	U	Sidechain
34	AA	3203	C	Sidechain
34	AA	3205	U	Sidechain
34	AA	3212	G	Sidechain
34	AA	3219	U	Sidechain
34	AA	3220	U	Sidechain
34	AA	3241	U	Sidechain
34	AA	3247	U	Sidechain
34	AA	3255	A	Sidechain
34	AA	3257	G	Sidechain
34	AA	3264	U	Sidechain
34	AA	3277	G	Sidechain
34	AA	3278	A	Sidechain
34	AA	3279	U	Sidechain
34	AA	3280	U	Sidechain
34	AA	3281	G	Sidechain
34	AA	3300	A	Sidechain
34	AA	3309	G	Sidechain
34	AA	331	A	Sidechain
34	AA	332	A	Sidechain
34	AA	3323	G	Sidechain
34	AA	3325	G	Sidechain
34	AA	3328	A	Sidechain
34	AA	3335	A	Sidechain
34	AA	3359	A	Sidechain
34	AA	3362	A	Sidechain
34	AA	3365	U	Sidechain
34	AA	3374	U	Sidechain
34	AA	3387	U	Sidechain
34	AA	339	G	Sidechain
34	AA	3391	G	Sidechain
34	AA	3402	A	Sidechain
34	AA	3413	A	Sidechain
34	AA	3418	A	Sidechain
34	AA	3427	U	Sidechain
34	AA	3441	A	Sidechain
34	AA	3444	G	Sidechain
34	AA	3449	U	Sidechain
34	AA	3452	U	Sidechain
34	AA	3470	G	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	3472	A	Sidechain
34	AA	3480	C	Sidechain
34	AA	3483	U	Sidechain
34	AA	3484	U	Sidechain
34	AA	3488	U	Sidechain
34	AA	349	G	Sidechain
34	AA	3495	U	Sidechain
34	AA	3499	C	Sidechain
34	AA	3503	U	Sidechain
34	AA	3505	U	Sidechain
34	AA	3508	A	Sidechain
34	AA	351	U	Sidechain
34	AA	3515	A	Sidechain
34	AA	3516	A	Sidechain
34	AA	352	A	Sidechain
34	AA	3526	U	Sidechain
34	AA	3532	A	Sidechain
34	AA	3535	A	Sidechain
34	AA	3545	U	Sidechain
34	AA	3546	C	Sidechain
34	AA	3549	U	Sidechain
34	AA	356	A	Sidechain
34	AA	357	A	Sidechain
34	AA	3571	A	Sidechain
34	AA	3574	G	Sidechain
34	AA	3581	A	Sidechain
34	AA	3585	A	Sidechain
34	AA	3591	U	Sidechain
34	AA	3594	G	Sidechain
34	AA	361	G	Sidechain
34	AA	362	U	Sidechain
34	AA	3624	U	Sidechain
34	AA	3629	U	Sidechain
34	AA	3632	U	Sidechain
34	AA	3639	G	Sidechain
34	AA	3646	G	Sidechain
34	AA	3648	U	Sidechain
34	AA	3658	G	Sidechain
34	AA	366	G	Sidechain
34	AA	3660	A	Sidechain
34	AA	3666	U	Sidechain
34	AA	367	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	3672	A	Sidechain
34	AA	368	G	Sidechain
34	AA	3688	G	Sidechain
34	AA	3692	A	Sidechain
34	AA	3698	U	Sidechain
34	AA	37	U	Sidechain
34	AA	3706	U	Sidechain
34	AA	3707	U	Sidechain
34	AA	3708	U	Sidechain
34	AA	3709	U	Sidechain
34	AA	3726	U	Sidechain
34	AA	3736	A	Sidechain
34	AA	3738	U	Sidechain
34	AA	3739	A	Sidechain
34	AA	374	A	Sidechain
34	AA	3740	A	Sidechain
34	AA	3749	U	Sidechain
34	AA	3754	A	Sidechain
34	AA	3767	U	Sidechain
34	AA	3775	G	Sidechain
34	AA	3776	U	Sidechain
34	AA	3782	A	Sidechain
34	AA	3783	G	Sidechain
34	AA	379	G	Sidechain
34	AA	38	U	Sidechain
34	AA	380	A	Sidechain
34	AA	389	U	Sidechain
34	AA	392	G	Sidechain
34	AA	393	G	Sidechain
34	AA	406	A	Sidechain
34	AA	416	G	Sidechain
34	AA	418	A	Sidechain
34	AA	422	G	Sidechain
34	AA	424	U	Sidechain
34	AA	439	U	Sidechain
34	AA	440	A	Sidechain
34	AA	441	A	Sidechain
34	AA	446	G	Sidechain
34	AA	449	A	Sidechain
34	AA	458	A	Sidechain
34	AA	490	U	Sidechain
34	AA	495	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	498	U	Sidechain
34	AA	500	A	Sidechain
34	AA	507	G	Sidechain
34	AA	520	U	Sidechain
34	AA	525	U	Sidechain
34	AA	527	A	Sidechain
34	AA	544	C	Sidechain
34	AA	55	G	Sidechain
34	AA	578	U	Sidechain
34	AA	579	C	Sidechain
34	AA	582	U	Sidechain
34	AA	583	U	Sidechain
34	AA	596	A	Sidechain
34	AA	60	A	Sidechain
34	AA	606	A	Sidechain
34	AA	607	A	Sidechain
34	AA	609	C	Sidechain
34	AA	614	U	Sidechain
34	AA	623	U	Sidechain
34	AA	629	A	Sidechain
34	AA	630	U	Sidechain
34	AA	633	U	Sidechain
34	AA	634	U	Sidechain
34	AA	637	U	Sidechain
34	AA	640	U	Sidechain
34	AA	641	G	Sidechain
34	AA	644	G	Sidechain
34	AA	649	U	Sidechain
34	AA	65	A	Sidechain
34	AA	656	U	Sidechain
34	AA	670	U	Sidechain
34	AA	671	U	Sidechain
34	AA	673	U	Sidechain
34	AA	679	U	Sidechain
34	AA	68	A	Sidechain
34	AA	683	A	Sidechain
34	AA	684	G	Sidechain
34	AA	688	U	Sidechain
34	AA	69	U	Sidechain
34	AA	696	C	Sidechain
34	AA	70	A	Sidechain
34	AA	702	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	703	U	Sidechain
34	AA	704	U	Sidechain
34	AA	706	U	Sidechain
34	AA	708	A	Sidechain
34	AA	71	A	Sidechain
34	AA	714	C	Sidechain
34	AA	716	C	Sidechain
34	AA	722	G	Sidechain
34	AA	729	G	Sidechain
34	AA	734	A	Sidechain
34	AA	739	G	Sidechain
34	AA	744	G	Sidechain
34	AA	746	A	Sidechain
34	AA	75	U	Sidechain
34	AA	754	A	Sidechain
34	AA	760	A	Sidechain
34	AA	764	G	Sidechain
34	AA	77	A	Sidechain
34	AA	770	U	Sidechain
34	AA	771	U	Sidechain
34	AA	773	A	Sidechain
34	AA	774	A	Sidechain
34	AA	825	G	Sidechain
34	AA	826	U	Sidechain
34	AA	828	G	Sidechain
34	AA	831	U	Sidechain
34	AA	835	G	Sidechain
34	AA	86	G	Sidechain
34	AA	869	A	Sidechain
34	AA	888	A	Sidechain
34	AA	911	U	Sidechain
34	AA	912	U	Sidechain
34	AA	913	U	Sidechain
34	AA	92	G	Sidechain
34	AA	920	A	Sidechain
34	AA	925	A	Sidechain
34	AA	926	G	Sidechain
34	AA	93	C	Sidechain
34	AA	931	U	Sidechain
34	AA	933	U	Sidechain
34	AA	937	C	Sidechain
34	AA	938	U	Sidechain

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Mol	Chain	Res	Type	Group
34	AA	94	G	Sidechain
34	AA	943	G	Sidechain
34	AA	95	A	Sidechain
34	AA	950	G	Sidechain
34	AA	954	G	Sidechain
34	AA	965	A	Sidechain
34	AA	966	A	Sidechain
34	AA	977	A	Sidechain
34	AA	981	U	Sidechain
36	AB	109	U	Sidechain
36	AB	11	A	Sidechain
36	AB	22	G	Sidechain
36	AB	24	U	Sidechain
36	AB	26	C	Sidechain
36	AB	48	G	Sidechain
36	AB	53	U	Sidechain
36	AB	55	A	Sidechain
36	AB	61	G	Sidechain
36	AB	69	U	Sidechain
36	AB	73	U	Sidechain
36	AB	75	G	Sidechain
36	AB	97	G	Sidechain
36	AB	98	G	Sidechain
35	AC	106	G	Sidechain
35	AC	12	U	Sidechain
35	AC	125	U	Sidechain
35	AC	127	C	Sidechain
35	AC	129	U	Sidechain
35	AC	156	A	Sidechain
35	AC	20	G	Sidechain
35	AC	25	C	Sidechain
35	AC	27	U	Sidechain
35	AC	3	G	Sidechain
35	AC	30	U	Sidechain
35	AC	31	U	Sidechain
35	AC	4	C	Sidechain
35	AC	40	G	Sidechain
35	AC	42	U	Sidechain
35	AC	53	G	Sidechain
35	AC	64	U	Sidechain
35	AC	78	U	Sidechain
35	AC	85	A	Sidechain

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Mol	Chain	Res	Type	Group
69	AD	11	GLY	Peptide
69	AD	163	ARG	Sidechain
69	AD	20	ASN	Peptide
69	AD	23	ARG	Sidechain
69	AD	242	ARG	Sidechain
69	AD	54	ARG	Sidechain
70	AE	119	TYR	Sidechain
70	AE	241	ARG	Sidechain
70	AE	272	ARG	Sidechain
70	AE	331	ARG	Sidechain
71	AF	140	ARG	Sidechain
71	AF	199	ARG	Sidechain
71	AF	264	TYR	Peptide
71	AF	48	ARG	Sidechain
71	AF	49	ARG	Sidechain
71	AF	60	TYR	Sidechain
72	AG	141	ARG	Peptide
72	AG	32	ARG	Sidechain
72	AG	41	THR	Peptide
74	AH	144	TYR	Sidechain
74	AH	179	TYR	Sidechain
74	AH	39	ARG	Sidechain
54	AI	11	TYR	Sidechain
54	AI	48	ARG	Sidechain
55	AJ	116	TYR	Sidechain
55	AJ	172	ASN	Peptide
57	AK	17	ARG	Sidechain
57	AK	31	ARG	Sidechain
57	AK	58	ARG	Sidechain
57	AK	81	ARG	Sidechain
57	AK	84	ARG	Sidechain
37	AL	197	ARG	Sidechain
37	AL	34	ARG	Sidechain
37	AL	63	ARG	Sidechain
37	AL	69	ARG	Sidechain
37	AL	96	TYR	Peptide
58	AM	122	ARG	Sidechain
58	AM	37	TYR	Sidechain
58	AM	50	ARG	Sidechain
58	AM	72	ARG	Sidechain
58	AM	82	ARG	Sidechain
43	AN	35	TYR	Sidechain

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Mol	Chain	Res	Type	Group
43	AN	66	ARG	Sidechain
43	AN	93	ARG	Sidechain
60	AO	127	ARG	Sidechain
60	AO	28	HIS	Peptide
60	AO	48	TYR	Sidechain
51	AP	160	ARG	Sidechain
51	AP	176	ARG	Sidechain
51	AP	186	ARG	Sidechain
51	AP	44	ARG	Sidechain
51	AP	49	ARG	Sidechain
51	AP	68	ARG	Sidechain
61	AQ	154	ARG	Sidechain
61	AQ	189	ARG	Sidechain
61	AQ	3	ARG	Sidechain
61	AQ	34	TYR	Sidechain
62	AR	181	ARG	Sidechain
62	AR	24	ARG	Sidechain
62	AR	278	ARG	Sidechain
62	AR	50	ARG	Sidechain
59	AS	111	ARG	Sidechain
59	AS	139	ARG	Sidechain
59	AS	157	LYS	Peptide
59	AS	165	TYR	Sidechain
59	AS	177	ARG	Sidechain
59	AS	183	ARG	Sidechain
59	AS	39	ARG	Sidechain
59	AS	57	ARG	Sidechain
65	AT	109	ARG	Sidechain
65	AT	116	ARG	Sidechain
65	AT	162	ARG	Sidechain
65	AT	37	ARG	Sidechain
65	AT	87	ARG	Sidechain
65	AT	99	ARG	Sidechain
73	AU	122	ARG	Sidechain
73	AU	134	ARG	Sidechain
73	AU	157	ARG	Sidechain
73	AU	170	TYR	Sidechain
73	AU	21	ARG	Sidechain
73	AU	35	ARG	Sidechain
73	AU	76	ARG	Sidechain
75	AV	109	ARG	Sidechain
75	AV	13	ARG	Sidechain

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Mol	Chain	Res	Type	Group
75	AV	21	ARG	Sidechain
75	AV	71	ARG	Sidechain
75	AV	80	ARG	Sidechain
63	AW	131	LYS	Peptide
63	AW	30	TYR	Sidechain
63	AW	37	ARG	Sidechain
63	AW	47	TYR	Sidechain
63	AW	56	ARG	Sidechain
63	AW	63	TYR	Peptide
77	AX	101	ARG	Sidechain
64	AY	173	ARG	Sidechain
66	AZ	114	ARG	Sidechain
66	AZ	15	ARG	Sidechain
66	AZ	83	ARG	Sidechain
66	AZ	86	ARG	Sidechain
46	Aa	4	ARG	Sidechain
46	Aa	74	ARG	Sidechain
46	Aa	76	TYR	Sidechain
46	Aa	88	ARG	Sidechain
47	Ab	106	ARG	Sidechain
56	Ac	14	ARG	Sidechain
56	Ac	48	ARG	Sidechain
56	Ac	69	TYR	Sidechain
49	Ae	18	ARG	Sidechain
49	Ae	28	ARG	Sidechain
49	Ae	42	ARG	Sidechain
49	Ae	45	ARG	Sidechain
49	Ae	6	ARG	Sidechain
50	Af	41	ARG	Sidechain
50	Af	46	ARG	Sidechain
76	Ag	16	ARG	Sidechain
76	Ag	37	ARG	Sidechain
52	Ah	17	ARG	Sidechain
52	Ah	7	LYS	Peptide
53	Ai	40	ARG	Sidechain
53	Ai	42	TYR	Sidechain
53	Ai	54	LYS	Peptide
20	B	146	ARG	Peptide
20	B	190	PRO	Peptide
20	B	213	ARG	Sidechain
20	B	64	ARG	Sidechain
33	C	103	THR	Peptide

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Mol	Chain	Res	Type	Group
33	C	119	ARG	Sidechain
33	C	151	SER	Peptide
33	C	62	ARG	Sidechain
33	C	79	ARG	Sidechain
33	C	84	ARG	Sidechain
3	D	117	ARG	Sidechain
4	E	108	ARG	Sidechain
4	E	14	ASN	Peptide
4	E	168	ARG	Peptide
4	E	171	ARG	Sidechain
4	E	69	ARG	Sidechain
4	E	78	ARG	Sidechain
21	F	100	ARG	Sidechain
21	F	103	TYR	Sidechain
21	F	108	ARG	Sidechain
21	F	11	ARG	Sidechain
21	F	191	ARG	Sidechain
5	G	107	ARG	Sidechain
5	G	236	TYR	Sidechain
5	G	63	TYR	Sidechain
5	G	80	GLN	Peptide
22	H	137	ARG	Sidechain
22	H	154	ARG	Sidechain
22	H	82	LYS	Peptide
6	I	136	ARG	Sidechain
6	I	150	ARG	Sidechain
6	I	195	ARG	Sidechain
6	I	62	ARG	Sidechain
23	J	115	ARG	Sidechain
23	J	12	ASN	Peptide
23	J	123	TYR	Sidechain
23	J	69	TYR	Sidechain
23	J	98	ARG	Sidechain
7	K	118	ARG	Sidechain
7	K	46	TYR	Sidechain
24	L	217	ARG	Sidechain
24	L	25	ARG	Sidechain
24	L	53	TYR	Sidechain
8	M	115	ARG	Sidechain
25	N	82	ARG	Sidechain
11	O	63	ARG	Sidechain
26	P	149	ARG	Sidechain

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Mol	Chain	Res	Type	Group
26	P	37	PHE	Peptide
26	P	50	ARG	Sidechain
27	Q	109	ARG	Sidechain
27	Q	137	LYS	Peptide
29	T	54	ARG	Sidechain
30	U	114	ARG	Sidechain
30	U	141	TYR	Sidechain
31	V	102	ARG	Sidechain
31	V	106	ARG	Sidechain
31	V	11	ARG	Sidechain
31	V	36	ARG	Sidechain
31	V	70	ARG	Sidechain
31	V	90	ARG	Sidechain
9	W	11	ARG	Sidechain
9	W	21	TYR	Sidechain
9	W	3	ARG	Sidechain
32	X	40	ARG	Sidechain
12	Y	108	ARG	Sidechain
12	Y	141	LYS	Peptide
12	Y	148	THR	Peptide
12	Y	161	TYR	Sidechain
12	Y	39	ARG	Sidechain
12	Y	53	TYR	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	34207	0	17266	124	0
2	7	1571	0	797	12	0
3	D	1229	0	1311	0	0
4	E	1515	0	1605	2	0
5	G	1758	0	1811	1	0
6	I	1424	0	1471	0	0
7	K	1037	0	1099	2	0
8	M	1099	0	1183	2	0
9	W	786	0	858	1	0
10	R	747	0	754	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	O	687	0	695	0	0
12	Y	1267	0	1316	1	0
13	Z	557	0	558	0	0
14	1	986	0	1076	0	0
15	2	321	0	338	0	0
16	3	782	0	820	0	0
17	4	586	0	604	1	0
18	5	458	0	496	0	0
19	6	346	0	381	0	0
20	B	1714	0	1838	1	0
21	F	2062	0	2200	3	0
22	H	1648	0	1803	1	0
23	J	1529	0	1680	0	0
24	L	1383	0	1434	4	0
25	N	772	0	813	2	0
26	P	954	0	997	0	0
27	Q	1129	0	1196	0	0
28	S	1047	0	1101	2	0
29	T	405	0	419	0	0
30	U	1202	0	1299	1	0
31	V	1206	0	1239	1	0
32	X	777	0	832	1	0
33	C	1539	0	1600	1	0
34	AA	67884	0	34244	322	0
35	AC	3215	0	1633	8	0
36	AB	2522	0	1275	9	0
37	AL	1757	0	1888	1	0
38	A1	1134	0	1245	2	0
39	A2	831	0	887	2	0
40	A4	555	0	599	4	0
41	A6	741	0	763	1	0
42	A7	794	0	869	2	0
43	AN	1202	0	1316	3	0
44	A8	1037	0	1139	2	0
45	A9	845	0	886	3	0
46	Aa	859	0	912	0	0
47	Ab	757	0	842	0	0
48	Ad	604	0	686	0	0
49	Ae	388	0	421	0	0
50	Af	414	0	452	0	0
51	AP	1697	0	1802	2	0
52	Ah	659	0	727	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	Ai	779	0	861	1	0
54	AI	1685	0	1849	1	0
55	AJ	1813	0	1985	1	0
56	Ac	710	0	761	0	0
57	AK	1660	0	1785	2	0
58	AM	996	0	1044	0	0
59	AS	1503	0	1636	2	0
60	AO	1172	0	1230	3	0
61	AQ	1545	0	1582	0	0
62	AR	2050	0	2140	2	0
63	AW	1319	0	1304	1	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	0	0
66	AZ	1001	0	1099	1	0
67	A3	995	0	1121	0	0
68	A5	1879	0	2005	4	0
69	AD	1867	0	1964	5	0
70	AE	3062	0	3205	6	0
71	AF	3095	0	3333	1	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	2	0
75	AV	1276	0	1355	0	0
76	Ag	343	0	388	1	0
77	AX	825	0	882	0	0
78	A0	522	0	539	0	0
All	All	193012	0	144279	538	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 2.

All (538) 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)
70:AE:353:LEU:H	70:AE:353:LEU:HD23	1.55	0.71
34:AA:3632:U:H3	34:AA:3653:G:H1	1.42	0.65
34:AA:123:A:H3'	34:AA:124:U:H5''	1.81	0.62
34:AA:744:G:H1	34:AA:915:G:H1	1.47	0.62
34:AA:642:A:C6	34:AA:684:G:C8	2.89	0.61
28:S:29:ILE:HD13	28:S:29:ILE:H	1.65	0.61
34:AA:440:A:H2'	34:AA:441:A:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1982:G:H1	1:A:2008:U:H3	1.48	0.60
34:AA:2735:G:H1	34:AA:2814:U:H3	1.50	0.59
34:AA:3626:A:H3'	34:AA:3627:C:H5''	1.86	0.58
34:AA:746:A:H2'	34:AA:747:A:C8	2.39	0.58
1:A:955:U:H2'	1:A:956:A:C8	2.39	0.57
1:A:1022:A:H2'	1:A:1023:A:C8	2.39	0.57
2:7:6:A:H61	2:7:65:A:H61	1.51	0.57
34:AA:1072:A:H4'	34:AA:1073:G:H21	1.70	0.57
40:A4:7:HIS:CG	40:A4:8:THR:N	2.72	0.57
34:AA:1259:G:C4	34:AA:2666:A:C2	2.93	0.57
34:AA:1822:A:N1	34:AA:2004:U:C4	2.73	0.56
34:AA:681:U:C6	34:AA:681:U:H5''	2.40	0.56
9:W:99:GLU:H	9:W:99:GLU:CD	2.12	0.56
39:A2:119:TYR:C	44:A8:111:ARG:HH22	2.13	0.56
1:A:1187:A:H2'	1:A:1188:A:C8	2.40	0.56
74:AH:46:ARG:HH11	74:AH:46:ARG:HB3	1.70	0.56
34:AA:1644:U:C4	34:AA:2102:A:N1	2.74	0.55
21:F:36:HIS:CD2	21:F:86:LEU:H	2.24	0.55
34:AA:445:A:C2	34:AA:446:G:C4	2.95	0.55
12:Y:44:HIS:CE1	12:Y:48:HIS:CE1	2.94	0.54
70:AE:85:VAL:HB	70:AE:160:HIS:CE1	2.41	0.54
1:A:149:A:C2	1:A:161:U:C4	2.95	0.54
62:AR:49:LEU:H	62:AR:49:LEU:HD12	1.71	0.54
34:AA:136:U:C4	34:AA:141:A:C2	2.96	0.54
35:AC:30:U:H2'	35:AC:31:U:C6	2.43	0.54
34:AA:124:U:H5'	34:AA:124:U:C6	2.43	0.53
34:AA:343:G:H2'	34:AA:344:A:H5''	1.90	0.53
63:AW:20:VAL:O	63:AW:145:HIS:CD2	2.62	0.53
34:AA:320:C:H2'	34:AA:321:A:C8	2.44	0.53
73:AU:107:THR:HG23	73:AU:110:GLY:H	1.73	0.53
7:K:115:GLU:CD	7:K:118:ARG:HH22	2.16	0.53
34:AA:2506:A:H2'	34:AA:2507:A:C8	2.43	0.53
34:AA:965:A:C6	34:AA:966:A:C2	2.97	0.53
34:AA:506:A:H2'	34:AA:507:G:C8	2.43	0.53
34:AA:173:A:H3'	34:AA:174:U:H5''	1.91	0.53
34:AA:1031:G:H1	69:AD:208:GLU:CD	2.17	0.52
41:A6:54:ILE:HD12	41:A6:54:ILE:H	1.74	0.52
1:A:520:U:H2'	1:A:521:G:C8	2.44	0.52
1:A:1734:G:H3'	1:A:1811:A:H61	1.74	0.52
30:U:101:HIS:CE1	30:U:105:ASN:HD22	2.28	0.52
34:AA:1531:G:H1	34:AA:1573:C:H5	1.55	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:AG:43:GLN:CD	72:AG:43:GLN:H	2.17	0.52
34:AA:445:A:N1	34:AA:702:U:C4	2.77	0.52
34:AA:912:U:H2'	34:AA:913:U:C6	2.45	0.52
34:AA:3164:G:C5	34:AA:3165:U:C5	2.97	0.52
34:AA:3768:A:C5	42:A7:29:HIS:CE1	2.98	0.52
24:L:168:ILE:HG12	24:L:169:ASP:H	1.75	0.51
34:AA:1675:C:H4'	34:AA:1737:A:C5	2.45	0.51
34:AA:2525:A:H2'	34:AA:2526:A:C8	2.45	0.51
1:A:1040:A:H61	34:AA:965:A:H61	1.58	0.51
1:A:2072:G:H2'	1:A:2073:A:C8	2.45	0.51
34:AA:445:A:C2	34:AA:702:U:C4	2.98	0.51
34:AA:914:G:H2'	34:AA:915:G:C8	2.45	0.51
34:AA:1588:U:H2'	34:AA:1589:G:C8	2.46	0.51
34:AA:2709:U:H2'	34:AA:2710:U:C6	2.45	0.51
34:AA:3054:A:C2	34:AA:3092:G:C6	2.99	0.51
34:AA:3555:U:C4	45:A9:91:HIS:CE1	2.99	0.51
1:A:1976:G:H3'	1:A:1977:G:C8	2.46	0.51
34:AA:1786:A:C5	34:AA:1787:A:C6	2.99	0.50
40:A4:7:HIS:CG	40:A4:8:THR:H	2.29	0.50
1:A:1859:A:H2'	1:A:1860:A:C8	2.46	0.50
34:AA:1770:G:H1'	34:AA:1797:A:H61	1.76	0.50
1:A:808:U:C5	1:A:809:U:C5	2.99	0.50
2:7:6:A:N1	2:7:65:A:N1	2.59	0.50
34:AA:1219:A:C5	34:AA:1220:U:C5	2.99	0.50
1:A:1041:G:H1'	34:AA:966:A:H61	1.76	0.50
34:AA:136:U:O4	34:AA:141:A:C2	2.65	0.50
34:AA:2657:G:H22	34:AA:2689:G:H1'	1.75	0.50
1:A:107:A:C5	1:A:108:A:C5	3.00	0.50
1:A:1261:A:H2'	1:A:1262:C:C6	2.47	0.50
1:A:597:C:H2'	1:A:598:A:C8	2.46	0.50
34:AA:1064:U:H2'	34:AA:1065:U:C6	2.46	0.50
34:AA:66:A:C2	34:AA:68:A:H1'	2.46	0.50
35:AC:13:A:H2'	35:AC:14:A:C8	2.47	0.50
24:L:213:ASP:C	24:L:217:ARG:HE	2.19	0.50
34:AA:1511:U:H2'	34:AA:1512:A:C8	2.47	0.50
34:AA:75:U:C4	34:AA:76:G:C6	3.00	0.49
34:AA:1433:U:C2	70:AE:254:PRO:HB3	2.47	0.49
34:AA:606:A:H2'	34:AA:607:A:C8	2.47	0.49
36:AB:24:U:C5	36:AB:25:A:C8	3.01	0.49
43:AN:79:GLU:CD	43:AN:79:GLU:H	2.20	0.49
2:7:15:G:H21	2:7:19:G:H1	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:1738:A:C4	34:AA:1739:C:C5	3.01	0.49
34:AA:2158:U:H2'	34:AA:2159:A:C8	2.48	0.49
69:AD:50:HIS:CG	69:AD:51:ASP:H	2.30	0.49
34:AA:642:A:C5	34:AA:684:G:C8	3.01	0.49
34:AA:715:U:H2'	34:AA:716:C:C5	2.48	0.49
4:E:141:VAL:HG22	4:E:143:ILE:H	1.77	0.49
34:AA:2401:C:H1'	34:AA:3736:A:C8	2.48	0.49
34:AA:2950:U:H2'	34:AA:2951:U:C6	2.48	0.49
1:A:952:U:H2'	1:A:953:C:C6	2.48	0.49
34:AA:3241:U:H2'	34:AA:3242:U:C6	2.48	0.49
34:AA:3402:A:H2'	34:AA:3403:A:C8	2.48	0.49
1:A:755:A:C2	1:A:756:A:C4	3.01	0.49
34:AA:983:G:C5	34:AA:1012:U:C4	3.01	0.49
34:AA:1416:U:H2'	34:AA:1417:G:C8	2.47	0.49
1:A:886:U:H2'	1:A:887:A:C8	2.48	0.48
34:AA:220:G:C6	34:AA:230:G:C5	3.01	0.48
21:F:249:ILE:HD12	21:F:249:ILE:H	1.78	0.48
34:AA:1093:G:H2'	34:AA:1094:U:C6	2.48	0.48
34:AA:1541:A:C2	34:AA:1542:A:C4	3.02	0.48
34:AA:2430:U:C6	34:AA:2434:U:C4	3.01	0.48
34:AA:3320:G:H2'	34:AA:3321:U:C6	2.48	0.48
1:A:1061:A:C2	1:A:1082:A:C4	3.02	0.48
34:AA:2132:A:C5	34:AA:2134:A:C5	3.01	0.48
57:AK:84:ARG:HE	57:AK:89:HIS:CD2	2.32	0.48
34:AA:909:U:H2'	34:AA:910:A:C8	2.49	0.48
51:AP:189:ILE:HD12	51:AP:189:ILE:H	1.79	0.48
1:A:246:A:H2'	1:A:247:G:C8	2.49	0.48
34:AA:687:G:H2'	34:AA:688:U:C6	2.49	0.48
51:AP:140:HIS:CD2	51:AP:142:ALA:H	2.32	0.48
1:A:993:A:H2'	1:A:994:G:C8	2.48	0.48
34:AA:352:A:C5	34:AA:353:G:C5	3.01	0.48
34:AA:1536:U:H3'	34:AA:1537:G:H5''	1.95	0.48
34:AA:3726:U:H4'	34:AA:3727:A:H5''	1.94	0.48
34:AA:2679:A:C4	34:AA:3353:A:C2	3.01	0.47
34:AA:2926:A:H2'	34:AA:2927:U:C6	2.48	0.47
2:7:45:A:H3'	2:7:46:G:H5'	1.96	0.47
34:AA:1106:A:C5	40:A4:17:HIS:CG	3.02	0.47
34:AA:2183:A:H2'	34:AA:2184:U:C6	2.49	0.47
34:AA:525:U:H2'	34:AA:526:U:C6	2.49	0.47
34:AA:1506:C:H2'	34:AA:1507:U:C6	2.49	0.47
34:AA:2569:G:C5	34:AA:2570:C:C5	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:A:C5	1:A:263:A:H1'	2.50	0.47
34:AA:1302:G:C6	34:AA:1446:A:C2	3.03	0.47
34:AA:2134:A:C6	34:AA:2135:G:C5	3.02	0.47
34:AA:3451:G:C6	34:AA:3452:U:C4	3.02	0.47
34:AA:1109:U:H2'	34:AA:1110:U:C6	2.50	0.47
1:A:149:A:N1	1:A:161:U:C4	2.83	0.47
1:A:930:A:C2	1:A:1032:A:C4	3.02	0.47
34:AA:593:A:H4'	34:AA:594:C:H5'	1.96	0.47
34:AA:2473:A:H2'	34:AA:2474:C:C6	2.50	0.47
44:A8:98:HIS:CD2	44:A8:99:ASN:H	2.33	0.47
60:AO:61:LEU:HD22	60:AO:61:LEU:H	1.79	0.47
34:AA:1034:A:C5	34:AA:1036:A:H1'	2.49	0.47
4:E:90:GLU:CD	4:E:90:GLU:H	2.23	0.47
34:AA:1100:A:C5	68:A5:185:HIS:CE1	3.03	0.47
34:AA:1905:C:H2'	34:AA:1906:A:C8	2.50	0.47
34:AA:2441:U:H2'	34:AA:2442:A:C5	2.50	0.47
34:AA:2663:G:C6	34:AA:2664:G:C6	3.03	0.47
1:A:1424:A:H2'	1:A:1425:C:C6	2.50	0.47
8:M:44:ILE:HD12	8:M:44:ILE:H	1.80	0.47
34:AA:1210:A:H2'	34:AA:1211:U:C6	2.50	0.47
1:A:491:A:H2'	1:A:492:A:C8	2.50	0.46
2:7:23:G:C5	2:7:24:C:C5	3.04	0.46
34:AA:1103:A:C5	34:AA:1231:A:C2	3.03	0.46
34:AA:1203:A:C6	34:AA:1204:A:C6	3.03	0.46
34:AA:1628:U:C5	34:AA:1629:G:C5	3.03	0.46
34:AA:1683:A:H2'	34:AA:1684:A:C8	2.50	0.46
34:AA:3263:G:H2'	34:AA:3264:U:C6	2.50	0.46
34:AA:1083:G:H2'	34:AA:1084:A:C8	2.50	0.46
34:AA:2020:A:H2'	34:AA:2021:A:C8	2.51	0.46
34:AA:2433:U:C2	34:AA:3337:U:C5	3.03	0.46
1:A:149:A:C2	1:A:150:C:C2	3.04	0.46
1:A:1214:A:HO2'	76:Ag:3:HIS:N	2.13	0.46
34:AA:3325:G:C5	34:AA:3326:A:C6	3.04	0.46
34:AA:40:A:C5	34:AA:1056:G:C6	3.03	0.46
36:AB:75:G:C4	36:AB:99:G:C6	3.04	0.46
69:AD:235:VAL:HG13	69:AD:236:GLY:H	1.81	0.46
1:A:995:A:H2'	1:A:996:C:C6	2.51	0.46
1:A:1444:C:H3'	1:A:1445:U:H5'	1.98	0.46
34:AA:1644:U:C5	34:AA:2102:A:C2	3.04	0.46
1:A:458:A:H3'	1:A:459:A:C5'	2.45	0.46
1:A:1743:A:H2'	1:A:1744:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:967:A:C5	34:AA:968:G:H1'	2.51	0.46
34:AA:1106:A:C4	40:A4:17:HIS:CD2	3.03	0.46
34:AA:3242:U:H2'	34:AA:3243:C:C6	2.51	0.46
1:A:122:C:C5	1:A:123:U:C5	3.04	0.46
24:L:13:LEU:HD22	24:L:13:LEU:H	1.81	0.46
34:AA:1043:G:C4	34:AA:3168:C:C2	3.03	0.46
34:AA:1786:A:H4'	38:A1:79:HIS:CE1	2.51	0.46
34:AA:1118:A:C2	34:AA:1177:A:C4	3.03	0.46
34:AA:2176:A:C5	34:AA:2177:A:C5	3.04	0.46
1:A:441:U:C4	1:A:442:A:C6	3.04	0.45
34:AA:918:G:C6	34:AA:920:A:C4	3.04	0.45
34:AA:1980:G:C8	34:AA:1981:U:C4	3.04	0.45
36:AB:95:U:H2'	36:AB:96:C:C6	2.51	0.45
1:A:1251:G:C6	1:A:2060:G:C5	3.04	0.45
34:AA:3386:A:H2'	34:AA:3387:U:C6	2.51	0.45
45:A9:66:LYS:HA	57:AK:2:TYR:CZ	2.51	0.45
1:A:118:U:H2'	1:A:119:C:C6	2.51	0.45
52:Ah:18:TYR:CG	69:AD:180:LEU:HD11	2.51	0.45
1:A:1208:G:C5	1:A:1209:G:C6	3.05	0.45
1:A:1873:A:C5	1:A:1874:A:H1'	2.52	0.45
2:7:14:A:C6	2:7:15:G:C2	3.04	0.45
31:V:10:GLU:CD	31:V:10:GLU:H	2.23	0.45
34:AA:1216:C:H2'	34:AA:1217:U:H5'	1.98	0.45
1:A:1272:A:H2'	1:A:1273:G:C8	2.51	0.45
34:AA:1259:G:C2	34:AA:2666:A:C4	3.05	0.45
34:AA:1831:G:C5	34:AA:1832:U:C5	3.04	0.45
34:AA:2106:A:C4	34:AA:2110:C:C5	3.05	0.45
34:AA:3140:U:H4'	34:AA:3141:G:OP1	2.16	0.45
1:A:1957:A:C2	1:A:2033:U:C2	3.05	0.45
34:AA:307:G:C5	34:AA:308:U:C4	3.05	0.45
34:AA:1036:A:C5	34:AA:1037:C:C5	3.04	0.45
34:AA:1214:C:H3'	34:AA:1215:A:H5''	1.99	0.45
34:AA:1662:G:C6	34:AA:1664:A:C5	3.05	0.45
34:AA:1793:A:C6	34:AA:1797:A:C8	3.05	0.45
1:A:392:G:H2'	1:A:393:A:C8	2.52	0.45
34:AA:262:A:H2'	34:AA:263:U:C6	2.52	0.45
34:AA:2590:U:H2'	34:AA:2590:U:O2	2.15	0.45
1:A:1008:A:C6	1:A:1009:A:C6	3.05	0.45
34:AA:70:A:C6	34:AA:71:A:C6	3.05	0.45
34:AA:510:A:H2'	34:AA:511:C:C6	2.52	0.45
34:AA:3164:G:C6	34:AA:3165:U:C4	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AN:26:GLU:CD	43:AN:80:ARG:HH12	2.24	0.45
45:A9:134:LEU:H	45:A9:134:LEU:HD22	1.82	0.45
1:A:1239:A:C4	1:A:1240:A:N7	2.85	0.45
34:AA:63:A:H2'	34:AA:64:G:C8	2.52	0.45
34:AA:378:U:C4	34:AA:379:G:C5	3.05	0.45
34:AA:1244:G:C4	34:AA:3176:A:C2	3.05	0.45
1:A:413:A:H2'	1:A:414:C:C6	2.52	0.44
1:A:805:A:C2	1:A:806:A:C4	3.04	0.44
1:A:1225:A:H2'	1:A:1226:A:C8	2.52	0.44
34:AA:734:A:H2'	34:AA:735:A:C8	2.52	0.44
34:AA:965:A:N6	34:AA:966:A:C2	2.85	0.44
34:AA:1646:C:H2'	34:AA:1647:U:C6	2.52	0.44
1:A:1378:G:C4	1:A:1682:A:C2	3.05	0.44
25:N:21:ILE:HD13	25:N:23:LEU:HD21	1.99	0.44
34:AA:609:C:H3'	34:AA:610:U:H5'	2.00	0.44
34:AA:2723:G:H2'	34:AA:2724:C:C6	2.52	0.44
34:AA:3022:U:H2'	34:AA:3023:C:C6	2.52	0.44
1:A:91:G:C6	1:A:92:C:C4	3.06	0.44
1:A:850:G:H2'	1:A:851:A:C8	2.52	0.44
1:A:1400:U:H5	1:A:1401:G:C5	2.36	0.44
1:A:1692:A:C4	1:A:1694:G:C8	3.05	0.44
34:AA:88:A:C2	34:AA:99:A:C4	3.05	0.44
34:AA:1186:A:C5	34:AA:1224:A:C6	3.05	0.44
34:AA:2181:A:C5	34:AA:2413:A:C2	3.05	0.44
34:AA:2189:A:C6	34:AA:2200:A:C2	3.05	0.44
1:A:872:A:C6	1:A:873:A:C2	3.06	0.44
1:A:1188:A:H2'	1:A:1189:A:C8	2.52	0.44
34:AA:350:A:C5	34:AA:376:G:C5	3.06	0.44
34:AA:1681:C:H2'	34:AA:1682:U:C6	2.53	0.44
34:AA:2737:C:H2'	34:AA:2738:U:C6	2.51	0.44
34:AA:2946:G:C6	34:AA:2947:G:C5	3.05	0.44
34:AA:3768:A:C6	42:A7:29:HIS:CE1	3.06	0.44
1:A:598:A:H2'	1:A:599:A:C8	2.53	0.44
1:A:1109:G:H4'	33:C:31:ASN:HD22	1.83	0.44
34:AA:916:U:H2'	34:AA:917:A:C8	2.52	0.44
34:AA:1572:U:C5	34:AA:1573:C:C5	3.06	0.44
24:L:213:ASP:C	24:L:217:ARG:HH11	2.25	0.44
34:AA:685:U:C5	34:AA:686:U:C4	3.06	0.44
34:AA:1121:G:C2	34:AA:1122:A:C2	3.06	0.44
34:AA:2439:C:H2'	34:AA:2440:A:C8	2.53	0.44
34:AA:3347:C:H2'	34:AA:3348:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:F:36:HIS:CG	21:F:85:GLY:HA2	2.52	0.44
34:AA:3615:A:H3'	34:AA:3615:A:C8	2.51	0.44
34:AA:3727:A:C2	34:AA:3728:A:C4	3.05	0.44
1:A:43:A:C2	1:A:384:A:C5	3.05	0.44
1:A:95:A:C6	1:A:404:G:C6	3.06	0.44
1:A:161:U:O4	1:A:162:A:C6	2.70	0.44
1:A:970:G:C6	1:A:971:G:C5	3.06	0.44
34:AA:3086:A:H2'	34:AA:3087:A:C8	2.53	0.44
34:AA:3171:C:H2'	34:AA:3172:A:C8	2.52	0.44
34:AA:202:C:H2'	34:AA:203:A:C8	2.53	0.44
34:AA:228:A:C5	34:AA:1537:G:C6	3.06	0.44
34:AA:1793:A:C6	34:AA:1795:A:C4	3.06	0.44
35:AC:29:G:C5	35:AC:30:U:C5	3.05	0.44
55:AJ:44:LEU:HD23	55:AJ:44:LEU:H	1.82	0.44
68:A5:141:PRO:HA	68:A5:242:TRP:CD2	2.52	0.44
1:A:943:U:H2'	1:A:944:G:C8	2.52	0.43
34:AA:1184:A:H2'	34:AA:1185:A:C8	2.53	0.43
34:AA:2577:C:C5	34:AA:2578:C:C2	3.06	0.43
34:AA:1113:C:H2'	34:AA:1114:A:C8	2.53	0.43
34:AA:1875:A:H2'	34:AA:1876:A:C8	2.53	0.43
34:AA:3035:A:H3'	34:AA:3036:A:C8	2.54	0.43
1:A:26:A:C4	1:A:27:U:C5	3.05	0.43
1:A:162:A:C6	1:A:163:G:C5	3.07	0.43
1:A:1061:A:C2	1:A:1081:U:O4	2.70	0.43
2:7:12:G:N2	2:7:22:A:C2	2.86	0.43
34:AA:1844:G:C5	34:AA:1845:C:C5	3.06	0.43
34:AA:3387:U:H2'	34:AA:3388:U:C6	2.54	0.43
59:AS:145:ARG:HH11	59:AS:148:GLU:CD	2.26	0.43
70:AE:68:HIS:CG	70:AE:69:LYS:N	2.86	0.43
1:A:1904:G:H2'	1:A:1905:C:C6	2.53	0.43
2:7:54:G:C6	2:7:55:U:C2	3.07	0.43
34:AA:1973:G:C6	34:AA:1974:U:C4	3.05	0.43
34:AA:1974:U:H2'	34:AA:1975:A:C8	2.53	0.43
34:AA:3066:A:C6	34:AA:3068:A:C5	3.06	0.43
1:A:1040:A:H61	34:AA:965:A:N6	2.15	0.43
1:A:2033:U:H2'	1:A:2034:U:C6	2.52	0.43
20:B:34:ALA:C	20:B:232:HIS:CE1	2.96	0.43
34:AA:1237:C:H2'	34:AA:1238:C:C6	2.54	0.43
69:AD:50:HIS:CG	69:AD:51:ASP:N	2.86	0.43
1:A:1061:A:C2	1:A:1082:A:C5	3.06	0.43
34:AA:141:A:C2	34:AA:142:C:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:205:G:C6	34:AA:405:A:C5	3.07	0.43
34:AA:723:A:C8	34:AA:727:A:C6	3.07	0.43
36:AB:13:A:C5	36:AB:110:G:C6	3.06	0.43
36:AB:77:A:C2	36:AB:100:A:C4	3.07	0.43
34:AA:2079:A:H2'	34:AA:2080:C:C6	2.54	0.43
34:AA:2516:A:H2'	34:AA:2517:A:C8	2.54	0.43
34:AA:3268:A:H3'	34:AA:3269:A:H5''	2.00	0.43
36:AB:66:G:C6	36:AB:67:C:C4	3.06	0.43
1:A:403:A:H2'	1:A:404:G:C8	2.53	0.43
1:A:1968:A:C4	1:A:1969:A:C8	3.07	0.43
25:N:71:GLU:H	25:N:71:GLU:CD	2.27	0.43
34:AA:30:G:C6	34:AA:55:G:C6	3.07	0.43
34:AA:344:A:C2	34:AA:345:G:C5	3.07	0.43
34:AA:2700:C:H5'	34:AA:2958:G:H21	1.83	0.43
34:AA:3055:U:H2'	34:AA:3056:U:C6	2.53	0.43
34:AA:888:A:C8	34:AA:890:G:H1'	2.53	0.43
34:AA:999:G:C4	34:AA:1001:A:C6	3.07	0.43
34:AA:1696:A:H2'	34:AA:1697:A:C8	2.54	0.43
34:AA:1699:G:C5	34:AA:1700:U:C5	3.07	0.43
35:AC:44:A:H2'	35:AC:45:A:C8	2.54	0.43
1:A:107:A:C4	1:A:108:A:C8	3.07	0.43
34:AA:423:U:H2'	34:AA:424:U:C6	2.54	0.43
34:AA:583:U:H5''	34:AA:583:U:H6	1.84	0.43
34:AA:983:G:C6	34:AA:1012:U:C5	3.07	0.43
68:A5:129:ASN:CG	68:A5:130:LYS:H	2.27	0.43
1:A:1386:U:C4	1:A:1667:A:C5	3.07	0.42
34:AA:48:A:C4	34:AA:50:U:C4	3.07	0.42
34:AA:977:A:C6	34:AA:978:G:C6	3.06	0.42
34:AA:1212:U:H2'	34:AA:1213:U:C6	2.54	0.42
34:AA:3165:U:H2'	34:AA:3166:U:C6	2.53	0.42
34:AA:3443:A:H2'	34:AA:3444:G:H5'	2.01	0.42
22:H:39:ASP:CG	22:H:47:GLY:H	2.27	0.42
34:AA:714:C:C2	34:AA:724:A:H1'	2.53	0.42
34:AA:1331:A:H2'	34:AA:1332:A:C8	2.54	0.42
34:AA:2021:A:C2	34:AA:2022:A:C4	3.07	0.42
34:AA:2400:A:C5	34:AA:2401:C:C5	3.08	0.42
1:A:887:A:C2	1:A:916:G:C2	3.06	0.42
1:A:1304:A:C6	1:A:1852:A:C6	3.07	0.42
34:AA:332:A:H2'	34:AA:333:A:C8	2.54	0.42
34:AA:1431:A:C4	34:AA:1432:A:C2	3.08	0.42
34:AA:3262:A:C2	34:AA:3263:G:H1'	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AN:76:LEU:H	43:AN:76:LEU:HD12	1.85	0.42
70:AE:11:HIS:CD2	70:AE:232:VAL:HA	2.54	0.42
74:AH:40:HIS:CE1	74:AH:41:LEU:HB2	2.54	0.42
1:A:632:C:H2'	1:A:633:U:C6	2.54	0.42
1:A:1271:G:C2	1:A:1272:A:C8	3.07	0.42
1:A:1401:G:H2'	1:A:1402:A:C8	2.54	0.42
34:AA:302:A:H2'	34:AA:303:A:C8	2.54	0.42
34:AA:1103:A:C6	34:AA:1231:A:C2	3.07	0.42
34:AA:1120:A:C2	34:AA:1121:G:C4	3.07	0.42
34:AA:1598:A:C2	34:AA:2649:A:C4	3.07	0.42
34:AA:2932:A:H4'	34:AA:2933:C:O5'	2.19	0.42
34:AA:3578:A:C2	34:AA:3579:A:C4	3.08	0.42
1:A:318:A:C4	1:A:320:C:C5	3.08	0.42
8:M:51:GLU:CD	8:M:83:ARG:HH21	2.28	0.42
34:AA:382:A:C2	34:AA:384:A:C4	3.08	0.42
34:AA:1683:A:C2	34:AA:1684:A:C4	3.08	0.42
34:AA:2573:A:C6	34:AA:2575:U:C4	3.08	0.42
34:AA:2801:C:H2'	34:AA:2802:U:C6	2.55	0.42
34:AA:3717:A:H2'	34:AA:3718:G:C8	2.54	0.42
2:7:6:A:N6	2:7:65:A:H61	2.17	0.42
34:AA:229:A:C5	34:AA:232:C:C4	3.07	0.42
34:AA:695:A:C5	34:AA:696:C:C4	3.08	0.42
34:AA:2021:A:H2'	34:AA:2022:A:C8	2.55	0.42
34:AA:3333:U:H2'	34:AA:3334:U:C6	2.54	0.42
34:AA:3776:U:H2'	34:AA:3777:G:C8	2.54	0.42
1:A:643:A:C2	1:A:929:U:C2	3.08	0.42
1:A:1379:G:C5	1:A:1380:C:C4	3.08	0.42
34:AA:26:A:H2'	34:AA:27:U:C6	2.55	0.42
34:AA:706:U:H2'	34:AA:707:U:C6	2.55	0.42
34:AA:718:U:H2'	34:AA:719:C:C6	2.54	0.42
34:AA:742:U:H2'	34:AA:743:A:C8	2.55	0.42
34:AA:2004:U:O4	34:AA:2005:A:C6	2.72	0.42
34:AA:2571:C:C5	34:AA:2598:G:C6	3.08	0.42
54:AI:115:GLU:CD	54:AI:115:GLU:H	2.27	0.42
1:A:116:A:C6	1:A:249:A:C6	3.08	0.42
1:A:970:G:C6	1:A:971:G:C6	3.08	0.42
1:A:1046:A:C2	1:A:1047:A:H1'	2.55	0.42
34:AA:302:A:C2	34:AA:303:A:C4	3.08	0.42
34:AA:607:A:H2'	34:AA:608:A:C8	2.55	0.42
34:AA:1423:G:H5'	73:AU:93:ARG:NH2	2.34	0.42
34:AA:1781:A:C6	34:AA:1782:U:C5	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:3635:G:H1	34:AA:3650:U:H3	1.68	0.42
1:A:379:G:C6	1:A:380:U:C4	3.07	0.42
1:A:806:A:C6	1:A:807:A:C5	3.08	0.42
1:A:1189:A:C5	1:A:1190:U:H1'	2.54	0.42
34:AA:84:U:C4	34:AA:85:A:C5	3.08	0.42
34:AA:658:U:C4	34:AA:659:U:C4	3.08	0.42
34:AA:949:A:C2	34:AA:984:A:C5	3.07	0.42
1:A:1846:U:C5	32:X:39:ALA:HB3	2.54	0.42
1:A:2058:A:C4	1:A:2086:A:C2	3.08	0.42
34:AA:69:U:H2'	34:AA:70:A:O4'	2.20	0.42
34:AA:207:A:C2	34:AA:209:G:C5	3.07	0.42
34:AA:280:U:H2'	34:AA:281:G:C8	2.54	0.42
34:AA:659:U:H2'	34:AA:660:U:C6	2.54	0.42
34:AA:995:A:C5	34:AA:996:C:C5	3.08	0.42
34:AA:1053:U:O2	34:AA:1053:U:H2'	2.20	0.42
34:AA:1219:A:C6	34:AA:1220:U:C4	3.08	0.42
34:AA:1301:U:H2'	34:AA:1308:A:C8	2.55	0.42
34:AA:3200:G:C5	34:AA:3203:C:C4	3.07	0.42
1:A:34:G:H3'	1:A:35:U:H5''	2.01	0.41
1:A:1703:U:H1'	28:S:137:HIS:CE1	2.55	0.41
1:A:2072:G:C6	1:A:2073:A:C6	3.07	0.41
1:A:2082:A:H2'	1:A:2083:A:C8	2.55	0.41
17:4:44:LEU:HD12	17:4:45:PHE:H	1.85	0.41
34:AA:219:A:C5	34:AA:237:A:C2	3.08	0.41
34:AA:733:C:H2'	34:AA:734:A:C8	2.55	0.41
34:AA:1813:A:C4	34:AA:2018:G:C5	3.08	0.41
34:AA:2613:A:C6	34:AA:2614:A:C4	3.08	0.41
34:AA:2621:U:H2'	34:AA:2622:C:C6	2.55	0.41
39:A2:53:ASN:HD22	39:A2:69:LYS:C	2.27	0.41
1:A:638:G:C5	1:A:639:U:C5	3.08	0.41
1:A:2034:U:C4	1:A:2035:U:C4	3.08	0.41
34:AA:374:A:C5	34:AA:375:A:C5	3.08	0.41
34:AA:418:A:C2	34:AA:419:A:C4	3.08	0.41
34:AA:703:U:H2'	34:AA:704:U:C6	2.54	0.41
34:AA:1203:A:C5	34:AA:1204:A:C5	3.07	0.41
34:AA:1285:U:C4	34:AA:1286:A:C5	3.08	0.41
34:AA:2712:A:H2'	34:AA:2713:C:C6	2.55	0.41
34:AA:3638:A:H61	34:AA:3647:C:H42	1.66	0.41
1:A:1193:A:C5	1:A:1195:G:C8	3.08	0.41
2:7:70:A:C2	2:7:71:C:C6	3.08	0.41
34:AA:934:G:C5	34:AA:1025:A:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:1170:A:N7	34:AA:1171:A:C5	2.88	0.41
34:AA:1683:A:C2	34:AA:1684:A:C5	3.08	0.41
34:AA:2601:C:C4	34:AA:2602:A:C5	3.08	0.41
34:AA:3248:C:C5	34:AA:3295:A:C4	3.07	0.41
1:A:1054:G:C6	1:A:1055:G:C4	3.07	0.41
1:A:1083:A:C5	1:A:1084:U:C5	3.09	0.41
34:AA:60:A:C8	34:AA:335:A:C6	3.08	0.41
34:AA:795:G:C5	34:AA:796:C:C4	3.08	0.41
34:AA:1302:G:C6	34:AA:1303:C:C4	3.08	0.41
34:AA:1540:G:C8	34:AA:1565:G:C2	3.09	0.41
34:AA:2593:G:C5	34:AA:2594:U:C5	3.08	0.41
34:AA:3316:G:C5	34:AA:3317:A:C8	3.08	0.41
1:A:1188:A:C2	1:A:1189:A:C4	3.09	0.41
34:AA:700:A:C5	34:AA:701:C:C5	3.08	0.41
34:AA:702:U:O4	34:AA:703:U:C2	2.74	0.41
34:AA:2014:C:C2	34:AA:2017:U:C5	3.08	0.41
34:AA:2083:U:H2'	34:AA:2084:U:C6	2.56	0.41
34:AA:2491:A:C8	34:AA:2563:A:H1'	2.56	0.41
35:AC:44:A:C2	35:AC:45:A:C4	3.08	0.41
38:A1:13:ILE:HG22	38:A1:15:ASN:H	1.85	0.41
1:A:10:G:C2	1:A:11:A:C4	3.08	0.41
1:A:608:A:C5	1:A:609:U:C5	3.09	0.41
34:AA:63:A:C6	34:AA:64:G:C6	3.08	0.41
34:AA:110:G:C2	34:AA:111:C:H1'	2.56	0.41
34:AA:113:C:C2	34:AA:114:A:C8	3.08	0.41
34:AA:221:A:C6	34:AA:222:G:C4	3.09	0.41
34:AA:350:A:C6	34:AA:376:G:C4	3.09	0.41
34:AA:643:G:N7	34:AA:644:G:C6	2.89	0.41
34:AA:2131:A:N7	34:AA:2132:A:C5	2.89	0.41
34:AA:3399:U:H2'	34:AA:3400:C:C6	2.56	0.41
34:AA:3471:A:C4	34:AA:3472:A:C8	3.09	0.41
36:AB:82:G:H2'	36:AB:83:G:C8	2.55	0.41
1:A:97:G:C6	1:A:98:G:C4	3.08	0.41
1:A:857:A:H2'	1:A:858:U:C6	2.56	0.41
1:A:1082:A:C4	1:A:1083:A:C8	3.09	0.41
1:A:1101:G:C6	1:A:1102:C:C4	3.08	0.41
1:A:1225:A:C6	1:A:1226:A:C6	3.08	0.41
1:A:1376:A:C2	1:A:1684:G:H1'	2.54	0.41
34:AA:141:A:C2	34:AA:142:C:N3	2.89	0.41
34:AA:1015:A:C2	34:AA:1032:A:C2	3.09	0.41
34:AA:1060:G:C5	34:AA:1061:U:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:3001:A:H2'	34:AA:3002:G:C8	2.56	0.41
34:AA:3763:G:C6	34:AA:3764:G:C5	3.09	0.41
34:AA:1730:A:C5	34:AA:1733:G:C5	3.09	0.41
34:AA:2492:G:C6	34:AA:2493:U:C4	3.08	0.41
34:AA:2695:A:C2	34:AA:3230:G:C5	3.09	0.41
34:AA:3198:G:C6	34:AA:3199:C:C5	3.09	0.41
70:AE:305:MET:HE1	70:AE:370:SER:HA	2.02	0.41
71:AF:211:TYR:O	71:AF:232:VAL:HG23	2.20	0.41
1:A:1305:A:N6	1:A:1894:A:H62	2.18	0.41
1:A:1832:U:H1'	1:A:1833:G:C2	2.56	0.41
1:A:1837:G:C6	1:A:1838:G:C4	3.09	0.41
1:A:1957:A:H2'	1:A:1958:A:C8	2.56	0.41
2:7:25:G:C6	2:7:26:C:C4	3.09	0.41
34:AA:26:A:C5	34:AA:338:U:C2	3.09	0.41
34:AA:331:A:C6	34:AA:332:A:C6	3.09	0.41
34:AA:997:G:H1'	34:AA:999:G:H21	1.86	0.41
34:AA:1067:U:H2'	34:AA:1068:C:C6	2.56	0.41
34:AA:1070:A:C4	34:AA:1518:A:C2	3.09	0.41
34:AA:1435:G:C5	34:AA:1436:A:C6	3.09	0.41
34:AA:1740:A:H2'	34:AA:1741:G:C8	2.56	0.41
34:AA:1781:A:C5	34:AA:1782:U:C5	3.09	0.41
34:AA:2460:A:H2'	34:AA:2461:A:C8	2.56	0.41
34:AA:2516:A:C2	34:AA:2517:A:C4	3.09	0.41
34:AA:3443:A:C5	34:AA:3471:A:C5	3.09	0.41
35:AC:148:C:H2'	35:AC:149:C:C6	2.56	0.41
59:AS:156:GLY:HA3	60:AO:50:PRO:HG3	2.03	0.41
68:A5:232:HIS:CE1	68:A5:238:ARG:NH2	2.88	0.41
1:A:2072:G:C5	1:A:2073:A:C6	3.09	0.41
34:AA:163:G:C5	34:AA:269:A:C2	3.09	0.41
34:AA:200:A:C6	34:AA:201:G:C5	3.09	0.41
34:AA:345:G:C6	34:AA:347:C:C4	3.08	0.41
34:AA:352:A:C6	34:AA:353:G:C5	3.09	0.41
34:AA:1736:A:N7	34:AA:1737:A:C5	2.88	0.41
34:AA:2004:U:O4	34:AA:2005:A:C5	2.73	0.41
34:AA:2613:A:C6	34:AA:2614:A:C5	3.09	0.41
34:AA:2710:U:C4	34:AA:2945:G:C6	3.09	0.41
34:AA:3153:G:C5	34:AA:3154:U:C4	3.09	0.41
34:AA:3161:A:C8	53:AI:55:PRO:HA	2.56	0.41
35:AC:8:G:C6	35:AC:9:U:C4	3.09	0.41
36:AB:88:A:C6	36:AB:89:G:C4	3.08	0.41
34:AA:307:G:C6	34:AA:308:U:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:380:A:C6	34:AA:381:A:C5	3.10	0.40
34:AA:1535:G:C6	34:AA:1569:A:C6	3.09	0.40
34:AA:2401:C:H1'	34:AA:3736:A:H8	1.86	0.40
34:AA:2563:A:C6	34:AA:2564:A:C6	3.09	0.40
35:AC:143:G:C5	35:AC:144:U:C5	3.09	0.40
1:A:1009:A:C6	1:A:1010:A:C5	3.10	0.40
1:A:1444:C:C5	1:A:1445:U:C5	3.10	0.40
2:7:36:A:H2'	2:7:37:U:H5'	2.02	0.40
34:AA:3444:G:C5	34:AA:3445:C:C5	3.09	0.40
1:A:161:U:O4	1:A:162:A:C5	2.75	0.40
1:A:593:G:C6	1:A:594:C:C4	3.10	0.40
1:A:865:G:H21	7:K:107:PRO:HG3	1.86	0.40
1:A:1043:A:C5	1:A:1044:C:C5	3.09	0.40
1:A:1729:A:C2	1:A:1730:A:C4	3.09	0.40
34:AA:261:A:H2'	34:AA:262:A:C8	2.57	0.40
34:AA:363:A:C2	34:AA:373:A:C4	3.09	0.40
34:AA:3316:G:C5	34:AA:3335:A:C2	3.09	0.40
34:AA:3701:A:C5	34:AA:3702:C:C5	3.10	0.40
37:AL:51:GLU:H	37:AL:51:GLU:CD	2.29	0.40
1:A:1008:A:H2'	1:A:1009:A:C8	2.55	0.40
1:A:1239:A:C6	1:A:1240:A:C5	3.10	0.40
1:A:2073:A:C2	1:A:2074:A:C4	3.09	0.40
34:AA:3697:G:C4	34:AA:3699:A:C5	3.10	0.40
34:AA:3778:G:C5	34:AA:3779:U:C4	3.10	0.40
60:AO:13:GLY:O	60:AO:14:HIS:CD2	2.74	0.40
62:AR:70:GLU:H	62:AR:70:GLU:CD	2.30	0.40
66:AZ:83:ARG:C	66:AZ:85:THR:H	2.28	0.40
1:A:98:G:C6	1:A:99:C:C4	3.09	0.40
1:A:1045:G:C6	1:A:1092:A:C4	3.09	0.40
1:A:2068:A:H2'	1:A:2069:G:C8	2.57	0.40
5:G:75:ILE:H	5:G:75:ILE:HD12	1.86	0.40
34:AA:519:A:C2	34:AA:520:U:H1'	2.56	0.40
34:AA:906:G:H2'	34:AA:907:C:C6	2.57	0.40
34:AA:2981:A:H2'	34:AA:2982:A:C8	2.56	0.40
34:AA:3455:A:C5	34:AA:3456:C:C5	3.09	0.40
34:AA:3479:U:H2'	34:AA:3480:C:C6	2.57	0.40
34:AA:3641:U:H3	34:AA:3644:G:H1	1.70	0.40
34:AA:3762:A:C2	34:AA:3763:G:C4	3.10	0.40
36:AB:13:A:C8	36:AB:110:G:C5	3.10	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	149/209 (71%)	142 (95%)	7 (5%)	0	100	100
4	E	183/185 (99%)	171 (93%)	11 (6%)	1 (0%)	24	63
5	G	222/224 (99%)	204 (92%)	16 (7%)	2 (1%)	14	51
6	I	176/189 (93%)	165 (94%)	9 (5%)	2 (1%)	11	46
7	K	127/129 (98%)	113 (89%)	9 (7%)	5 (4%)	2	18
8	M	136/138 (99%)	125 (92%)	9 (7%)	2 (2%)	8	40
9	W	91/108 (84%)	82 (90%)	6 (7%)	3 (3%)	3	21
10	R	92/114 (81%)	80 (87%)	7 (8%)	5 (5%)	1	14
11	O	77/79 (98%)	69 (90%)	5 (6%)	3 (4%)	2	18
12	Y	152/154 (99%)	145 (95%)	4 (3%)	3 (2%)	6	31
13	Z	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	9	40
14	1	118/120 (98%)	112 (95%)	5 (4%)	1 (1%)	16	54
15	2	35/68 (52%)	33 (94%)	2 (6%)	0	100	100
16	3	93/95 (98%)	82 (88%)	10 (11%)	1 (1%)	11	46
17	4	74/76 (97%)	62 (84%)	8 (11%)	4 (5%)	1	14
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
19	6	41/43 (95%)	33 (80%)	7 (17%)	1 (2%)	4	27
20	B	208/210 (99%)	189 (91%)	11 (5%)	8 (4%)	2	19
21	F	255/257 (99%)	232 (91%)	18 (7%)	5 (2%)	6	31
22	H	200/214 (94%)	187 (94%)	10 (5%)	3 (2%)	8	40
23	J	186/188 (99%)	169 (91%)	9 (5%)	8 (4%)	2	17
24	L	165/214 (77%)	146 (88%)	14 (8%)	5 (3%)	3	22
25	N	96/98 (98%)	90 (94%)	4 (4%)	2 (2%)	5	30
26	P	125/127 (98%)	109 (87%)	13 (10%)	3 (2%)	4	27
27	Q	142/144 (99%)	127 (89%)	13 (9%)	2 (1%)	9	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	S	126/128 (98%)	107 (85%)	12 (10%)	7 (6%)	1	14
29	T	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
30	U	147/149 (99%)	141 (96%)	4 (3%)	2 (1%)	9	40
31	V	142/156 (91%)	128 (90%)	11 (8%)	3 (2%)	5	30
32	X	92/103 (89%)	78 (85%)	11 (12%)	3 (3%)	3	21
33	C	193/195 (99%)	171 (89%)	17 (9%)	5 (3%)	4	25
37	AL	209/211 (99%)	191 (91%)	14 (7%)	4 (2%)	6	32
38	A1	136/145 (94%)	125 (92%)	8 (6%)	3 (2%)	5	29
39	A2	96/118 (81%)	90 (94%)	4 (4%)	2 (2%)	5	30
40	A4	64/66 (97%)	60 (94%)	1 (2%)	3 (5%)	2	16
41	A6	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
42	A7	92/102 (90%)	87 (95%)	5 (5%)	0	100	100
43	AN	144/146 (99%)	137 (95%)	5 (4%)	2 (1%)	9	40
44	A8	123/125 (98%)	102 (83%)	21 (17%)	0	100	100
45	A9	101/103 (98%)	92 (91%)	7 (7%)	2 (2%)	6	31
46	Aa	104/106 (98%)	96 (92%)	6 (6%)	2 (2%)	6	32
47	Ab	91/105 (87%)	85 (93%)	5 (6%)	1 (1%)	11	46
48	Ad	68/76 (90%)	65 (96%)	3 (4%)	0	100	100
49	Ae	39/50 (78%)	36 (92%)	3 (8%)	0	100	100
50	Af	49/51 (96%)	43 (88%)	6 (12%)	0	100	100
51	AP	202/204 (99%)	187 (93%)	7 (4%)	8 (4%)	2	18
52	Ah	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	44
53	Ai	93/95 (98%)	87 (94%)	4 (4%)	2 (2%)	5	29
54	AI	203/213 (95%)	183 (90%)	17 (8%)	3 (2%)	8	40
55	AJ	216/244 (88%)	202 (94%)	12 (6%)	2 (1%)	14	51
56	Ac	87/89 (98%)	76 (87%)	7 (8%)	4 (5%)	2	16
57	AK	199/201 (99%)	192 (96%)	5 (2%)	2 (1%)	12	48
58	AM	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
59	AS	184/186 (99%)	168 (91%)	14 (8%)	2 (1%)	11	46
60	AO	145/147 (99%)	132 (91%)	12 (8%)	1 (1%)	18	56
61	AQ	185/205 (90%)	161 (87%)	19 (10%)	5 (3%)	4	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	3	23
63	AW	149/170 (88%)	133 (89%)	10 (7%)	6 (4%)	2	18
64	AY	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12	48
65	AT	179/181 (99%)	171 (96%)	5 (3%)	3 (2%)	7	36
66	AZ	119/121 (98%)	110 (92%)	7 (6%)	2 (2%)	7	36
67	A3	117/119 (98%)	107 (92%)	9 (8%)	1 (1%)	14	51
68	A5	221/223 (99%)	195 (88%)	21 (10%)	5 (2%)	5	28
69	AD	245/247 (99%)	223 (91%)	20 (8%)	2 (1%)	16	54
70	AE	378/380 (100%)	353 (93%)	21 (6%)	4 (1%)	11	46
71	AF	388/390 (100%)	356 (92%)	26 (7%)	6 (2%)	8	40
72	AG	116/159 (73%)	104 (90%)	11 (10%)	1 (1%)	14	51
73	AU	178/180 (99%)	169 (95%)	6 (3%)	3 (2%)	7	36
74	AH	183/185 (99%)	166 (91%)	14 (8%)	3 (2%)	7	38
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	6	31
76	Ag	35/37 (95%)	30 (86%)	3 (9%)	2 (6%)	1	14
77	AX	95/97 (98%)	88 (93%)	5 (5%)	2 (2%)	5	30
78	A0	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
All	All	10111/10698 (94%)	9269 (92%)	652 (6%)	190 (2%)	8	32

All (190) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	I	42	HIS
6	I	70	HIS
8	M	41	GLU
9	W	4	VAL
10	R	42	ILE
17	4	10	PRO
17	4	20	LYS
20	B	93	ASN
20	B	146	ARG
22	H	25	LEU
23	J	13	PRO
23	J	112	ILE
23	J	156	ASP
26	P	100	SER

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Mol	Chain	Res	Type
27	Q	137	LYS
32	X	52	LYS
37	AL	169	PRO
45	A9	66	LYS
51	AP	51	LEU
51	AP	149	ILE
55	AJ	57	VAL
55	AJ	65	LEU
56	Ac	42	TYR
61	AQ	57	TYR
65	AT	129	ASN
68	A5	116	ARG
70	AE	196	LEU
73	AU	183	ARG
76	Ag	7	ARG
4	E	167	ALA
5	G	41	TRP
7	K	57	ARG
7	K	120	HIS
7	K	121	THR
8	M	99	ASP
10	R	41	GLY
17	4	18	LYS
19	6	28	LYS
20	B	50	LYS
22	H	178	LEU
23	J	157	SER
23	J	165	ILE
24	L	119	THR
24	L	168	ILE
28	S	17	ILE
28	S	101	ILE
30	U	10	GLY
31	V	41	VAL
32	X	51	LYS
33	C	116	THR
37	AL	144	ASP
39	A2	95	GLN
40	A4	38	ASN
46	Aa	77	GLY
51	AP	72	LYS
51	AP	138	PRO

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Mol	Chain	Res	Type
51	AP	150	ASN
51	AP	188	SER
53	Ai	85	LYS
54	AI	88	PRO
56	Ac	5	GLY
62	AR	114	ASN
62	AR	152	ILE
62	AR	229	ASN
63	AW	106	ASN
65	AT	15	LYS
71	AF	19	VAL
71	AF	95	MET
71	AF	313	LEU
72	AG	26	SER
74	AH	43	ILE
74	AH	110	ARG
74	AH	166	CYS
75	AV	134	GLU
7	K	29	PRO
9	W	62	GLN
11	O	70	TYR
13	Z	76	LYS
17	4	47	HIS
20	B	49	THR
21	F	104	ASP
21	F	177	VAL
23	J	132	SER
26	P	39	ASP
28	S	13	HIS
28	S	24	GLY
28	S	34	ALA
28	S	120	ARG
30	U	141	TYR
32	X	121	ILE
33	C	27	LYS
37	AL	61	THR
38	A1	42	LEU
40	A4	8	THR
43	AN	87	CYS
47	Ab	10	ALA
51	AP	108	LYS
54	AI	19	VAL

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Mol	Chain	Res	Type
56	Ac	48	ARG
60	AO	24	LYS
61	AQ	24	ARG
62	AR	59	GLN
62	AR	172	GLY
62	AR	233	ASP
63	AW	132	ALA
65	AT	4	THR
67	A3	37	LEU
68	A5	83	CYS
68	A5	172	ALA
71	AF	68	GLY
71	AF	346	SER
5	G	121	GLY
9	W	69	ILE
12	Y	142	LYS
14	1	11	LYS
21	F	176	GLN
23	J	106	LYS
24	L	29	LEU
24	L	86	SER
25	N	52	PRO
26	P	57	THR
28	S	40	LYS
31	V	56	TYR
33	C	29	LEU
33	C	30	GLU
37	AL	129	LYS
38	A1	30	GLU
39	A2	17	ASN
40	A4	36	ASP
46	Aa	52	GLN
51	AP	183	ALA
53	Ai	95	ASP
61	AQ	13	LYS
61	AQ	47	SER
62	AR	183	PRO
63	AW	37	ARG
63	AW	61	ARG
66	AZ	84	VAL
70	AE	12	GLY
70	AE	239	THR

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Mol	Chain	Res	Type
71	AF	268	HIS
73	AU	167	GLN
75	AV	13	ARG
77	AX	78	LYS
7	K	58	SER
10	R	36	ASP
10	R	37	GLY
11	O	35	GLU
20	B	98	THR
20	B	150	THR
21	F	195	ILE
22	H	105	ASP
23	J	58	LYS
25	N	67	SER
27	Q	143	PRO
33	C	143	VAL
45	A9	47	LEU
54	AI	49	LYS
57	AK	72	LEU
61	AQ	60	ILE
63	AW	9	ARG
63	AW	20	VAL
68	A5	168	VAL
69	AD	199	VAL
75	AV	56	ASN
10	R	127	ALA
12	Y	21	PRO
12	Y	49	ASN
16	3	46	ASP
20	B	209	ASN
31	V	9	HIS
38	A1	37	PRO
56	Ac	40	CYS
57	AK	88	PRO
59	AS	130	PRO
64	AY	89	ARG
66	AZ	70	VAL
70	AE	107	ALA
73	AU	134	ARG
76	Ag	9	LYS
59	AS	82	VAL
69	AD	127	VAL

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Mol	Chain	Res	Type
77	AX	68	ILE
11	O	41	PRO
20	B	190	PRO
21	F	189	VAL
43	AN	46	VAL
24	L	202	GLY
52	Ah	52	VAL
68	A5	100	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	
3	D	132/177 (75%)	130 (98%)	2 (2%)	57	72
4	E	161/164 (98%)	155 (96%)	6 (4%)	30	51
5	G	191/191 (100%)	184 (96%)	7 (4%)	30	51
6	I	154/160 (96%)	151 (98%)	3 (2%)	50	67
7	K	115/115 (100%)	114 (99%)	1 (1%)	70	79
8	M	116/116 (100%)	115 (99%)	1 (1%)	70	79
9	W	86/99 (87%)	82 (95%)	4 (5%)	23	45
10	R	83/97 (86%)	81 (98%)	2 (2%)	43	64
11	O	76/76 (100%)	73 (96%)	3 (4%)	28	49
12	Y	137/137 (100%)	133 (97%)	4 (3%)	37	58
13	Z	60/60 (100%)	60 (100%)	0	100	100
14	1	104/104 (100%)	101 (97%)	3 (3%)	37	58
15	2	35/61 (57%)	34 (97%)	1 (3%)	37	58
16	3	87/87 (100%)	86 (99%)	1 (1%)	65	76
17	4	70/70 (100%)	69 (99%)	1 (1%)	59	72
18	5	47/52 (90%)	47 (100%)	0	100	100
19	6	36/36 (100%)	35 (97%)	1 (3%)	38	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	B	195/195 (100%)	191 (98%)	4 (2%)	47	65
21	F	233/233 (100%)	224 (96%)	9 (4%)	28	49
22	H	182/190 (96%)	175 (96%)	7 (4%)	29	50
23	J	177/177 (100%)	171 (97%)	6 (3%)	32	54
24	L	151/190 (80%)	146 (97%)	5 (3%)	33	55
25	N	91/91 (100%)	88 (97%)	3 (3%)	33	55
26	P	99/99 (100%)	98 (99%)	1 (1%)	68	78
27	Q	120/120 (100%)	119 (99%)	1 (1%)	73	80
28	S	114/114 (100%)	109 (96%)	5 (4%)	25	47
29	T	43/43 (100%)	42 (98%)	1 (2%)	44	64
30	U	132/132 (100%)	130 (98%)	2 (2%)	57	72
31	V	131/140 (94%)	127 (97%)	4 (3%)	35	56
32	X	88/94 (94%)	88 (100%)	0	100	100
33	C	167/167 (100%)	162 (97%)	5 (3%)	36	57
37	AL	190/190 (100%)	187 (98%)	3 (2%)	55	70
38	A1	127/131 (97%)	123 (97%)	4 (3%)	35	56
39	A2	97/109 (89%)	96 (99%)	1 (1%)	68	78
40	A4	60/60 (100%)	58 (97%)	2 (3%)	33	55
41	A6	83/83 (100%)	78 (94%)	5 (6%)	17	39
42	A7	90/96 (94%)	86 (96%)	4 (4%)	25	47
43	AN	135/135 (100%)	130 (96%)	5 (4%)	30	51
44	A8	114/114 (100%)	109 (96%)	5 (4%)	25	47
45	A9	90/90 (100%)	87 (97%)	3 (3%)	33	55
46	Aa	89/89 (100%)	87 (98%)	2 (2%)	45	64
47	Ab	82/92 (89%)	80 (98%)	2 (2%)	43	64
48	Ad	69/73 (94%)	66 (96%)	3 (4%)	26	47
49	Ae	40/47 (85%)	38 (95%)	2 (5%)	22	43
50	Af	45/45 (100%)	44 (98%)	1 (2%)	45	64
51	AP	179/179 (100%)	176 (98%)	3 (2%)	53	69
52	Ah	70/70 (100%)	69 (99%)	1 (1%)	59	72
53	Ai	87/87 (100%)	86 (99%)	1 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	AI	189/195 (97%)	185 (98%)	4 (2%)	47	65
55	AJ	204/224 (91%)	202 (99%)	2 (1%)	68	78
56	Ac	74/74 (100%)	70 (95%)	4 (5%)	20	41
57	AK	181/181 (100%)	180 (99%)	1 (1%)	78	83
58	AM	106/106 (100%)	103 (97%)	3 (3%)	38	60
59	AS	158/158 (100%)	150 (95%)	8 (5%)	21	42
60	AO	121/121 (100%)	118 (98%)	3 (2%)	42	63
61	AQ	165/176 (94%)	160 (97%)	5 (3%)	36	57
62	AR	215/250 (86%)	210 (98%)	5 (2%)	44	64
63	AW	128/128 (100%)	126 (98%)	2 (2%)	55	70
64	AY	90/90 (100%)	88 (98%)	2 (2%)	45	64
65	AT	162/162 (100%)	161 (99%)	1 (1%)	78	83
66	AZ	111/111 (100%)	110 (99%)	1 (1%)	70	79
67	A3	110/110 (100%)	109 (99%)	1 (1%)	70	79
68	A5	201/201 (100%)	194 (96%)	7 (4%)	32	53
69	AD	191/191 (100%)	187 (98%)	4 (2%)	47	65
70	AE	335/335 (100%)	329 (98%)	6 (2%)	51	68
71	AF	336/336 (100%)	330 (98%)	6 (2%)	51	68
72	AG	110/142 (78%)	107 (97%)	3 (3%)	39	61
73	AU	162/162 (100%)	158 (98%)	4 (2%)	42	63
74	AH	168/168 (100%)	164 (98%)	4 (2%)	43	64
75	AV	140/140 (100%)	139 (99%)	1 (1%)	76	81
76	Ag	34/34 (100%)	34 (100%)	0	100	100
77	AX	92/92 (100%)	91 (99%)	1 (1%)	65	76
78	A0	53/53 (100%)	52 (98%)	1 (2%)	50	67
All	All	9096/9417 (97%)	8877 (98%)	219 (2%)	43	64

All (219) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	107	ARG
3	D	158	LEU
4	E	36	LEU

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Mol	Chain	Res	Type
4	E	37	LYS
4	E	69	ARG
4	E	90	GLU
4	E	160	THR
4	E	181	LYS
5	G	41	TRP
5	G	149	ILE
5	G	168	MET
5	G	179	ILE
5	G	182	VAL
5	G	234	TYR
5	G	242	TRP
6	I	16	TYR
6	I	89	GLU
6	I	136	ARG
7	K	46	TYR
8	M	116	SER
9	W	18	GLU
9	W	45	ARG
9	W	99	GLU
9	W	101	ASP
10	R	43	ARG
10	R	61	ASP
11	O	17	GLN
11	O	26	LEU
11	O	68	GLU
12	Y	27	ASN
12	Y	64	LYS
12	Y	72	ASN
12	Y	105	LYS
14	1	20	ARG
14	1	113	LYS
14	1	118	LYS
15	2	99	LYS
16	3	2	PRO
17	4	77	PHE
19	6	17	GLN
20	B	49	THR
20	B	161	ILE
20	B	209	ASN
20	B	210	VAL
21	F	5	ILE

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Mol	Chain	Res	Type
21	F	18	TRP
21	F	42	ILE
21	F	93	THR
21	F	108	ARG
21	F	132	ARG
21	F	174	LYS
21	F	224	ASN
21	F	249	ILE
22	H	14	LYS
22	H	25	LEU
22	H	68	LEU
22	H	136	LYS
22	H	158	ILE
22	H	159	ILE
22	H	191	LEU
23	J	50	ILE
23	J	51	GLU
23	J	111	LYS
23	J	142	SER
23	J	165	ILE
23	J	166	GLU
24	L	37	LYS
24	L	92	ARG
24	L	119	THR
24	L	176	PHE
24	L	201	GLU
25	N	21	ILE
25	N	31	ILE
25	N	43	LYS
26	P	34	PHE
27	Q	103	LEU
28	S	29	ILE
28	S	36	LYS
28	S	86	LEU
28	S	94	GLU
28	S	121	LEU
29	T	35	ASN
30	U	3	ARG
30	U	47	PRO
31	V	10	GLU
31	V	25	LYS
31	V	70	ARG

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Mol	Chain	Res	Type
31	V	130	GLN
33	C	22	VAL
33	C	75	VAL
33	C	121	LEU
33	C	135	GLU
33	C	172	LEU
37	AL	91	THR
37	AL	160	ILE
37	AL	193	LYS
38	A1	86	GLN
38	A1	101	VAL
38	A1	105	LYS
38	A1	121	LYS
39	A2	94	GLN
40	A4	5	LYS
40	A4	30	MET
41	A6	14	ASN
41	A6	19	LEU
41	A6	44	LEU
41	A6	65	LEU
41	A6	89	ARG
42	A7	41	ILE
42	A7	52	MET
42	A7	74	ASN
42	A7	95	GLU
43	AN	56	VAL
43	AN	76	LEU
43	AN	79	GLU
43	AN	80	ARG
43	AN	82	LYS
44	A8	4	LYS
44	A8	34	LYS
44	A8	61	LYS
44	A8	77	LYS
44	A8	113	LYS
45	A9	54	ARG
45	A9	134	LEU
45	A9	136	TYR
46	Aa	32	ILE
46	Aa	91	ARG
47	Ab	8	LYS
47	Ab	106	ARG

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Mol	Chain	Res	Type
48	Ad	38	ILE
48	Ad	40	LYS
48	Ad	47	LYS
49	Ae	17	ARG
49	Ae	30	LYS
50	Af	19	ILE
51	AP	56	ILE
51	AP	85	LYS
51	AP	162	LEU
52	Ah	84	ILE
53	Ai	68	VAL
54	AI	10	HIS
54	AI	63	LEU
54	AI	88	PRO
54	AI	149	LEU
55	AJ	55	ILE
55	AJ	120	SER
56	Ac	48	ARG
56	Ac	49	ARG
56	Ac	55	LYS
56	Ac	90	LYS
57	AK	134	TYR
58	AM	15	ILE
58	AM	29	ASP
58	AM	49	ASN
59	AS	26	LEU
59	AS	28	LEU
59	AS	58	TYR
59	AS	74	HIS
59	AS	96	GLN
59	AS	133	LYS
59	AS	177	ARG
59	AS	187	LYS
60	AO	32	ARG
60	AO	61	LEU
60	AO	63	LEU
61	AQ	35	ASP
61	AQ	59	GLN
61	AQ	125	VAL
61	AQ	126	VAL
61	AQ	193	ASP
62	AR	39	GLN

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Mol	Chain	Res	Type
62	AR	56	THR
62	AR	77	GLU
62	AR	152	ILE
62	AR	207	MET
63	AW	22	LEU
63	AW	94	ILE
64	AY	96	ILE
64	AY	133	MET
65	AT	162	ARG
66	AZ	43	LYS
67	A3	111	GLN
68	A5	99	LYS
68	A5	118	LEU
68	A5	149	THR
68	A5	167	LYS
68	A5	169	ARG
68	A5	195	GLU
68	A5	224	ARG
69	AD	12	ARG
69	AD	137	VAL
69	AD	207	VAL
69	AD	242	ARG
70	AE	71	GLU
70	AE	140	THR
70	AE	214	VAL
70	AE	272	ARG
70	AE	353	LEU
70	AE	361	LYS
71	AF	77	PRO
71	AF	86	ARG
71	AF	190	ARG
71	AF	266	LYS
71	AF	313	LEU
71	AF	344	ARG
72	AG	71	VAL
72	AG	134	SER
72	AG	166	LYS
73	AU	90	TYR
73	AU	107	THR
73	AU	157	ARG
73	AU	166	LEU
74	AH	46	ARG

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Mol	Chain	Res	Type
74	AH	47	LEU
74	AH	57	VAL
74	AH	159	LEU
75	AV	97	VAL
77	AX	44	LEU
78	A0	37	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	180	GLN
3	D	212	ASN
4	E	133	HIS
4	E	155	HIS
5	G	101	GLN
5	G	106	GLN
5	G	158	ASN
6	I	101	GLN
6	I	108	GLN
7	K	56	HIS
7	K	113	HIS
8	M	36	ASN
9	W	56	HIS
10	R	31	ASN
11	O	52	HIS
12	Y	26	ASN
12	Y	44	HIS
12	Y	48	HIS
13	Z	81	GLN
13	Z	82	ASN
14	1	31	ASN
14	1	52	ASN
15	2	38	HIS
16	3	43	ASN
16	3	63	GLN
18	5	28	GLN
20	B	90	HIS
20	B	132	ASN
26	P	38	ASN
28	S	19	ASN
28	S	87	ASN
28	S	137	HIS

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Mol	Chain	Res	Type
30	U	105	ASN
31	V	141	ASN
31	V	149	GLN
33	C	140	ASN
37	AL	4	HIS
37	AL	18	GLN
37	AL	58	HIS
37	AL	130	ASN
38	A1	79	HIS
39	A2	53	ASN
40	A4	11	ASN
40	A4	17	HIS
40	A4	27	HIS
42	A7	29	HIS
42	A7	103	HIS
42	A7	114	ASN
44	A8	50	ASN
44	A8	98	HIS
46	Aa	12	HIS
48	Ad	4	GLN
50	Af	28	HIS
50	Af	43	ASN
51	AP	157	HIS
52	Ah	33	GLN
53	Ai	46	GLN
55	AJ	96	GLN
55	AJ	172	ASN
56	Ac	15	ASN
57	AK	173	ASN
57	AK	192	GLN
59	AS	14	HIS
60	AO	19	HIS
60	AO	40	HIS
60	AO	60	HIS
60	AO	118	HIS
60	AO	119	ASN
61	AQ	14	ASN
61	AQ	59	GLN
61	AQ	143	ASN
62	AR	17	GLN
62	AR	193	GLN
63	AW	25	HIS

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Mol	Chain	Res	Type
63	AW	97	ASN
63	AW	145	HIS
64	AY	139	ASN
64	AY	149	ASN
65	AT	170	ASN
67	A3	39	ASN
67	A3	81	ASN
68	A5	212	ASN
68	A5	232	HIS
69	AD	50	HIS
69	AD	118	HIS
69	AD	139	GLN
69	AD	216	HIS
70	AE	276	ASN
70	AE	338	ASN
71	AF	146	HIS
71	AF	294	HIS
71	AF	353	ASN
72	AG	15	ASN
72	AG	152	HIS
73	AU	58	ASN
73	AU	97	HIS
74	AH	40	HIS
74	AH	168	ASN
77	AX	114	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1588/1608 (98%)	481 (30%)	86 (5%)
2	7	73/74 (98%)	24 (32%)	3 (4%)
34	AA	3167/3193 (99%)	984 (31%)	190 (5%)
35	AC	148/151 (98%)	51 (34%)	6 (4%)
36	AB	117/118 (99%)	30 (25%)	4 (3%)
All	All	5093/5144 (99%)	1570 (30%)	289 (5%)

All (1570) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	17	C
1	A	25	C

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Mol	Chain	Res	Type
1	A	26	A
1	A	27	U
1	A	34	G
1	A	35	U
1	A	39	A
1	A	40	A
1	A	42	G
1	A	43	A
1	A	47	A
1	A	50	C
1	A	52	U
1	A	57	G
1	A	59	G
1	A	60	A
1	A	67	A
1	A	68	U
1	A	71	A
1	A	79	U
1	A	81	U
1	A	82	G
1	A	84	A
1	A	106	A
1	A	113	U
1	A	116	A
1	A	125	G
1	A	128	A
1	A	129	U
1	A	130	U
1	A	138	U
1	A	139	A
1	A	140	A
1	A	142	G
1	A	143	A
1	A	144	U
1	A	151	G
1	A	157	G
1	A	158	C
1	A	159	U
1	A	161	U
1	A	164	C
1	A	165	U
1	A	168	U

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Mol	Chain	Res	Type
1	A	182	U
1	A	183	C
1	A	206	A
1	A	207	G
1	A	208	U
1	A	209	A
1	A	217	G
1	A	247	G
1	A	249	A
1	A	251	U
1	A	252	U
1	A	254	U
1	A	255	A
1	A	258	A
1	A	260	A
1	A	262	A
1	A	264	G
1	A	266	A
1	A	267	A
1	A	268	C
1	A	272	U
1	A	273	A
1	A	274	A
1	A	292	G
1	A	305	G
1	A	308	U
1	A	320	C
1	A	322	G
1	A	323	C
1	A	326	U
1	A	330	U
1	A	335	G
1	A	339	A
1	A	342	G
1	A	343	G
1	A	344	C
1	A	345	C
1	A	349	C
1	A	358	G
1	A	361	G
1	A	365	A
1	A	367	C

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Mol	Chain	Res	Type
1	A	375	U
1	A	378	A
1	A	379	G
1	A	384	A
1	A	385	U
1	A	396	G
1	A	399	C
1	A	405	A
1	A	406	A
1	A	407	A
1	A	408	U
1	A	409	A
1	A	410	G
1	A	422	A
1	A	423	A
1	A	424	G
1	A	430	C
1	A	431	A
1	A	432	G
1	A	434	A
1	A	440	G
1	A	441	U
1	A	445	U
1	A	446	U
1	A	450	C
1	A	451	A
1	A	454	U
1	A	458	A
1	A	459	A
1	A	466	A
1	A	467	G
1	A	470	A
1	A	475	C
1	A	483	A
1	A	488	U
1	A	508	U
1	A	509	U
1	A	515	U
1	A	516	G
1	A	521	G
1	A	526	G
1	A	527	A

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Mol	Chain	Res	Type
1	A	543	A
1	A	545	A
1	A	546	G
1	A	547	U
1	A	548	A
1	A	549	A
1	A	562	A
1	A	564	G
1	A	565	U
1	A	566	C
1	A	568	G
1	A	575	G
1	A	584	G
1	A	587	A
1	A	590	C
1	A	601	A
1	A	602	G
1	A	613	A
1	A	614	A
1	A	615	U
1	A	616	U
1	A	617	G
1	A	618	U
1	A	620	G
1	A	626	A
1	A	627	A
1	A	629	A
1	A	630	C
1	A	631	G
1	A	641	G
1	A	642	A
1	A	646	U
1	A	648	A
1	A	752	U
1	A	753	U
1	A	756	A
1	A	760	C
1	A	790	U
1	A	791	U
1	A	792	U
1	A	793	G
1	A	794	U

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Mol	Chain	Res	Type
1	A	800	U
1	A	801	G
1	A	804	U
1	A	805	A
1	A	806	A
1	A	815	G
1	A	816	U
1	A	824	A
1	A	828	A
1	A	832	A
1	A	833	A
1	A	837	A
1	A	844	G
1	A	845	U
1	A	846	G
1	A	849	U
1	A	851	A
1	A	852	A
1	A	853	U
1	A	857	A
1	A	858	U
1	A	866	A
1	A	867	A
1	A	869	A
1	A	870	A
1	A	875	A
1	A	876	U
1	A	877	U
1	A	879	A
1	A	881	C
1	A	882	A
1	A	887	A
1	A	888	A
1	A	896	U
1	A	908	U
1	A	915	G
1	A	917	C
1	A	920	A
1	A	921	G
1	A	922	U
1	A	924	A
1	A	925	C

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Mol	Chain	Res	Type
1	A	927	A
1	A	928	U
1	A	929	U
1	A	930	A
1	A	931	A
1	A	941	C
1	A	942	U
1	A	945	G
1	A	962	A
1	A	965	U
1	A	966	C
1	A	967	A
1	A	973	G
1	A	974	A
1	A	982	A
1	A	983	G
1	A	984	A
1	A	990	U
1	A	999	A
1	A	1002	A
1	A	1003	C
1	A	1004	U
1	A	1011	G
1	A	1013	A
1	A	1021	A
1	A	1029	U
1	A	1035	A
1	A	1038	C
1	A	1051	U
1	A	1054	G
1	A	1057	A
1	A	1061	A
1	A	1062	A
1	A	1065	C
1	A	1072	A
1	A	1073	U
1	A	1074	A
1	A	1082	A
1	A	1089	A
1	A	1090	C
1	A	1092	A
1	A	1093	U

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Mol	Chain	Res	Type
1	A	1094	A
1	A	1095	A
1	A	1097	C
1	A	1098	U
1	A	1099	A
1	A	1100	U
1	A	1101	G
1	A	1107	U
1	A	1108	A
1	A	1109	G
1	A	1112	G
1	A	1116	G
1	A	1119	G
1	A	1175	G
1	A	1177	A
1	A	1183	U
1	A	1193	A
1	A	1195	G
1	A	1197	C
1	A	1198	U
1	A	1199	U
1	A	1209	G
1	A	1210	G
1	A	1212	C
1	A	1227	G
1	A	1230	A
1	A	1239	A
1	A	1247	G
1	A	1251	G
1	A	1252	A
1	A	1255	G
1	A	1259	C
1	A	1260	C
1	A	1261	A
1	A	1265	G
1	A	1268	G
1	A	1271	G
1	A	1274	C
1	A	1279	G
1	A	1284	A
1	A	1285	A
1	A	1286	U

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Mol	Chain	Res	Type
1	A	1287	U
1	A	1292	U
1	A	1295	A
1	A	1296	C
1	A	1297	A
1	A	1301	G
1	A	1302	G
1	A	1303	A
1	A	1304	A
1	A	1307	U
1	A	1308	C
1	A	1315	U
1	A	1318	A
1	A	1319	G
1	A	1321	C
1	A	1363	U
1	A	1366	A
1	A	1367	U
1	A	1374	G
1	A	1375	C
1	A	1382	G
1	A	1383	U
1	A	1384	U
1	A	1385	U
1	A	1386	U
1	A	1387	U
1	A	1388	A
1	A	1401	G
1	A	1409	U
1	A	1414	A
1	A	1415	A
1	A	1416	U
1	A	1417	U
1	A	1422	U
1	A	1423	A
1	A	1424	A
1	A	1427	A
1	A	1431	A
1	A	1432	G
1	A	1433	A
1	A	1437	U
1	A	1443	G

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Mol	Chain	Res	Type
1	A	1444	C
1	A	1445	U
1	A	1449	U
1	A	1450	A
1	A	1451	G
1	A	1453	G
1	A	1454	G
1	A	1456	G
1	A	1459	U
1	A	1462	A
1	A	1463	C
1	A	1464	U
1	A	1607	U
1	A	1623	U
1	A	1624	U
1	A	1625	C
1	A	1626	U
1	A	1635	C
1	A	1636	A
1	A	1644	U
1	A	1645	C
1	A	1646	U
1	A	1648	A
1	A	1649	C
1	A	1656	A
1	A	1659	U
1	A	1660	U
1	A	1661	U
1	A	1664	G
1	A	1668	A
1	A	1673	A
1	A	1674	G
1	A	1677	C
1	A	1678	U
1	A	1679	G
1	A	1691	G
1	A	1692	A
1	A	1693	U
1	A	1703	U
1	A	1705	C
1	A	1706	A
1	A	1715	A

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Mol	Chain	Res	Type
1	A	1716	C
1	A	1717	A
1	A	1718	C
1	A	1719	U
1	A	1720	G
1	A	1721	A
1	A	1723	A
1	A	1727	A
1	A	1728	U
1	A	1732	G
1	A	1735	U
1	A	1742	A
1	A	1749	C
1	A	1750	U
1	A	1787	U
1	A	1790	C
1	A	1792	U
1	A	1795	G
1	A	1796	C
1	A	1801	A
1	A	1802	G
1	A	1806	U
1	A	1810	U
1	A	1812	A
1	A	1813	U
1	A	1817	U
1	A	1818	A
1	A	1819	U
1	A	1820	C
1	A	1824	A
1	A	1825	U
1	A	1830	C
1	A	1833	G
1	A	1834	A
1	A	1835	U
1	A	1837	G
1	A	1846	U
1	A	1850	G
1	A	1854	U
1	A	1856	A
1	A	1861	U
1	A	1866	A

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Mol	Chain	Res	Type
1	A	1868	C
1	A	1870	A
1	A	1871	G
1	A	1881	G
1	A	1882	U
1	A	1887	A
1	A	1892	U
1	A	1897	A
1	A	1898	G
1	A	1899	A
1	A	1902	G
1	A	1904	G
1	A	1907	A
1	A	1908	A
1	A	1911	A
1	A	1912	C
1	A	1913	G
1	A	1915	C
1	A	1916	C
1	A	1927	U
1	A	1928	A
1	A	1929	C
1	A	1930	A
1	A	1932	A
1	A	1938	C
1	A	1944	U
1	A	1954	U
1	A	1955	G
1	A	1961	U
1	A	1977	G
1	A	1978	A
1	A	1979	C
1	A	1980	A
1	A	1981	A
1	A	1982	G
1	A	1983	A
1	A	2012	G
1	A	2016	A
1	A	2019	C
1	A	2020	G
1	A	2021	U
1	A	2028	U

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Mol	Chain	Res	Type
1	A	2034	U
1	A	2042	A
1	A	2048	A
1	A	2049	G
1	A	2053	U
1	A	2054	A
1	A	2058	A
1	A	2061	U
1	A	2072	G
1	A	2075	C
1	A	2084	G
1	A	2085	G
1	A	2086	A
1	A	2087	U
1	A	2088	C
1	A	2089	A
1	A	2090	U
2	7	8	U
2	7	13	C
2	7	16	U
2	7	17	U
2	7	18	G
2	7	19	G
2	7	20	U
2	7	21	U
2	7	32	U
2	7	33	C
2	7	34	U
2	7	41	C
2	7	43	C
2	7	46	G
2	7	50	G
2	7	53	A
2	7	55	U
2	7	56	U
2	7	57	C
2	7	69	U
2	7	70	A
2	7	72	C
2	7	73	C
2	7	74	A
34	AA	11	A

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Mol	Chain	Res	Type
34	AA	12	U
34	AA	13	G
34	AA	14	U
34	AA	16	A
34	AA	18	G
34	AA	25	A
34	AA	26	A
34	AA	30	G
34	AA	32	C
34	AA	40	A
34	AA	43	A
34	AA	44	U
34	AA	45	A
34	AA	49	U
34	AA	55	G
34	AA	57	A
34	AA	59	G
34	AA	60	A
34	AA	62	A
34	AA	63	A
34	AA	66	A
34	AA	73	U
34	AA	75	U
34	AA	83	U
34	AA	85	A
34	AA	87	U
34	AA	92	G
34	AA	105	G
34	AA	109	A
34	AA	110	G
34	AA	111	C
34	AA	113	C
34	AA	121	U
34	AA	122	A
34	AA	124	U
34	AA	125	C
34	AA	130	G
34	AA	133	U
34	AA	134	G
34	AA	135	G
34	AA	136	U
34	AA	137	G

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Mol	Chain	Res	Type
34	AA	144	U
34	AA	145	U
34	AA	147	C
34	AA	148	G
34	AA	149	A
34	AA	150	C
34	AA	152	G
34	AA	157	G
34	AA	162	U
34	AA	163	G
34	AA	165	A
34	AA	167	U
34	AA	168	A
34	AA	172	C
34	AA	173	A
34	AA	174	U
34	AA	175	G
34	AA	180	C
34	AA	182	U
34	AA	183	U
34	AA	185	A
34	AA	186	A
34	AA	189	U
34	AA	190	G
34	AA	191	A
34	AA	192	G
34	AA	195	A
34	AA	197	G
34	AA	198	U
34	AA	199	G
34	AA	200	A
34	AA	201	G
34	AA	207	A
34	AA	208	U
34	AA	211	U
34	AA	215	C
34	AA	216	C
34	AA	219	A
34	AA	220	G
34	AA	221	A
34	AA	226	G
34	AA	227	A

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Mol	Chain	Res	Type
34	AA	228	A
34	AA	229	A
34	AA	231	G
34	AA	235	A
34	AA	239	U
34	AA	242	U
34	AA	246	U
34	AA	247	A
34	AA	250	U
34	AA	258	U
34	AA	263	U
34	AA	265	U
34	AA	268	C
34	AA	269	A
34	AA	271	G
34	AA	276	G
34	AA	290	G
34	AA	292	U
34	AA	293	U
34	AA	302	A
34	AA	303	A
34	AA	304	U
34	AA	305	A
34	AA	307	G
34	AA	308	U
34	AA	309	G
34	AA	310	U
34	AA	313	U
34	AA	315	C
34	AA	317	U
34	AA	319	U
34	AA	324	U
34	AA	325	A
34	AA	333	A
34	AA	336	U
34	AA	337	A
34	AA	338	U
34	AA	342	G
34	AA	344	A
34	AA	345	G
34	AA	347	C
34	AA	351	U

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Mol	Chain	Res	Type
34	AA	354	C
34	AA	358	C
34	AA	359	A
34	AA	360	A
34	AA	362	U
34	AA	378	U
34	AA	382	A
34	AA	384	A
34	AA	385	G
34	AA	386	U
34	AA	392	G
34	AA	396	U
34	AA	400	C
34	AA	401	A
34	AA	402	A
34	AA	405	A
34	AA	408	U
34	AA	409	A
34	AA	411	U
34	AA	412	A
34	AA	413	C
34	AA	416	G
34	AA	417	A
34	AA	431	G
34	AA	432	A
34	AA	433	A
34	AA	439	U
34	AA	442	G
34	AA	444	G
34	AA	447	A
34	AA	448	A
34	AA	449	A
34	AA	450	A
34	AA	451	C
34	AA	458	A
34	AA	459	G
34	AA	462	G
34	AA	463	G
34	AA	467	U
34	AA	489	U
34	AA	494	U
34	AA	495	U

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Mol	Chain	Res	Type
34	AA	497	U
34	AA	498	U
34	AA	499	U
34	AA	500	A
34	AA	501	U
34	AA	502	U
34	AA	503	A
34	AA	504	A
34	AA	505	A
34	AA	506	A
34	AA	509	A
34	AA	510	A
34	AA	514	C
34	AA	521	U
34	AA	522	A
34	AA	523	A
34	AA	527	A
34	AA	530	U
34	AA	532	C
34	AA	534	A
34	AA	536	A
34	AA	538	A
34	AA	539	G
34	AA	542	A
34	AA	543	U
34	AA	545	C
34	AA	547	C
34	AA	549	G
34	AA	573	U
34	AA	579	C
34	AA	580	A
34	AA	581	C
34	AA	582	U
34	AA	583	U
34	AA	584	U
34	AA	585	C
34	AA	586	U
34	AA	592	C
34	AA	593	A
34	AA	594	C
34	AA	595	U
34	AA	598	U

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Mol	Chain	Res	Type
34	AA	599	G
34	AA	601	G
34	AA	604	G
34	AA	605	A
34	AA	608	A
34	AA	609	C
34	AA	610	U
34	AA	615	U
34	AA	617	A
34	AA	618	U
34	AA	620	U
34	AA	621	C
34	AA	622	U
34	AA	623	U
34	AA	628	U
34	AA	631	U
34	AA	636	U
34	AA	637	U
34	AA	641	G
34	AA	642	A
34	AA	645	A
34	AA	646	A
34	AA	648	U
34	AA	649	U
34	AA	650	U
34	AA	651	A
34	AA	653	A
34	AA	659	U
34	AA	662	A
34	AA	666	U
34	AA	671	U
34	AA	672	C
34	AA	674	U
34	AA	675	A
34	AA	677	A
34	AA	678	A
34	AA	679	U
34	AA	681	U
34	AA	682	A
34	AA	683	A
34	AA	684	G
34	AA	685	U

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Mol	Chain	Res	Type
34	AA	694	U
34	AA	697	A
34	AA	698	G
34	AA	699	U
34	AA	704	U
34	AA	707	U
34	AA	708	A
34	AA	714	C
34	AA	715	U
34	AA	716	C
34	AA	722	G
34	AA	727	A
34	AA	729	G
34	AA	738	A
34	AA	755	A
34	AA	760	A
34	AA	761	U
34	AA	763	U
34	AA	765	A
34	AA	767	U
34	AA	769	U
34	AA	771	U
34	AA	773	A
34	AA	774	A
34	AA	778	U
34	AA	779	U
34	AA	793	A
34	AA	794	C
34	AA	806	G
34	AA	809	A
34	AA	810	U
34	AA	811	A
34	AA	812	U
34	AA	813	G
34	AA	822	A
34	AA	825	G
34	AA	833	G
34	AA	834	U
34	AA	835	G
34	AA	859	C
34	AA	860	A
34	AA	862	U

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Mol	Chain	Res	Type
34	AA	873	U
34	AA	874	A
34	AA	880	A
34	AA	885	A
34	AA	889	U
34	AA	890	G
34	AA	893	U
34	AA	896	U
34	AA	899	A
34	AA	900	G
34	AA	903	C
34	AA	905	A
34	AA	918	G
34	AA	920	A
34	AA	925	A
34	AA	927	A
34	AA	934	G
34	AA	936	A
34	AA	937	C
34	AA	945	G
34	AA	946	A
34	AA	951	A
34	AA	955	A
34	AA	956	A
34	AA	965	A
34	AA	966	A
34	AA	968	G
34	AA	970	C
34	AA	976	G
34	AA	980	A
34	AA	984	A
34	AA	988	G
34	AA	989	A
34	AA	993	U
34	AA	998	U
34	AA	999	G
34	AA	1013	U
34	AA	1014	C
34	AA	1015	A
34	AA	1016	A
34	AA	1024	U
34	AA	1026	G

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Mol	Chain	Res	Type
34	AA	1027	G
34	AA	1033	A
34	AA	1034	A
34	AA	1035	G
34	AA	1036	A
34	AA	1040	A
34	AA	1042	C
34	AA	1043	G
34	AA	1053	U
34	AA	1056	G
34	AA	1062	U
34	AA	1063	A
34	AA	1070	A
34	AA	1072	A
34	AA	1073	G
34	AA	1078	C
34	AA	1079	U
34	AA	1080	C
34	AA	1081	A
34	AA	1086	C
34	AA	1087	G
34	AA	1092	A
34	AA	1099	U
34	AA	1100	A
34	AA	1101	A
34	AA	1102	U
34	AA	1106	A
34	AA	1109	U
34	AA	1111	A
34	AA	1113	C
34	AA	1114	A
34	AA	1115	G
34	AA	1116	G
34	AA	1121	G
34	AA	1122	A
34	AA	1123	U
34	AA	1124	A
34	AA	1132	G
34	AA	1136	A
34	AA	1158	G
34	AA	1164	U
34	AA	1168	C

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Mol	Chain	Res	Type
34	AA	1169	A
34	AA	1170	A
34	AA	1172	C
34	AA	1174	C
34	AA	1186	A
34	AA	1187	A
34	AA	1188	A
34	AA	1193	G
34	AA	1194	A
34	AA	1196	A
34	AA	1197	U
34	AA	1198	A
34	AA	1199	A
34	AA	1200	C
34	AA	1202	C
34	AA	1205	U
34	AA	1206	U
34	AA	1207	U
34	AA	1210	A
34	AA	1215	A
34	AA	1217	U
34	AA	1218	C
34	AA	1219	A
34	AA	1221	A
34	AA	1222	U
34	AA	1223	U
34	AA	1224	A
34	AA	1225	A
34	AA	1226	A
34	AA	1229	A
34	AA	1230	A
34	AA	1231	A
34	AA	1232	U
34	AA	1233	A
34	AA	1234	A
34	AA	1235	C
34	AA	1239	A
34	AA	1240	A
34	AA	1245	G
34	AA	1257	A
34	AA	1259	G
34	AA	1263	A

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Mol	Chain	Res	Type
34	AA	1272	U
34	AA	1273	G
34	AA	1279	U
34	AA	1281	C
34	AA	1283	C
34	AA	1287	A
34	AA	1288	C
34	AA	1291	U
34	AA	1295	A
34	AA	1299	G
34	AA	1300	G
34	AA	1306	A
34	AA	1309	U
34	AA	1310	A
34	AA	1313	C
34	AA	1314	G
34	AA	1320	G
34	AA	1321	A
34	AA	1324	U
34	AA	1325	C
34	AA	1329	U
34	AA	1334	G
34	AA	1337	G
34	AA	1340	G
34	AA	1341	G
34	AA	1344	C
34	AA	1345	A
34	AA	1346	U
34	AA	1416	U
34	AA	1418	A
34	AA	1420	C
34	AA	1422	A
34	AA	1423	G
34	AA	1431	A
34	AA	1432	A
34	AA	1433	U
34	AA	1435	G
34	AA	1436	A
34	AA	1437	U
34	AA	1441	G
34	AA	1444	A
34	AA	1445	A

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Mol	Chain	Res	Type
34	AA	1450	G
34	AA	1451	A
34	AA	1453	U
34	AA	1458	A
34	AA	1460	A
34	AA	1473	A
34	AA	1476	A
34	AA	1480	G
34	AA	1481	A
34	AA	1486	A
34	AA	1498	U
34	AA	1499	U
34	AA	1503	A
34	AA	1504	A
34	AA	1506	C
34	AA	1524	U
34	AA	1535	G
34	AA	1537	G
34	AA	1539	U
34	AA	1540	G
34	AA	1549	U
34	AA	1550	A
34	AA	1556	G
34	AA	1565	G
34	AA	1567	A
34	AA	1572	U
34	AA	1575	C
34	AA	1578	G
34	AA	1583	G
34	AA	1586	C
34	AA	1592	G
34	AA	1595	A
34	AA	1599	G
34	AA	1601	A
34	AA	1602	A
34	AA	1605	A
34	AA	1619	U
34	AA	1626	A
34	AA	1630	A
34	AA	1631	A
34	AA	1635	G
34	AA	1636	A

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Mol	Chain	Res	Type
34	AA	1637	G
34	AA	1642	G
34	AA	1643	U
34	AA	1644	U
34	AA	1649	G
34	AA	1651	C
34	AA	1657	U
34	AA	1659	A
34	AA	1661	U
34	AA	1668	G
34	AA	1676	C
34	AA	1677	G
34	AA	1685	G
34	AA	1688	A
34	AA	1691	G
34	AA	1693	U
34	AA	1703	U
34	AA	1704	U
34	AA	1705	A
34	AA	1706	A
34	AA	1707	A
34	AA	1721	C
34	AA	1725	U
34	AA	1730	A
34	AA	1732	A
34	AA	1733	G
34	AA	1736	A
34	AA	1737	A
34	AA	1739	C
34	AA	1748	A
34	AA	1750	U
34	AA	1751	C
34	AA	1756	G
34	AA	1762	A
34	AA	1763	G
34	AA	1766	U
34	AA	1767	U
34	AA	1768	A
34	AA	1769	U
34	AA	1770	G
34	AA	1771	A
34	AA	1774	U

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Mol	Chain	Res	Type
34	AA	1780	G
34	AA	1781	A
34	AA	1782	U
34	AA	1783	G
34	AA	1788	C
34	AA	1794	U
34	AA	1797	A
34	AA	1798	A
34	AA	1799	A
34	AA	1800	U
34	AA	1801	G
34	AA	1805	U
34	AA	1806	C
34	AA	1812	C
34	AA	1817	G
34	AA	1832	U
34	AA	1842	U
34	AA	1850	U
34	AA	1852	C
34	AA	1855	U
34	AA	1856	U
34	AA	1857	A
34	AA	1871	A
34	AA	1872	A
34	AA	1874	C
34	AA	1881	C
34	AA	1882	U
34	AA	1886	A
34	AA	1887	G
34	AA	1888	A
34	AA	1898	U
34	AA	1899	U
34	AA	1900	G
34	AA	1902	A
34	AA	1903	C
34	AA	1904	U
34	AA	1905	C
34	AA	1914	A
34	AA	1915	A
34	AA	1963	U
34	AA	1964	G
34	AA	1965	U

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Mol	Chain	Res	Type
34	AA	1966	A
34	AA	1969	A
34	AA	1970	A
34	AA	1971	U
34	AA	1976	A
34	AA	1978	U
34	AA	1981	U
34	AA	1990	A
34	AA	1991	U
34	AA	1996	C
34	AA	1997	G
34	AA	1998	A
34	AA	1999	A
34	AA	2000	G
34	AA	2003	G
34	AA	2010	C
34	AA	2018	G
34	AA	2019	A
34	AA	2030	G
34	AA	2034	G
34	AA	2072	U
34	AA	2082	C
34	AA	2084	U
34	AA	2090	U
34	AA	2092	G
34	AA	2093	U
34	AA	2096	G
34	AA	2097	A
34	AA	2102	A
34	AA	2106	A
34	AA	2107	C
34	AA	2108	A
34	AA	2109	A
34	AA	2113	C
34	AA	2114	A
34	AA	2115	U
34	AA	2125	A
34	AA	2136	C
34	AA	2145	A
34	AA	2146	A
34	AA	2147	A
34	AA	2148	U

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Mol	Chain	Res	Type
34	AA	2149	A
34	AA	2154	A
34	AA	2160	G
34	AA	2161	G
34	AA	2174	G
34	AA	2181	A
34	AA	2186	C
34	AA	2203	G
34	AA	2218	C
34	AA	2219	A
34	AA	2220	U
34	AA	2389	G
34	AA	2394	C
34	AA	2395	U
34	AA	2400	A
34	AA	2403	G
34	AA	2404	A
34	AA	2405	A
34	AA	2410	A
34	AA	2415	G
34	AA	2419	A
34	AA	2424	A
34	AA	2427	G
34	AA	2433	U
34	AA	2437	A
34	AA	2438	A
34	AA	2451	A
34	AA	2453	A
34	AA	2463	U
34	AA	2464	G
34	AA	2465	G
34	AA	2477	U
34	AA	2486	U
34	AA	2489	C
34	AA	2500	A
34	AA	2501	A
34	AA	2510	U
34	AA	2516	A
34	AA	2518	U
34	AA	2521	A
34	AA	2524	C
34	AA	2536	A

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Mol	Chain	Res	Type
34	AA	2537	A
34	AA	2539	G
34	AA	2542	G
34	AA	2544	G
34	AA	2545	A
34	AA	2548	A
34	AA	2549	A
34	AA	2550	C
34	AA	2552	A
34	AA	2555	A
34	AA	2556	C
34	AA	2565	G
34	AA	2566	G
34	AA	2573	A
34	AA	2574	A
34	AA	2575	U
34	AA	2581	G
34	AA	2584	A
34	AA	2589	A
34	AA	2591	U
34	AA	2596	A
34	AA	2600	G
34	AA	2602	A
34	AA	2603	U
34	AA	2606	A
34	AA	2608	G
34	AA	2618	G
34	AA	2627	U
34	AA	2628	G
34	AA	2629	U
34	AA	2640	U
34	AA	2665	A
34	AA	2666	A
34	AA	2667	C
34	AA	2668	G
34	AA	2671	C
34	AA	2676	C
34	AA	2681	U
34	AA	2684	G
34	AA	2686	G
34	AA	2690	A
34	AA	2695	A

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Mol	Chain	Res	Type
34	AA	2696	G
34	AA	2697	A
34	AA	2698	C
34	AA	2703	U
34	AA	2704	U
34	AA	2705	G
34	AA	2710	U
34	AA	2711	U
34	AA	2712	A
34	AA	2727	U
34	AA	2728	G
34	AA	2730	G
34	AA	2745	G
34	AA	2803	A
34	AA	2809	A
34	AA	2810	A
34	AA	2811	A
34	AA	2817	U
34	AA	2822	U
34	AA	2823	U
34	AA	2824	A
34	AA	2833	U
34	AA	2835	G
34	AA	2837	G
34	AA	2884	G
34	AA	2886	A
34	AA	2887	U
34	AA	2888	U
34	AA	2920	A
34	AA	2928	G
34	AA	2932	A
34	AA	2933	C
34	AA	2945	G
34	AA	2946	G
34	AA	2953	G
34	AA	2959	G
34	AA	2960	G
34	AA	2967	A
34	AA	2968	U
34	AA	2975	A
34	AA	2980	U
34	AA	2981	A

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Mol	Chain	Res	Type
34	AA	2987	G
34	AA	2990	G
34	AA	2991	U
34	AA	2995	A
34	AA	2996	A
34	AA	3005	C
34	AA	3013	A
34	AA	3015	A
34	AA	3016	G
34	AA	3017	A
34	AA	3018	A
34	AA	3019	A
34	AA	3020	U
34	AA	3028	A
34	AA	3029	G
34	AA	3030	A
34	AA	3033	A
34	AA	3034	A
34	AA	3035	A
34	AA	3044	A
34	AA	3053	G
34	AA	3059	U
34	AA	3068	A
34	AA	3076	G
34	AA	3079	A
34	AA	3081	C
34	AA	3086	A
34	AA	3088	G
34	AA	3091	U
34	AA	3092	G
34	AA	3094	C
34	AA	3100	G
34	AA	3108	A
34	AA	3111	U
34	AA	3112	U
34	AA	3113	U
34	AA	3116	A
34	AA	3118	A
34	AA	3123	C
34	AA	3124	G
34	AA	3126	A
34	AA	3127	A

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Mol	Chain	Res	Type
34	AA	3130	U
34	AA	3131	A
34	AA	3135	A
34	AA	3138	A
34	AA	3139	C
34	AA	3140	U
34	AA	3141	G
34	AA	3146	U
34	AA	3155	G
34	AA	3158	U
34	AA	3159	G
34	AA	3160	A
34	AA	3161	A
34	AA	3167	A
34	AA	3168	C
34	AA	3169	C
34	AA	3173	G
34	AA	3175	G
34	AA	3176	A
34	AA	3180	C
34	AA	3187	G
34	AA	3193	G
34	AA	3201	C
34	AA	3204	C
34	AA	3208	C
34	AA	3209	G
34	AA	3212	G
34	AA	3220	U
34	AA	3222	G
34	AA	3225	C
34	AA	3229	C
34	AA	3230	G
34	AA	3231	A
34	AA	3232	U
34	AA	3233	G
34	AA	3235	C
34	AA	3245	U
34	AA	3246	A
34	AA	3248	C
34	AA	3253	G
34	AA	3257	G
34	AA	3258	C

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Mol	Chain	Res	Type
34	AA	3269	A
34	AA	3277	G
34	AA	3282	U
34	AA	3287	C
34	AA	3292	A
34	AA	3294	U
34	AA	3295	A
34	AA	3297	G
34	AA	3301	C
34	AA	3302	G
34	AA	3304	G
34	AA	3305	A
34	AA	3306	G
34	AA	3309	G
34	AA	3310	G
34	AA	3330	A
34	AA	3336	G
34	AA	3337	U
34	AA	3342	C
34	AA	3343	C
34	AA	3349	G
34	AA	3351	U
34	AA	3353	A
34	AA	3356	U
34	AA	3357	U
34	AA	3358	U
34	AA	3359	A
34	AA	3361	U
34	AA	3362	A
34	AA	3374	U
34	AA	3375	A
34	AA	3378	C
34	AA	3379	A
34	AA	3380	U
34	AA	3381	A
34	AA	3382	U
34	AA	3383	A
34	AA	3389	G
34	AA	3391	G
34	AA	3398	A
34	AA	3414	G
34	AA	3415	A

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Mol	Chain	Res	Type
34	AA	3416	G
34	AA	3418	A
34	AA	3421	A
34	AA	3432	A
34	AA	3434	A
34	AA	3435	A
34	AA	3442	C
34	AA	3443	A
34	AA	3444	G
34	AA	3445	C
34	AA	3459	A
34	AA	3463	G
34	AA	3464	U
34	AA	3468	G
34	AA	3471	A
34	AA	3472	A
34	AA	3476	A
34	AA	3477	A
34	AA	3483	U
34	AA	3488	U
34	AA	3493	G
34	AA	3500	G
34	AA	3507	A
34	AA	3510	C
34	AA	3513	G
34	AA	3515	A
34	AA	3516	A
34	AA	3526	U
34	AA	3527	U
34	AA	3528	A
34	AA	3530	A
34	AA	3568	G
34	AA	3571	A
34	AA	3573	U
34	AA	3575	U
34	AA	3576	A
34	AA	3578	A
34	AA	3580	G
34	AA	3581	A
34	AA	3582	G
34	AA	3585	A
34	AA	3586	U

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Mol	Chain	Res	Type
34	AA	3588	A
34	AA	3589	U
34	AA	3590	A
34	AA	3591	U
34	AA	3594	G
34	AA	3597	C
34	AA	3612	U
34	AA	3615	A
34	AA	3616	U
34	AA	3617	A
34	AA	3618	A
34	AA	3623	A
34	AA	3624	U
34	AA	3626	A
34	AA	3627	C
34	AA	3628	C
34	AA	3632	U
34	AA	3635	G
34	AA	3658	G
34	AA	3659	C
34	AA	3663	A
34	AA	3664	G
34	AA	3665	U
34	AA	3667	C
34	AA	3668	U
34	AA	3670	U
34	AA	3671	A
34	AA	3676	C
34	AA	3677	A
34	AA	3680	A
34	AA	3683	G
34	AA	3684	A
34	AA	3689	C
34	AA	3697	G
34	AA	3698	U
34	AA	3707	U
34	AA	3711	U
34	AA	3712	G
34	AA	3716	C
34	AA	3727	A
34	AA	3728	A
34	AA	3732	U

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Mol	Chain	Res	Type
34	AA	3733	G
34	AA	3736	A
34	AA	3737	G
34	AA	3739	A
34	AA	3740	A
34	AA	3741	A
34	AA	3752	C
34	AA	3761	G
34	AA	3767	U
34	AA	3768	A
34	AA	3770	C
34	AA	3774	A
34	AA	3775	G
34	AA	3778	G
34	AA	3779	U
34	AA	3782	A
34	AA	3783	G
35	AC	5	A
35	AC	25	C
35	AC	36	C
35	AC	37	A
35	AC	38	G
35	AC	39	C
35	AC	43	G
35	AC	44	A
35	AC	50	G
35	AC	53	G
35	AC	55	A
35	AC	56	A
35	AC	63	A
35	AC	64	U
35	AC	66	C
35	AC	67	G
35	AC	73	A
35	AC	75	A
35	AC	78	U
35	AC	79	G
35	AC	80	C
35	AC	82	G
35	AC	85	A
35	AC	90	G
35	AC	91	A

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Mol	Chain	Res	Type
35	AC	92	A
35	AC	94	C
35	AC	98	A
35	AC	99	G
35	AC	107	A
35	AC	108	A
35	AC	109	U
35	AC	111	U
35	AC	112	A
35	AC	114	A
35	AC	115	C
35	AC	116	U
35	AC	117	A
35	AC	119	A
35	AC	122	A
35	AC	123	A
35	AC	135	G
35	AC	136	A
35	AC	137	A
35	AC	138	U
35	AC	139	A
35	AC	140	G
35	AC	142	G
35	AC	145	A
35	AC	146	C
35	AC	156	A
36	AB	3	A
36	AB	7	G
36	AB	13	A
36	AB	16	A
36	AB	18	A
36	AB	22	G
36	AB	25	A
36	AB	26	C
36	AB	27	A
36	AB	33	U
36	AB	38	U
36	AB	39	C
36	AB	40	A
36	AB	48	G
36	AB	51	G
36	AB	53	U

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Mol	Chain	Res	Type
36	AB	54	A
36	AB	63	A
36	AB	64	A
36	AB	69	U
36	AB	71	G
36	AB	74	A
36	AB	76	U
36	AB	84	U
36	AB	85	G
36	AB	89	G
36	AB	93	G
36	AB	97	G
36	AB	100	A
36	AB	110	G

All (289) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	25	C
1	A	39	A
1	A	45	U
1	A	105	A
1	A	116	A
1	A	138	U
1	A	139	A
1	A	156	A
1	A	157	G
1	A	161	U
1	A	206	A
1	A	246	A
1	A	248	G
1	A	250	A
1	A	251	U
1	A	273	A
1	A	291	A
1	A	383	G
1	A	386	U
1	A	423	A
1	A	474	A
1	A	525	G
1	A	544	G
1	A	586	A

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Mol	Chain	Res	Type
1	A	589	U
1	A	614	A
1	A	752	U
1	A	753	U
1	A	789	U
1	A	790	U
1	A	793	G
1	A	805	A
1	A	815	G
1	A	844	G
1	A	876	U
1	A	919	U
1	A	930	A
1	A	973	G
1	A	975	A
1	A	981	U
1	A	983	G
1	A	1028	U
1	A	1071	G
1	A	1073	U
1	A	1099	A
1	A	1100	U
1	A	1182	A
1	A	1209	G
1	A	1259	C
1	A	1283	U
1	A	1284	A
1	A	1295	A
1	A	1381	C
1	A	1386	U
1	A	1400	U
1	A	1413	U
1	A	1414	A
1	A	1421	A
1	A	1423	A
1	A	1430	G
1	A	1431	A
1	A	1448	U
1	A	1455	C
1	A	1623	U
1	A	1624	U
1	A	1645	C

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Mol	Chain	Res	Type
1	A	1660	U
1	A	1673	A
1	A	1692	A
1	A	1703	U
1	A	1705	C
1	A	1786	U
1	A	1817	U
1	A	1818	A
1	A	1819	U
1	A	1834	A
1	A	1865	G
1	A	1870	A
1	A	1897	A
1	A	1898	G
1	A	1912	C
1	A	1976	G
1	A	1977	G
1	A	2048	A
1	A	2053	U
1	A	2071	U
2	7	32	U
2	7	33	C
2	7	56	U
34	AA	10	G
34	AA	11	A
34	AA	13	G
34	AA	21	G
34	AA	25	A
34	AA	40	A
34	AA	43	A
34	AA	61	A
34	AA	62	A
34	AA	65	A
34	AA	124	U
34	AA	149	A
34	AA	162	U
34	AA	179	G
34	AA	181	C
34	AA	206	A
34	AA	215	C
34	AA	257	U
34	AA	270	U

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Mol	Chain	Res	Type
34	AA	289	A
34	AA	337	A
34	AA	344	A
34	AA	353	G
34	AA	358	C
34	AA	385	G
34	AA	411	U
34	AA	416	G
34	AA	432	A
34	AA	500	A
34	AA	501	U
34	AA	504	A
34	AA	505	A
34	AA	579	C
34	AA	580	A
34	AA	581	C
34	AA	583	U
34	AA	593	A
34	AA	594	C
34	AA	597	A
34	AA	607	A
34	AA	608	A
34	AA	620	U
34	AA	621	C
34	AA	641	G
34	AA	645	A
34	AA	652	A
34	AA	666	U
34	AA	667	U
34	AA	673	U
34	AA	674	U
34	AA	681	U
34	AA	683	A
34	AA	697	A
34	AA	698	G
34	AA	702	U
34	AA	703	U
34	AA	715	U
34	AA	721	U
34	AA	754	A
34	AA	764	G
34	AA	809	A

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Mol	Chain	Res	Type
34	AA	821	C
34	AA	859	C
34	AA	888	A
34	AA	889	U
34	AA	935	A
34	AA	965	A
34	AA	998	U
34	AA	1013	U
34	AA	1032	A
34	AA	1035	G
34	AA	1042	C
34	AA	1078	C
34	AA	1080	C
34	AA	1101	A
34	AA	1115	G
34	AA	1197	U
34	AA	1204	A
34	AA	1205	U
34	AA	1206	U
34	AA	1217	U
34	AA	1222	U
34	AA	1224	A
34	AA	1230	A
34	AA	1234	A
34	AA	1272	U
34	AA	1336	U
34	AA	1422	A
34	AA	1431	A
34	AA	1435	G
34	AA	1457	G
34	AA	1459	U
34	AA	1503	A
34	AA	1504	A
34	AA	1538	U
34	AA	1566	A
34	AA	1574	C
34	AA	1632	G
34	AA	1642	G
34	AA	1643	U
34	AA	1658	G
34	AA	1705	A
34	AA	1736	A

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Mol	Chain	Res	Type
34	AA	1748	A
34	AA	1750	U
34	AA	1779	A
34	AA	1794	U
34	AA	1805	U
34	AA	1841	U
34	AA	1873	U
34	AA	1881	C
34	AA	1898	U
34	AA	1913	A
34	AA	1964	G
34	AA	1980	G
34	AA	1989	A
34	AA	1990	A
34	AA	1996	C
34	AA	1999	A
34	AA	2015	C
34	AA	2033	C
34	AA	2096	G
34	AA	2109	A
34	AA	2146	A
34	AA	2153	A
34	AA	2180	U
34	AA	2193	U
34	AA	2219	A
34	AA	2394	C
34	AA	2437	A
34	AA	2523	U
34	AA	2590	U
34	AA	2618	G
34	AA	2665	A
34	AA	2696	G
34	AA	2697	A
34	AA	2727	U
34	AA	2816	U
34	AA	2822	U
34	AA	2832	A
34	AA	2883	U
34	AA	2885	A
34	AA	2886	A
34	AA	2919	A
34	AA	2932	A

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Mol	Chain	Res	Type
34	AA	2958	G
34	AA	2959	G
34	AA	3016	G
34	AA	3018	A
34	AA	3034	A
34	AA	3067	G
34	AA	3111	U
34	AA	3130	U
34	AA	3137	U
34	AA	3139	C
34	AA	3140	U
34	AA	3160	A
34	AA	3167	A
34	AA	3229	C
34	AA	3230	G
34	AA	3232	U
34	AA	3245	U
34	AA	3309	G
34	AA	3361	U
34	AA	3379	A
34	AA	3381	A
34	AA	3382	U
34	AA	3391	G
34	AA	3414	G
34	AA	3434	A
34	AA	3476	A
34	AA	3505	U
34	AA	3526	U
34	AA	3575	U
34	AA	3577	A
34	AA	3585	A
34	AA	3588	A
34	AA	3590	A
34	AA	3627	C
34	AA	3658	G
34	AA	3662	U
34	AA	3664	G
34	AA	3667	C
34	AA	3698	U
34	AA	3711	U
34	AA	3727	A
34	AA	3736	A

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Mol	Chain	Res	Type
34	AA	3767	U
34	AA	3769	U
34	AA	3782	A
35	AC	35	A
35	AC	37	A
35	AC	75	A
35	AC	134	G
35	AC	139	A
35	AC	145	A
36	AB	13	A
36	AB	39	C
36	AB	84	U
36	AB	88	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	30.56

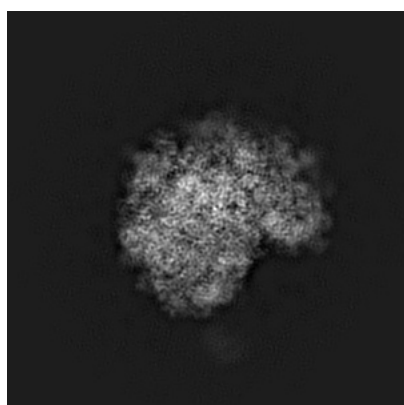
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6454. These allow visual inspection of the internal detail of the map and identification of artifacts.

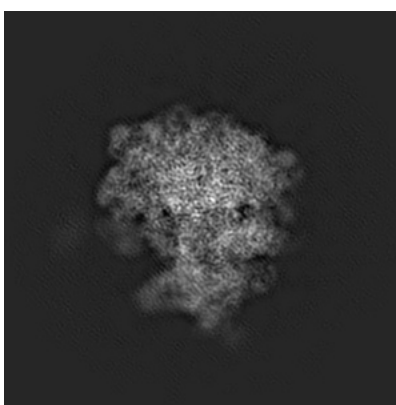
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

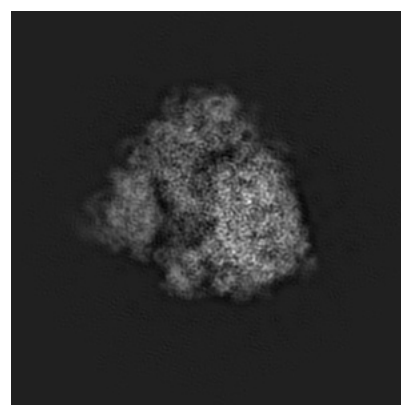
6.1.1 Primary map



X



Y

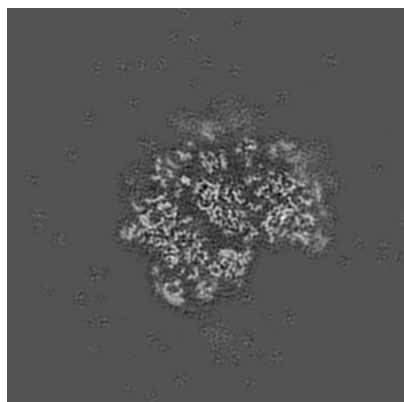


Z

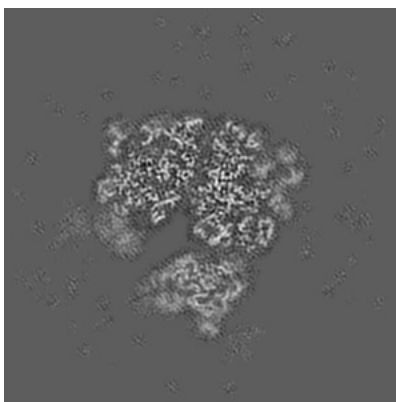
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

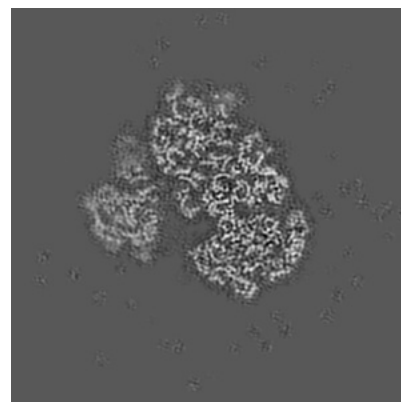
6.2.1 Primary map



X Index: 148



Y Index: 148

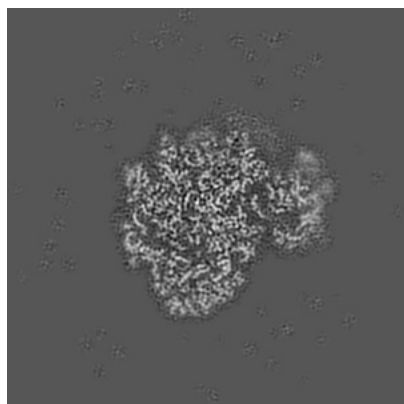


Z Index: 148

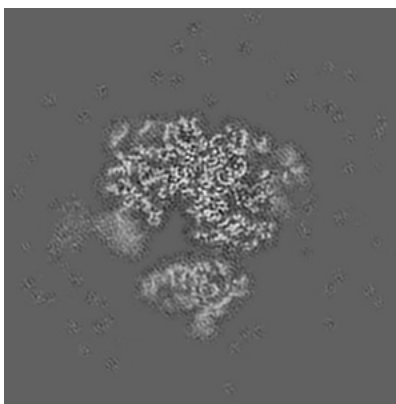
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

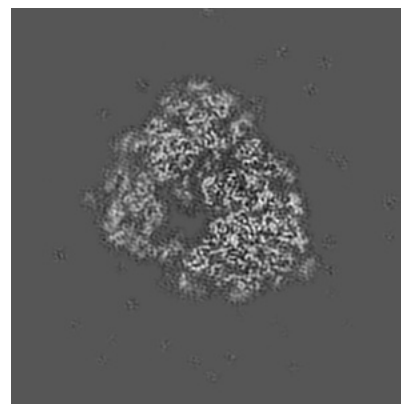
6.3.1 Primary map



X Index: 160



Y Index: 153

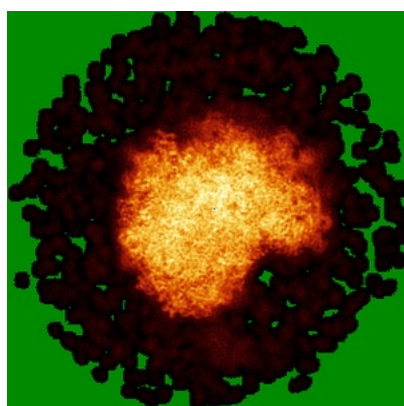


Z Index: 139

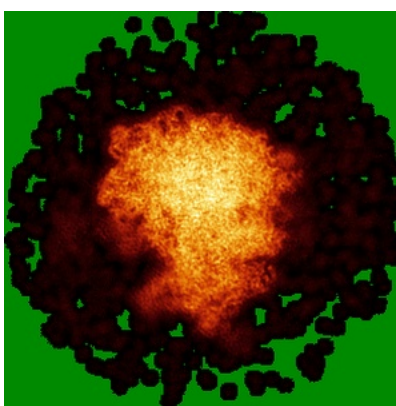
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

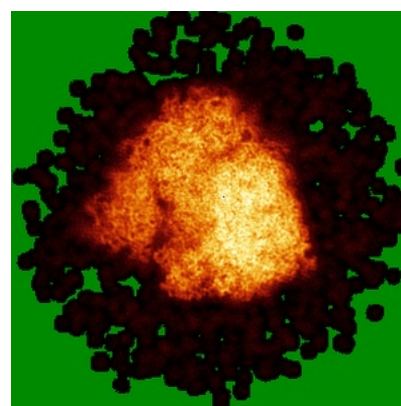
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

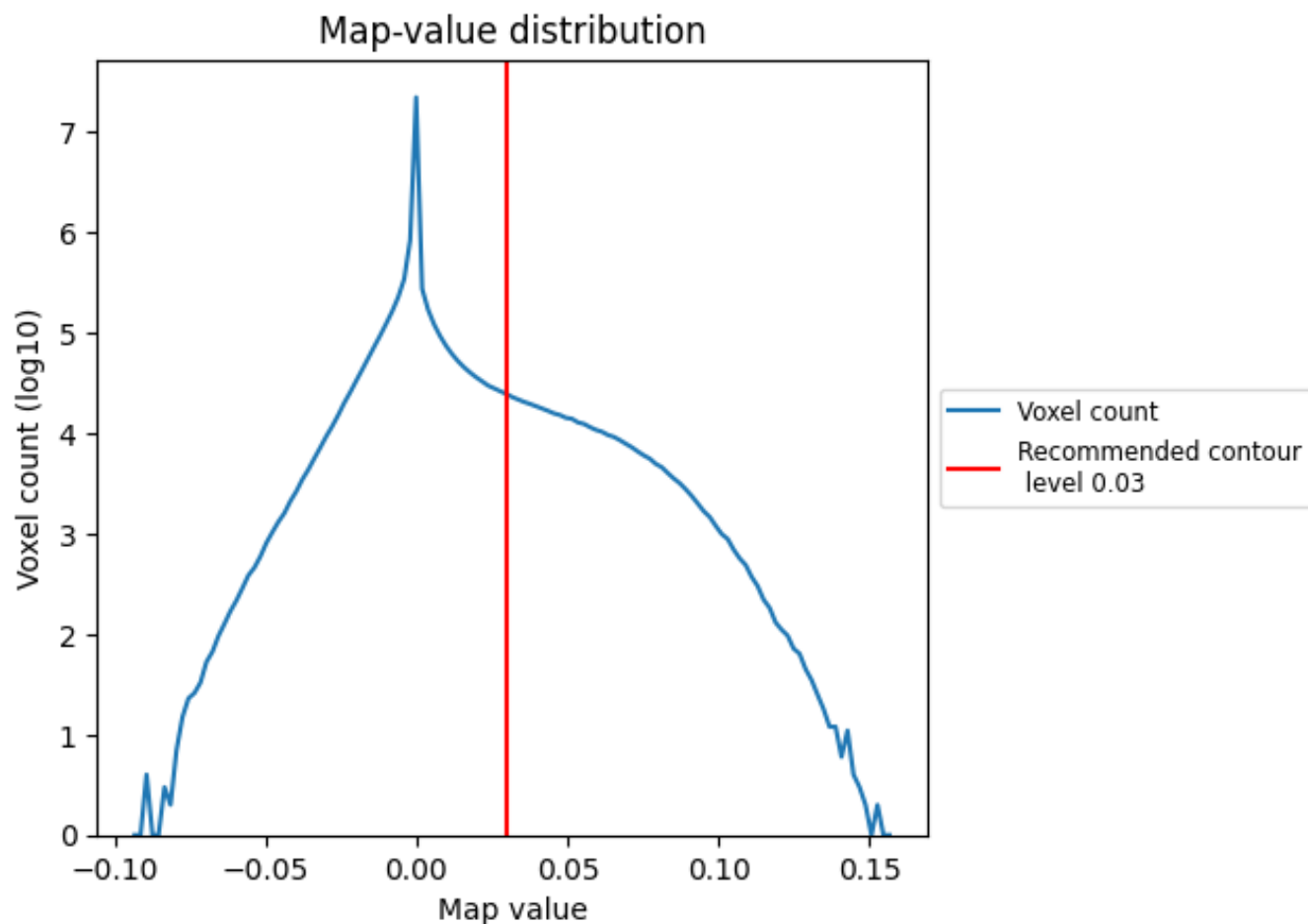
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

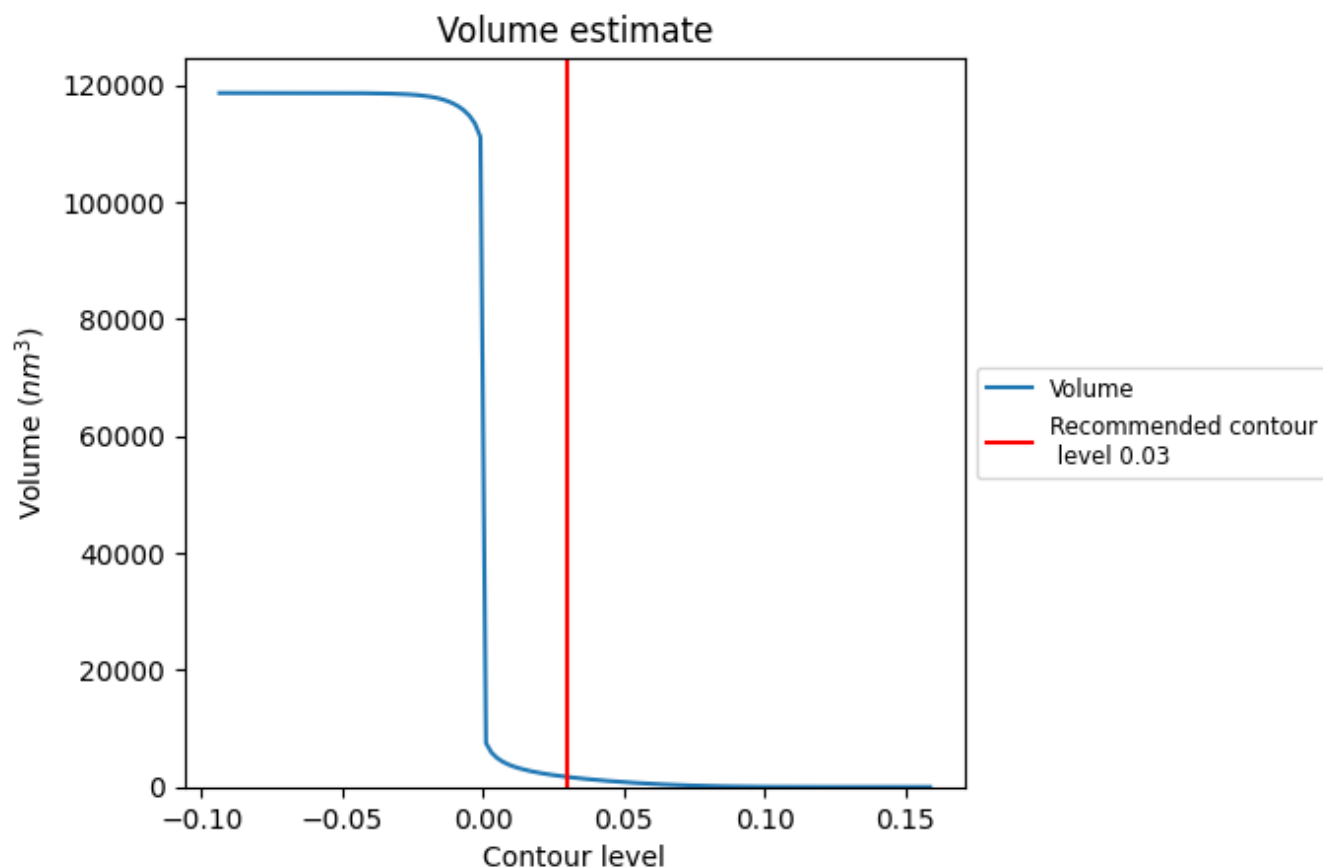
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

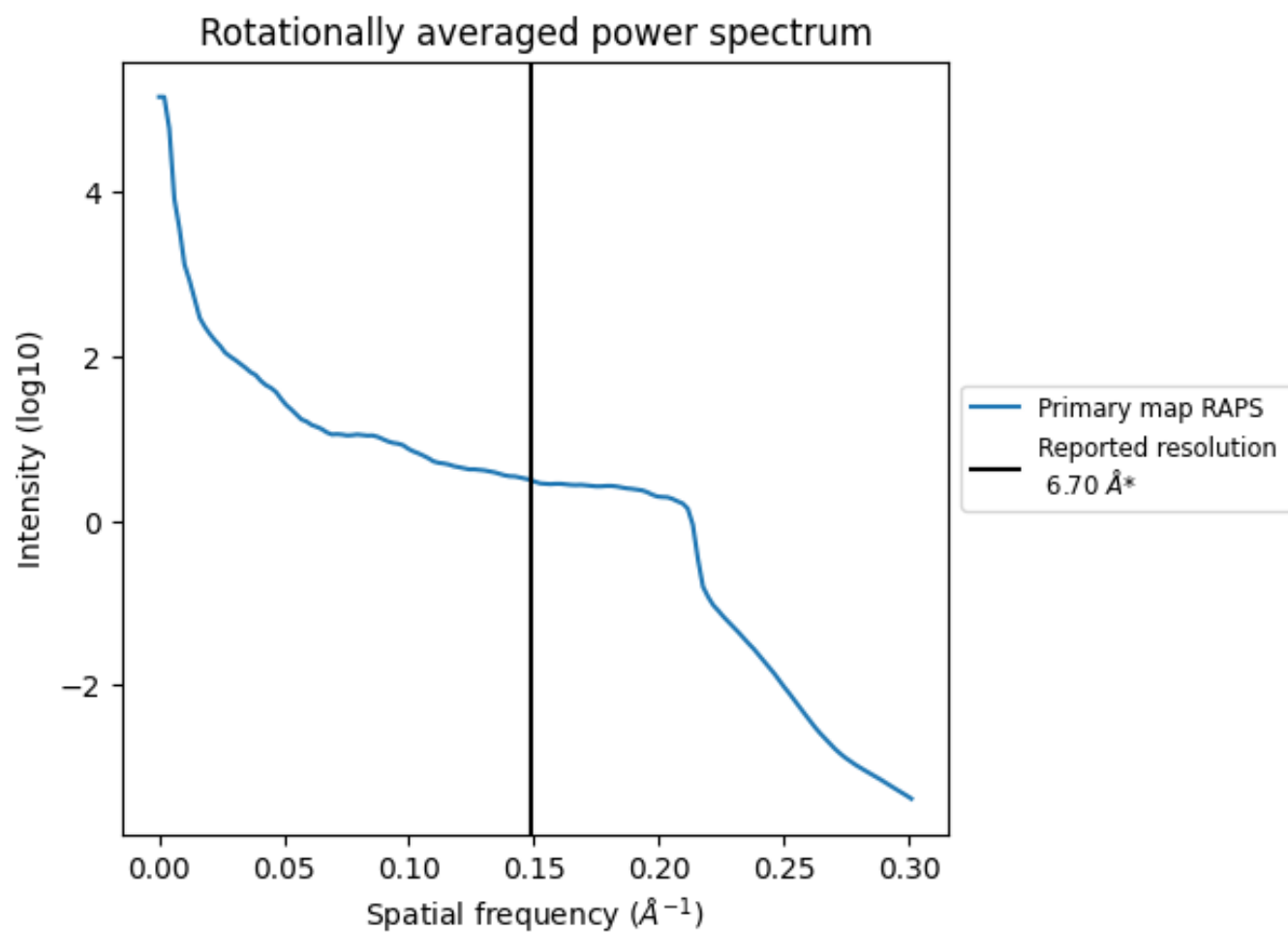
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1717 nm³; this corresponds to an approximate mass of 1551 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.149 Å⁻¹

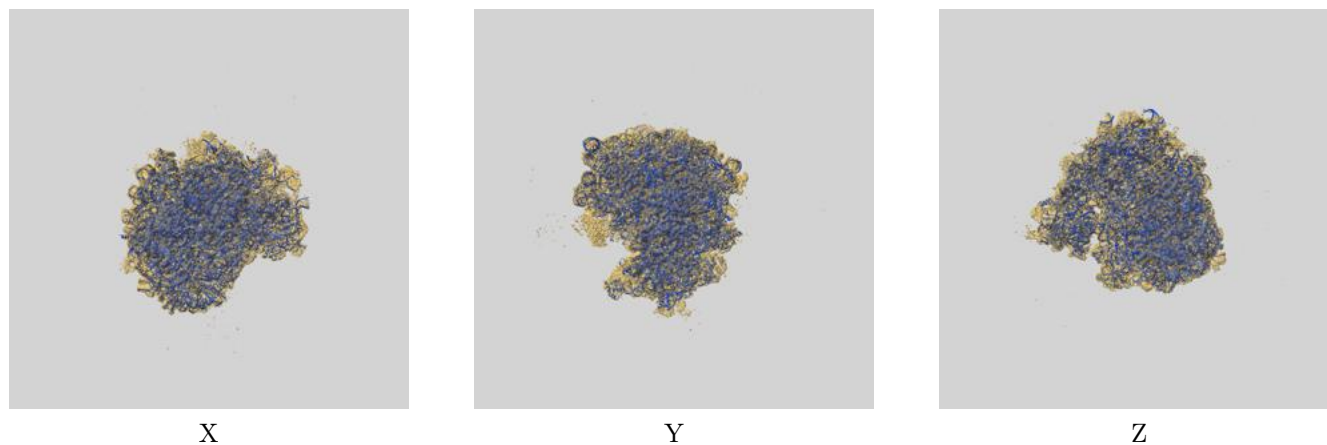
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

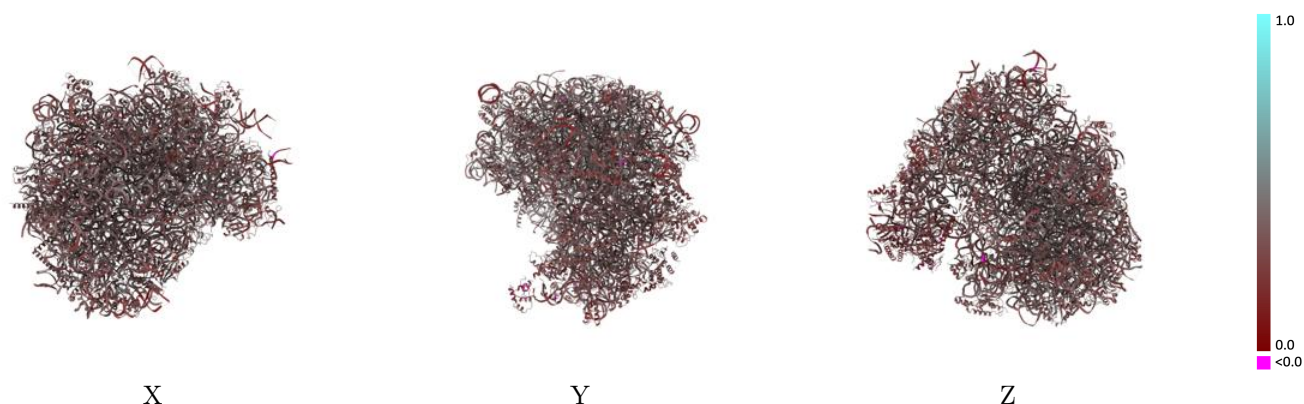
This section contains information regarding the fit between EMDB map EMD-6454 and PDB model 3JBP. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



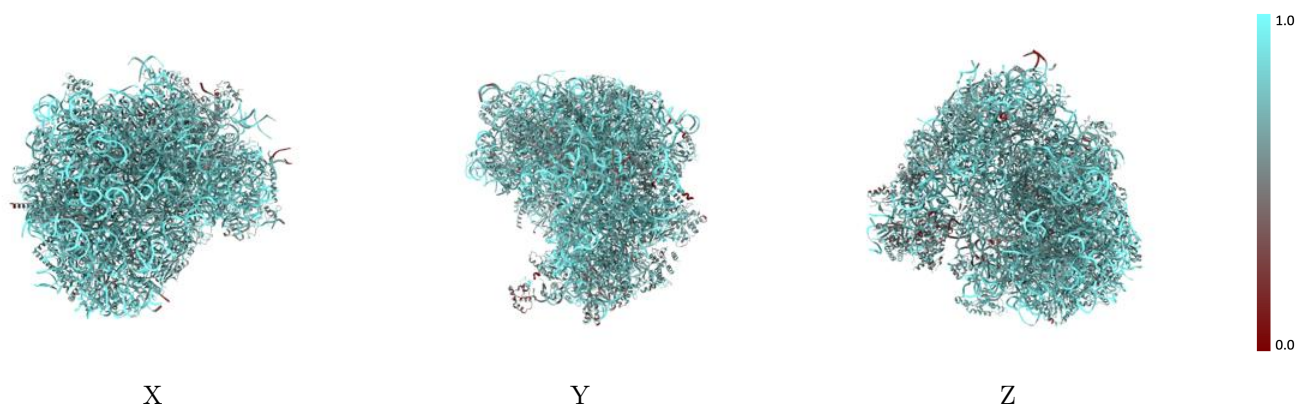
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



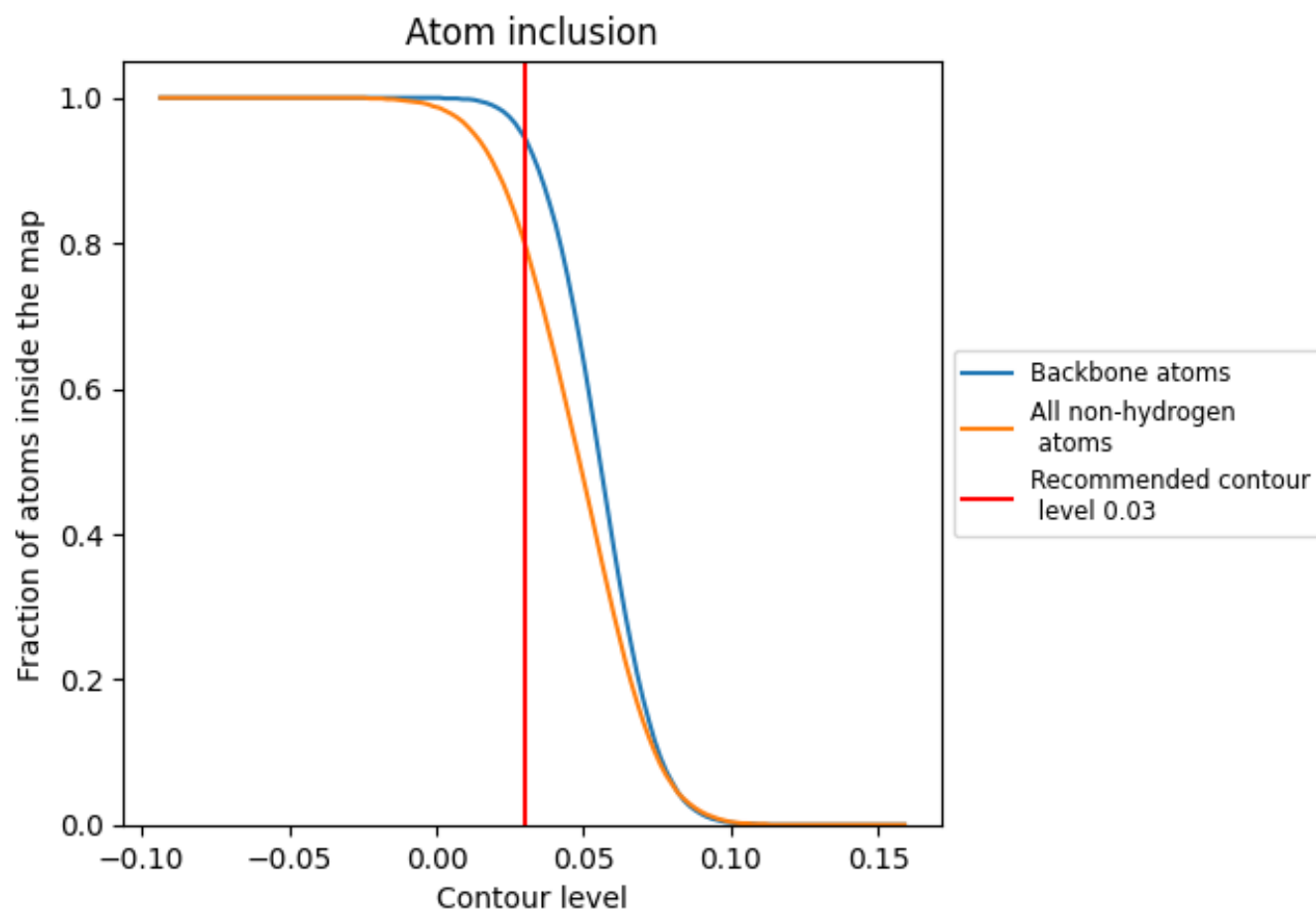
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.3520
1	 0.6760	 0.3380
2	 0.6370	 0.2980
3	 0.6670	 0.3600
4	 0.7040	 0.3540
5	 0.4570	 0.3260
6	 0.6580	 0.3710
7	 0.5700	 0.2680
A	 0.8930	 0.3460
A0	 0.6860	 0.3770
A1	 0.6750	 0.3570
A2	 0.7010	 0.3550
A3	 0.7070	 0.3420
A4	 0.6200	 0.3400
A5	 0.7040	 0.3520
A6	 0.6790	 0.3630
A7	 0.7160	 0.3780
A8	 0.6480	 0.3580
A9	 0.7020	 0.3770
AA	 0.8990	 0.3660
AB	 0.9510	 0.3610
AC	 0.9270	 0.3650
AD	 0.6490	 0.3740
AE	 0.7000	 0.3650
AF	 0.6930	 0.3480
AG	 0.7330	 0.3340
AH	 0.7280	 0.3640
AI	 0.7060	 0.3380
AJ	 0.6680	 0.3400
AK	 0.6850	 0.3410
AL	 0.7490	 0.3720
AM	 0.6650	 0.3760
AN	 0.7310	 0.3340
AO	 0.7030	 0.3640
AP	 0.6910	 0.3430



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Chain	Atom inclusion	Q-score
AQ	 0.6920	 0.3720
AR	 0.7240	 0.3270
AS	 0.6880	 0.3580
AT	 0.6330	 0.3350
AU	 0.7040	 0.3650
AV	 0.6920	 0.3650
AW	 0.7160	 0.3660
AX	 0.6330	 0.3480
AY	 0.6790	 0.3640
AZ	 0.7230	 0.3540
Aa	 0.6880	 0.3600
Ab	 0.6940	 0.3490
Ac	 0.7020	 0.3570
Ad	 0.6820	 0.3580
Ae	 0.6920	 0.3630
Af	 0.7250	 0.3480
Ag	 0.5820	 0.3290
Ah	 0.6670	 0.3530
Ai	 0.6810	 0.3850
B	 0.6540	 0.3510
C	 0.6860	 0.3270
D	 0.6270	 0.3180
E	 0.7030	 0.3360
F	 0.6960	 0.3520
G	 0.7180	 0.3610
H	 0.6390	 0.3200
I	 0.5590	 0.2760
J	 0.6410	 0.3310
K	 0.6740	 0.3530
L	 0.7000	 0.3570
M	 0.5500	 0.2640
N	 0.5800	 0.2690
O	 0.6280	 0.2740
P	 0.6550	 0.3560
Q	 0.6430	 0.3710
R	 0.4640	 0.2790
S	 0.5760	 0.2620
T	 0.6310	 0.2910
U	 0.6490	 0.3530
V	 0.6690	 0.3700
W	 0.6450	 0.3020
X	 0.5250	 0.2950

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Chain	Atom inclusion	Q-score
Y	 0.6300	 0.2640
Z	 0.6960	 0.3570