



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Jan 31, 2017 – 11:49 AM EST

PDB ID : 3JBU  
EMDB ID: : EMD-6483  
Title : Mechanisms of Ribosome Stalling by SecM at Multiple Elongation Steps  
Authors : Zhang, J.; Pan, X.J.; Yan, K.G.; Sun, S.; Gao, N.; Sui, S.F.  
Deposited on : 2015-10-16  
Resolution : 3.64 Å(reported)  
Based on PDB ID : 4V7T

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028442

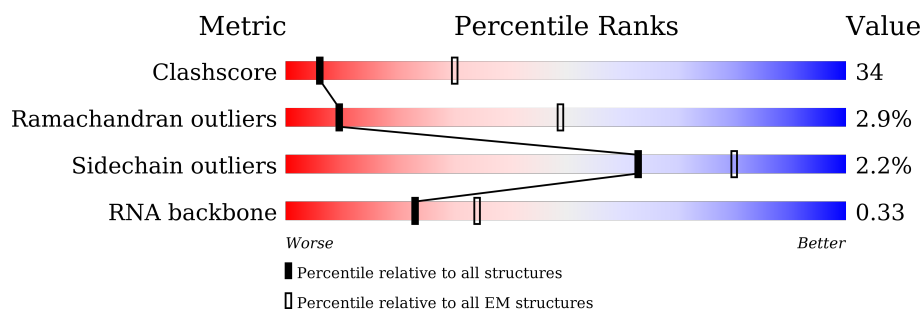
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.64 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.









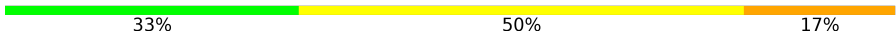

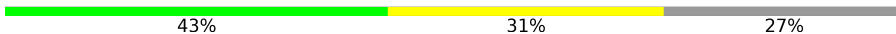
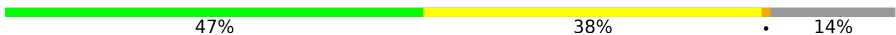

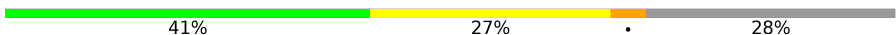








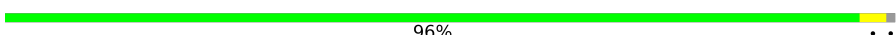
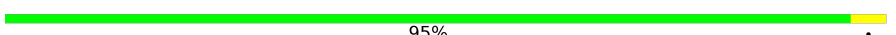
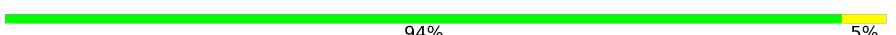

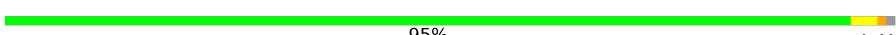
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	B	241	56% 32% • 10%
2	C	233	60% 27% • 12%
3	D	206	55% 43% •
4	E	167	58% 30% • 10%
5	F	131	42% 34% • 24%
6	G	156	67% 28% • •
7	H	130	66% 31% • •
8	I	130	50% 42% 5% •


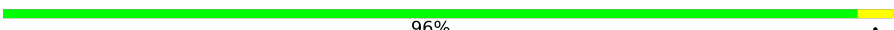
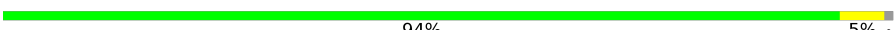
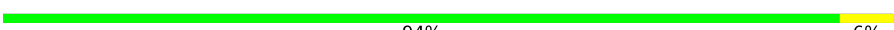
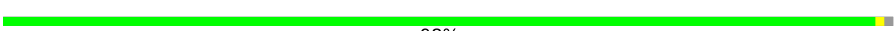







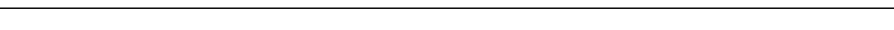
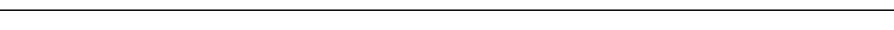
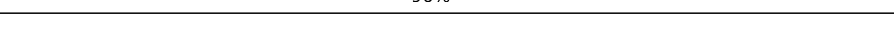






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Mol	Chain	Length	Quality of chain
9	J	103	
10	K	129	
11	L	124	
12	M	118	
13	N	101	
14	O	89	
15	P	82	
16	Q	84	
17	R	75	
18	S	92	
19	T	87	
20	U	71	
21	0	78	
22	1	63	
23	2	59	
24	3	57	
25	4	55	
26	6	46	
27	7	65	
28	8	38	
29	c	273	
30	d	209	
31	e	201	
32	f	179	
33	g	177	

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Mol	Chain	Length	Quality of chain
34	h	149	 90% 10%
35	j	142	 96% .
36	k	123	 94% 5% .
37	l	144	 94% 6%
38	m	136	 98% ..
39	n	127	 91% . . 6%
40	o	117	 92% 7% .
41	p	115	 95% . .
42	q	118	 97% ..
43	r	103	 94% 6%
44	s	110	 95% 5%
45	t	100	 89% . 7%
46	u	104	 89% 8% ..
47	w	94	 96% .
48	y	85	 88% 12%
49	z	87	 14% 16% 70%
50	A	1542	 36% 46% 17% .
51	X	11	 9% 27% 36% 27%
52	a	120	 62% 34% . .
53	b	2904	 55% 37% 6% .
54	v	76	 61% 39%

## 2 Entry composition [i](#)

There are 54 unique types of molecules in this entry. The entry contains 143334 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 30S ribosomal protein S2.

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 8 is a protein called 30S ribosomal protein S9.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 14 is a protein called 30S ribosomal protein S15.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	79	ARG	GLN	ENGINEERED MUTATION	UNP P0ADZ4

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

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

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

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

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

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

- Molecule 18 is a protein called 30S ribosomal protein S19.

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

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

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

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

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

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 25 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.



Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 30 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 31 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 32 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 33 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 34 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	135	Total	C	N	O	S	0	0
			1063	680	201	176	6		

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 49 is a protein called SecM-glycine.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	26	Total	C	N	O	0	0
			203	129	33	41		

- Molecule 50 is a RNA chain called 16S rRNA.

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

- Molecule 51 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	X	11	Total	C	N	O	P	0	0
			232	103	39	79	11		

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	118	Total	C	N	O	P	0	0
			2528	1126	464	821	117		

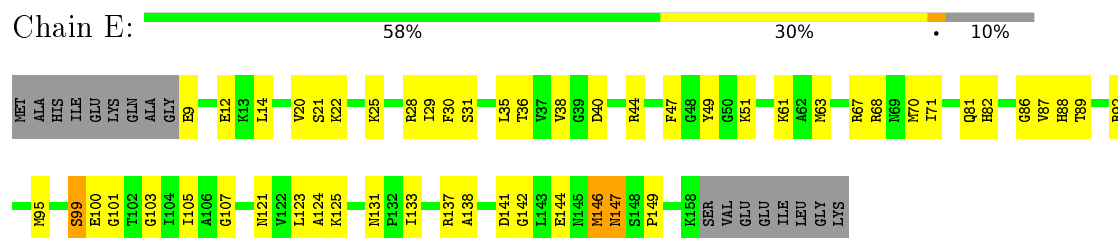
- Molecule 53 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

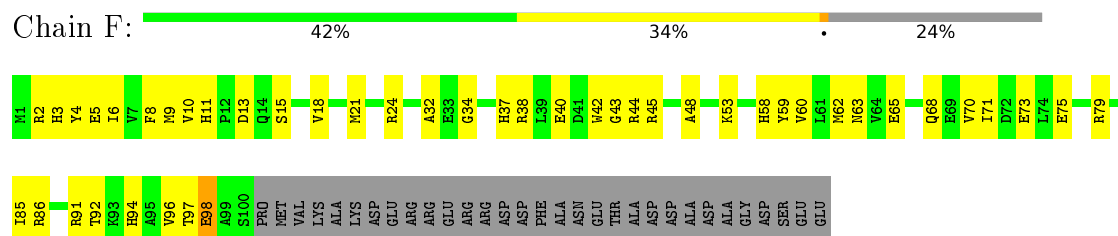
- Molecule 54 is a RNA chain called glycine-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	76	Total	C	N	O	P	0	0
			1623	722	291	534	76		

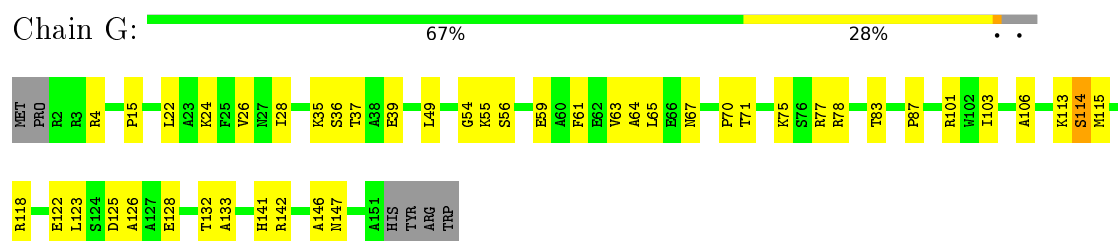




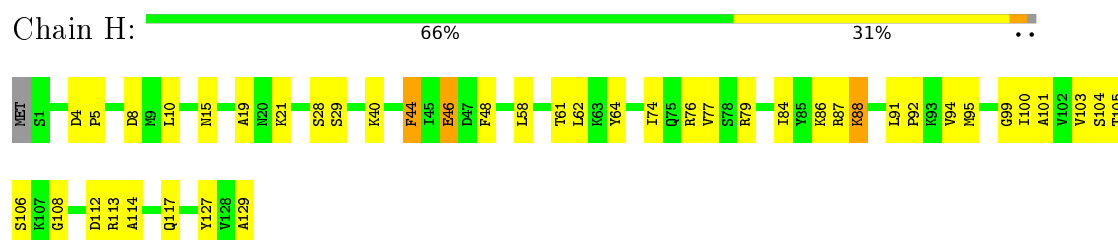
- Molecule 5: 30S ribosomal protein S6



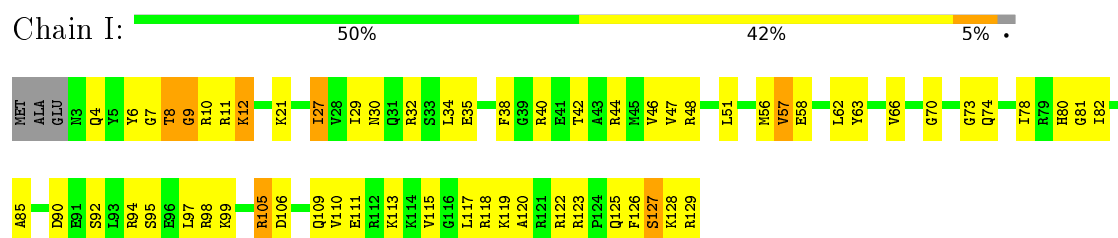
- Molecule 6: 30S ribosomal protein S7



- Molecule 7: 30S ribosomal protein S8

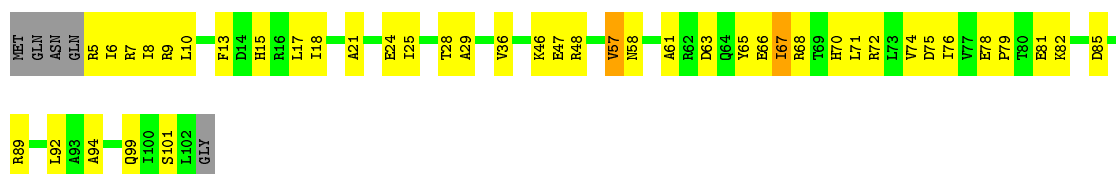


- Molecule 8: 30S ribosomal protein S9



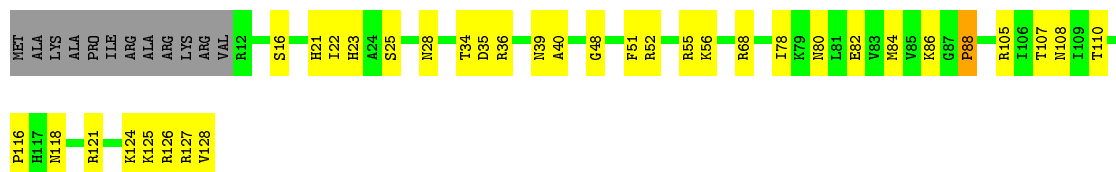
- Molecule 9: 30S ribosomal protein S10





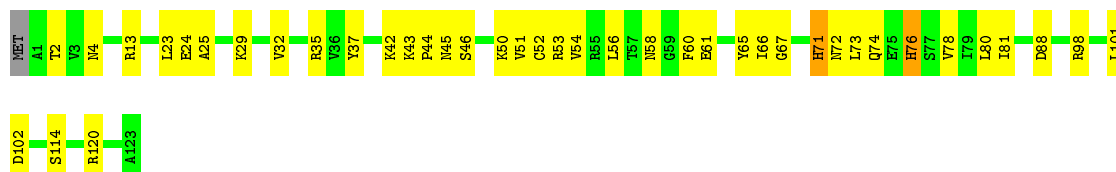
- Molecule 10: 30S ribosomal protein S11

Chain K: 64% 26% 9%



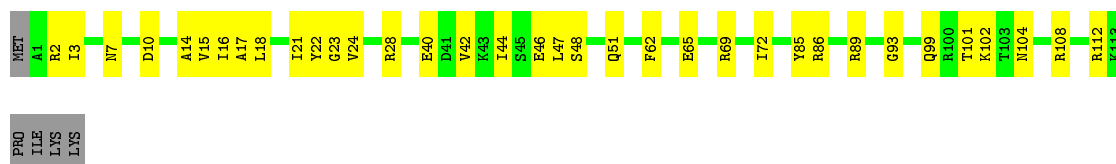
- Molecule 11: 30S ribosomal protein S12

Chain L: 66% 31% ..



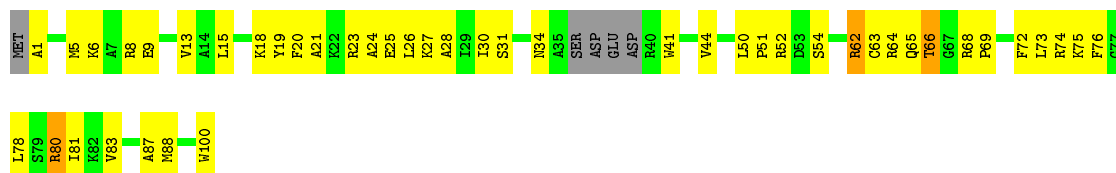
- Molecule 12: 30S ribosomal protein S13

Chain M: 66% 30% .



- Molecule 13: 30S ribosomal protein S14

Chain N: 50% 42% . 5%

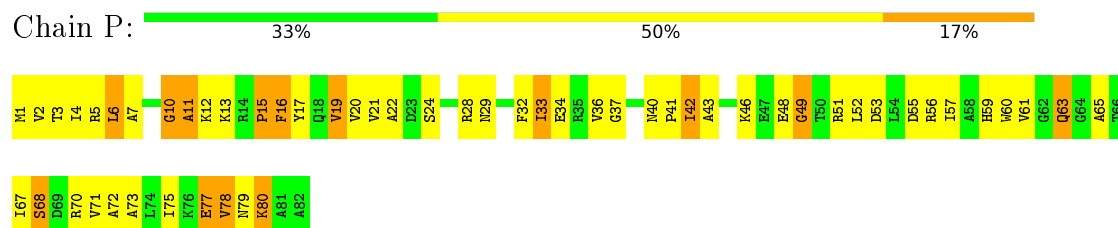


- Molecule 14: 30S ribosomal protein S15

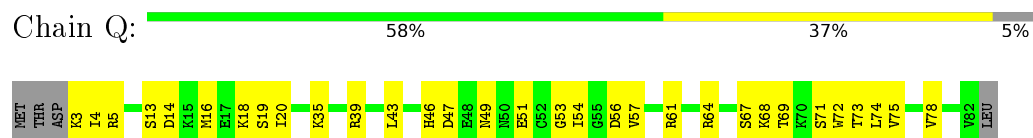
Chain O: 79% 18% ..



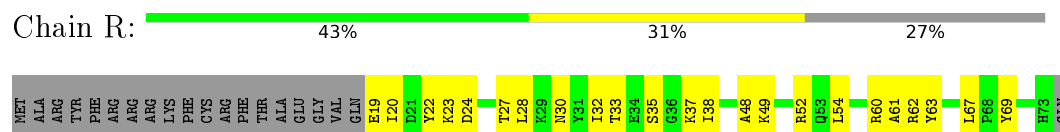
- Molecule 15: 30S ribosomal protein S16



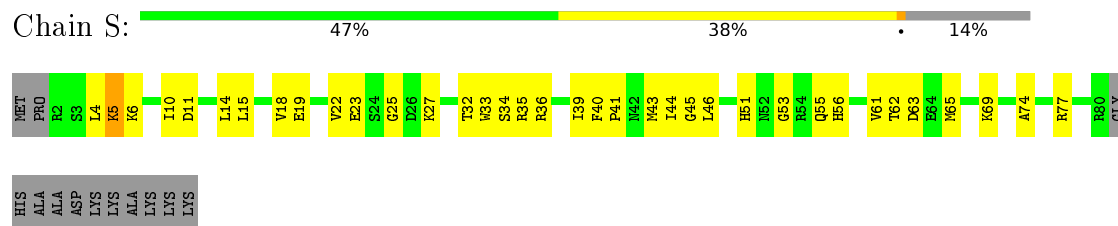
- Molecule 16: 30S ribosomal protein S17



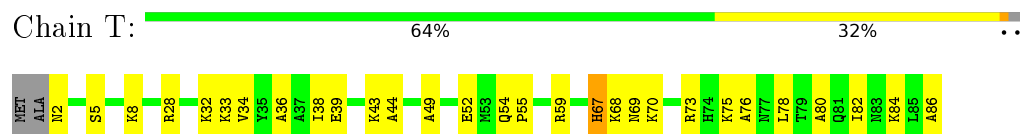
- Molecule 17: 30S ribosomal protein S18



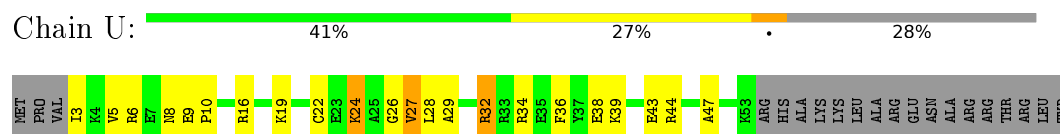
- Molecule 18: 30S ribosomal protein S19



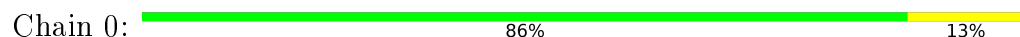
- Molecule 19: 30S ribosomal protein S20



- Molecule 20: 30S ribosomal protein S21



- Molecule 21: 50S ribosomal protein L28







- Molecule 22: 50S ribosomal protein L29

Chain 1: 78% 21% .



- Molecule 23: 50S ribosomal protein L30

Chain 2: 86% 8% . .



- Molecule 24: 50S ribosomal protein L32

Chain 3: 86% 12% .



- Molecule 25: 50S ribosomal protein L33

Chain 4: 87% . 9%



- Molecule 26: 50S ribosomal protein L34

Chain 6: 87% 7% 7%



- Molecule 27: 50S ribosomal protein L35

Chain 7: 89% 9% .



- Molecule 28: 50S ribosomal protein L36

Chain 8: 82% 18%



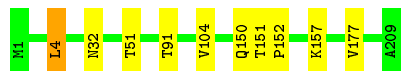
- Molecule 29: 50S ribosomal protein L2

Chain c:  96% ..



- Molecule 30: 50S ribosomal protein L3

Chain d:  95% .




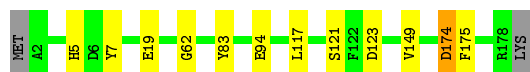
- Molecule 31: 50S ribosomal protein L4

Chain e:  94% 5%



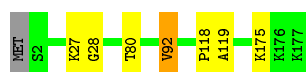
- Molecule 32: 50S ribosomal protein L5

Chain f:  92% 6% ..



- Molecule 33: 50S ribosomal protein L6

Chain g:  95% ..



- Molecule 34: 50S ribosomal protein L9

Chain h:  90% 10%



- Molecule 35: 50S ribosomal protein L13

Chain j:  96% .



- Molecule 36: 50S ribosomal protein L14

Chain k:  94% 5%



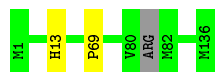
- Molecule 37: 50S ribosomal protein L15

Chain l:  94% 6%




- Molecule 38: 50S ribosomal protein L16

Chain m:  98% ..



- Molecule 39: 50S ribosomal protein L17

Chain n:  91% .. 6%



- Molecule 40: 50S ribosomal protein L18

Chain o:  92% 7%



- Molecule 41: 50S ribosomal protein L19

Chain p:  95% ..



- Molecule 42: 50S ribosomal protein L20

Chain q:  97% ..



- Molecule 43: 50S ribosomal protein L21

Chain r:  94% 6%



- Molecule 44: 50S ribosomal protein L22

Chain s: 95% 5%



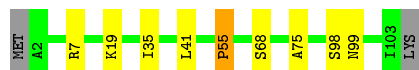
- Molecule 45: 50S ribosomal protein L23

Chain t: 89% 7%



- Molecule 46: 50S ribosomal protein L24

Chain u: 89% 8% ..



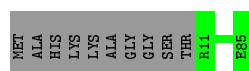
- Molecule 47: 50S ribosomal protein L25

Chain w: 96% .



- Molecule 48: 50S ribosomal protein L27

Chain y: 88% 12%



- Molecule 49: SecM-glycine

Chain z: 14% 16% 70%

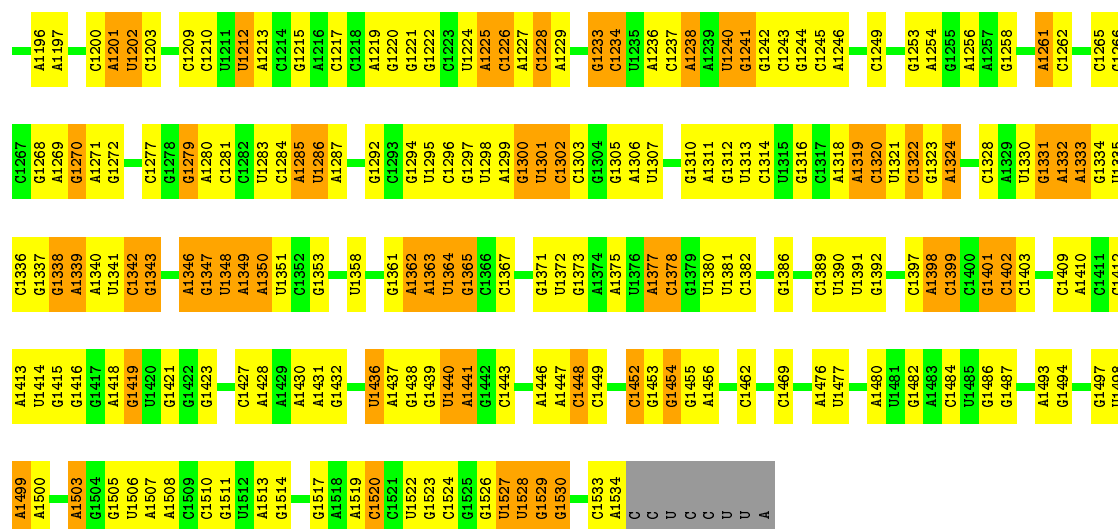


- Molecule 50: 16S rRNA

Chain A: 36% 46% 17% .



G1124	U1066	C990	C848	G771	A896	U619	G541	U473	G410	G347	U268	G201	C136	G64	A
U1125	G1057	U991	G849	U772	U697	C620	G542	G474	A411	G346	C272	G202	U137	A65	A
G1127	G993	U992	U850	G773	G698	A621	U543	U475	A412	A349		G203	G138	C67	U
G1128	G927	G994	G851	G779	G699	C623	C545	U476	A413			G204	G139	G68	U5
G1129	G928	G995	G853	U780	U701		A546	G477	A414	C352	G275	A205	U140	G69	G6
A1130	U1062	A996	C857	A781	A702	G626	A547	U479	G415	G354	C277	U209	G143	U70	A7
G1131	C1063	U997	G858	A782	G703	G627	G548	U480	G417	C355	C278	G211	G142	A8	G9
G1132	C998	C998	G859	G786	A704	G628	C549	C549	C418	C356	A279	G212	A143	G9	
G1133	C999	C999	G860	G787	U705	A629	G550	A482	C420	C357	G276	G215	G146	G10	G11
G1134	U1066	A1000	A860	U788	U706	A630	G551	C483	U420			C216	G147	U12	U12
U1135	A1067	G1001	G861	U789	U707	C631	U552	G484	U421	G360		U217	G148	U13	U13
C1136	C936	G1002	G862	U790	C708	U632	A553	U485	C422	G361		C218	G149	U14	U14
G1137	C1069	G1003	A864	A790	U709	G633	C556	U486	G423	G362	C286	U219	U150	G15	
G1138	U1070	A1004	A865	G791	G710		G557	A487	G424	A363	U287	U218	G151	A80	
G1139	C1071	A1005	C866	A792	G721	U636	G558	C488	G425	A364	A288	U219	A152	A81	
G1140	G1072	G1006	G867	U793	U723	C637	G559	C489	U426	U365	C290	C221	A153	G82	
C1141	C940	U1007	G869	A794	C719	A640	U561	C490	U427	A366	U291	C222	C153	C83	
G1142	G942	U1008	U870	U795	C720	U641	U562	G491	G428	U367	C292	U223	U154	U84	
G1143	G1074	U1009	U871	C797	G721	U642	U563	C492	U429	U368	U296	U224	A155	U85	
U1075	U1076	U1010	A872	U798	G722	A643	U564	G493	A430	G369		C225	C156	G86	
A1145			G873	U801	G724	U644	U565	A494	A431	C370			U157	C87	
			U874	A802	G725	G645	G566	A495	U432	C371		A228	A160	C90	
			U875	C806	A728	G646	G567	A496	A433	C372	A300	U229	A161	C95	
			G877		U729	G647		G497	A434	A373	G301	G230	A162	A26	
			U878		A729	C651	U571	A498	C435	A374	G302	U231	C163	G27	
			G879		U730	U652	U572	A499	C436	U375	U304	G232	G164	U96	
					C731	U653	A573	A500	U437	G376		G233	G165	U29	
			C882		C732	U657	A574	C503	U438	G377		C234	U166	G97	
					G733		G575	C504	U439	G378	A309	C235	G167	U30	
			G886		G734		C576	G505	C440	C379	G310	A236	A174	G31	
			G887		C735		C577	G506		G380	C311		C175	A32	
			G888		U736		G578	C507	G444	A382		U239	G176	A101	
			A889		C737		A579	U508	G445	A383	C314	G240	U170	G102	
			G890		C738		G584	A510	G446	A384		G241	G177	U103	
			U891				G585	C511	G447	G385	U317	G242	C178	G35	
			A892		G741		G586	U512	G448	G386	G318	A243	A174	G104	
			C893		G742		G587		G449	U387		U244	C175	G106	
			G894		A743		G588	U516	A450	U388	C322	U245	C176	G107	
			C895				G589	U517	A451	A389	U323	A246	G177	G108	
			G896		A747		U590	C518	A452	U390	A325	G247	C178	A109	
			A900		G748		U591		G455	U391	G326	U249	A181	C43	
			A901		A749		G592		A456	C392	A327	A250	A182	A44	
			G902		C750				G457	A393	C328	G251	C183	G45	
					U751		A600		U458	C396	A329	U252	G184	G46	
			A906		G752		G601	C525	A459	A397	C330	A253	U185	C47	
			G907		A753		A602	G527	A461	U398	G331	G254	G186	A119	
			A908		C754		U603	C528	G462	G399	G332	G255			
			U909		G755			G529	U463	G400	C335	U256	A190	A51	
			C910		U757		A607		U464	C401			G191	C52	
			U911				A608	U531	A465	G402		G259	A192	A53	
			C912		C764		A609	A532	A466	A403	C339	G260	C125	C54	
			A913		U842		U610	A533	U467	G404	U340	U261	C194	U56	
			G914		G765		C611	U534	A468	U405	C341	A263	A195	G128	
					A767		C614	A535	C469	G406	C342	A264	A197	A129	
			G917		A768			U539	U470	U407	U343	G265	G198	A130	
			A918		G693			A539	C471	A908	C345	G266	A199	G61	
			A919		A695		C618	G540	U472	U409	G346	C267	G200	U133	



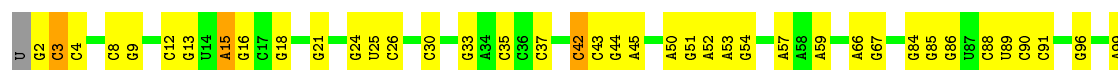
### • Molecule 51: mRNA

Chain X: 9% 27% 36% 27%



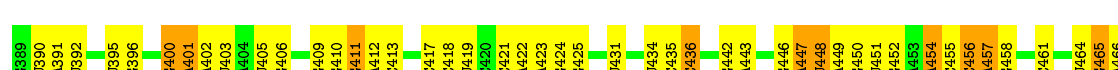
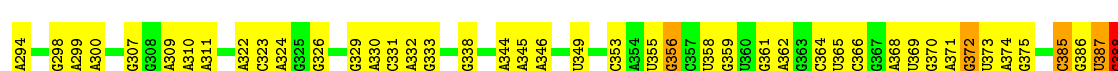
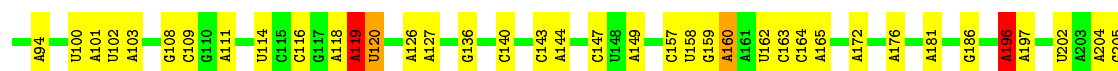
### • Molecule 52: 5S rRNA

Chain a: 62% 34%

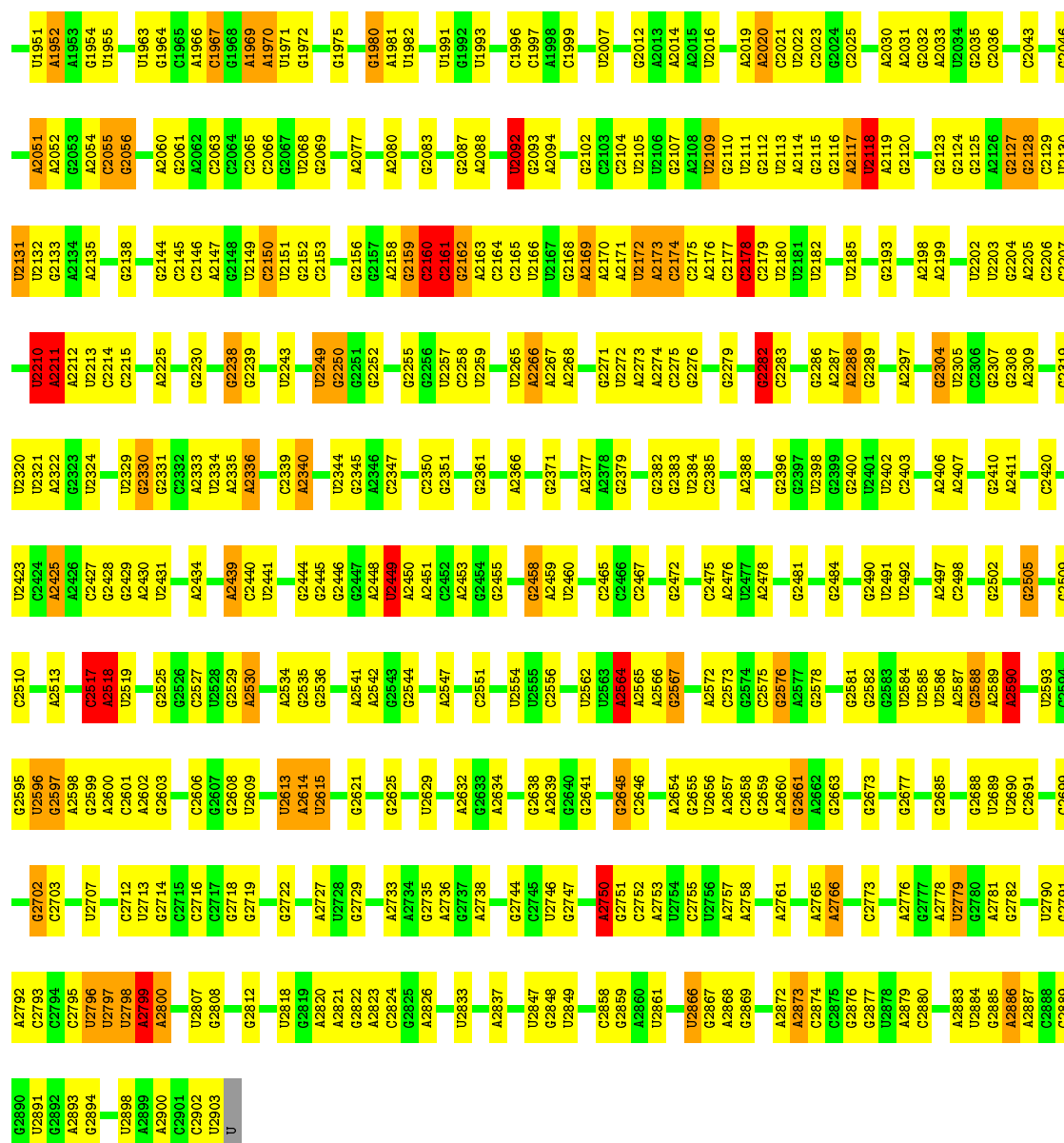


### • Molecule 53: 23S rRNA

Chain b: 55% 37% 6%



G1840	G1750	U1648	G1555	C1454	U1352	U1267	U1101	G1036	C951	G858	C758	U658	G570	C475
G1843	A1754	G1653	C1556	U1458	G1355	A1268	C1101	G1037	C951	G859	C763	G659	U571	C476
G1846	A1755	G1654	C1557	G1459	G1355	G1185	A1103	G1038	C957	A866	A764	G662	U572	A477
A1848	A1756	A1654	C1558	U1460	G1358	G1186	C1104	A1039	U958	C867	C765	G663	A574	A478
U1849	U1758	C1655	U1562	C1461	A1365	G1187	U1105	G1044	A959	U868	U766	G664	A575	A479
	U1759	C1656	A1566	U1467	A1368	G1188	G1107	G1047	A960	G869	G770	A688	U576	A480
A1858	G1760	C1657	G1567	A1275	G1368	G1189	U1108	G1048	C961	U872		G669	G583	A481
U1859	A1761	G1658	G1567	A1276	G1369	G1110	C1109	A1048	G962	A878		A670	C584	A482
G1860	A1762	A1569	A1568	A1287	A1373	G1111	C1110	C1049	G963	C874	G775	A671	G585	A483
G1861	G1763	G1661	A1570	U1476	G1374	A1111	A1050	A1050	C964	G875	G776	C672	A586	G489
G1862	C1764	U1662	A1571	A1477	G1374	G1112	G1112	G1051	C965	C876	G777	G673	C587	G490
	U1765	G1663	A1572	G1478	A1203	G1115	C1052	C1052	C965	C877	U778	G674	U588	G491
	G1766				A1205	G1115	C1053	C1053	C968	A877		A675		A492
U1865		G1667	U1576	U1481	G1377	G1116	G1054	G1054	G969	A878	G780		A603	G500
A1866	A1773	A1668	C1577	A1378	A1276	C1117	A1054	G1055	A972	A879		U686	G604	A501
G1867	C1774	A1669	U1578	G1482	C1207	C1117	G1055	G1056	A973	A781		A607	A502	A502
C1868	U1775	G1674	A1583	G1483	C1208	G1121	G1056	G1056	A974	G881	G784	G696	A503	A504
G1869	G1776	C1675	U1584	U1487	U1209	G1122	U1058	U1058	G974	G882	G785		A608	A505
C1870		C1675	C1585	U1494	G1289	G1125	G1059	G1059	A975	G883		G701		
A1871	A1780	A1678		A1494	A1302	A1126	U1061	U1061	A979	U887	C787		G612	A514
G1873				A1495	A1302	A1126	G1062	G1062	A980	A788		G704	A613	A508
	A1783			A1496	U1391	U1130	G1063	G1063	A981	A789	A705	G704	A614	A509
A1880	A1784	G1681	C1592	U1497	A1392	G1131	C1064	C1064	C982	A790	U790	A706	U615	C509
	A1785	G1682	G1595	C1498	A1393	U1132	U1065	U1065	A983	G791	G707		A616	C510
G1897	A1786	U1683	C1596	U1499	U1394	U1133	U1066	U1066	A984	G792			G617	
	A1787		A1598	A1500	A1395	A1133	U1067	G1068	C986	A794			G618	A514
C1905	G1792	G1687	U1599	G1499	G1227	G1136	A1069	G1070	G989	G798		U714	A621	G518
G1906	C1793	U1693	C1600	U1503	U1231	G1137	A1142	G1071	C995	G799		A715	G622	U519
G1907	A1794	G1694	G1601	C1507	G1232	G1138	G1139	G1072	A996	A800		A717	G625	A526
C1908		G1695	A1602	U1508	U1316	G1139	A1073	A1073	A996	G801		C717	A626	C527
	A1800	G1696	A1603	A1509	U1318	U1141	G1074	G1074	G1003	G805		C719	G628	A528
A1913	A1801	G1697	C1606	C1510	C1320	A1142	G1075	G1075	U1004			U720		A529
G1914	A1802	G1698	C1607	G1517	A1321	A1143	C1076	C1076	U1004				A631	A529
U1915	A1803	G1699	A1608	U1522	A1322	A1144	A1077	A1077	C1005				A632	G630
A1916	G1804	A1700	A1609	U1523	A1323	G1145	C1078	C1078	C1006				A637	G631
U1917				U1524	U1327	U1148	C1079	C1079	A1010				G636	A532
A1918	G1807	G1703	C1611	U1525	U1327	U1148	U1081	U1081	A1011				A637	A538
A1919	A1808	C1704	C1612	G1526	A1419	A1156	A1084	A1084	U1012				U639	
	A1810	A1706	A1616	C1526	A1420	G1157	A1085	A1085	U1013				C640	C644
C1924	G1811	G1707	C1617	G1529	U1329	G1163	A1086	A1086	U1018				U641	U545
A1927			A1618	G1530	C1330	U1248	G1087	G1087	U1019				U642	U546
A1928	G1814		U1624	G1531	G1332	U1249	G1250	G1250	A1165				A643	A547
G1929	A1815	G1740	U1624	U1534	G1251	G1251	A1088	A1088	A1069				A644	G548
C1930	G1816	A1713	U1624	G1425	G1251	G1251	A1088	A1088	U1069				C645	C549
U1931	G1817	U1714	G1631	G1426	G1337	G1253	A1090	A1090	G1022				U646	C550
A1932		G1715	U1632	A1427	G1338	A1253	A1091	A1091	U1023				G647	
	G1823		A1633	G1428	G1338	A1254	G1091	G1091	G1024					
A1936	G1824	G1731	G1633	G1429	G1341	U1255	G1092	G1092	G1025				G651	G559
A1937	U1825	C1732	A1634	U1539	A1342	C1172	G1093	G1093	G1026				U652	C560
A1938	G1826	G1733	A1635	G1435	G1257	U1173	U1094	U1094	A1027				U653	A563
U1939			C1541	U1344	G1258	U1174	A1095	A1095	A1028				A654	C564
U1940	A1829	G1738	U1643	U1542	G1259	A1175	A1096	A1096	A1028				U655	
C1941		A1739	C1644	U1542	A1260	U1176	U1097	U1097	A1032				A656	
U1942	G1833		A1645	A1552	A1265	G1177	A1098	A1098	U1033				A657	U568
C1943		A1746	C1646	C1452	A1265	C1178	G1099	G1099	A1034					
U1944	G1839		U1647	U1554	A1453	G1179	C1100	C1100	U1035				G757	



• Molecule 54: glycine-tRNA

Chain v: 61% 39%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	60354	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	16	Depositor
Minimum defocus (nm)	3500	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	37878	Depositor
Image detector	GATAN K2 Summit (4K X 4K)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
1	B	0.29	0/1735	0.51	0/2338
10	K	0.30	0/893	0.53	0/1205
11	L	0.36	0/969	0.59	0/1300
12	M	0.31	0/884	0.52	0/1181
13	N	0.34	0/785	0.54	0/1043
14	O	0.33	0/724	0.54	0/966
15	P	0.29	0/659	0.49	0/884
16	Q	0.34	0/657	0.53	0/881
17	R	0.37	0/462	0.58	0/621
18	S	0.32	0/652	0.55	0/877
19	T	0.33	0/671	0.52	0/888
2	C	0.33	0/1651	0.55	0/2225
20	U	0.33	0/430	0.63	0/570
21	0	0.38	0/635	0.67	0/848
22	1	0.37	0/502	0.65	0/667
23	2	0.39	0/453	0.61	0/605
24	3	0.41	0/450	0.73	0/599
25	4	0.38	0/416	0.58	0/554
26	6	0.44	0/380	0.77	0/498
27	7	0.37	0/513	0.62	0/676
28	8	0.38	0/303	0.74	0/397
29	c	0.39	0/2121	0.70	1/2852 (0.0%)
3	D	0.34	0/1665	0.55	0/2227
30	d	0.38	0/1586	0.63	1/2134 (0.0%)
31	e	0.39	0/1571	0.62	1/2113 (0.0%)
32	f	0.39	0/1434	0.66	0/1926
33	g	0.37	0/1343	0.56	0/1816
34	h	0.37	0/1122	0.68	5/1515 (0.3%)
35	j	0.37	0/1152	0.58	0/1551
36	k	0.38	0/947	0.68	1/1268 (0.1%)
37	l	0.38	0/1062	0.68	0/1413
38	m	0.38	0/1081	0.63	0/1443
39	n	0.39	0/973	0.67	0/1301
4	E	0.38	0/1118	0.56	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
40	o	0.39	0/902	0.70	0/1209
41	p	0.37	0/929	0.66	0/1242
42	q	0.39	0/960	0.69	1/1278 (0.1%)
43	r	0.40	0/829	0.67	1/1107 (0.1%)
44	s	0.35	0/864	0.67	1/1156 (0.1%)
45	t	0.40	0/744	0.66	1/994 (0.1%)
46	u	0.39	0/787	0.67	0/1051
47	w	0.36	0/766	0.58	0/1025
48	y	0.37	0/576	0.60	0/762
49	z	0.49	0/206	0.83	2/277 (0.7%)
5	F	0.32	0/835	0.56	0/1128
50	A	0.87	6/36762 (0.0%)	0.86	20/57350 (0.0%)
51	X	1.07	4/257 (1.6%)	0.91	0/396
52	a	0.45	1/2824 (0.0%)	0.93	7/4402 (0.2%)
53	b	0.55	52/69800 (0.1%)	1.03	441/108892 (0.4%)
54	v	0.36	1/1812 (0.1%)	0.85	4/2822 (0.1%)
6	G	0.31	0/1187	0.53	0/1591
7	H	0.35	0/989	0.55	0/1326
8	I	0.32	0/1034	0.61	0/1375
9	J	0.33	0/796	0.59	0/1077
All	All	0.60	64/155858 (0.0%)	0.89	487/233346 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	L	0	1
23	2	0	1
29	c	0	1
30	d	0	1
36	k	0	1
37	l	0	1
43	r	0	1
52	a	0	1
53	b	0	72
All	All	0	80

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	A	230	G	C6-N1	60.83	1.82	1.39
50	A	230	G	N3-C4	58.56	1.76	1.35
50	A	230	G	C2-N3	55.19	1.76	1.32
50	A	230	G	N1-C2	53.83	1.80	1.37
50	A	230	G	C5-C4	53.10	1.75	1.38
50	A	230	G	C5-C6	39.86	1.82	1.42
53	b	1087	G	O3'-P	16.62	1.81	1.61
53	b	2055	C	O3'-P	16.06	1.80	1.61
53	b	1055	G	O5'-C5'	11.59	1.62	1.44
53	b	1349	C	C4-N4	-10.90	1.24	1.33
53	b	2131	U	N1-C2	10.86	1.48	1.38
51	X	12	G	OP3-P	-10.81	1.48	1.61
53	b	2131	U	C4-C5	10.37	1.52	1.43
53	b	1	G	OP3-P	-10.10	1.49	1.61
54	v	1	C	OP3-P	-9.99	1.49	1.61
53	b	1088	A	O5'-C5'	9.14	1.59	1.44
53	b	2455	G	O3'-P	-8.96	1.50	1.61
53	b	1057	A	O3'-P	8.87	1.71	1.61
53	b	1349	C	N3-C4	-8.77	1.27	1.33
53	b	1055	G	C5'-C4'	8.63	1.61	1.51
53	b	1103	A	O3'-P	8.44	1.71	1.61
53	b	2056	G	O3'-P	-8.42	1.51	1.61
53	b	1087	G	C3'-O3'	8.37	1.53	1.42
53	b	2451	A	O3'-P	-8.29	1.51	1.61
53	b	1088	A	C5'-C4'	8.16	1.61	1.51
53	b	1078	U	O3'-P	7.67	1.70	1.61
53	b	2109	U	N1-C6	7.65	1.44	1.38
53	b	1349	C	N1-C2	7.42	1.47	1.40
53	b	2109	U	N3-C4	7.30	1.45	1.38
53	b	1086	A	O3'-P	7.06	1.69	1.61
53	b	780	G	O3'-P	6.73	1.69	1.61
53	b	1349	C	C2-N3	-6.71	1.30	1.35
53	b	2575	C	O3'-P	6.70	1.69	1.61
53	b	2178	C	O3'-P	6.62	1.69	1.61
52	a	2	G	O3'-P	6.58	1.69	1.61
53	b	1349	C	C2-O2	6.37	1.30	1.24
53	b	400	G	O3'-P	6.33	1.68	1.61
51	X	14	U	C1'-N1	6.21	1.58	1.48
53	b	569	U	O3'-P	-5.96	1.54	1.61
53	b	1100	C	O3'-P	5.93	1.68	1.61
53	b	1055	G	P-O5'	5.89	1.65	1.59
53	b	401	A	O5'-C5'	5.86	1.53	1.44
53	b	1661	G	O3'-P	5.81	1.68	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	b	2446	G	O3'-P	5.80	1.68	1.61
53	b	1826	G	O3'-P	5.80	1.68	1.61
53	b	1080	A	N1-C2	5.78	1.39	1.34
53	b	1088	A	P-O5'	5.73	1.65	1.59
53	b	778	G	O3'-P	5.66	1.68	1.61
53	b	1773	A	O3'-P	5.48	1.67	1.61
53	b	979	A	O3'-P	5.46	1.67	1.61
53	b	1054	A	O3'-P	5.46	1.67	1.61
53	b	1054	A	C3'-O3'	5.40	1.49	1.42
53	b	87	U	O3'-P	5.37	1.67	1.61
51	X	13	C	C1'-N1	5.37	1.56	1.48
53	b	247	G	O3'-P	-5.29	1.54	1.61
53	b	514	A	N3-C4	5.28	1.38	1.34
53	b	2384	U	O3'-P	5.26	1.67	1.61
53	b	1088	A	O4'-C1'	5.24	1.48	1.41
53	b	2444	G	O3'-P	-5.20	1.54	1.61
53	b	1060	U	O3'-P	5.17	1.67	1.61
53	b	779	U	O3'-P	5.16	1.67	1.61
53	b	2109	U	C2-O2	5.12	1.26	1.22
53	b	2330	G	O3'-P	5.11	1.67	1.61
51	X	20	U	C1'-N1	5.09	1.56	1.48

All (487) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	A	230	G	N7-C8-N9	21.72	123.96	113.10
50	A	230	G	C2-N3-C4	19.69	121.75	111.90
50	A	230	G	N3-C4-N9	18.99	137.39	126.00
53	b	1509	A	N9-C1'-C2'	17.94	137.32	114.00
53	b	1275	A	N9-C1'-C2'	17.27	136.46	114.00
53	b	1943	U	N1-C1'-C2'	16.93	136.01	114.00
53	b	1102	C	N1-C1'-C2'	16.51	135.47	114.00
54	v	74	C	O3'-P-O5'	-15.69	74.20	104.00
53	b	1060	U	N1-C1'-C2'	15.38	134.00	114.00
53	b	2092	U	N1-C1'-C2'	14.95	133.43	114.00
54	v	74	C	OP2-P-O3'	14.00	136.01	105.20
53	b	1395	A	N9-C1'-C2'	13.75	131.88	114.00
53	b	1204	A	N9-C1'-C2'	13.69	131.79	114.00
53	b	2455	G	P-O3'-C3'	-13.40	103.62	119.70
50	A	230	G	N3-C4-C5	-13.17	122.02	128.60
50	A	230	G	N1-C2-N3	-12.74	116.26	123.90
53	b	1079	C	N1-C1'-C2'	-12.69	97.50	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	1272	A	N9-C1'-C2'	12.39	130.10	114.00
53	b	250	G	N9-C1'-C2'	12.34	130.04	114.00
53	b	1349	C	N1-C2-O2	12.22	126.23	118.90
50	A	230	G	N9-C4-C5	-12.10	100.56	105.40
53	b	2597	G	N9-C1'-C2'	12.03	129.64	114.00
53	b	2613	U	N1-C1'-C2'	11.68	129.18	114.00
53	b	1205	A	N9-C1'-C2'	11.56	129.03	114.00
50	A	230	G	C4-C5-N7	-11.46	106.22	110.80
53	b	2118	U	O4'-C1'-N1	11.29	117.23	108.20
53	b	2210	U	N1-C1'-C2'	11.25	128.63	114.00
53	b	2178	C	N1-C1'-C2'	-11.23	99.40	114.00
53	b	1667	G	N9-C1'-C2'	-11.15	99.50	114.00
53	b	2449	U	N1-C1'-C2'	-11.08	99.60	114.00
53	b	1069	A	O4'-C1'-N9	10.94	116.95	108.20
53	b	1349	C	C2-N1-C1'	10.93	130.82	118.80
53	b	2799	A	N9-C1'-C2'	10.93	128.20	114.00
53	b	1080	A	C8-N9-C1'	-10.92	108.05	127.70
53	b	782	A	N9-C1'-C2'	10.73	127.94	114.00
53	b	1080	A	C4-N9-C1'	10.63	145.43	126.30
53	b	1349	C	N3-C4-N4	-10.61	110.57	118.00
52	a	3	C	C4'-C3'-O3'	10.55	134.09	113.00
53	b	1080	A	O4'-C1'-N9	10.47	116.57	108.20
53	b	2161	C	N1-C1'-C2'	10.33	127.43	114.00
53	b	119	A	N9-C1'-C2'	10.26	127.33	114.00
53	b	2517	C	N1-C1'-C2'	-10.20	100.73	114.00
53	b	2798	U	N1-C1'-C2'	10.19	127.25	114.00
53	b	1266	G	O4'-C1'-N9	10.17	116.33	108.20
53	b	1299	G	C2'-C3'-O3'	9.94	131.37	109.50
53	b	614	A	N9-C1'-C2'	9.92	126.89	114.00
53	b	246	C	N1-C1'-C2'	9.64	126.53	114.00
53	b	1616	A	N9-C1'-C2'	9.54	126.39	114.00
53	b	1079	C	C6-N1-C1'	-9.52	109.38	120.80
53	b	1349	C	C6-N1-C1'	-9.49	109.42	120.80
53	b	973	A	N9-C1'-C2'	9.43	126.26	114.00
53	b	877	A	N9-C1'-C2'	-9.41	101.65	112.00
54	v	74	C	P-O3'-C3'	-9.38	108.44	119.70
53	b	2161	C	O4'-C1'-N1	9.29	115.63	108.20
53	b	1225	G	N9-C1'-C2'	9.16	125.91	114.00
53	b	456	C	N1-C1'-C2'	9.13	125.86	114.00
53	b	25	U	N1-C1'-C2'	9.09	125.82	114.00
53	b	2282	G	N9-C1'-C2'	-9.05	102.05	112.00
53	b	788	A	N9-C1'-C2'	-9.03	102.07	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	1395	A	O4'-C1'-N9	8.84	115.27	108.20
53	b	1055	G	C8-N9-C1'	-8.83	115.52	127.00
53	b	1088	A	C5'-C4'-O4'	8.83	119.69	109.10
53	b	640	C	N1-C1'-C2'	8.81	125.46	114.00
53	b	959	A	N9-C1'-C2'	8.81	125.46	114.00
53	b	1458	U	N1-C1'-C2'	8.81	125.46	114.00
53	b	979	A	N9-C1'-C2'	-8.81	102.31	112.00
53	b	1088	A	O4'-C1'-N9	-8.79	101.17	108.20
53	b	457	A	N9-C1'-C2'	8.77	125.40	114.00
53	b	2451	A	P-O3'-C3'	8.75	130.20	119.70
53	b	1522	A	N9-C1'-C2'	8.72	125.33	114.00
53	b	479	A	C4'-C3'-O3'	-8.68	91.18	109.40
53	b	983	A	N9-C1'-C2'	8.68	125.28	114.00
53	b	2505	G	P-O3'-C3'	-8.67	109.30	119.70
50	A	230	G	C5-C6-N1	8.63	115.81	111.50
53	b	2467	C	N1-C1'-C2'	-8.61	102.53	112.00
53	b	401	A	P-O5'-C5'	8.53	134.54	120.90
53	b	49	A	N9-C1'-C2'	8.43	124.96	114.00
53	b	242	G	N9-C1'-C2'	-8.41	102.75	112.00
53	b	1084	A	N9-C1'-C2'	8.36	124.86	114.00
53	b	1097	U	O4'-C1'-N1	8.31	114.85	108.20
53	b	544	C	N1-C1'-C2'	8.29	124.78	114.00
53	b	2750	A	O4'-C1'-N9	-8.27	101.58	108.20
53	b	2779	U	N1-C1'-C2'	8.25	124.72	114.00
53	b	931	U	N1-C1'-C2'	8.24	124.72	114.00
53	b	1272	A	O4'-C1'-N9	-8.24	101.61	108.20
53	b	1055	G	O5'-C5'-C4'	8.22	127.32	111.70
53	b	1773	A	C2'-C3'-O3'	8.22	127.58	109.50
53	b	1952	A	N9-C1'-C2'	8.15	124.60	114.00
53	b	2596	U	N1-C1'-C2'	8.12	124.56	114.00
53	b	1970	A	N9-C1'-C2'	8.12	124.55	114.00
53	b	2250	G	N9-C1'-C2'	8.10	124.54	114.00
53	b	618	G	N9-C1'-C2'	8.08	124.50	114.00
53	b	1055	G	C5'-C4'-O4'	8.08	118.79	109.10
53	b	1055	G	C4-N9-C1'	8.04	136.96	126.50
53	b	1265	A	N9-C1'-C2'	8.01	124.41	114.00
53	b	1103	A	C2'-C3'-O3'	8.01	127.12	109.50
53	b	2178	C	C2'-C3'-O3'	8.00	127.11	109.50
53	b	858	G	N9-C1'-C2'	-7.98	103.22	112.00
53	b	2162	G	O4'-C1'-N9	7.89	114.51	108.20
53	b	1459	G	N9-C1'-C2'	7.88	124.25	114.00
53	b	1143	A	N9-C1'-C2'	7.84	124.19	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	A	1158	C	N1-C2-O2	7.83	123.60	118.90
53	b	388	G	O4'-C1'-N9	7.82	114.46	108.20
53	b	1087	G	C4'-C3'-O3'	7.82	128.64	113.00
53	b	783	A	O4'-C1'-N9	7.81	114.44	108.20
53	b	1459	G	C1'-O4'-C4'	-7.79	103.67	109.90
53	b	241	A	N9-C1'-C2'	7.77	124.10	114.00
53	b	2056	G	OP2-P-O3'	7.76	122.28	105.20
53	b	1079	C	C2-N1-C1'	7.74	127.32	118.80
53	b	1392	A	N9-C1'-C2'	7.72	124.04	114.00
53	b	160	A	N9-C1'-C2'	7.72	124.03	114.00
53	b	1301	A	O4'-C1'-N9	7.71	114.37	108.20
53	b	1057	A	N9-C1'-C2'	-7.71	103.52	112.00
53	b	801	G	O4'-C1'-N9	-7.70	102.04	108.20
53	b	2128	G	N9-C1'-C2'	7.66	123.95	114.00
53	b	1567	G	N9-C1'-C2'	7.63	123.93	114.00
53	b	787	C	N1-C1'-C2'	7.63	123.92	114.00
53	b	979	A	C2'-C3'-O3'	7.63	126.28	109.50
53	b	108	G	N9-C1'-C2'	-7.62	103.61	112.00
53	b	2211	A	N9-C1'-C2'	7.57	123.84	114.00
53	b	72	U	N1-C1'-C2'	7.55	123.81	114.00
53	b	2172	U	C4'-C3'-O3'	7.55	128.09	113.00
53	b	2458	G	N9-C1'-C2'	-7.53	103.72	112.00
53	b	1088	A	C8-N9-C1'	-7.51	114.18	127.70
50	A	230	G	N3-C2-N2	7.51	125.16	119.90
34	h	62	LEU	N-CA-C	7.50	131.26	111.00
53	b	281	C	N1-C1'-C2'	7.50	123.75	114.00
53	b	783	A	C4'-C3'-O3'	7.49	127.97	113.00
53	b	1087	G	P-O3'-C3'	7.47	128.66	119.70
53	b	417	C	N1-C1'-C2'	-7.46	103.79	112.00
53	b	2117	A	N9-C1'-C2'	7.42	123.65	114.00
53	b	2211	A	O4'-C1'-N9	-7.41	102.28	108.20
53	b	603	A	N9-C1'-C2'	7.39	123.61	114.00
53	b	639	U	N1-C1'-C2'	7.39	123.61	114.00
50	A	1158	C	C2-N1-C1'	7.38	126.92	118.80
53	b	1102	C	C6-N1-C1'	-7.33	112.00	120.80
53	b	1054	A	O4'-C1'-N9	7.32	114.05	108.20
53	b	2645	G	N9-C1'-C2'	-7.32	103.95	112.00
53	b	1088	A	C2'-C3'-O3'	7.29	125.55	109.50
53	b	1055	G	P-O5'-C5'	7.29	132.57	120.90
53	b	2051	A	N9-C1'-C2'	-7.26	104.02	112.00
53	b	1300	G	O4'-C1'-N9	-7.25	102.40	108.20
53	b	247	G	N9-C1'-C2'	7.24	123.41	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	277	G	C2'-C3'-O3'	7.22	125.39	109.50
53	b	1967	C	N1-C1'-C2'	7.22	123.39	114.00
53	b	1057	A	C2'-C3'-O3'	7.22	125.38	109.50
53	b	2439	A	N9-C1'-C2'	-7.21	104.07	112.00
29	c	156	ARG	NE-CZ-NH2	-7.20	116.70	120.30
53	b	1300	G	N9-C1'-C2'	7.20	123.36	114.00
53	b	957	C	N1-C1'-C2'	7.16	123.31	114.00
53	b	242	G	O4'-C1'-N9	7.14	113.91	108.20
53	b	2541	A	C2'-C3'-O3'	7.13	125.19	109.50
53	b	2178	C	C4'-C3'-O3'	7.12	127.23	113.00
53	b	1076	C	N1-C1'-C2'	7.10	123.23	114.00
53	b	1055	G	N9-C1'-C2'	7.10	123.23	114.00
53	b	2160	C	O4'-C1'-N1	7.08	113.87	108.20
53	b	574	A	N9-C1'-C2'	7.07	123.19	114.00
53	b	603	A	O4'-C1'-N9	-7.06	102.56	108.20
53	b	2455	G	OP2-P-O3'	7.05	120.70	105.20
53	b	1698	A	N9-C1'-C2'	7.02	123.13	114.00
53	b	1088	A	C4'-C3'-O3'	-7.02	94.66	109.40
53	b	500	G	N9-C1'-C2'	-7.02	104.28	112.00
53	b	574	A	O4'-C1'-N9	-7.01	102.59	108.20
53	b	2205	A	C2'-C3'-O3'	7.00	124.90	113.70
53	b	2796	U	N1-C1'-C2'	6.98	123.07	114.00
53	b	873	C	C2'-C3'-O3'	6.98	124.86	113.70
53	b	1349	C	N3-C2-O2	-6.98	117.02	121.90
53	b	1392	A	O4'-C1'-N9	6.97	113.78	108.20
53	b	2661	G	N9-C1'-C2'	6.94	123.02	114.00
53	b	158	U	N1-C1'-C2'	6.89	122.96	114.00
53	b	559	G	N9-C1'-C2'	-6.87	104.44	112.00
53	b	2702	G	C2'-C3'-O3'	6.85	124.66	113.70
53	b	1156	A	N9-C1'-C2'	6.85	122.90	114.00
53	b	1080	A	C5'-C4'-O4'	6.83	117.30	109.10
34	h	61	VAL	N-CA-C	6.83	129.45	111.00
53	b	1918	A	N9-C1'-C2'	-6.83	104.49	112.00
53	b	1377	G	N9-C1'-C2'	6.81	122.86	114.00
53	b	1069	A	C1'-O4'-C4'	-6.81	104.45	109.90
53	b	215	G	N9-C1'-C2'	6.80	122.84	114.00
53	b	564	C	N1-C1'-C2'	6.80	122.84	114.00
53	b	1080	A	C1'-O4'-C4'	-6.77	104.48	109.90
53	b	2879	A	N9-C1'-C2'	6.77	122.80	114.00
53	b	2304	G	C2'-C3'-O3'	6.76	124.52	113.70
53	b	2012	G	C2'-C3'-O3'	6.76	124.52	113.70
53	b	2530	A	N9-C1'-C2'	6.75	122.78	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	783	A	O5'-P-OP1	-6.74	99.64	105.70
53	b	2425	A	N9-C1'-C2'	6.73	122.75	114.00
53	b	544	C	O4'-C1'-N1	6.72	113.58	108.20
53	b	2455	G	OP1-P-O3'	-6.70	90.46	105.20
53	b	388	G	C1'-O4'-C4'	-6.70	104.54	109.90
53	b	1078	U	C2'-C3'-O3'	6.69	124.41	113.70
53	b	2272	U	N1-C1'-C2'	6.69	122.70	114.00
53	b	2162	G	C1'-O4'-C4'	-6.69	104.55	109.90
52	a	15	A	N9-C1'-C2'	6.68	122.68	114.00
53	b	2118	U	C1'-O4'-C4'	-6.66	104.57	109.90
53	b	1508	A	N9-C1'-C2'	6.64	122.63	114.00
53	b	2797	U	O4'-C1'-C2'	-6.64	99.16	105.80
53	b	2518	A	O4'-C1'-N9	-6.61	102.91	108.20
53	b	2589	A	C2'-C3'-O3'	6.60	124.26	113.70
53	b	1349	C	C5'-C4'-O4'	6.57	116.98	109.10
53	b	1311	G	N9-C1'-C2'	-6.56	104.78	112.00
53	b	2127	G	N9-C1'-C2'	6.56	122.53	114.00
53	b	1098	A	C2'-C3'-O3'	6.54	124.16	113.70
53	b	1392	A	C1'-O4'-C4'	-6.52	104.69	109.90
53	b	241	A	O4'-C1'-N9	-6.48	103.02	108.20
53	b	1301	A	C1'-O4'-C4'	-6.47	104.72	109.90
53	b	2564	A	N9-C1'-C2'	6.46	122.39	114.00
53	b	387	U	N1-C1'-C2'	6.45	122.38	114.00
50	A	1158	C	N3-C2-O2	-6.42	117.40	121.90
53	b	1023	U	C5'-C4'-O4'	6.40	116.78	109.10
53	b	450	G	N9-C1'-C2'	-6.38	104.98	112.00
53	b	477	A	N9-C1'-C2'	6.35	122.25	114.00
53	b	986	C	N1-C1'-C2'	6.35	122.25	114.00
53	b	1348	C	C4'-C3'-O3'	6.33	125.67	113.00
53	b	1080	A	O4'-C4'-C3'	-6.33	97.67	104.00
53	b	87	U	C2'-C3'-O3'	6.32	123.81	113.70
53	b	464	U	N1-C1'-C2'	6.31	122.20	114.00
53	b	877	A	O4'-C4'-C3'	-6.30	97.70	104.00
53	b	1087	G	O4'-C1'-N9	6.28	113.23	108.20
53	b	196	A	O4'-C1'-N9	6.27	113.21	108.20
53	b	1704	C	C2'-C3'-O3'	6.25	123.70	113.70
52	a	3	C	OP1-P-O3'	6.25	118.94	105.20
53	b	2798	U	O4'-C1'-N1	6.25	113.20	108.20
53	b	448	U	N1-C1'-C2'	-6.24	105.14	112.00
53	b	1055	G	O5'-P-OP1	6.24	118.19	110.70
53	b	1773	A	N9-C1'-C2'	-6.23	105.15	112.00
53	b	674	G	N9-C1'-C2'	-6.22	105.16	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	z	15	THR	C-N-CD	6.21	141.45	128.40
53	b	2178	C	C4'-C3'-C2'	-6.21	96.39	102.60
53	b	2822	G	N9-C1'-C2'	6.20	122.06	114.00
53	b	2873	A	O4'-C1'-N9	6.19	113.15	108.20
53	b	2178	C	O4'-C4'-C3'	-6.19	97.81	104.00
53	b	1496	A	N9-C1'-C2'	6.18	122.04	114.00
53	b	1618	A	N9-C1'-C2'	6.18	122.03	114.00
53	b	2848	G	N9-C1'-C2'	-6.18	105.21	112.00
53	b	1103	A	N9-C1'-C2'	-6.16	105.22	112.00
53	b	2128	G	C4'-C3'-O3'	6.14	125.29	113.00
53	b	2889	C	N1-C1'-C2'	6.14	121.99	114.00
34	h	67	ALA	N-CA-C	6.14	127.59	111.00
53	b	458	G	O4'-C1'-N9	6.14	113.11	108.20
53	b	1266	G	C1'-O4'-C4'	-6.14	104.99	109.90
53	b	1927	A	N9-C1'-C2'	6.13	121.97	114.00
53	b	2750	A	C5'-C4'-O4'	6.13	116.46	109.10
53	b	1459	G	O4'-C1'-N9	6.12	113.10	108.20
52	a	66	A	C2'-C3'-O3'	6.12	123.49	113.70
50	A	390	U	N3-C2-O2	-6.11	117.92	122.20
53	b	273	G	N9-C1'-C2'	6.11	121.94	114.00
53	b	2336	A	N9-C1'-C2'	6.11	121.94	114.00
53	b	2446	G	N9-C1'-C2'	-6.10	105.29	112.00
53	b	576	U	N1-C1'-C2'	6.09	121.92	114.00
53	b	1125	G	N9-C1'-C2'	6.09	121.92	114.00
53	b	786	C	N1-C1'-C2'	6.07	121.90	114.00
53	b	801	G	C2'-C3'-O3'	6.07	123.42	113.70
53	b	2431	U	N1-C1'-C2'	-6.07	105.33	112.00
53	b	2800	A	C4'-C3'-O3'	6.07	125.13	113.00
53	b	1088	A	P-O5'-C5'	6.06	130.60	120.90
53	b	1033	U	C3'-C2'-C1'	6.04	106.33	101.50
50	A	365	U	C2-N1-C1'	6.04	124.94	117.70
53	b	1395	A	C1'-O4'-C4'	-6.02	105.08	109.90
53	b	1980	G	N9-C1'-C2'	-6.02	105.38	112.00
53	b	1756	G	C5'-C4'-O4'	6.02	116.32	109.10
53	b	974	G	O4'-C1'-N9	6.01	113.01	108.20
53	b	1400	U	N1-C1'-C2'	6.01	121.81	114.00
53	b	2210	U	O4'-C1'-N1	-6.01	103.39	108.20
53	b	454	A	N9-C1'-C2'	5.99	121.79	114.00
53	b	914	G	N9-C1'-C2'	-5.99	105.41	112.00
53	b	1675	C	N1-C1'-C2'	5.99	121.78	114.00
53	b	2798	U	C1'-O4'-C4'	-5.98	105.11	109.90
53	b	385	C	N1-C1'-C2'	5.98	121.78	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	2249	U	N1-C1'-C2'	-5.98	105.43	112.00
53	b	800	A	N9-C1'-C2'	5.97	121.77	114.00
31	e	61	ARG	N-CA-C	5.97	127.12	111.00
53	b	1600	C	N1-C1'-C2'	5.97	121.76	114.00
53	b	2654	A	N9-C1'-C2'	5.97	121.76	114.00
53	b	877	A	C4'-C3'-C2'	-5.97	96.63	102.60
53	b	2567	G	N9-C1'-C2'	5.96	121.75	114.00
30	d	4	LEU	CB-CG-CD1	5.96	121.13	111.00
53	b	253	C	N1-C1'-C2'	-5.95	105.45	112.00
53	b	1698	A	O4'-C1'-N9	-5.94	103.45	108.20
53	b	1057	A	C4'-C3'-O3'	5.94	124.88	113.00
53	b	2271	G	N9-C1'-C2'	5.93	121.71	114.00
53	b	196	A	N9-C1'-C2'	-5.93	105.48	112.00
53	b	1249	U	N1-C1'-C2'	5.93	121.71	114.00
53	b	465	G	N9-C1'-C2'	5.92	121.69	114.00
53	b	479	A	N9-C1'-C2'	5.91	121.69	114.00
53	b	1756	G	C5'-C4'-C3'	5.91	125.46	116.00
53	b	2131	U	C5-C6-N1	-5.91	119.75	122.70
53	b	2025	C	N1-C1'-C2'	5.90	121.67	114.00
53	b	1057	A	C4'-C3'-C2'	-5.89	96.71	102.60
53	b	1078	U	N1-C1'-C2'	5.89	121.65	114.00
53	b	1204	A	O4'-C1'-N9	-5.88	103.50	108.20
53	b	608	A	N9-C1'-C2'	5.88	121.64	114.00
53	b	1253	A	N9-C1'-C2'	5.87	121.63	114.00
53	b	1814	G	N9-C1'-C2'	5.86	121.61	114.00
53	b	51	G	N9-C1'-C2'	-5.86	105.56	112.00
53	b	2329	U	N1-C1'-C2'	-5.85	105.56	112.00
53	b	2161	C	C1'-O4'-C4'	-5.84	105.23	109.90
53	b	2180	U	O4'-C1'-C2'	-5.84	99.96	105.80
53	b	877	A	C5'-C4'-O4'	5.83	116.10	109.10
53	b	2307	G	N9-C1'-C2'	5.83	121.58	114.00
53	b	2873	A	C1'-O4'-C4'	-5.83	105.24	109.90
53	b	1272	A	C4-N9-C1'	-5.83	115.81	126.30
53	b	84	A	N9-C1'-C2'	-5.83	105.59	112.00
53	b	1070	A	N9-C1'-C2'	5.83	121.57	114.00
53	b	1100	C	C4'-C3'-O3'	5.83	124.65	113.00
53	b	1056	G	N9-C1'-C2'	5.82	121.57	114.00
53	b	1495	A	N9-C1'-C2'	5.82	121.57	114.00
53	b	2750	A	N9-C1'-C2'	5.81	121.55	114.00
53	b	390	U	N1-C1'-C2'	-5.81	105.61	112.00
53	b	2160	C	O4'-C4'-C3'	-5.80	98.20	104.00
53	b	1087	G	C5'-C4'-C3'	5.79	125.26	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	411	G	N9-C1'-C2'	5.79	121.52	114.00
53	b	985	C	N1-C1'-C2'	5.78	121.52	114.00
52	a	33	G	N9-C1'-C2'	-5.77	105.65	112.00
53	b	1058	U	O4'-C1'-N1	5.77	112.82	108.20
53	b	704	G	N9-C1'-C2'	-5.77	105.65	112.00
53	b	1055	G	O5'-P-OP2	-5.77	100.50	105.70
53	b	1348	C	N1-C1'-C2'	-5.77	105.65	112.00
53	b	1801	A	N9-C1'-C2'	5.77	121.50	114.00
53	b	2172	U	O4'-C1'-N1	5.77	112.82	108.20
53	b	1103	A	O4'-C1'-N9	5.77	112.81	108.20
53	b	1996	C	N1-C1'-C2'	5.77	121.50	114.00
53	b	1761	C	N1-C1'-C2'	5.76	121.49	114.00
53	b	2340	A	C8-N9-C1'	-5.76	117.33	127.70
53	b	2151	U	C4'-C3'-O3'	5.76	124.51	113.00
53	b	75	G	O4'-C1'-C2'	-5.75	100.05	105.80
53	b	2178	C	O4'-C1'-N1	5.74	112.79	108.20
53	b	1133	A	O4'-C1'-N9	5.73	112.79	108.20
53	b	1678	A	N9-C1'-C2'	-5.73	105.70	112.00
49	z	16	PRO	CB-CA-C	5.73	126.32	112.00
53	b	479	A	C2'-C3'-O3'	5.72	122.86	113.70
53	b	1401	G	N9-C1'-C2'	5.69	121.40	114.00
53	b	400	G	N9-C1'-C2'	5.68	121.39	114.00
52	a	42	C	N1-C1'-C2'	5.68	121.38	114.00
50	A	1158	C	C6-N1-C2	-5.67	118.03	120.30
53	b	400	G	C2'-C3'-O3'	5.67	122.77	113.70
53	b	280	U	N1-C1'-C2'	5.66	121.36	114.00
53	b	1060	U	C3'-C2'-C1'	-5.66	96.97	101.50
44	s	88	ARG	NE-CZ-NH1	-5.66	117.47	120.30
53	b	1754	A	N9-C1'-C2'	5.66	121.36	114.00
53	b	447	A	N9-C1'-C2'	-5.65	105.79	112.00
53	b	1057	A	O4'-C1'-C2'	-5.64	100.16	105.80
53	b	1839	G	O4'-C1'-C2'	-5.64	100.16	105.80
53	b	2551	C	N1-C1'-C2'	-5.64	105.80	112.00
53	b	423	A	N9-C1'-C2'	5.64	121.33	114.00
53	b	1097	U	C5'-C4'-O4'	5.61	115.84	109.10
53	b	830	G	N9-C1'-C2'	5.61	121.29	114.00
53	b	1098	A	O4'-C4'-C3'	-5.60	98.40	104.00
53	b	1103	A	C4'-C3'-C2'	-5.58	97.02	102.60
53	b	845	A	C4'-C3'-O3'	5.58	124.15	113.00
50	A	365	U	N1-C2-O2	5.57	126.70	122.80
53	b	196	A	C1'-O4'-C4'	-5.56	105.45	109.90
53	b	877	A	C4'-C3'-O3'	5.54	124.09	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	2266	A	N9-C1'-C2'	5.53	121.19	114.00
53	b	544	C	C1'-O4'-C4'	-5.53	105.48	109.90
53	b	410	G	C2'-C3'-O3'	5.53	122.54	113.70
53	b	1055	G	C3'-C2'-C1'	5.53	105.92	101.50
53	b	1069	A	O4'-C1'-C2'	-5.53	100.27	105.80
53	b	2252	G	N9-C1'-C2'	-5.52	105.93	112.00
53	b	531	C	N1-C1'-C2'	5.52	121.17	114.00
53	b	777	G	C2'-C3'-O3'	5.52	122.53	113.70
53	b	2877	G	N9-C1'-C2'	-5.52	105.93	112.00
53	b	866	A	O4'-C1'-C2'	-5.51	100.29	105.80
53	b	1234	U	N1-C1'-C2'	5.51	121.16	114.00
53	b	1758	U	N1-C1'-C2'	5.50	121.15	114.00
53	b	2211	A	C4'-C3'-O3'	-5.50	97.86	109.40
53	b	62	U	O4'-C1'-N1	5.49	112.59	108.20
53	b	791	C	N1-C1'-C2'	5.48	121.13	114.00
53	b	571	U	O4'-C1'-N1	5.47	112.58	108.20
53	b	1023	U	C5'-C4'-C3'	5.47	124.76	116.00
53	b	2590	A	C5'-C4'-O4'	5.47	115.67	109.10
53	b	2172	U	C2'-C3'-O3'	-5.47	97.47	109.50
53	b	1104	C	C5'-C4'-O4'	5.46	115.66	109.10
53	b	1287	A	N9-C1'-C2'	5.46	121.09	114.00
50	A	230	G	C4-N9-C1'	5.46	133.59	126.50
53	b	1239	G	N9-C1'-C2'	-5.45	106.00	112.00
53	b	2152	G	C5'-C4'-O4'	5.45	115.64	109.10
53	b	979	A	C4'-C3'-C2'	-5.45	97.15	102.60
53	b	1204	A	O4'-C4'-C3'	-5.45	98.55	104.00
53	b	1054	A	C4'-C3'-O3'	5.44	123.88	113.00
53	b	372	G	O4'-C1'-N9	5.43	112.55	108.20
53	b	2340	A	C4-N9-C1'	5.43	136.07	126.30
53	b	9	G	C2'-C3'-O3'	5.42	122.37	113.70
53	b	1032	A	N9-C1'-C2'	-5.42	106.04	112.00
53	b	2656	U	N1-C1'-C2'	-5.42	106.04	112.00
53	b	2160	C	N1-C1'-C2'	-5.41	106.05	112.00
53	b	2614	A	N9-C1'-C2'	-5.40	106.06	112.00
53	b	119	A	O4'-C1'-N9	-5.40	103.88	108.20
53	b	388	G	O4'-C4'-C3'	-5.38	98.62	104.00
53	b	1969	A	N9-C1'-C2'	5.37	120.98	114.00
53	b	2173	A	O5'-P-OP2	-5.37	100.87	105.70
53	b	401	A	C5'-C4'-O4'	5.36	115.53	109.10
53	b	2152	G	C8-N9-C1'	-5.35	120.05	127.00
53	b	805	G	N9-C1'-C2'	5.34	120.94	114.00
53	b	1205	A	C4'-C3'-O3'	-5.34	98.18	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	910	A	N9-C1'-C2'	5.34	120.94	114.00
53	b	1103	A	O4'-C4'-C3'	-5.34	98.66	104.00
53	b	2449	U	O4'-C1'-N1	5.33	112.47	108.20
53	b	1865	U	N1-C1'-C2'	-5.33	106.14	112.00
53	b	2288	A	N9-C1'-C2'	5.33	120.92	114.00
53	b	1058	U	N1-C1'-C2'	5.32	120.92	114.00
53	b	1081	U	O4'-C4'-C3'	-5.32	98.68	104.00
53	b	1569	A	N9-C1'-C2'	5.32	120.91	114.00
53	b	2866	U	N1-C1'-C2'	5.31	120.91	114.00
50	A	230	G	C6-C5-N7	5.31	133.58	130.40
53	b	1425	G	N9-C1'-C2'	5.31	120.90	114.00
53	b	925	A	N9-C1'-C2'	-5.29	106.18	112.00
53	b	583	G	N9-C1'-C2'	-5.29	106.18	112.00
53	b	1238	G	C2'-C3'-O3'	5.29	122.16	113.70
53	b	801	G	C5'-C4'-O4'	5.29	115.45	109.10
36	k	70	ARG	NE-CZ-NH2	-5.28	117.66	120.30
53	b	1079	C	C3'-C2'-C1'	5.28	105.72	101.50
53	b	2869	G	N9-C1'-C2'	5.26	120.84	114.00
53	b	157	C	N1-C1'-C2'	5.26	120.83	114.00
53	b	531	C	O4'-C1'-N1	-5.25	104.00	108.20
53	b	934	U	C5'-C4'-O4'	5.25	115.40	109.10
53	b	1585	C	N1-C1'-C2'	5.25	120.83	114.00
53	b	1461	C	N1-C1'-C2'	5.25	120.82	114.00
53	b	2128	G	O4'-C1'-C2'	-5.24	100.56	105.80
53	b	1204	A	C4'-C3'-O3'	-5.23	98.41	109.40
53	b	674	G	C4'-C3'-C2'	-5.23	97.37	102.60
53	b	2238	G	N9-C1'-C2'	5.23	120.80	114.00
53	b	1102	C	C2-N1-C1'	5.22	124.55	118.80
50	A	1322	C	C2-N1-C1'	5.22	124.54	118.80
53	b	2127	G	O4'-C1'-N9	-5.21	104.03	108.20
53	b	989	G	N9-C1'-C2'	-5.21	106.27	112.00
53	b	1088	A	C1'-O4'-C4'	5.21	114.07	109.90
34	h	66	ASN	N-CA-C	5.20	125.05	111.00
53	b	365	U	C4'-C3'-O3'	5.20	123.40	113.00
53	b	1238	G	N9-C1'-C2'	-5.20	106.28	112.00
53	b	1583	A	N9-C1'-C2'	-5.19	106.29	112.00
53	b	2340	A	N9-C1'-C2'	5.19	120.75	114.00
53	b	372	G	C1'-O4'-C4'	-5.19	105.75	109.90
53	b	1393	A	N9-C1'-C2'	5.19	120.74	114.00
53	b	782	A	C4'-C3'-O3'	-5.17	98.54	109.40
53	b	1344	U	N1-C1'-C2'	5.17	120.71	114.00
52	a	3	C	P-O3'-C3'	-5.16	113.50	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	q	11	ARG	NE-CZ-NH2	-5.16	117.72	120.30
53	b	250	G	O4'-C1'-N9	-5.16	104.08	108.20
53	b	43	G	N9-C1'-C2'	5.15	120.70	114.00
53	b	1133	A	C1'-O4'-C4'	-5.15	105.78	109.90
53	b	2020	A	N9-C1'-C2'	-5.15	106.33	112.00
53	b	783	A	O4'-C4'-C3'	-5.15	98.85	104.00
53	b	1224	U	N1-C1'-C2'	5.15	120.69	114.00
54	v	33	U	P-O3'-C3'	5.14	125.87	119.70
50	A	754	C	C2-N1-C1'	5.14	124.45	118.80
53	b	2174	C	N1-C1'-C2'	5.14	120.68	114.00
53	b	395	U	N1-C1'-C2'	-5.13	106.36	112.00
53	b	1801	A	O4'-C1'-N9	-5.13	104.10	108.20
53	b	809	G	N9-C1'-C2'	5.12	120.66	114.00
45	t	3	ARG	NE-CZ-NH1	5.12	122.86	120.30
53	b	2210	U	C4'-C3'-O3'	-5.12	98.66	109.40
53	b	1780	A	N9-C1'-C2'	5.11	120.65	114.00
53	b	1801	A	C4'-C3'-O3'	-5.10	98.70	109.40
53	b	2330	G	O4'-C1'-C2'	-5.10	100.70	105.80
53	b	2384	U	C3'-C2'-C1'	5.09	105.58	101.50
53	b	2180	U	N1-C1'-C2'	-5.09	106.40	112.00
53	b	24	G	N9-C1'-C2'	5.09	120.62	114.00
53	b	450	G	C2'-C3'-O3'	5.09	121.84	113.70
53	b	356	G	N9-C1'-C2'	5.08	120.61	114.00
53	b	2518	A	N9-C1'-C2'	5.08	120.61	114.00
53	b	995	C	N1-C1'-C2'	5.08	120.61	114.00
43	r	10	LYS	CD-CE-NZ	5.08	123.38	111.70
53	b	877	A	C2'-C3'-O3'	5.08	121.83	113.70
53	b	1427	A	N9-C1'-C2'	5.08	120.60	114.00
53	b	1815	A	N9-C1'-C2'	5.08	120.60	114.00
53	b	2576	G	N9-C1'-C2'	5.08	120.60	114.00
53	b	254	G	N9-C1'-C2'	-5.07	106.43	112.00
53	b	1330	C	N1-C1'-C2'	5.07	120.59	114.00
53	b	1804	C	C2'-C3'-O3'	5.07	121.81	113.70
53	b	1266	G	O4'-C1'-C2'	-5.06	100.74	105.80
34	h	31	VAL	C-N-CD	-5.06	109.47	120.60
53	b	2150	C	O4'-C1'-C2'	-5.06	100.74	105.80
53	b	436	C	C5'-C4'-O4'	5.06	115.17	109.10
53	b	2750	A	C2'-C3'-O3'	5.06	121.79	113.70
53	b	2588	G	N9-C1'-C2'	-5.06	106.44	112.00
53	b	2282	G	O4'-C1'-C2'	-5.05	100.75	105.80
53	b	873	C	N1-C1'-C2'	-5.05	106.45	112.00
53	b	896	A	O4'-C4'-C3'	-5.05	98.95	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	b	120	U	N1-C1'-C2'	5.03	120.53	114.00
53	b	914	G	C4'-C3'-C2'	-5.03	97.57	102.60
53	b	896	A	N9-C1'-C2'	-5.02	106.47	112.00
53	b	94	A	C4-N9-C1'	5.02	135.34	126.30
53	b	2169	A	C3'-C2'-C1'	5.02	105.51	101.50
53	b	2238	G	O4'-C1'-N9	-5.02	104.19	108.20
53	b	2497	A	N9-C1'-C2'	-5.02	106.48	112.00
53	b	94	A	C8-N9-C1'	-5.00	118.69	127.70

There are no chirality outliers.

All (80) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	2	3	LYS	Peptide
11	L	71	HIS	Peptide
52	a	45	A	Sidechain
53	b	1057	A	Sidechain
53	b	1060	U	Sidechain
53	b	1069	A	Sidechain
53	b	1079	C	Sidechain
53	b	1088	A	Sidechain
53	b	1102	C	Sidechain
53	b	1103	A	Sidechain
53	b	1104	C	Sidechain
53	b	1143	A	Sidechain
53	b	1186	G	Sidechain
53	b	119	A	Sidechain
53	b	1204	A	Sidechain
53	b	1225	G	Sidechain
53	b	1266	G	Sidechain
53	b	1272	A	Sidechain
53	b	1275	A	Sidechain
53	b	1300	G	Sidechain
53	b	1392	A	Sidechain
53	b	1395	A	Sidechain
53	b	1509	A	Sidechain
53	b	1667	G	Sidechain
53	b	1678	A	Sidechain
53	b	1698	A	Sidechain
53	b	1759	A	Sidechain
53	b	1774	C	Sidechain
53	b	1829	A	Sidechain

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Mol	Chain	Res	Type	Group
53	b	1927	A	Sidechain
53	b	1943	U	Sidechain
53	b	196	A	Sidechain
53	b	2092	U	Sidechain
53	b	210	C	Sidechain
53	b	2118	U	Sidechain
53	b	2159	G	Sidechain
53	b	2160	C	Sidechain
53	b	2161	C	Sidechain
53	b	2178	C	Sidechain
53	b	2210	U	Sidechain
53	b	2211	A	Sidechain
53	b	2282	G	Sidechain
53	b	2330	G	Sidechain
53	b	241	A	Sidechain
53	b	242	G	Sidechain
53	b	2449	U	Sidechain
53	b	246	C	Sidechain
53	b	247	G	Sidechain
53	b	25	U	Sidechain
53	b	250	G	Sidechain
53	b	2517	C	Sidechain
53	b	2518	A	Sidechain
53	b	2564	A	Sidechain
53	b	2590	A	Sidechain
53	b	2597	G	Sidechain
53	b	2615	U	Sidechain
53	b	2750	A	Sidechain
53	b	2766	A	Sidechain
53	b	277	G	Sidechain
53	b	2796	U	Sidechain
53	b	2799	A	Sidechain
53	b	2886	A	Sidechain
53	b	388	G	Sidechain
53	b	574	A	Sidechain
53	b	603	A	Sidechain
53	b	674	G	Sidechain
53	b	75	G	Sidechain
53	b	779	U	Sidechain
53	b	782	A	Sidechain
53	b	783	A	Sidechain
53	b	788	A	Sidechain

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Mol	Chain	Res	Type	Group
53	b	801	G	Sidechain
53	b	959	A	Sidechain
53	b	973	A	Sidechain
53	b	979	A	Sidechain
29	c	232	HIS	Peptide
30	d	151	THR	Peptide
36	k	34	GLY	Peptide
37	l	102	GLY	Peptide
43	r	50	GLY	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1704	0	1732	61	0
2	C	1624	0	1699	49	0
3	D	1643	0	1710	83	0
4	E	1105	0	1148	44	0
5	F	817	0	808	32	0
6	G	1174	0	1230	29	0
7	H	979	0	1034	32	0
8	I	1022	0	1067	125	0
9	J	786	0	828	42	0
10	K	877	0	887	34	0
11	L	955	0	1019	35	0
12	M	876	0	935	27	0
13	N	774	0	827	39	0
14	O	716	0	742	14	0
15	P	649	0	663	119	0
16	Q	648	0	691	30	0
17	R	455	0	478	23	0
18	S	637	0	665	36	0
19	T	665	0	714	26	0
20	U	425	0	449	32	0
21	0	625	0	652	6	0
22	1	501	0	531	12	0
23	2	449	0	488	12	0
24	3	444	0	457	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	4	409	0	440	0	0
26	6	377	0	418	2	0
27	7	504	0	572	2	0
28	8	302	0	343	6	0
29	c	2082	0	2154	0	0
30	d	1565	0	1616	0	0
31	e	1552	0	1619	0	0
32	f	1410	0	1444	0	0
33	g	1323	0	1371	0	0
34	h	1111	0	1148	0	0
35	j	1129	0	1162	0	0
36	k	938	0	1012	0	0
37	l	1053	0	1129	0	0
38	m	1063	0	1143	0	0
39	n	960	0	1000	0	0
40	o	892	0	923	0	0
41	p	917	0	960	0	0
42	q	947	0	1019	0	0
43	r	816	0	839	0	0
44	s	857	0	922	0	0
45	t	738	0	807	0	0
46	u	779	0	831	0	0
47	w	753	0	780	0	0
48	y	569	0	581	0	0
49	z	203	0	198	0	0
50	A	32831	0	16518	889	0
51	X	232	0	118	22	0
52	a	2528	0	1283	0	0
53	b	62321	0	31336	0	0
54	v	1623	0	823	0	0
All	All	143334	0	95963	1594	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 34.

All (1594) 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)
50:A:230:G:C6	50:A:230:G:C5	1.82	1.68
8:I:111:GLU:CB	50:A:1348:U:C4'	1.75	1.65
15:P:70:ARG:HG2	50:A:375:U:C5'	1.15	1.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:230:G:N3	50:A:230:G:C4	1.76	1.50
50:A:230:G:C5	50:A:230:G:C4	1.75	1.50
50:A:230:G:N3	50:A:230:G:C2	1.76	1.50
50:A:230:G:C2	50:A:230:G:N1	1.80	1.48
15:P:70:ARG:CG	50:A:375:U:H5'	1.08	1.45
50:A:230:G:C6	50:A:230:G:N1	1.82	1.44
8:I:111:GLU:CB	50:A:1348:U:H4'	0.95	1.42
8:I:111:GLU:CG	50:A:1348:U:H4'	1.50	1.40
15:P:5:ARG:CD	50:A:377:G:OP1	1.71	1.38
50:A:996:A:C5	50:A:997:U:H5	1.42	1.38
15:P:12:LYS:HG3	50:A:392:C:P	1.66	1.34
8:I:111:GLU:HB3	50:A:1348:U:C5'	1.58	1.31
10:K:88:PRO:CG	20:U:28:LEU:HD11	1.59	1.31
8:I:105:ARG:HD3	8:I:106:ASP:N	1.46	1.30
10:K:88:PRO:HG3	20:U:28:LEU:CD1	1.59	1.30
8:I:111:GLU:N	50:A:1348:U:P	2.05	1.29
15:P:5:ARG:HD3	50:A:377:G:P	1.71	1.29
15:P:3:THR:CG2	50:A:377:G:OP2	1.82	1.27
50:A:996:A:C5	50:A:997:U:C5	2.24	1.26
8:I:111:GLU:N	50:A:1348:U:O5'	1.72	1.22
8:I:111:GLU:HB3	50:A:1348:U:C4'	1.44	1.22
50:A:996:A:C6	50:A:997:U:C5	2.30	1.18
15:P:70:ARG:HH12	50:A:374:A:C2'	1.52	1.16
8:I:11:ARG:HA	8:I:105:ARG:HH22	1.11	1.15
4:E:125:LYS:NZ	50:A:9:G:OP2	1.80	1.15
8:I:11:ARG:HA	8:I:105:ARG:NH2	1.63	1.13
8:I:111:GLU:CB	50:A:1348:U:C5'	2.18	1.13
15:P:13:LYS:N	50:A:392:C:OP1	1.82	1.12
8:I:111:GLU:HB2	50:A:1348:U:C4'	1.53	1.09
15:P:70:ARG:HH12	50:A:374:A:H2'	1.11	1.08
15:P:5:ARG:HD3	50:A:377:G:OP1	0.91	1.08
50:A:686:U:O4	50:A:703:G:O2'	1.73	1.07
15:P:3:THR:HG21	50:A:377:G:OP2	0.90	1.06
15:P:70:ARG:HB3	50:A:376:G:OP1	1.53	1.06
21:O:68:LEU:HD23	21:O:71:LEU:HD12	1.37	1.04
8:I:11:ARG:HH22	50:A:1347:G:N2	1.55	1.02
15:P:70:ARG:CG	50:A:375:U:C5'	1.84	1.01
7:H:4:ASP:OD1	7:H:76:ARG:NH1	1.94	1.00
3:D:9:LYS:NZ	50:A:542:G:OP1	1.95	0.99
19:T:73:ARG:NH2	50:A:261:U:OP2	1.95	0.99
1:B:72:LYS:NZ	1:B:164:ASP:OD2	1.94	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:11:ARG:HH22	50:A:1347:G:H22	1.08	0.97
17:R:52:ARG:NH1	50:A:664:G:OP1	1.97	0.96
5:F:38:ARG:NH1	5:F:96:VAL:O	1.97	0.96
15:P:3:THR:HG21	50:A:377:G:P	2.04	0.96
15:P:70:ARG:NH1	50:A:374:A:C2'	2.29	0.95
14:O:87:ARG:NH1	14:O:88:ARG:O	2.01	0.94
15:P:12:LYS:HA	50:A:392:C:OP1	1.68	0.94
19:T:68:LYS:NZ	50:A:224:U:OP1	2.01	0.94
50:A:997:U:C4	50:A:1044:A:N6	2.36	0.92
5:F:3:HIS:NE2	5:F:5:GLU:OE2	2.01	0.92
15:P:70:ARG:CG	50:A:375:U:H5''	1.97	0.92
8:I:94:ARG:NH2	50:A:1179:A:OP2	2.03	0.92
11:L:53:ARG:HH21	11:L:61:GLU:HG2	1.33	0.92
15:P:12:LYS:CA	50:A:392:C:OP1	2.18	0.91
8:I:111:GLU:HG2	50:A:1348:U:H4'	1.53	0.91
12:M:10:ASP:HB3	12:M:44:ILE:HG21	1.53	0.91
7:H:88:LYS:NZ	50:A:601:G:OP1	2.03	0.91
4:E:100:GLU:HA	4:E:121:ASN:HD21	1.35	0.90
8:I:95:SER:O	8:I:99:LYS:NZ	2.04	0.90
8:I:11:ARG:NE	8:I:106:ASP:OD1	2.05	0.90
15:P:5:ARG:NH1	50:A:377:G:OP1	2.02	0.90
5:F:42:TRP:HB3	5:F:45:ARG:HH21	1.36	0.90
15:P:6:LEU:O	50:A:376:G:C8	2.25	0.90
15:P:60:TRP:HZ3	50:A:228:A:O2'	1.54	0.90
8:I:111:GLU:CB	50:A:1348:U:O5'	2.19	0.89
8:I:11:ARG:CA	8:I:105:ARG:HH22	1.85	0.89
8:I:111:GLU:HB3	50:A:1348:U:H4'	1.02	0.89
8:I:105:ARG:HD3	8:I:106:ASP:H	1.36	0.89
8:I:11:ARG:NH2	50:A:1347:G:N2	2.21	0.89
4:E:28:ARG:NH2	50:A:1397:C:OP2	2.04	0.88
50:A:996:A:C4	50:A:997:U:C5	2.62	0.88
8:I:111:GLU:HB3	50:A:1348:U:H5'	1.55	0.88
22:1:7:ARG:CZ	22:1:56:LEU:HD22	2.03	0.88
50:A:1013:G:N2	50:A:1016:A:OP2	2.07	0.87
50:A:1266:G:N2	50:A:1269:A:OP2	2.06	0.87
9:J:46:LYS:NZ	9:J:48:ARG:HB3	1.88	0.87
3:D:21:LYS:NZ	50:A:429:U:O2'	2.09	0.86
8:I:113:LYS:NZ	8:I:120:ALA:O	2.09	0.86
15:P:12:LYS:HG3	50:A:392:C:OP1	1.73	0.86
3:D:69:ARG:NH1	50:A:402:G:OP2	2.09	0.86
50:A:996:A:C4	50:A:997:U:C6	2.65	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:23:LEU:HD12	11:L:29:LYS:HE2	1.59	0.85
19:T:43:LYS:HD2	19:T:86:ALA:HB2	1.58	0.85
20:U:27:VAL:C	20:U:28:LEU:HD22	1.95	0.85
8:I:56:MET:HG2	8:I:57:VAL:HG23	1.59	0.85
22:1:14:LEU:O	22:1:18:LEU:HG	1.77	0.84
12:M:102:LYS:NZ	50:A:953:G:O6	2.09	0.84
15:P:28:ARG:HE	15:P:29:ASN:HD21	1.23	0.84
50:A:1391:U:H2'	50:A:1392:G:H8	1.41	0.84
50:A:996:A:C2'	50:A:997:U:H5'	2.07	0.83
15:P:70:ARG:CB	50:A:376:G:OP1	2.26	0.83
16:Q:53:GLY:N	16:Q:56:ASP:OD2	2.09	0.83
18:S:36:ARG:NH1	50:A:1220:G:OP1	2.12	0.83
51:X:16:G:O2'	51:X:17:C:O5'	1.94	0.83
50:A:997:U:O4	50:A:1044:A:N6	2.12	0.82
11:L:50:LYS:NZ	50:A:521:G:OP1	2.13	0.82
4:E:40:ASP:OD2	4:E:44:ARG:NE	2.12	0.82
50:A:944:G:N1	50:A:1338:G:OP2	2.12	0.82
8:I:11:ARG:NH2	50:A:1347:G:H22	1.78	0.82
8:I:111:GLU:HB2	50:A:1348:U:H4'	1.15	0.82
6:G:101:ARG:NH1	50:A:939:G:OP1	2.12	0.81
1:B:138:ARG:O	1:B:142:LYS:NZ	2.11	0.81
3:D:181:PHE:HZ	3:D:184:LYS:HZ2	1.24	0.81
28:8:3:VAL:HG22	28:8:36:ARG:HB3	1.60	0.81
50:A:1070:U:O2	50:A:1106:G:N1	2.13	0.81
6:G:70:PRO:HA	6:G:141:HIS:HE1	1.42	0.81
15:P:28:ARG:NE	15:P:29:ASN:HD21	1.79	0.80
8:I:105:ARG:CD	8:I:106:ASP:N	2.40	0.80
51:X:19:C:H5''	51:X:19:C:O2	1.81	0.80
50:A:1346:A:N6	50:A:1375:A:OP2	2.14	0.80
11:L:72:ASN:ND2	11:L:102:ASP:O	2.14	0.79
23:2:5:ILE:CG2	23:2:57:VAL:HG13	2.13	0.79
50:A:1347:G:H5'	50:A:1348:U:O4'	1.83	0.79
50:A:446:G:H1	50:A:488:C:H42	1.31	0.79
8:I:11:ARG:HA	8:I:105:ARG:CZ	2.13	0.79
50:A:510:A:HO2'	50:A:542:G:HO2'	1.30	0.79
3:D:139:ASN:H	3:D:182:LYS:HA	1.48	0.79
50:A:181:A:N6	50:A:195:A:OP2	2.16	0.79
15:P:70:ARG:NH1	50:A:374:A:H2'	1.92	0.79
15:P:60:TRP:HZ3	50:A:228:A:HO2'	0.80	0.79
8:I:105:ARG:NH1	8:I:106:ASP:HB2	1.97	0.79
18:S:5:LYS:HE2	18:S:6:LYS:HE2	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1072:G:O6	50:A:1102:A:N6	2.15	0.78
50:A:1073:U:H3	50:A:1102:A:H61	1.28	0.78
15:P:12:LYS:C	50:A:392:C:OP1	2.22	0.78
15:P:22:ALA:HA	15:P:33:ILE:HG13	1.65	0.78
8:I:113:LYS:HZ1	8:I:117:LEU:HD22	1.46	0.78
15:P:70:ARG:HG2	50:A:375:U:C4'	2.13	0.78
50:A:373:A:H61	50:A:482:A:H5'	1.47	0.78
8:I:113:LYS:HE3	8:I:117:LEU:HD13	1.66	0.78
50:A:614:C:N4	50:A:626:G:O6	2.17	0.78
15:P:12:LYS:HG3	50:A:392:C:OP2	1.82	0.77
15:P:6:LEU:O	50:A:376:G:N9	2.18	0.77
8:I:63:TYR:HE2	50:A:1130:A:H5''	1.48	0.77
15:P:12:LYS:HD2	50:A:392:C:C5'	2.15	0.77
15:P:60:TRP:CZ3	50:A:228:A:O2'	2.34	0.77
9:J:9:ARG:NH1	9:J:71:LEU:HD21	1.99	0.77
50:A:1498:U:OP2	51:X:15:G:O2'	2.03	0.77
13:N:15:LEU:HD23	13:N:18:LYS:HD2	1.66	0.77
50:A:251:G:H4'	50:A:252:U:H5'	1.67	0.76
1:B:101:THR:N	1:B:174:GLU:OE2	2.16	0.76
15:P:12:LYS:HD2	50:A:392:C:H5'	1.67	0.76
15:P:17:TYR:CE2	50:A:375:U:O2'	2.39	0.76
3:D:87:GLU:OE1	3:D:187:ARG:NH2	2.17	0.76
15:P:13:LYS:HE2	50:A:392:C:H4'	1.67	0.76
51:X:16:G:C2	51:X:17:C:C5	2.74	0.76
50:A:1423:G:O6	50:A:1476:A:N6	2.18	0.76
50:A:457:G:O6	50:A:475:C:N4	2.19	0.76
5:F:6:ILE:HD11	5:F:71:ILE:HD11	1.67	0.76
50:A:69:G:O6	50:A:98:A:N6	2.20	0.75
4:E:12:GLU:OE2	4:E:63:MET:HG2	1.85	0.75
7:H:99:GLY:HA2	7:H:129:ALA:HB3	1.66	0.75
5:F:10:VAL:HB	5:F:58:HIS:HB3	1.69	0.75
18:S:32:THR:HG22	18:S:34:SER:H	1.52	0.75
2:C:160:GLU:HG3	2:C:161:ILE:HG12	1.69	0.75
2:C:31:ASN:OD1	2:C:58:ARG:NH1	2.20	0.75
9:J:70:HIS:HB2	9:J:72:ARG:HH12	1.51	0.75
8:I:105:ARG:HH11	8:I:106:ASP:H	1.34	0.75
1:B:187:ASP:HB3	1:B:203:ASP:HB3	1.69	0.74
1:B:45:THR:HG22	1:B:200:PRO:HG2	1.69	0.74
8:I:111:GLU:CA	50:A:1348:U:O5'	2.35	0.74
50:A:1347:G:H5'	50:A:1348:U:H6	1.53	0.74
3:D:43:ARG:NH2	50:A:512:U:OP1	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:28:ARG:HH21	12:M:62:PHE:HB2	1.53	0.73
23:2:5:ILE:CD1	23:2:40:ASP:OD1	2.36	0.73
14:O:79:ARG:HD2	14:O:82:GLU:OE2	1.88	0.73
50:A:1240:U:H5''	50:A:1241:G:OP2	1.88	0.73
50:A:201:G:HO2'	50:A:469:C:HO2'	1.35	0.73
50:A:374:A:H1'	50:A:451:A:P	2.28	0.73
50:A:996:A:C6	50:A:997:U:H5	1.84	0.73
21:O:9:GLY:O	21:O:11:ARG:HG3	1.89	0.73
2:C:26:LYS:HZ2	13:N:75:LYS:HA	1.52	0.73
50:A:700:G:H5'	50:A:701:U:OP2	1.89	0.73
6:G:35:LYS:HD2	50:A:1373:G:H5''	1.70	0.73
11:L:42:LYS:HG2	11:L:43:LYS:HG3	1.71	0.73
50:A:996:A:C2	50:A:997:U:C6	2.76	0.73
50:A:230:G:H21	50:A:231:U:H1'	1.53	0.72
9:J:46:LYS:HZ1	9:J:48:ARG:HB3	1.54	0.72
19:T:82:ILE:O	19:T:86:ALA:N	2.23	0.72
9:J:36:VAL:HG12	9:J:76:ILE:HA	1.70	0.72
51:X:16:G:C2	51:X:17:C:C4	2.78	0.72
24:3:25:VAL:O	24:3:26:THR:OG1	2.08	0.71
17:R:62:ARG:HB3	17:R:69:TYR:HD1	1.55	0.71
8:I:118:ARG:HG3	8:I:119:LYS:H	1.55	0.71
10:K:34:THR:HG22	10:K:40:ALA:HA	1.71	0.71
10:K:80:ASN:OD1	10:K:105:ARG:NH2	2.23	0.71
50:A:1241:G:H8	50:A:1241:G:OP2	1.73	0.71
50:A:147:G:H1	50:A:175:C:H42	1.37	0.70
5:F:2:ARG:HH11	5:F:68:GLN:HE21	1.39	0.70
8:I:109:GLN:O	50:A:1348:U:OP1	2.03	0.70
50:A:843:U:OP1	50:A:846:G:N2	2.24	0.70
15:P:4:ILE:HG12	15:P:21:VAL:HG22	1.74	0.70
23:2:5:ILE:HD11	23:2:45:ARG:NH1	2.06	0.70
2:C:69:THR:C	2:C:106:ARG:HH12	1.94	0.70
19:T:59:ARG:HH12	50:A:178:C:P	2.13	0.70
20:U:27:VAL:O	20:U:28:LEU:HD13	1.91	0.70
50:A:1347:G:C5'	50:A:1348:U:H6	2.05	0.70
50:A:1414:U:H2'	50:A:1415:G:H8	1.57	0.70
50:A:960:U:H4'	50:A:961:U:OP2	1.91	0.70
51:X:16:G:C2'	51:X:17:C:O5'	2.40	0.70
50:A:840:C:H5''	50:A:841:C:OP2	1.91	0.70
22:1:18:LEU:HD21	22:1:53:VAL:CG1	2.22	0.69
8:I:98:ARG:NH1	50:A:1178:G:OP2	2.25	0.69
50:A:46:G:N2	50:A:396:C:O2	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1178:G:N2	50:A:1181:G:OP2	2.24	0.69
8:I:127:SER:H	50:A:1341:U:H6	1.41	0.69
1:B:17:HIS:HE1	1:B:189:ASN:HD22	1.40	0.69
15:P:51:ARG:NH2	15:P:53:ASP:HB2	2.06	0.69
50:A:1050:G:N2	50:A:1209:C:O2	2.25	0.69
50:A:973:G:H3'	50:A:974:A:H5''	1.75	0.69
3:D:131:ILE:HG22	3:D:133:SER:H	1.57	0.69
8:I:111:GLU:HB2	50:A:1348:U:O4'	1.92	0.69
1:B:70:GLY:HA3	1:B:163:ILE:HG22	1.75	0.69
3:D:151:GLN:O	3:D:155:LYS:NZ	2.21	0.69
15:P:73:ALA:O	15:P:77:GLU:HB2	1.93	0.69
11:L:4:ASN:HD21	16:Q:35:LYS:HE2	1.57	0.69
50:A:507:C:H3'	50:A:508:U:H5''	1.75	0.69
50:A:191:G:OP2	50:A:191:G:H8	1.75	0.68
15:P:12:LYS:CG	50:A:392:C:P	2.63	0.68
51:X:16:G:N1	51:X:17:C:N4	2.41	0.68
8:I:111:GLU:HB2	50:A:1348:U:C5'	2.04	0.68
18:S:14:LEU:HD11	18:S:32:THR:HG23	1.74	0.68
16:Q:5:ARG:NH1	50:A:636:U:OP1	2.27	0.68
15:P:5:ARG:CD	50:A:377:G:P	2.61	0.68
3:D:90:LEU:HD23	3:D:93:LEU:HD12	1.76	0.68
50:A:996:A:C4	50:A:997:U:H6	2.12	0.68
8:I:113:LYS:NZ	8:I:117:LEU:HD22	2.09	0.68
8:I:111:GLU:HB2	50:A:1348:U:O5'	1.90	0.68
50:A:1527:U:O2'	50:A:1528:U:OP1	2.10	0.68
50:A:219:U:H2'	50:A:220:G:H8	1.58	0.68
15:P:12:LYS:CG	50:A:392:C:OP1	2.41	0.68
50:A:564:C:N4	50:A:565:U:O4	2.27	0.68
16:Q:46:HIS:HB3	16:Q:73:THR:HG22	1.75	0.68
17:R:62:ARG:HB3	17:R:69:TYR:CD1	2.28	0.68
18:S:35:ARG:HH12	18:S:74:ALA:HB3	1.59	0.68
22:1:7:ARG:NH2	22:1:56:LEU:HD22	2.07	0.68
50:A:123:U:OP1	50:A:311:C:O2'	2.11	0.68
7:H:19:ALA:HB2	50:A:827:U:H4'	1.75	0.68
3:D:141:VAL:HG22	3:D:180:THR:HG22	1.75	0.67
3:D:187:ARG:NH1	3:D:196:GLU:OE1	2.27	0.67
19:T:76:ALA:HB2	50:A:186:C:H4'	1.77	0.67
50:A:592:G:O6	50:A:647:C:N4	2.25	0.67
50:A:1144:G:O6	50:A:1145:A:N6	2.28	0.67
50:A:99:C:HO2'	50:A:100:G:H8	1.42	0.67
50:A:747:A:OP2	50:A:747:A:H8	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:124:VAL:HA	3:D:142:VAL:HA	1.75	0.67
18:S:18:VAL:HG21	18:S:43:MET:HG2	1.74	0.67
50:A:996:A:N3	50:A:997:U:C6	2.62	0.67
5:F:75:GLU:OE2	5:F:79:ARG:NE	2.28	0.67
11:L:78:VAL:HG12	11:L:101:LEU:HD13	1.76	0.67
20:U:34:ARG:HH12	50:A:1524:C:P	2.17	0.67
10:K:23:HIS:NE2	10:K:25:SER:OG	2.27	0.67
50:A:27:G:H1	50:A:556:C:H42	1.42	0.67
50:A:374:A:H5'	50:A:452:A:C2	2.30	0.67
4:E:51:LYS:NZ	50:A:1080:A:OP1	2.27	0.67
2:C:175:HIS:HD2	50:A:1108:G:H5'	1.60	0.67
8:I:48:ARG:NH2	8:I:56:MET:SD	2.68	0.67
15:P:59:HIS:CE1	15:P:63:GLN:HE22	2.13	0.67
21:O:68:LEU:CD2	21:O:71:LEU:HD12	2.20	0.67
50:A:374:A:H5''	50:A:375:U:C5	2.30	0.67
23:2:5:ILE:HD11	23:2:45:ARG:HH12	1.59	0.66
50:A:908:A:H2'	50:A:909:A:H8	1.60	0.66
50:A:186:C:N4	50:A:191:G:O6	2.19	0.66
4:E:47:PHE:HE2	4:E:137:ARG:NH1	1.93	0.66
8:I:111:GLU:CG	50:A:1348:U:C4'	2.42	0.66
8:I:74:GLN:NE2	50:A:1249:C:O2'	2.29	0.66
11:L:13:ARG:HH11	50:A:562:U:H5''	1.61	0.66
10:K:126:ARG:HD3	10:K:128:VAL:HB	1.77	0.66
7:H:62:LEU:C	7:H:62:LEU:HD23	4.01	0.66
50:A:374:A:OP1	50:A:452:A:N6	2.29	0.66
1:B:119:GLN:HB3	1:B:136:ARG:HD2	1.78	0.66
5:F:91:ARG:HG3	5:F:92:THR:HG23	1.78	0.66
50:A:977:A:N6	50:A:1224:U:O5'	2.29	0.66
50:A:1398:A:O2'	50:A:1399:C:OP1	2.13	0.66
2:C:149:LYS:HD2	2:C:166:TRP:HE1	1.62	0.66
3:D:2:ARG:NH1	3:D:114:ARG:HD2	2.10	0.66
8:I:105:ARG:HD3	8:I:106:ASP:CA	2.26	0.66
50:A:203:G:H21	50:A:205:A:H61	1.44	0.65
50:A:201:G:O2'	50:A:469:C:O2'	2.12	0.65
50:A:413:G:O3'	50:A:428:G:N2	2.29	0.65
16:Q:61:ARG:HH11	16:Q:75:VAL:HG22	1.62	0.65
19:T:67:HIS:CE1	19:T:69:ASN:HD22	2.15	0.65
50:A:1347:G:H5'	50:A:1348:U:C6	2.32	0.65
5:F:53:LYS:NZ	50:A:710:G:OP1	2.24	0.65
2:C:4:VAL:HG13	50:A:1190:G:OP2	1.96	0.65
51:X:16:G:O2'	51:X:17:C:C5'	2.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:123:ARG:H	50:A:1343:G:H1'	1.62	0.65
15:P:17:TYR:HE2	50:A:375:U:O2'	1.80	0.65
3:D:56:GLU:HG2	3:D:198:LEU:HB2	1.78	0.65
8:I:12:LYS:H	8:I:105:ARG:HH22	1.44	0.65
50:A:1332:A:O2'	50:A:1333:A:OP1	2.16	0.64
50:A:1363:A:O2'	50:A:1365:G:N7	2.28	0.64
1:B:66:ILE:HG12	1:B:159:ALA:HB3	1.79	0.64
8:I:12:LYS:N	8:I:105:ARG:HH22	1.95	0.64
8:I:11:ARG:CD	8:I:106:ASP:OD1	2.46	0.64
50:A:662:U:O2'	50:A:836:G:OP1	2.15	0.64
5:F:9:MET:HG2	5:F:59:TYR:HE1	1.63	0.64
8:I:126:PHE:HB3	50:A:1342:C:OP2	1.97	0.64
15:P:79:ASN:O	15:P:80:LYS:HB2	1.98	0.64
8:I:126:PHE:HA	50:A:1341:U:H3'	1.79	0.64
21:O:68:LEU:HD23	21:O:71:LEU:CD1	2.21	0.64
19:T:59:ARG:NH1	50:A:178:C:OP2	2.31	0.64
4:E:99:SER:HG	50:A:6:G:H1	0.69	0.64
9:J:15:HIS:HA	9:J:18:ILE:HG22	1.79	0.64
9:J:46:LYS:HZ3	9:J:48:ARG:HB3	1.62	0.64
12:M:48:SER:HB2	12:M:51:GLN:HB2	1.79	0.64
12:M:22:TYR:O	12:M:69:ARG:NH2	2.29	0.64
50:A:1348:U:H2'	50:A:1349:A:H5''	1.79	0.64
5:F:37:HIS:HE1	5:F:97:THR:HA	1.61	0.64
15:P:22:ALA:HB2	15:P:32:PHE:HA	1.80	0.64
4:E:49:TYR:HE2	50:A:1079:G:H5''	1.63	0.64
15:P:59:HIS:HE1	15:P:63:GLN:HE22	1.45	0.64
50:A:1030:U:OP2	50:A:1031:C:N4	2.31	0.63
8:I:10:ARG:HH21	50:A:1148:U:H5'	1.62	0.63
2:C:33:ASP:OD2	13:N:64:ARG:HD2	1.98	0.63
9:J:46:LYS:NZ	9:J:48:ARG:HE	1.95	0.63
23:2:5:ILE:HD12	23:2:40:ASP:OD1	1.98	0.63
50:A:664:G:H22	50:A:741:G:H1	1.45	0.63
1:B:13:VAL:HG12	1:B:15:PHE:H	1.64	0.63
8:I:105:ARG:HD3	8:I:105:ARG:C	2.16	0.63
50:A:1130:A:H2'	50:A:1131:G:C8	2.34	0.63
5:F:43:GLY:HA2	5:F:58:HIS:CE1	2.32	0.63
50:A:102:G:C2	50:A:103:U:C5	3.75	0.63
7:H:105:THR:OG1	7:H:108:GLY:O	2.17	0.63
50:A:967:C:OP2	50:A:968:A:O2'	2.15	0.63
7:H:79:ARG:NH1	50:A:878:A:OP1	2.31	0.63
8:I:120:ALA:HB1	50:A:1349:A:OP2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:414:A:OP2	50:A:428:G:N1	2.32	0.63
50:A:483:C:H3'	50:A:484:G:H2'	1.81	0.63
13:N:78:LEU:HB3	13:N:83:VAL:HG21	1.80	0.63
9:J:9:ARG:H	9:J:99:GLN:HB3	1.62	0.63
14:O:79:ARG:HA	14:O:82:GLU:OE2	1.99	0.63
50:A:948:C:H42	50:A:1233:G:H1	1.44	0.62
50:A:1414:U:H2'	50:A:1415:G:C8	2.34	0.62
3:D:196:GLU:O	3:D:199:ILE:HG12	1.99	0.62
4:E:67:ARG:HE	4:E:68:ARG:HH12	1.47	0.62
50:A:197:A:N1	50:A:220:G:O2'	2.30	0.62
50:A:667:G:H2'	50:A:668:G:H8	1.63	0.62
50:A:1201:A:H1'	50:A:1202:U:OP2	2.00	0.62
15:P:70:ARG:HG3	50:A:375:U:H5'	1.59	0.62
50:A:517:G:N2	50:A:530:G:OP1	2.33	0.62
8:I:11:ARG:HG3	8:I:105:ARG:HH12	1.64	0.62
11:L:120:ARG:HH12	50:A:500:G:H5''	1.64	0.62
50:A:1004:A:H1'	50:A:1026:G:C6	2.34	0.62
15:P:5:ARG:CG	50:A:377:G:OP1	2.46	0.62
50:A:63:C:C2	50:A:64:G:C8	7.94	0.62
50:A:859:G:OP2	50:A:869:G:N1	2.30	0.62
2:C:26:LYS:NZ	13:N:75:LYS:HA	2.13	0.62
14:O:15:GLY:HA3	14:O:20:ASP:OD2	2.00	0.62
19:T:2:ASN:HA	50:A:332:G:OP2	1.98	0.62
4:E:35:LEU:HD11	4:E:133:ILE:HD13	1.82	0.62
50:A:132:C:H2'	50:A:133:U:C6	2.34	0.62
8:I:111:GLU:HG2	50:A:1348:U:C4'	2.17	0.62
12:M:24:VAL:HG13	12:M:28:ARG:HB3	1.82	0.62
2:C:175:HIS:CD2	50:A:1108:G:H5'	2.35	0.62
50:A:147:G:N2	50:A:176:C:O2	2.32	0.62
50:A:720:C:H5''	50:A:721:G:OP2	2.00	0.62
50:A:1129:C:H1'	50:A:1130:A:OP1	2.00	0.62
50:A:1130:A:H8	50:A:1130:A:OP1	1.82	0.62
50:A:701:U:O2'	50:A:702:A:OP2	2.14	0.62
15:P:57:ILE:O	15:P:61:VAL:HG23	2.00	0.61
50:A:574:A:H5''	50:A:575:G:OP2	2.00	0.61
1:B:22:TRP:HB2	1:B:188:THR:HG22	1.81	0.61
5:F:70:VAL:HG13	5:F:73:GLU:OE2	2.00	0.61
50:A:757:U:O2'	50:A:879:C:O2	2.19	0.61
9:J:46:LYS:HZ1	9:J:48:ARG:NE	1.97	0.61
50:A:1301:U:O2'	50:A:1302:C:O5'	2.19	0.61
16:Q:5:ARG:HH12	50:A:636:U:H4'	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:88:LYS:HB2	50:A:600:A:OP1	2.00	0.61
9:J:7:ARG:NH2	50:A:1126:U:OP1	2.33	0.61
16:Q:47:ASP:OD1	16:Q:74:LEU:HB2	2.00	0.61
15:P:37:GLY:HA2	15:P:51:ARG:NH1	2.16	0.61
50:A:1528:U:O2'	50:A:1530:G:OP2	2.17	0.61
50:A:301:G:O2'	50:A:302:G:O5'	2.18	0.61
15:P:17:TYR:CE1	50:A:374:A:C2	2.88	0.61
50:A:1068:G:H1	50:A:1107:C:H42	1.49	0.61
3:D:182:LYS:NZ	3:D:183:ARG:NH1	2.47	0.61
20:U:16:ARG:HA	20:U:19:LYS:NZ	2.16	0.61
3:D:58:GLN:HG3	3:D:62:ARG:NH1	2.16	0.61
5:F:3:HIS:HA	5:F:65:GLU:HG3	1.83	0.61
8:I:12:LYS:H	8:I:105:ARG:NH2	1.98	0.61
15:P:67:ILE:CG2	15:P:72:ALA:HB2	2.31	0.61
50:A:936:C:H2'	50:A:937:A:H8	1.66	0.60
3:D:58:GLN:HG3	3:D:62:ARG:HH11	1.65	0.60
4:E:9:GLU:N	4:E:40:ASP:OD1	2.33	0.60
50:A:82:G:C5	50:A:83:C:H1'	2.36	0.60
50:A:996:A:H2'	50:A:997:U:H5'	1.79	0.60
50:A:1040:U:H2'	50:A:1041:G:H8	1.67	0.60
50:A:184:G:H4'	50:A:185:U:OP1	2.01	0.60
50:A:440:C:H42	50:A:497:G:H1	1.47	0.60
50:A:572:A:OP2	50:A:573:A:OP2	2.18	0.60
50:A:890:G:O2'	50:A:906:A:N6	2.34	0.60
51:X:16:G:C2	51:X:17:C:N4	2.69	0.60
20:U:27:VAL:O	20:U:28:LEU:HD22	2.01	0.60
12:M:104:ASN:ND2	50:A:949:A:OP2	2.31	0.60
7:H:92:PRO:HB2	7:H:94:VAL:HG13	1.83	0.60
10:K:82:GLU:HG3	10:K:108:ASN:HB2	1.84	0.60
8:I:10:ARG:NH2	50:A:1149:C:OP2	2.34	0.60
50:A:372:C:N4	50:A:387:U:O4	2.35	0.60
50:A:391:G:H2'	50:A:392:C:O4'	2.02	0.60
5:F:70:VAL:O	5:F:73:GLU:HG2	2.02	0.60
7:H:21:LYS:O	7:H:64:TYR:OH	2.19	0.60
9:J:81:GLU:OE2	9:J:82:LYS:NZ	2.27	0.60
15:P:20:VAL:CG2	15:P:32:PHE:HB2	2.32	0.60
50:A:102:G:C2	50:A:103:U:C6	3.83	0.60
50:A:462:G:H1	50:A:470:C:H42	1.47	0.60
50:A:927:G:O2'	50:A:1503:A:N7	2.33	0.60
50:A:997:U:O2'	50:A:998:C:O5'	2.19	0.60
22:1:7:ARG:NH2	22:1:56:LEU:CD2	2.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:277:C:H2'	50:A:278:G:H8	1.67	0.59
1:B:89:PHE:CZ	1:B:153:MET:HA	2.37	0.59
20:U:34:ARG:NH1	50:A:1524:C:P	2.74	0.59
50:A:1529:G:OP2	50:A:1530:G:OP2	2.20	0.59
50:A:147:G:N2	50:A:175:C:N3	2.41	0.59
50:A:18:C:N3	50:A:917:G:N2	2.38	0.59
11:L:23:LEU:HD13	11:L:58:ASN:HB2	1.83	0.59
50:A:1121:U:H2'	50:A:1122:U:C6	2.37	0.59
50:A:301:G:H4'	50:A:302:G:OP1	2.00	0.59
15:P:5:ARG:CZ	50:A:377:G:OP1	2.50	0.59
50:A:996:A:O2'	50:A:997:U:H5'	2.02	0.59
20:U:9:GLU:HG3	20:U:10:PRO:HD2	1.85	0.59
51:X:16:G:N3	51:X:17:C:C5	2.70	0.59
13:N:76:PHE:HB2	13:N:78:LEU:HG	1.85	0.59
50:A:1013:G:H2'	50:A:1015:G:OP2	2.03	0.59
8:I:11:ARG:NH2	50:A:1347:G:C2	2.71	0.59
19:T:36:ALA:HA	19:T:39:GLU:OE2	2.01	0.59
50:A:457:G:N7	50:A:458:U:N3	2.51	0.59
23:2:5:ILE:HD11	23:2:40:ASP:OD1	2.01	0.59
50:A:801:U:H2'	50:A:802:A:H8	1.68	0.59
9:J:21:ALA:HA	9:J:24:GLU:OE2	2.03	0.59
13:N:51:PRO:HB2	13:N:54:SER:HB3	1.85	0.59
4:E:21:SER:O	50:A:15:G:N2	2.33	0.58
4:E:86:GLY:HA3	4:E:141:ASP:HB3	1.84	0.58
11:L:120:ARG:HH12	50:A:500:G:C5'	2.16	0.58
14:O:45:HIS:CE1	50:A:668:G:H21	2.21	0.58
15:P:59:HIS:CE1	15:P:63:GLN:NE2	2.71	0.58
50:A:1261:A:H5''	50:A:1262:C:OP2	2.03	0.58
4:E:47:PHE:CE2	4:E:137:ARG:NH1	2.70	0.58
15:P:77:GLU:C	15:P:79:ASN:H	2.07	0.58
50:A:610:U:H5'	50:A:611:C:OP2	2.03	0.58
50:A:1133:G:H2'	50:A:1134:G:C8	2.38	0.58
18:S:5:LYS:HE3	50:A:1314:C:P	2.44	0.58
50:A:877:G:H2'	50:A:878:A:H8	1.67	0.58
3:D:106:PHE:HD1	3:D:158:LEU:HD21	1.68	0.58
3:D:182:LYS:HZ2	3:D:183:ARG:HH11	1.50	0.58
6:G:122:GLU:OE2	6:G:133:ALA:HB2	2.04	0.58
10:K:35:ASP:OD1	10:K:36:ARG:N	2.36	0.58
50:A:844:G:H3'	50:A:846:G:H1'	1.85	0.58
1:B:202:ASN:HD22	1:B:205:ALA:HB3	1.69	0.58
2:C:19:SER:HB3	2:C:21:TRP:NE1	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:94:ARG:HA	8:I:97:LEU:HB2	1.86	0.58
23:2:5:ILE:HG21	23:2:57:VAL:CG1	2.34	0.58
50:A:193:C:H2'	50:A:194:C:C6	2.39	0.58
3:D:125:ASN:N	3:D:141:VAL:O	2.37	0.58
13:N:20:PHE:HA	13:N:24:ALA:HA	1.85	0.58
15:P:5:ARG:HA	15:P:68:SER:OG	2.04	0.58
50:A:1002:G:H2'	50:A:1003:G:H8	1.69	0.58
50:A:1060:U:H2'	50:A:1061:G:H8	1.69	0.58
50:A:1362:A:H2'	50:A:1362:A:OP2	2.04	0.58
15:P:12:LYS:CD	50:A:392:C:H5'	2.32	0.58
15:P:5:ARG:NE	50:A:377:G:OP1	2.35	0.57
11:L:25:ALA:O	50:A:553:A:O2'	2.21	0.57
50:A:1130:A:H2'	50:A:1131:G:H8	1.68	0.57
8:I:129:ARG:N	50:A:1341:U:O4'	2.38	0.57
1:B:115:ASP:O	1:B:118:THR:OG1	2.16	0.57
1:B:100:LEU:HB2	1:B:174:GLU:OE2	2.04	0.57
20:U:34:ARG:NH1	50:A:1524:C:OP2	2.24	0.57
17:R:60:ARG:NH1	50:A:736:C:OP1	2.37	0.57
50:A:996:A:N3	50:A:997:U:H6	2.00	0.57
15:P:19:VAL:HG13	15:P:37:GLY:C	2.24	0.57
18:S:11:ASP:OD2	18:S:34:SER:HB3	2.04	0.57
50:A:1242:G:H1	50:A:1295:U:H3	1.52	0.57
18:S:36:ARG:HD2	50:A:1318:A:O2'	2.04	0.57
28:8:19:ARG:NH1	28:8:26:ILE:HD11	2.20	0.57
8:I:115:VAL:HG12	50:A:1367:C:H5''	1.85	0.57
50:A:497:G:H5''	50:A:498:A:OP2	2.05	0.57
5:F:10:VAL:HG11	5:F:18:VAL:HG22	1.86	0.57
9:J:66:GLU:OE2	9:J:68:ARG:NE	2.38	0.57
15:P:10:GLY:O	15:P:11:ALA:HB2	2.05	0.57
50:A:1033:G:OP2	50:A:1033:G:H8	1.87	0.57
3:D:127:ARG:NH2	50:A:619:U:O2'	2.38	0.57
3:D:124:VAL:O	3:D:126:GLY:N	2.37	0.57
7:H:84:ILE:HD12	7:H:86:LYS:NZ	2.19	0.57
11:L:114:SER:OG	50:A:501:C:O3'	2.22	0.57
50:A:373:A:C6	50:A:481:G:H4'	2.40	0.57
1:B:120:SER:HA	1:B:136:ARG:HH12	1.70	0.57
8:I:11:ARG:HA	8:I:105:ARG:NH1	2.20	0.57
12:M:112:ARG:HD2	50:A:1229:A:OP2	2.05	0.57
50:A:1132:C:H2'	50:A:1133:G:C8	2.40	0.57
3:D:12:ARG:NH2	3:D:36:ALA:H	2.03	0.57
8:I:44:ARG:HA	8:I:47:VAL:HG22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1447:A:H5''	50:A:1448:C:H5	1.69	0.56
16:Q:39:ARG:NH1	50:A:280:C:O2	2.38	0.56
50:A:859:G:OP2	50:A:869:G:N2	2.36	0.56
50:A:996:A:N1	50:A:997:U:C5	2.70	0.56
7:H:91:LEU:HD12	7:H:92:PRO:HD2	1.86	0.56
9:J:8:ILE:HD11	9:J:74:VAL:HB	1.87	0.56
13:N:63:CYS:SG	13:N:66:THR:HG22	2.45	0.56
2:C:69:THR:H	2:C:103:ALA:HB1	1.71	0.56
11:L:53:ARG:HB3	11:L:61:GLU:OE2	2.06	0.56
1:B:69:VAL:HG12	1:B:161:PHE:O	2.05	0.56
50:A:976:G:N1	50:A:1362:A:O2'	2.37	0.56
8:I:127:SER:N	50:A:1341:U:H5''	2.21	0.56
50:A:386:C:H5''	50:A:387:U:OP2	2.06	0.56
15:P:10:GLY:HA3	15:P:15:PRO:HA	1.88	0.56
23:2:5:ILE:CD1	23:2:45:ARG:NH1	2.68	0.56
50:A:449:G:H2'	50:A:450:G:O4'	2.06	0.56
13:N:72:PHE:CE2	13:N:74:ARG:HA	2.40	0.56
14:O:17:ASP:OD1	14:O:18:ALA:N	2.38	0.56
15:P:12:LYS:HD2	50:A:392:C:H5''	1.87	0.56
22:1:18:LEU:HD21	22:1:53:VAL:HG11	1.88	0.56
28:8:19:ARG:CZ	28:8:26:ILE:CD1	2.83	0.56
50:A:954:G:N2	50:A:1228:C:N3	2.54	0.56
2:C:137:VAL:HG11	2:C:167:TYR:HE2	1.71	0.56
15:P:51:ARG:O	15:P:52:LEU:HD12	2.06	0.56
16:Q:61:ARG:NH1	16:Q:75:VAL:HG22	2.21	0.56
5:F:2:ARG:HG3	5:F:91:ARG:HH21	1.71	0.55
50:A:451:A:H1'	50:A:452:A:N7	2.20	0.55
8:I:113:LYS:HZ1	8:I:117:LEU:HB3	1.71	0.55
51:X:13:C:H3'	51:X:14:U:H5''	1.87	0.55
50:A:590:U:O2'	50:A:591:U:H5''	2.06	0.55
20:U:26:GLY:C	20:U:28:LEU:H	2.10	0.55
23:2:5:ILE:CG2	23:2:57:VAL:CG1	2.83	0.55
50:A:1266:G:H2'	50:A:1268:G:OP2	2.06	0.55
1:B:101:THR:HG23	1:B:174:GLU:OE2	2.07	0.55
51:X:16:G:N2	51:X:17:C:C4	2.74	0.55
18:S:5:LYS:HE3	50:A:1314:C:OP2	2.06	0.55
50:A:410:G:N2	50:A:431:A:OP2	2.36	0.55
50:A:769:G:H4'	50:A:1513:A:H4'	1.87	0.55
19:T:70:LYS:HG3	19:T:73:ARG:HH21	1.72	0.55
50:A:14:U:O2	50:A:14:U:H2'	3.14	0.55
50:A:228:A:H5''	50:A:229:U:OP2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:28:ASN:ND2	50:A:689:C:H5"	2.22	0.55
9:J:5:ARG:NH1	9:J:79:PRO:HG2	2.21	0.55
9:J:9:ARG:HH11	9:J:71:LEU:HD21	1.69	0.55
11:L:53:ARG:NH2	11:L:61:GLU:HG2	2.13	0.55
15:P:12:LYS:CG	50:A:392:C:OP2	2.54	0.55
50:A:496:A:H5'	50:A:497:G:OP2	2.06	0.55
50:A:996:A:C6	50:A:997:U:C4	2.93	0.55
10:K:126:ARG:HG2	10:K:128:VAL:H	1.70	0.55
50:A:100:G:N2	50:A:101:A:H1'	2.75	0.55
12:M:47:LEU:HD12	12:M:51:GLN:HB3	1.88	0.55
50:A:908:A:H2'	50:A:909:A:C8	2.41	0.55
13:N:5:MET:HE2	50:A:982:U:H5"	1.88	0.55
3:D:182:LYS:HZ2	3:D:183:ARG:NH1	2.04	0.55
5:F:37:HIS:CE1	5:F:97:THR:HA	2.41	0.55
6:G:71:THR:HG22	6:G:141:HIS:NE2	2.22	0.55
15:P:67:ILE:HG21	15:P:72:ALA:HB2	1.88	0.55
50:A:52:C:N3	50:A:360:G:N2	2.54	0.54
50:A:621:A:H3'	50:A:622:A:H8	1.72	0.54
14:O:68:TYR:OH	50:A:753:A:OP1	2.25	0.54
50:A:1265:C:H2'	50:A:1266:G:C8	2.42	0.54
8:I:111:GLU:HG2	50:A:1348:U:O3'	2.07	0.54
2:C:26:LYS:HZ2	13:N:75:LYS:HG2	1.72	0.54
3:D:36:ALA:HA	3:D:41:GLY:HA3	1.89	0.54
8:I:27:ILE:HA	8:I:62:LEU:HB2	1.89	0.54
22:1:18:LEU:CD2	22:1:53:VAL:HG11	2.37	0.54
2:C:127:VAL:O	2:C:129:PHE:N	2.38	0.54
2:C:153:SER:HB2	2:C:195:ILE:HG23	1.89	0.54
18:S:45:GLY:H	18:S:61:VAL:HG23	1.73	0.54
50:A:184:G:HO2'	50:A:185:U:H6	1.54	0.54
3:D:170:LEU:HD22	3:D:181:PHE:HD1	1.72	0.54
3:D:7:LYS:H	50:A:430:A:P	2.30	0.54
11:L:13:ARG:NH1	50:A:562:U:OP1	2.40	0.54
2:C:69:THR:H	2:C:103:ALA:CB	2.20	0.54
50:A:1124:G:O2'	50:A:1145:A:N6	2.41	0.54
50:A:1133:G:H2'	50:A:1134:G:H8	1.72	0.54
6:G:70:PRO:HA	6:G:141:HIS:CE1	2.33	0.54
14:O:73:ASP:OD2	14:O:76:ARG:HB2	2.07	0.54
15:P:20:VAL:HG21	15:P:32:PHE:HB2	1.90	0.54
18:S:5:LYS:HG3	50:A:1314:C:OP2	2.07	0.54
50:A:1158:C:H2'	50:A:1159:U:H4'	1.90	0.54
50:A:163:C:H2'	50:A:164:G:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:362:G:N2	50:A:365:U:OP2	2.41	0.54
11:L:78:VAL:N	11:L:102:ASP:OD2	2.41	0.54
50:A:1023:U:N3	50:A:1024:G:N7	2.55	0.54
50:A:533:A:O2'	50:A:535:A:OP2	2.24	0.54
9:J:48:ARG:NH1	13:N:100:TRP:CD2	2.76	0.54
12:M:102:LYS:NZ	50:A:954:G:C6	2.76	0.54
50:A:1097:C:HO2'	50:A:1169:A:HO2'	1.56	0.54
50:A:1175:G:H2'	50:A:1176:A:H8	1.72	0.54
50:A:1265:C:H2'	50:A:1266:G:H8	1.73	0.54
18:S:69:LYS:NZ	50:A:1319:A:H5'	2.23	0.54
50:A:502:A:H61	50:A:543:U:H3	1.56	0.54
5:F:15:SER:HB2	5:F:44:ARG:HD2	1.90	0.54
9:J:47:GLU:HG3	50:A:1254:A:OP1	2.08	0.54
9:J:9:ARG:NH2	50:A:1126:U:O4	2.41	0.54
11:L:23:LEU:HD13	11:L:58:ASN:HD22	1.73	0.54
50:A:403:C:H2'	50:A:404:G:C8	2.43	0.53
8:I:129:ARG:OXT	50:A:1341:U:H4'	2.08	0.53
9:J:25:ILE:O	9:J:28:THR:OG1	2.17	0.53
12:M:89:ARG:O	12:M:93:GLY:N	2.39	0.53
2:C:5:HIS:NE2	13:N:88:MET:HG2	2.24	0.53
50:A:1409:C:H2'	50:A:1410:A:C8	2.42	0.53
50:A:374:A:N7	50:A:375:U:C2	2.76	0.53
1:B:67:LEU:HD11	1:B:91:VAL:HG23	1.90	0.53
3:D:57:LYS:HD3	3:D:202:LEU:HD23	1.90	0.53
18:S:5:LYS:HG2	18:S:6:LYS:HG2	1.89	0.53
50:A:1131:G:H1	50:A:1144:G:HO2'	1.57	0.53
3:D:201:GLU:O	50:A:8:A:N6	2.41	0.53
50:A:1075:U:H2'	50:A:1076:U:C6	2.44	0.53
50:A:1130:A:H8	50:A:1130:A:P	2.32	0.53
50:A:139:A:H2'	50:A:140:U:H6	1.74	0.53
2:C:89:VAL:O	2:C:93:ILE:HG12	2.08	0.53
15:P:3:THR:CG2	50:A:377:G:P	2.82	0.53
16:Q:68:LYS:HG3	16:Q:69:THR:HG23	1.91	0.53
50:A:484:G:O2'	50:A:485:U:OP2	2.23	0.53
1:B:72:LYS:HD2	1:B:204:ASP:OD2	2.09	0.53
8:I:111:GLU:HG2	50:A:1348:U:C3'	2.38	0.53
50:A:1279:G:N3	50:A:1279:G:H2'	2.23	0.53
50:A:928:G:O2'	50:A:1533:C:H5'	2.09	0.53
13:N:80:ARG:HE	13:N:81:ILE:HG23	1.74	0.53
18:S:35:ARG:HH12	18:S:74:ALA:CB	2.22	0.53
50:A:1162:C:H2'	50:A:1163:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:474:G:H2'	50:A:475:C:C2	2.44	0.53
50:A:846:G:N3	50:A:846:G:H2'	2.24	0.53
9:J:46:LYS:NZ	9:J:48:ARG:NE	2.56	0.53
9:J:63:ASP:OD2	9:J:65:TYR:CZ	2.62	0.53
16:Q:5:ARG:HH22	50:A:636:U:H4'	1.73	0.53
51:X:20:U:H6	51:X:21:C:C2	2.27	0.53
6:G:37:THR:OG1	50:A:1240:U:O2'	2.17	0.53
50:A:1412:C:H2'	50:A:1413:A:C8	2.43	0.53
2:C:31:ASN:HD21	2:C:58:ARG:HD3	1.74	0.53
10:K:88:PRO:CG	20:U:28:LEU:CD1	2.46	0.53
50:A:1346:A:H4'	50:A:1347:G:OP1	2.08	0.53
50:A:391:G:C6	50:A:392:C:C4	2.97	0.53
50:A:826:C:OP2	50:A:826:C:H6	1.91	0.53
51:X:19:C:C5'	51:X:19:C:O2	2.53	0.53
50:A:1003:G:N2	50:A:1037:C:O2	2.41	0.52
50:A:944:G:C2	50:A:1338:G:OP2	2.62	0.52
50:A:772:U:H2'	50:A:773:G:C8	2.44	0.52
15:P:6:LEU:C	50:A:376:G:C1'	2.77	0.52
50:A:1237:C:H42	50:A:1337:G:H1	1.57	0.52
10:K:126:ARG:HG2	10:K:128:VAL:N	2.25	0.52
50:A:1006:G:C2	50:A:1007:U:H1'	2.44	0.52
50:A:104:G:H2'	50:A:105:G:H8	1.74	0.52
50:A:1158:C:H2'	50:A:1158:C:O2	2.10	0.52
50:A:1453:G:H5'	50:A:1454:G:OP2	2.08	0.52
4:E:95:MET:HG3	4:E:124:ALA:HB2	1.91	0.52
19:T:28:ARG:O	19:T:32:LYS:NZ	2.32	0.52
50:A:999:C:H2'	50:A:1000:A:C8	2.44	0.52
50:A:1028:C:H2'	50:A:1029:U:O4'	2.09	0.52
50:A:992:U:O2'	50:A:1043:G:O6	2.16	0.52
50:A:1071:C:H42	50:A:1104:G:H1	1.57	0.52
50:A:1243:C:H2'	50:A:1244:G:H8	1.74	0.52
50:A:506:G:O6	50:A:525:C:N4	2.41	0.52
11:L:67:GLY:O	11:L:98:ARG:NH1	2.36	0.52
50:A:1294:G:H2'	50:A:1295:U:C6	2.44	0.52
50:A:464:U:H2'	50:A:466:A:OP2	2.09	0.52
50:A:893:C:H2'	50:A:894:G:C8	2.44	0.52
50:A:886:G:N2	50:A:912:C:O2	2.43	0.52
10:K:124:LYS:HA	20:U:34:ARG:HG3	1.90	0.52
13:N:73:LEU:HB2	13:N:78:LEU:HB2	1.91	0.52
15:P:6:LEU:HG	15:P:17:TYR:CB	2.40	0.52
16:Q:5:ARG:HH12	50:A:636:U:H5'	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1075:U:H2'	50:A:1076:U:H6	1.73	0.52
50:A:152:A:H62	50:A:169:C:H42	1.56	0.52
50:A:451:A:H1'	50:A:452:A:C8	2.45	0.52
50:A:296:U:O2'	50:A:556:C:O2	2.24	0.52
8:I:125:GLN:O	50:A:942:G:N2	2.42	0.52
3:D:173:ASP:OD2	3:D:176:LYS:HB2	2.10	0.52
4:E:67:ARG:HH21	4:E:68:ARG:HH22	1.57	0.52
6:G:24:LYS:HE3	50:A:1375:A:H5''	1.92	0.52
7:H:44:PHE:HE2	7:H:100:ILE:HG13	1.75	0.52
18:S:35:ARG:NH1	18:S:74:ALA:HB3	2.23	0.52
2:C:152:VAL:HG12	2:C:153:SER:O	2.09	0.52
3:D:8:LEU:O	3:D:12:ARG:HG3	2.10	0.52
4:E:20:VAL:HG22	4:E:31:SER:O	2.10	0.52
18:S:10:ILE:HG21	18:S:15:LEU:HD22	1.92	0.52
20:U:5:VAL:HB	20:U:19:LYS:HE3	1.91	0.52
50:A:700:G:C3'	50:A:701:U:H5''	2.40	0.52
50:A:737:C:H2'	50:A:738:C:C6	2.45	0.52
12:M:18:LEU:HG	12:M:21:ILE:HD11	1.92	0.52
15:P:1:MET:HG3	50:A:136:C:O4'	2.09	0.52
50:A:999:C:H42	50:A:1041:G:H1	1.57	0.51
50:A:1427:C:H2'	50:A:1428:A:C8	2.45	0.51
50:A:702:A:O2'	50:A:703:G:OP1	2.28	0.51
1:B:164:ASP:OD1	1:B:165:ALA:N	2.43	0.51
3:D:94:GLU:HG2	3:D:99:ASN:ND2	2.25	0.51
50:A:1003:G:H21	50:A:1005:A:H5'	1.74	0.51
18:S:77:ARG:NH2	50:A:1222:G:H5''	2.25	0.51
50:A:1339:A:OP2	50:A:1339:A:H8	1.93	0.51
50:A:455:G:H2'	50:A:456:A:C8	2.44	0.51
2:C:87:ARG:HG2	2:C:98:ALA:HB1	1.91	0.51
8:I:35:GLU:O	8:I:40:ARG:NE	2.28	0.51
20:U:8:ASN:OD1	20:U:9:GLU:N	2.42	0.51
5:F:21:MET:O	5:F:24:ARG:HG2	2.10	0.51
6:G:78:ARG:NH1	6:G:83:THR:O	2.43	0.51
9:J:48:ARG:HA	9:J:66:GLU:HA	1.93	0.51
11:L:71:HIS:HB3	11:L:73:LEU:H	1.75	0.51
12:M:15:VAL:HG13	12:M:16:ILE:HG12	1.93	0.51
15:P:28:ARG:HE	15:P:29:ASN:ND2	2.01	0.51
15:P:5:ARG:HH11	50:A:377:G:P	2.31	0.51
19:T:67:HIS:HE1	19:T:69:ASN:HD22	1.57	0.51
50:A:1129:C:N3	50:A:1144:G:N2	2.57	0.51
50:A:202:G:H1	50:A:215:C:H42	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:309:A:H2'	50:A:310:G:H8	1.75	0.51
50:A:702:A:HO2'	50:A:703:G:P	2.32	0.51
1:B:164:ASP:OD2	1:B:166:ASP:HB2	2.10	0.51
3:D:193:ASP:O	3:D:195:ASN:N	2.43	0.51
15:P:2:VAL:HG23	15:P:65:ALA:HA	1.92	0.51
20:U:36:PHE:HB2	20:U:39:LYS:HG2	1.91	0.51
51:X:14:U:H4'	51:X:15:G:OP1	2.11	0.51
28:8:19:ARG:CZ	28:8:26:ILE:HD11	2.39	0.51
50:A:401:C:H2'	50:A:402:G:H8	1.75	0.51
50:A:708:C:H2'	50:A:709:U:H6	1.74	0.51
50:A:1083:U:H3'	50:A:1084:G:C8	2.46	0.51
50:A:79:G:O6	50:A:80:A:N6	2.42	0.51
5:F:8:PHE:CZ	5:F:60:VAL:HG11	2.46	0.51
15:P:12:LYS:O	15:P:13:LYS:HB2	2.10	0.51
50:A:210:C:H4'	50:A:211:G:C2	2.46	0.51
20:U:24:LYS:O	20:U:28:LEU:HB2	2.10	0.51
23:2:40:ASP:OD1	23:2:45:ARG:NH1	2.44	0.51
50:A:1034:G:H3'	50:A:1035:A:H8	1.74	0.51
22:1:45:GLN:O	22:1:47:ARG:N	2.39	0.51
50:A:390:U:H2'	50:A:390:U:O2	2.11	0.51
50:A:511:C:O2'	50:A:512:U:OP2	2.25	0.51
50:A:684:U:H3	50:A:706:A:H61	1.59	0.51
10:K:86:LYS:NZ	50:A:707:U:OP1	2.34	0.51
3:D:187:ARG:HD2	3:D:196:GLU:OE2	2.11	0.51
15:P:22:ALA:CB	15:P:32:PHE:HA	2.41	0.51
15:P:6:LEU:HG	15:P:17:TYR:HB3	1.93	0.51
50:A:1348:U:C2'	50:A:1349:A:H5''	2.41	0.50
50:A:588:G:O2'	50:A:589:U:O5'	2.29	0.50
50:A:667:G:OP1	50:A:732:C:O2'	2.26	0.50
16:Q:68:LYS:HB3	50:A:254:G:P	2.51	0.50
23:2:3:LYS:O	23:2:4:THR:OG1	2.27	0.50
1:B:63:LYS:NZ	1:B:88:GLN:HE22	2.09	0.50
2:C:84:GLU:OE1	2:C:87:ARG:NH2	2.44	0.50
6:G:24:LYS:O	6:G:28:ILE:HG12	2.11	0.50
50:A:1065:U:H1'	50:A:1066:C:OP2	2.11	0.50
50:A:1175:G:H2'	50:A:1176:A:C8	2.47	0.50
50:A:1347:G:C4'	50:A:1348:U:H6	2.24	0.50
50:A:1436:U:O4	50:A:1437:A:N6	2.44	0.50
50:A:1510:C:H2'	50:A:1511:G:C8	2.47	0.50
50:A:487:A:H5''	50:A:488:C:OP2	2.10	0.50
50:A:694:A:H2'	50:A:695:A:H5'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:789:U:HO2'	50:A:790:A:H8	1.60	0.50
2:C:70:ALA:N	2:C:106:ARG:HH22	2.10	0.50
9:J:46:LYS:HE2	9:J:66:GLU:OE1	2.11	0.50
15:P:17:TYR:CE1	50:A:374:A:H2	2.28	0.50
15:P:20:VAL:HG21	15:P:32:PHE:CB	2.41	0.50
15:P:20:VAL:HG23	15:P:34:GLU:O	2.10	0.50
50:A:1399:C:C6	50:A:1399:C:OP2	2.65	0.50
50:A:767:A:O2'	50:A:1524:C:O2	2.24	0.50
50:A:209:U:H5''	50:A:210:C:OP2	2.11	0.50
2:C:38:VAL:HB	2:C:93:ILE:HG21	1.91	0.50
3:D:169:TRP:NE1	3:D:185:PRO:HG3	2.26	0.50
50:A:362:G:H2'	50:A:364:A:OP2	2.11	0.50
11:L:13:ARG:NH1	50:A:562:U:H5''	2.26	0.50
50:A:608:A:C6	50:A:609:A:C4	3.00	0.50
11:L:120:ARG:NH1	50:A:500:G:H5''	2.25	0.50
14:O:4:THR:OG1	14:O:5:GLU:OE1	2.29	0.50
19:T:67:HIS:HE1	19:T:69:ASN:HB2	1.77	0.50
23:2:5:ILE:HG21	23:2:57:VAL:HG13	1.88	0.50
3:D:2:ARG:NH2	50:A:404:G:OP1	2.38	0.50
50:A:458:U:H2'	50:A:459:A:C8	2.47	0.50
16:Q:3:LYS:HB3	50:A:637:C:OP2	2.12	0.50
50:A:861:G:HO2'	50:A:874:G:HO2'	1.59	0.50
8:I:125:GLN:CD	50:A:941:G:H1	2.15	0.50
9:J:46:LYS:HZ2	9:J:48:ARG:HE	1.60	0.50
13:N:19:TYR:CD2	13:N:51:PRO:HB3	2.46	0.50
15:P:20:VAL:HG21	15:P:32:PHE:CG	2.47	0.50
50:A:259:G:H2'	50:A:260:G:H8	1.76	0.50
50:A:401:C:H2'	50:A:402:G:C8	2.47	0.50
3:D:169:TRP:CE2	3:D:185:PRO:HG3	2.47	0.50
15:P:78:VAL:HG22	15:P:78:VAL:O	2.11	0.50
19:T:67:HIS:CE1	19:T:69:ASN:HB2	2.47	0.50
51:X:16:G:H8	51:X:16:G:O5'	1.95	0.50
50:A:1279:G:H4'	50:A:1281:C:H41	1.77	0.49
2:C:4:VAL:N	50:A:1190:G:OP2	2.45	0.49
3:D:60:VAL:O	3:D:63:ILE:HG22	2.12	0.49
8:I:27:ILE:CD1	8:I:48:ARG:HH11	2.25	0.49
18:S:44:ILE:HD13	18:S:63:ASP:OD1	2.11	0.49
50:A:155:A:H61	50:A:166:U:H3	1.60	0.49
50:A:266:G:H1'	50:A:268:U:OP2	2.11	0.49
50:A:279:A:H4'	50:A:280:C:OP2	2.11	0.49
50:A:373:A:H2	50:A:482:A:C8	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:115:GLN:HE21	3:D:119:HIS:CE1	2.30	0.49
4:E:51:LYS:NZ	50:A:1080:A:P	2.85	0.49
11:L:51:VAL:HG12	11:L:65:TYR:HA	1.94	0.49
50:A:1087:G:H22	50:A:1099:G:H1'	1.77	0.49
8:I:128:LYS:HD2	50:A:1341:U:N3	2.28	0.49
50:A:61:G:O2'	50:A:378:G:N2	2.44	0.49
2:C:19:SER:HB3	2:C:21:TRP:HE1	1.76	0.49
50:A:1346:A:C4'	50:A:1347:G:OP1	2.61	0.49
16:Q:68:LYS:NZ	50:A:253:A:OP1	2.35	0.49
50:A:503:C:H42	50:A:542:G:H1	1.61	0.49
50:A:957:U:H5''	50:A:958:A:OP2	2.12	0.49
1:B:138:ARG:O	1:B:142:LYS:HG2	2.12	0.49
2:C:52:SER:HB3	2:C:111:ASP:OD2	2.12	0.49
3:D:74:TYR:CE1	3:D:92:LEU:HB3	2.48	0.49
8:I:11:ARG:CA	8:I:105:ARG:NH2	2.51	0.49
26:6:1:MET:HE1	26:6:3:ARG:NH2	2.28	0.49
50:A:380:G:N2	50:A:383:A:OP2	2.45	0.49
50:A:411:A:N6	50:A:413:G:N3	2.61	0.49
50:A:468:A:N6	50:A:469:C:N3	2.60	0.49
50:A:601:G:H2'	50:A:602:A:C8	2.48	0.49
13:N:83:VAL:O	13:N:87:ALA:N	2.41	0.49
15:P:61:VAL:HA	15:P:65:ALA:H	1.76	0.49
15:P:70:ARG:HG2	50:A:375:U:H5''	1.53	0.49
50:A:983:A:H5''	50:A:984:C:OP2	2.12	0.49
3:D:18:LEU:HD22	3:D:63:ILE:HD13	1.93	0.49
8:I:51:LEU:HD11	8:I:62:LEU:HD11	1.94	0.49
10:K:28:ASN:HB2	50:A:690:G:OP2	2.13	0.49
13:N:63:CYS:SG	13:N:65:GLN:N	2.74	0.49
50:A:222:C:H2'	50:A:223:A:C8	2.48	0.49
50:A:402:G:H2'	50:A:403:C:H6	1.78	0.49
2:C:183:TYR:O	2:C:184:ASN:ND2	2.45	0.49
3:D:75:TYR:HE1	3:D:200:VAL:HG23	1.77	0.49
16:Q:14:ASP:OD2	16:Q:53:GLY:HA2	2.12	0.49
50:A:1380:U:H1'	50:A:1382:C:H41	1.78	0.49
50:A:1499:A:H1'	50:A:1520:C:H5'	1.94	0.49
1:B:150:ILE:HD11	1:B:153:MET:HE1	1.95	0.49
7:H:29:SER:HB2	50:A:589:U:H5''	1.95	0.49
8:I:125:GLN:NE2	50:A:941:G:O6	2.46	0.49
17:R:37:LYS:NZ	20:U:22:CYS:HB3	2.28	0.49
18:S:33:TRP:NE1	18:S:56:HIS:HE1	2.11	0.49
50:A:63:C:H42	50:A:104:G:H1	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:644:U:H2'	50:A:645:G:O4'	2.13	0.49
50:A:68:G:C2	50:A:69:G:H1'	2.47	0.49
50:A:720:C:OP2	50:A:721:G:H3'	2.13	0.49
4:E:105:ILE:HG21	4:E:123:LEU:HD12	1.94	0.49
6:G:125:ASP:HA	6:G:128:GLU:HG2	1.93	0.49
8:I:11:ARG:HD2	8:I:106:ASP:OD1	2.12	0.49
50:A:374:A:C5	50:A:375:U:H1'	2.48	0.49
50:A:374:A:H5''	50:A:375:U:H5	1.77	0.49
50:A:391:G:O6	50:A:392:C:N4	2.46	0.49
50:A:816:A:OP2	50:A:817:C:O2'	2.20	0.49
5:F:86:ARG:NH2	17:R:63:TYR:HB3	2.28	0.49
19:T:5:SER:O	19:T:8:LYS:HG2	2.13	0.49
17:R:38:ILE:N	50:A:719:C:O2	2.41	0.48
50:A:893:C:H2'	50:A:894:G:H8	1.78	0.48
50:A:895:G:C2	50:A:896:C:C2	3.01	0.48
50:A:900:A:H2'	50:A:901:A:H8	1.77	0.48
50:A:1036:A:H2'	50:A:1037:C:O4'	2.13	0.48
50:A:517:G:H21	50:A:530:G:P	2.37	0.48
6:G:64:ALA:HB1	6:G:126:ALA:HB3	1.94	0.48
15:P:12:LYS:HG2	15:P:13:LYS:HG2	1.94	0.48
8:I:128:LYS:HB2	50:A:1341:U:N1	2.28	0.48
50:A:910:C:H2'	50:A:911:U:C6	2.47	0.48
50:A:976:G:N2	50:A:1363:A:N3	2.60	0.48
50:A:987:G:H2'	50:A:988:G:H8	1.78	0.48
50:A:996:A:C2	50:A:997:U:C5	2.98	0.48
9:J:21:ALA:HA	9:J:24:GLU:HG2	1.95	0.48
9:J:70:HIS:HB2	9:J:72:ARG:NH1	2.23	0.48
13:N:41:TRP:O	13:N:44:VAL:HG12	2.14	0.48
15:P:42:ILE:HG22	15:P:43:ALA:N	2.28	0.48
17:R:60:ARG:HA	17:R:63:TYR:CD2	2.48	0.48
50:A:1007:U:H2'	50:A:1008:U:C6	2.48	0.48
50:A:35:G:H2'	50:A:36:C:H6	1.78	0.48
1:B:107:ARG:O	1:B:111:LYS:HG2	2.13	0.48
5:F:4:TYR:CZ	5:F:71:ILE:HG21	2.48	0.48
9:J:47:GLU:HB2	9:J:67:ILE:HG23	1.96	0.48
20:U:3:ILE:HG12	20:U:19:LYS:HG2	1.96	0.48
50:A:403:C:H2'	50:A:404:G:H8	1.78	0.48
1:B:124:THR:CB	1:B:136:ARG:HH21	2.26	0.48
6:G:103:ILE:HG21	6:G:123:LEU:HD21	1.95	0.48
8:I:34:LEU:HD22	8:I:38:PHE:HE2	1.78	0.48
16:Q:68:LYS:HB3	50:A:254:G:OP2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:54:GLN:HB3	19:T:55:PRO:HD3	1.96	0.48
50:A:109:A:OP2	50:A:110:C:H5	1.97	0.48
50:A:203:G:H21	50:A:205:A:N6	2.10	0.48
50:A:204:G:H2'	50:A:205:A:H8	1.77	0.48
13:N:66:THR:OG1	50:A:1202:U:O2'	2.25	0.48
50:A:1454:G:H2'	50:A:1455:G:C8	2.48	0.48
50:A:303:A:H5''	50:A:304:U:OP2	2.14	0.48
50:A:370:C:H2'	50:A:371:A:O4'	2.14	0.48
50:A:488:C:H2'	50:A:489:C:H6	1.79	0.48
3:D:123:MET:HG3	3:D:143:SER:HB2	1.95	0.48
4:E:71:ILE:HG21	4:E:144:GLU:HB2	1.96	0.48
50:A:70:U:O2'	50:A:94:G:O6	2.28	0.48
50:A:988:G:H1	50:A:1217:C:H42	1.62	0.48
1:B:127:LYS:HE3	1:B:129:THR:OG1	2.14	0.48
8:I:56:MET:O	8:I:58:GLU:N	2.46	0.48
10:K:116:PRO:C	10:K:118:ASN:H	2.17	0.48
19:T:54:GLN:HG3	19:T:75:LYS:HE3	1.96	0.48
24:3:43:ILE:HG22	24:3:49:TYR:HB2	1.96	0.48
50:A:1507:A:N7	50:A:1530:G:N2	2.61	0.48
4:E:22:LYS:HD3	4:E:29:ILE:HD11	1.95	0.48
8:I:111:GLU:OE1	8:I:111:GLU:HA	2.13	0.48
16:Q:20:ILE:HD12	16:Q:47:ASP:OD2	2.14	0.48
15:P:7:ALA:HB2	50:A:376:G:C2	2.48	0.48
50:A:782:A:C6	50:A:801:U:C2	3.02	0.48
1:B:124:THR:OG1	1:B:136:ARG:NH2	2.37	0.48
3:D:12:ARG:HH21	3:D:35:GLN:HB3	1.77	0.48
3:D:64:TYR:CE2	3:D:93:LEU:HB3	2.47	0.48
6:G:87:PRO:HD3	6:G:147:ASN:O	2.14	0.48
13:N:26:LEU:HA	13:N:30:ILE:HD12	1.96	0.48
50:A:1371:G:H2'	50:A:1372:U:C6	2.48	0.47
50:A:473:U:H2'	50:A:474:G:O4'	2.13	0.47
50:A:628:G:H2'	50:A:629:A:H8	1.78	0.47
50:A:824:G:H1	50:A:876:C:H42	1.62	0.47
7:H:15:ASN:ND2	50:A:826:C:O2	2.47	0.47
18:S:46:LEU:O	18:S:61:VAL:HG22	2.14	0.47
28:8:16:ILE:HD13	28:8:25:VAL:HG22	1.96	0.47
50:A:1021:A:H2'	50:A:1022:A:C8	2.49	0.47
50:A:1030:U:H5''	50:A:1031:C:C4	2.49	0.47
50:A:1341:U:H2'	50:A:1342:C:H4'	1.96	0.47
50:A:166:U:O4	50:A:167:A:N6	2.47	0.47
50:A:301:G:HO2'	50:A:302:G:C5'	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:17:TYR:HE1	50:A:374:A:H2	1.61	0.47
50:A:373:A:H5"	50:A:375:U:O4	2.14	0.47
15:P:5:ARG:HD2	50:A:376:G:H3'	1.44	0.47
10:K:126:ARG:NH1	50:A:693:G:OP1	2.42	0.47
6:G:106:ALA:HB1	6:G:132:THR:OG1	2.15	0.47
8:I:9:GLY:HA2	8:I:80:HIS:CD2	2.49	0.47
11:L:29:LYS:O	11:L:80:LEU:HD12	2.14	0.47
50:A:1253:G:H2'	50:A:1254:A:H8	1.79	0.47
18:S:40:PHE:CG	18:S:41:PRO:HD2	2.48	0.47
50:A:1219:A:N6	50:A:1220:G:O6	2.47	0.47
50:A:491:G:H2'	50:A:492:C:C6	2.50	0.47
50:A:742:G:H2'	50:A:743:A:H8	1.80	0.47
50:A:956:U:H3	50:A:960:U:H3	1.62	0.47
8:I:8:THR:O	8:I:81:GLY:HA2	2.14	0.47
15:P:11:ALA:O	15:P:12:LYS:C	2.52	0.47
50:A:1202:U:H2'	50:A:1203:C:O4'	2.15	0.47
50:A:1271:A:H5'	50:A:1314:C:H5"	1.96	0.47
50:A:932:C:O2	50:A:1386:G:N2	2.47	0.47
50:A:1486:G:H2'	50:A:1487:G:O4'	2.15	0.47
50:A:161:A:H2'	50:A:162:A:C8	2.49	0.47
3:D:7:LYS:NZ	50:A:408:A:OP2	2.37	0.47
50:A:692:U:O2	50:A:694:A:H5"	2.15	0.47
9:J:85:ASP:HA	9:J:89:ARG:HB2	1.96	0.47
18:S:32:THR:HG22	18:S:34:SER:N	2.27	0.47
19:T:33:LYS:HA	19:T:36:ALA:HB3	1.97	0.47
50:A:1237:C:H3'	50:A:1238:A:O4'	2.13	0.47
50:A:425:G:H2'	50:A:426:U:O4'	2.15	0.47
50:A:667:G:H2'	50:A:668:G:C8	2.47	0.47
50:A:696:A:N3	50:A:786:G:O2'	2.47	0.47
50:A:94:G:H5"	50:A:95:C:OP1	2.15	0.47
4:E:14:LEU:HB3	4:E:36:THR:HG22	1.96	0.47
7:H:101:ALA:HA	7:H:127:TYR:HB3	1.95	0.47
50:A:139:A:H2'	50:A:140:U:C6	2.50	0.47
1:B:217:ALA:HB1	1:B:221:ARG:HE	1.78	0.47
3:D:123:MET:O	3:D:143:SER:N	2.48	0.47
6:G:56:SER:HB2	6:G:59:GLU:HB2	1.97	0.47
7:H:91:LEU:HD11	7:H:103:VAL:HG21	1.96	0.47
8:I:6:TYR:CG	8:I:7:GLY:N	2.82	0.47
8:I:7:GLY:HA3	8:I:85:ALA:HB2	1.95	0.47
10:K:52:ARG:HE	10:K:56:LYS:HE2	1.80	0.47
15:P:75:ILE:C	15:P:77:GLU:H	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:5:ARG:HH12	50:A:636:U:C5'	2.27	0.47
10:K:108:ASN:CG	20:U:6:ARG:HE	2.17	0.47
50:A:1131:G:N1	50:A:1144:G:O2'	2.48	0.47
50:A:1277:C:O2'	50:A:1279:G:H8	1.97	0.47
50:A:1348:U:HO2'	50:A:1349:A:P	2.38	0.47
7:H:106:SER:HA	50:A:642:A:C5	2.48	0.47
1:B:75:ALA:HB1	1:B:163:ILE:HD13	1.97	0.47
10:K:121:ARG:NH2	20:U:34:ARG:HD2	2.29	0.47
13:N:81:ILE:HD11	50:A:1202:U:C2	2.49	0.47
18:S:15:LEU:HA	18:S:18:VAL:HG12	1.96	0.47
50:A:101:A:C4	50:A:102:G:C8	3.36	0.47
50:A:1342:C:H5'	50:A:1343:G:H5''	1.97	0.47
50:A:1391:U:H2'	50:A:1392:G:C8	2.33	0.47
50:A:584:G:H2'	50:A:585:G:H8	1.80	0.47
50:A:630:A:H2'	50:A:631:C:O4'	2.15	0.47
1:B:204:ASP:HA	1:B:209:VAL:HG21	1.96	0.47
2:C:76:ILE:HA	2:C:82:ASP:OD2	2.14	0.47
8:I:30:ASN:HD21	8:I:66:VAL:H	1.63	0.47
13:N:23:ARG:HB2	13:N:26:LEU:HD12	1.97	0.47
15:P:67:ILE:HG13	15:P:71:VAL:HG12	1.96	0.47
16:Q:5:ARG:HH12	50:A:636:U:C4'	2.27	0.47
50:A:822:U:O4	50:A:823:C:N4	2.48	0.47
16:Q:49:ASN:HB2	16:Q:51:GLU:OE2	2.14	0.47
28:8:22:VAL:HG11	28:8:36:ARG:HG3	1.98	0.46
50:A:1130:A:OP1	50:A:1130:A:C8	2.67	0.46
50:A:222:C:H2'	50:A:223:A:H8	1.79	0.46
4:E:14:LEU:HA	4:E:36:THR:HA	1.97	0.46
16:Q:13:SER:HA	16:Q:54:ILE:HG12	1.96	0.46
50:A:960:U:H2'	50:A:1225:A:H62	1.80	0.46
50:A:1439:G:C4	50:A:1440:U:H1'	2.50	0.46
50:A:691:G:O2'	50:A:696:A:N6	2.48	0.46
11:L:56:LEU:HD21	11:L:81:ILE:HG13	1.98	0.46
19:T:78:LEU:O	19:T:82:ILE:HG12	2.15	0.46
50:A:1361:G:O2'	50:A:1362:A:H5'	2.16	0.46
50:A:432:A:H2'	50:A:433:G:O4'	2.15	0.46
50:A:438:U:OP2	50:A:438:U:H6	1.98	0.46
50:A:53:A:H2'	50:A:53:A:N3	3.07	0.46
50:A:651:C:N4	50:A:752:G:O2'	2.49	0.46
2:C:22:PHE:HD1	9:J:13:PHE:CE2	2.33	0.46
15:P:48:GLU:CD	15:P:49:GLY:H	2.17	0.46
50:A:1371:G:H2'	50:A:1372:U:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1413:A:H2'	50:A:1414:U:H6	1.81	0.46
50:A:26:A:N6	50:A:558:G:H1'	2.30	0.46
50:A:39:G:C6	50:A:40:C:C4	3.03	0.46
50:A:63:C:N3	50:A:64:G:C8	8.41	0.46
8:I:125:GLN:HG2	50:A:941:G:H22	1.79	0.46
2:C:58:ARG:HG3	2:C:62:SER:O	2.15	0.46
3:D:84:ASN:OD1	4:E:101:GLY:HA3	2.15	0.46
4:E:44:ARG:HD2	4:E:70:MET:SD	2.55	0.46
50:A:412:A:C6	50:A:414:A:H1'	2.51	0.46
50:A:457:G:C2	50:A:476:U:C4	3.03	0.46
50:A:946:A:C6	50:A:947:G:C6	3.04	0.46
3:D:120:LYS:HE2	3:D:130:ASN:HD21	1.80	0.46
6:G:55:LYS:HE3	6:G:63:VAL:HG11	1.98	0.46
8:I:122:ARG:NH1	50:A:941:G:H1'	2.30	0.46
9:J:6:ILE:HG23	9:J:101:SER:O	2.16	0.46
14:O:76:ARG:O	14:O:79:ARG:HB3	2.16	0.46
20:U:27:VAL:O	20:U:27:VAL:HG12	2.16	0.46
50:A:107:G:O2'	50:A:378:G:O2'	2.34	0.46
12:M:101:THR:HG21	50:A:1226:C:OP2	2.15	0.46
50:A:154:U:H2'	50:A:155:A:C8	2.50	0.46
50:A:55:A:H5'	50:A:56:U:OP2	2.16	0.46
3:D:173:ASP:OD1	3:D:174:ALA:N	2.48	0.46
5:F:86:ARG:HH21	17:R:63:TYR:HB3	1.79	0.46
4:E:82:HIS:HE1	7:H:95:MET:SD	2.38	0.46
8:I:6:TYR:OH	8:I:8:THR:HG22	2.16	0.46
12:M:15:VAL:HB	12:M:40:GLU:HG2	1.97	0.46
13:N:24:ALA:O	13:N:28:ALA:N	2.47	0.46
17:R:32:ILE:HD13	17:R:67:LEU:HD13	1.98	0.46
22:1:18:LEU:HD21	22:1:53:VAL:CB	2.46	0.46
50:A:1124:G:H1'	50:A:1125:U:H5	1.80	0.46
50:A:956:U:H2'	50:A:957:U:O4'	2.16	0.46
18:S:25:GLY:O	18:S:27:LYS:HG2	2.16	0.46
50:A:1181:G:O2'	50:A:1182:G:N7	2.48	0.46
13:N:66:THR:HG1	50:A:1202:U:HO2'	1.58	0.46
50:A:730:G:H1'	50:A:765:G:O2'	2.16	0.46
50:A:773:G:N2	50:A:806:C:O2	2.49	0.46
9:J:10:LEU:HB3	9:J:18:ILE:HG13	1.98	0.46
10:K:127:ARG:NH2	50:A:1523:G:OP2	2.49	0.46
12:M:22:TYR:HB3	12:M:65:GLU:OE2	2.16	0.46
50:A:1096:C:O2	50:A:1170:A:O2'	2.33	0.46
50:A:1283:U:H2'	50:A:1284:C:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:109:A:C6	50:A:326:G:C6	3.04	0.46
50:A:968:A:H4'	50:A:969:A:OP2	2.15	0.46
1:B:203:ASP:OD1	1:B:204:ASP:N	2.49	0.46
1:B:71:THR:HG21	1:B:93:HIS:H	1.81	0.46
8:I:27:ILE:HD13	8:I:48:ARG:HH11	1.81	0.46
9:J:21:ALA:O	9:J:25:ILE:HG12	2.16	0.46
15:P:10:GLY:O	15:P:11:ALA:CB	2.64	0.46
17:R:49:LYS:HE3	50:A:663:A:H5''	1.97	0.46
50:A:1066:C:OP2	50:A:1066:C:C6	2.69	0.45
50:A:125:U:H2'	50:A:126:G:O4'	2.17	0.45
50:A:1427:C:H2'	50:A:1428:A:H8	1.80	0.45
50:A:199:A:H2'	50:A:200:G:H8	1.80	0.45
50:A:917:G:C6	50:A:918:A:C6	3.03	0.45
3:D:194:ILE:O	3:D:195:ASN:ND2	2.49	0.45
20:U:43:GLU:HG3	20:U:44:ARG:HG3	1.98	0.45
51:X:16:G:O2'	51:X:17:C:H5'	2.15	0.45
50:A:1060:U:H2'	50:A:1061:G:C8	2.49	0.45
50:A:153:C:H42	50:A:168:G:H1	1.64	0.45
50:A:209:U:OP2	50:A:210:C:H5	2.00	0.45
50:A:375:U:OP1	50:A:452:A:H1'	2.16	0.45
50:A:472:U:H2'	50:A:473:U:C6	2.51	0.45
16:Q:5:ARG:NH1	50:A:636:U:H5'	2.30	0.45
50:A:814:A:HO2'	50:A:1510:C:HO2'	1.64	0.45
1:B:121:GLN:HA	1:B:125:PHE:CE2	2.51	0.45
1:B:116:LEU:HD13	1:B:139:GLU:OE1	2.16	0.45
4:E:87:VAL:HG23	4:E:92:ARG:HG2	1.97	0.45
8:I:105:ARG:HD3	8:I:106:ASP:C	2.37	0.45
17:R:52:ARG:NH1	50:A:664:G:P	2.89	0.45
50:A:1300:G:O2'	50:A:1301:U:P	2.74	0.45
8:I:129:ARG:N	50:A:1341:U:O5'	2.39	0.45
50:A:1454:G:H2'	50:A:1455:G:H8	1.79	0.45
50:A:1526:G:H2'	50:A:1527:U:C6	2.52	0.45
50:A:299:G:H2'	50:A:300:A:C8	2.51	0.45
4:E:99:SER:HB2	50:A:6:G:H22	1.81	0.45
50:A:900:A:H2'	50:A:901:A:C8	2.51	0.45
1:B:17:HIS:CE1	1:B:189:ASN:HD22	2.27	0.45
50:A:1074:G:H1	50:A:1083:U:H3	1.65	0.45
50:A:487:A:H8	50:A:488:C:C6	2.35	0.45
50:A:790:A:H5''	50:A:791:G:OP2	2.16	0.45
3:D:139:ASN:N	3:D:181:PHE:O	2.49	0.45
4:E:25:LYS:HE2	50:A:923:A:OP1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:86:ARG:O	12:M:89:ARG:HB2	2.17	0.45
50:A:475:C:H2'	50:A:476:U:C6	2.51	0.45
1:B:70:GLY:HA2	1:B:168:GLU:HG3	1.99	0.45
2:C:35:ASP:HA	2:C:38:VAL:HG12	1.99	0.45
4:E:138:ALA:HA	4:E:141:ASP:HB2	1.98	0.45
8:I:11:ARG:CG	8:I:105:ARG:HH12	2.28	0.45
11:L:2:THR:HG22	11:L:4:ASN:H	1.82	0.45
17:R:23:LYS:HA	17:R:28:LEU:HD11	1.97	0.45
18:S:39:ILE:HD11	18:S:65:MET:HB3	1.99	0.45
19:T:34:VAL:O	19:T:38:ILE:HG12	2.17	0.45
50:A:117:G:N1	50:A:118:U:O2	2.50	0.45
15:P:6:LEU:C	50:A:376:G:N9	2.69	0.45
50:A:645:G:C2	50:A:646:G:C8	3.05	0.45
1:B:71:THR:OG1	1:B:92:ASN:HA	2.17	0.45
8:I:122:ARG:HA	50:A:1343:G:O2'	2.17	0.45
19:T:49:ALA:HA	19:T:52:GLU:HG2	1.98	0.45
50:A:1117:A:C6	50:A:1184:G:C6	3.04	0.45
50:A:1244:G:H2'	50:A:1245:C:C6	2.52	0.45
50:A:193:C:H2'	50:A:194:C:H6	1.78	0.45
50:A:243:A:H4'	50:A:244:U:O5'	2.16	0.45
50:A:550:G:H2'	50:A:551:U:H6	1.82	0.45
50:A:585:G:C2	50:A:586:C:C2	3.05	0.45
1:B:72:LYS:HE2	1:B:167:HIS:HD2	1.82	0.45
2:C:146:LYS:HG3	2:C:171:ARG:HG2	1.98	0.45
2:C:72:PRO:O	2:C:76:ILE:HG22	2.17	0.45
8:I:4:GLN:OE1	8:I:21:LYS:HG2	2.17	0.45
10:K:16:SER:HA	10:K:78:ILE:HA	1.98	0.45
15:P:37:GLY:HA2	15:P:51:ARG:HH11	1.82	0.45
10:K:88:PRO:CB	20:U:28:LEU:HD11	2.37	0.45
20:U:34:ARG:NH1	50:A:1524:C:OP1	2.49	0.45
50:A:1299:A:H5''	50:A:1300:G:OP2	2.17	0.45
12:M:99:GLN:NE2	50:A:1307:U:OP1	2.45	0.45
50:A:406:G:N2	50:A:437:U:O2	2.50	0.45
50:A:375:U:P	50:A:452:A:H1'	2.57	0.45
50:A:515:G:H2'	50:A:516:U:O4'	2.16	0.45
50:A:505:G:H4'	50:A:534:U:N3	2.31	0.45
50:A:63:C:N3	50:A:64:G:N7	8.57	0.45
50:A:997:U:HO2'	50:A:998:C:P	2.39	0.45
1:B:162:VAL:HB	1:B:184:ALA:HA	1.99	0.45
2:C:158:GLY:HA2	2:C:192:TYR:CD1	2.52	0.45
7:H:46:GLU:HB3	7:H:61:THR:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:18:LEU:HD21	22:1:53:VAL:HB	1.98	0.45
26:6:44:VAL:HG13	26:6:45:SER:H	1.82	0.45
50:A:1005:A:C2	50:A:1006:G:H1'	2.52	0.45
8:I:118:ARG:NH1	50:A:1234:C:OP1	2.49	0.45
50:A:43:C:H2'	50:A:44:A:O4'	2.16	0.45
50:A:575:G:OP1	50:A:575:G:H4'	2.17	0.45
50:A:584:G:H2'	50:A:585:G:C8	2.52	0.45
50:A:709:U:H2'	50:A:710:G:C8	2.52	0.45
3:D:173:ASP:HB3	3:D:178:GLU:H	1.82	0.45
3:D:90:LEU:HD11	3:D:196:GLU:HG2	1.98	0.45
7:H:40:LYS:HD3	7:H:48:PHE:CE1	2.52	0.45
9:J:57:VAL:HG11	50:A:964:A:O2'	2.17	0.45
9:J:6:ILE:HB	9:J:76:ILE:HG13	1.99	0.45
19:T:49:ALA:HA	19:T:52:GLU:OE2	2.16	0.45
50:A:109:A:OP2	50:A:110:C:C5	2.70	0.45
50:A:1124:G:O2'	50:A:1127:G:O6	2.33	0.45
50:A:368:U:O2'	50:A:369:G:OP1	2.34	0.45
50:A:562:U:H5''	50:A:563:A:OP1	2.17	0.45
50:A:608:A:H2'	50:A:609:A:O4'	2.17	0.45
2:C:190:THR:OG1	2:C:193:GLY:O	2.20	0.45
5:F:5:GLU:HA	5:F:63:ASN:HA	1.99	0.45
6:G:49:LEU:HD21	6:G:123:LEU:HB2	1.98	0.45
18:S:25:GLY:N	18:S:27:LYS:NZ	2.65	0.45
19:T:70:LYS:HG3	19:T:73:ARG:NH2	2.32	0.45
50:A:109:A:H4'	50:A:110:C:OP2	2.16	0.44
50:A:1200:C:H5''	50:A:1201:A:H3'	1.99	0.44
50:A:991:U:H3	50:A:1212:U:H4'	1.82	0.44
18:S:69:LYS:HZ1	50:A:1319:A:H5'	1.82	0.44
50:A:945:G:C2	50:A:946:A:C8	3.05	0.44
1:B:207:ARG:HG3	1:B:208:ALA:N	2.32	0.44
3:D:97:LEU:HA	3:D:100:VAL:HG22	1.99	0.44
5:F:6:ILE:HB	5:F:62:MET:HB2	1.99	0.44
15:P:29:ASN:ND2	50:A:376:G:O6	2.50	0.44
15:P:42:ILE:O	15:P:43:ALA:HB3	2.16	0.44
16:Q:43:LEU:HD21	16:Q:72:TRP:CG	2.53	0.44
51:X:20:U:C6	51:X:21:C:C2	3.05	0.44
50:A:1021:A:H2'	50:A:1022:A:H8	1.81	0.44
50:A:1347:G:OP1	50:A:1348:U:C6	2.70	0.44
1:B:46:VAL:HB	1:B:47:PRO:HD3	2.00	0.44
2:C:59:PRO:O	2:C:61:LYS:HG2	2.18	0.44
3:D:61:ARG:HA	3:D:71:PHE:HE2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:X:16:G:O5'	51:X:16:G:C8	2.70	0.44
50:A:1123:U:N3	50:A:1151:A:N1	2.66	0.44
50:A:702:A:C8	50:A:702:A:OP1	2.70	0.44
50:A:734:G:C2	50:A:735:C:C2	3.06	0.44
1:B:119:GLN:C	1:B:136:ARG:NH1	2.70	0.44
4:E:88:HIS:CE1	4:E:89:THR:HG23	2.52	0.44
11:L:35:ARG:HE	11:L:37:TYR:HE1	1.64	0.44
12:M:101:THR:OG1	50:A:1225:A:H5'	2.18	0.44
17:R:19:GLU:N	17:R:19:GLU:OE1	2.50	0.44
17:R:22:TYR:CE2	17:R:23:LYS:HD3	2.52	0.44
18:S:25:GLY:N	18:S:27:LYS:HZ3	2.16	0.44
50:A:374:A:H1'	50:A:451:A:O5'	2.17	0.44
3:D:131:ILE:HG12	50:A:620:C:C2	2.52	0.44
10:K:22:ILE:HG12	10:K:23:HIS:N	2.32	0.44
50:A:40:C:H2'	50:A:41:G:H8	1.83	0.44
50:A:5:U:H4'	50:A:6:G:O5'	2.16	0.44
7:H:112:ASP:OD1	7:H:113:ARG:N	2.51	0.44
13:N:68:ARG:HA	13:N:69:PRO:HD2	1.83	0.44
15:P:40:ASN:HA	15:P:41:PRO:HD2	1.86	0.44
15:P:56:ARG:HD2	15:P:56:ARG:HA	1.82	0.44
51:X:16:G:H2'	51:X:17:C:O5'	2.17	0.44
8:I:10:ARG:NH2	50:A:1148:U:H5'	2.29	0.44
50:A:1310:G:N2	50:A:1328:C:C2	2.86	0.44
50:A:1437:A:H2'	50:A:1438:G:H8	1.82	0.44
50:A:152:A:H62	50:A:169:C:N4	2.15	0.44
50:A:448:A:C6	50:A:487:A:C4	3.05	0.44
50:A:886:G:C6	50:A:887:G:C5	3.06	0.44
3:D:96:ARG:NH2	3:D:133:SER:OG	2.50	0.44
3:D:75:TYR:CE1	3:D:200:VAL:HG23	2.52	0.44
3:D:7:LYS:NZ	50:A:408:A:P	2.91	0.44
6:G:36:SER:O	6:G:39:GLU:HB3	2.17	0.44
8:I:120:ALA:HB1	50:A:1349:A:H5'	1.99	0.44
14:O:21:THR:O	50:A:750:C:O2'	2.34	0.44
50:A:101:A:C6	50:A:102:G:C5	3.43	0.44
50:A:217:C:OP2	50:A:217:C:H6	2.00	0.44
50:A:26:A:H5''	50:A:27:G:OP2	2.18	0.44
50:A:382:A:H2'	50:A:383:A:C8	2.53	0.44
50:A:98:A:H5'	50:A:99:C:OP2	2.18	0.44
1:B:116:LEU:HD23	1:B:119:GLN:HG3	2.00	0.44
3:D:14:GLU:HB2	3:D:62:ARG:NH2	2.32	0.44
15:P:16:PHE:O	15:P:16:PHE:CD1	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:71:VAL:O	15:P:75:ILE:HG13	2.18	0.44
50:A:1441:A:N6	50:A:1462:C:H1'	2.33	0.44
50:A:291:U:H2'	50:A:292:G:H8	1.81	0.44
6:G:63:VAL:HA	6:G:67:ASN:OD1	2.18	0.44
10:K:51:PHE:HD1	10:K:55:ARG:HB3	1.83	0.44
12:M:42:VAL:HB	12:M:46:GLU:HG3	2.00	0.44
13:N:9:GLU:O	13:N:13:VAL:HG23	2.18	0.44
3:D:106:PHE:CD1	3:D:158:LEU:HD21	2.51	0.44
6:G:22:LEU:O	6:G:26:VAL:HG23	2.17	0.44
9:J:5:ARG:HH11	9:J:79:PRO:HG2	1.81	0.44
9:J:48:ARG:NH1	13:N:100:TRP:CE3	2.86	0.44
13:N:25:GLU:HA	13:N:28:ALA:HB3	2.00	0.44
50:A:130:A:N1	50:A:233:C:O2'	2.47	0.43
16:Q:64:ARG:HD2	50:A:130:A:OP1	2.18	0.43
50:A:1348:U:O2'	50:A:1349:A:O5'	2.33	0.43
7:H:29:SER:OG	50:A:590:U:OP1	2.33	0.43
50:A:974:A:H8	50:A:974:A:OP1	2.01	0.43
3:D:12:ARG:HH22	3:D:36:ALA:H	1.64	0.43
50:A:1129:C:H4'	50:A:1130:A:OP2	2.17	0.43
50:A:1220:G:H2'	50:A:1221:G:H8	1.83	0.43
50:A:122:G:N3	50:A:122:G:H2'	2.32	0.43
50:A:1313:U:H3	50:A:1324:A:H61	1.66	0.43
50:A:462:G:H8	50:A:462:G:OP2	2.01	0.43
50:A:487:A:C8	50:A:488:C:C6	3.05	0.43
50:A:786:G:C6	50:A:787:A:C5	3.06	0.43
50:A:944:G:N2	50:A:1338:G:OP2	2.51	0.43
1:B:120:SER:CA	1:B:136:ARG:HH12	2.30	0.43
1:B:57:ASN:HA	1:B:60:ALA:HB3	2.00	0.43
8:I:105:ARG:HH11	8:I:106:ASP:N	2.10	0.43
10:K:107:THR:HG22	10:K:108:ASN:OD1	2.18	0.43
12:M:69:ARG:HA	12:M:72:ILE:HG22	2.00	0.43
17:R:33:THR:HG23	17:R:35:SER:H	1.83	0.43
18:S:55:GLN:N	18:S:55:GLN:OE1	2.52	0.43
50:A:1037:C:H2'	50:A:1038:C:C6	2.53	0.43
50:A:1135:U:O2	50:A:1138:G:N1	2.51	0.43
2:C:35:ASP:O	2:C:39:ARG:HG3	2.19	0.43
5:F:40:GLU:OE2	5:F:98:GLU:OE2	2.36	0.43
8:I:78:ILE:C	8:I:81:GLY:H	2.22	0.43
11:L:52:CYS:SG	11:L:66:ILE:HD11	2.58	0.43
50:A:1009:U:H5'	50:A:1010:U:OP2	2.18	0.43
50:A:1419:G:C4	50:A:1482:G:C2	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:549:C:C4	50:A:550:G:N7	2.86	0.43
50:A:811:C:O2'	50:A:901:A:N1	2.44	0.43
2:C:77:GLY:H	2:C:82:ASP:CG	2.21	0.43
4:E:61:LYS:HE2	50:A:1073:U:OP1	2.18	0.43
11:L:54:VAL:HG11	11:L:81:ILE:HD11	2.00	0.43
17:R:19:GLU:HG2	17:R:20:ILE:N	2.34	0.43
51:X:19:C:C4'	51:X:19:C:O2	2.66	0.43
22:1:15:ASN:HA	22:1:18:LEU:HD12	2.00	0.43
50:A:1004:A:H1'	50:A:1026:G:C5	2.53	0.43
50:A:1455:G:C2	50:A:1456:A:C4	3.07	0.43
50:A:317:U:H2'	50:A:318:G:C8	2.53	0.43
50:A:987:G:H2'	50:A:988:G:C8	2.52	0.43
5:F:45:ARG:HD2	5:F:59:TYR:HE2	1.84	0.43
9:J:5:ARG:N	9:J:79:PRO:HD3	2.33	0.43
12:M:14:ALA:HA	12:M:17:ALA:HB3	2.00	0.43
2:C:26:LYS:NZ	13:N:75:LYS:HG2	2.33	0.43
50:A:1157:A:N7	50:A:1180:A:N6	2.67	0.43
50:A:1306:A:C6	50:A:1307:U:C2	3.07	0.43
50:A:1234:C:HO2'	50:A:1364:U:H6	1.64	0.43
50:A:252:U:H2'	50:A:253:A:H8	1.84	0.43
50:A:54:C:H42	50:A:357:G:H1	1.66	0.43
12:M:2:ARG:HD3	12:M:7:ASN:HA	2.01	0.43
15:P:67:ILE:HG23	15:P:72:ALA:HB2	1.99	0.43
50:A:477:C:H2'	50:A:478:A:H8	1.83	0.43
50:A:499:A:C2	50:A:547:A:C5	3.07	0.43
7:H:114:ALA:HA	7:H:117:GLN:HE22	1.83	0.43
12:M:104:ASN:ND2	50:A:948:C:H3'	2.34	0.43
14:O:66:LEU:HD11	14:O:86:LEU:HD21	1.99	0.43
15:P:10:GLY:HA2	15:P:16:PHE:HB3	2.00	0.43
4:E:51:LYS:HZ1	50:A:1080:A:C5'	2.32	0.43
50:A:301:G:H2'	50:A:302:G:C8	2.54	0.43
50:A:348:G:O6	50:A:349:A:N6	2.52	0.43
50:A:412:A:H3'	50:A:413:G:H5''	1.99	0.43
50:A:419:C:H2'	50:A:420:U:O4'	2.18	0.43
50:A:636:U:H5'	50:A:637:C:OP2	2.19	0.43
4:E:40:ASP:OD2	4:E:44:ARG:HB2	2.19	0.43
5:F:42:TRP:HB3	5:F:45:ARG:NH2	2.18	0.43
6:G:61:PHE:O	6:G:65:LEU:N	2.49	0.43
8:I:11:ARG:CB	8:I:105:ARG:HH12	2.32	0.43
8:I:126:PHE:O	8:I:127:SER:HB2	2.18	0.43
15:P:48:GLU:CG	15:P:49:GLY:N	2.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1529:G:H5''	50:A:1530:G:OP2	2.18	0.43
50:A:224:U:H2'	50:A:225:C:C6	2.54	0.43
50:A:286:C:H2'	50:A:287:U:C6	2.53	0.43
50:A:421:U:H5''	50:A:422:C:H5	1.84	0.43
50:A:448:A:N6	50:A:487:A:C4	2.87	0.43
50:A:563:A:H2'	50:A:563:A:N3	2.33	0.43
8:I:122:ARG:HG2	50:A:1350:A:OP1	2.19	0.43
17:R:24:ASP:O	17:R:28:LEU:HG	2.19	0.43
50:A:1330:U:H5''	50:A:1331:G:OP2	2.18	0.43
50:A:202:G:H2'	50:A:203:G:O4'	2.18	0.43
50:A:631:C:H5''	50:A:632:U:H5'	2.01	0.43
50:A:892:A:C6	50:A:893:C:N3	2.87	0.43
1:B:8:MET:HG3	1:B:14:HIS:HE2	1.84	0.43
3:D:66:VAL:HG23	3:D:70:GLN:HB2	2.01	0.43
6:G:114:SER:O	6:G:118:ARG:HG3	2.18	0.43
15:P:6:LEU:O	50:A:376:G:C4	2.72	0.43
20:U:16:ARG:HA	20:U:19:LYS:HZ3	1.84	0.43
51:X:13:C:O2	51:X:13:C:H2'	2.19	0.43
50:A:20:U:H2'	50:A:21:G:O4'	2.19	0.42
50:A:241:G:C6	50:A:242:G:C5	3.07	0.42
16:Q:67:SER:OG	50:A:255:G:OP2	2.37	0.42
50:A:690:G:H2'	50:A:691:G:O4'	2.19	0.42
50:A:727:G:C2	50:A:731:G:C2	3.07	0.42
50:A:842:U:H3'	50:A:843:U:H4'	2.01	0.42
3:D:72:ARG:O	3:D:76:LYS:HG2	2.18	0.42
50:A:1066:C:H6	50:A:1066:C:OP2	2.02	0.42
50:A:1320:C:OP2	50:A:1321:U:OP2	2.38	0.42
50:A:1415:G:C2	50:A:1486:G:C5	3.07	0.42
50:A:6:G:H2'	50:A:6:G:N3	2.34	0.42
50:A:570:G:H1	50:A:866:C:H42	1.67	0.42
3:D:170:LEU:HD12	3:D:170:LEU:O	2.19	0.42
3:D:201:GLU:O	3:D:204:SER:OG	2.33	0.42
10:K:39:ASN:HD22	50:A:683:G:H21	1.67	0.42
15:P:77:GLU:C	15:P:79:ASN:N	2.73	0.42
50:A:99:C:O2'	50:A:100:G:H8	1.99	0.42
50:A:1162:C:H2'	50:A:1163:A:H8	1.84	0.42
18:S:77:ARG:HH21	50:A:1222:G:H5''	1.84	0.42
50:A:374:A:H5'	50:A:452:A:C6	2.54	0.42
50:A:33:A:OP2	50:A:398:U:H5'	2.20	0.42
50:A:82:G:N7	50:A:83:C:H1'	2.34	0.42
50:A:80:A:N6	50:A:90:C:H42	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:182:LYS:HZ1	3:D:183:ARG:HH12	1.66	0.42
3:D:63:ILE:HG23	3:D:64:TYR:CD1	2.55	0.42
4:E:88:HIS:CD2	4:E:137:ARG:HG3	2.55	0.42
7:H:28:SER:HB2	7:H:58:LEU:HB2	2.00	0.42
8:I:105:ARG:CD	8:I:106:ASP:H	2.18	0.42
8:I:42:THR:O	8:I:46:VAL:HG23	2.19	0.42
16:Q:16:MET:HB2	16:Q:19:SER:HB2	2.01	0.42
10:K:88:PRO:HG3	20:U:28:LEU:HD11	0.66	0.42
27:7:62:LEU:HB3	27:7:65:ALA:HB2	2.00	0.42
50:A:1099:G:C5	50:A:1100:C:C4	3.07	0.42
50:A:1110:A:N6	50:A:1111:A:C6	2.87	0.42
50:A:1111:A:O2'	50:A:1112:C:H6	2.01	0.42
50:A:47:C:O2	50:A:47:C:H2'	3.95	0.42
50:A:757:U:O2'	50:A:879:C:H1'	2.19	0.42
6:G:142:ARG:O	6:G:146:ALA:N	2.44	0.42
8:I:105:ARG:CD	8:I:106:ASP:O	2.67	0.42
14:O:5:GLU:O	14:O:9:LYS:HG2	2.19	0.42
17:R:23:LYS:HZ3	17:R:61:ALA:HA	1.83	0.42
50:A:1270:G:C2	50:A:1271:A:C4	3.07	0.42
50:A:1236:A:N6	50:A:1337:G:O6	2.52	0.42
50:A:190:A:C2	50:A:191:G:H1'	2.54	0.42
50:A:919:A:O5'	50:A:919:A:H8	2.02	0.42
50:A:97:G:C5	50:A:98:A:H1'	2.55	0.42
7:H:84:ILE:HD12	7:H:86:LYS:HZ3	1.83	0.42
15:P:17:TYR:CD1	15:P:17:TYR:N	2.86	0.42
15:P:33:ILE:O	15:P:34:GLU:HB3	2.18	0.42
16:Q:57:VAL:HG23	16:Q:78:VAL:HB	2.02	0.42
19:T:28:ARG:O	19:T:32:LYS:HG2	2.19	0.42
50:A:1242:G:H2'	50:A:1243:C:C6	2.54	0.42
50:A:1253:G:H2'	50:A:1254:A:C8	2.54	0.42
50:A:1526:G:H2'	50:A:1527:U:H6	1.82	0.42
50:A:235:C:H2'	50:A:236:A:H8	1.85	0.42
50:A:322:C:OP2	50:A:328:C:H5	2.01	0.42
50:A:374:A:H3'	50:A:375:U:H6	1.84	0.42
50:A:374:A:H5'	50:A:452:A:N1	2.34	0.42
50:A:571:U:O4	50:A:864:A:N6	2.53	0.42
50:A:73:C:H2'	50:A:74:A:C8	2.54	0.42
2:C:146:LYS:HB3	2:C:202:PHE:CD2	2.54	0.42
13:N:27:LYS:O	13:N:31:SER:HB2	2.20	0.42
21:O:67:VAL:O	21:O:71:LEU:HG	2.18	0.42
50:A:974:A:H4'	50:A:975:A:H5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:171:GLU:HB2	3:D:180:THR:OG1	2.20	0.42
11:L:23:LEU:HD22	11:L:58:ASN:HB2	2.01	0.42
13:N:20:PHE:CD2	13:N:24:ALA:HB1	2.54	0.42
20:U:16:ARG:HA	20:U:19:LYS:HZ2	1.85	0.42
9:J:61:ALA:HB2	50:A:1061:G:H5'	2.00	0.42
50:A:1129:C:H42	50:A:1143:G:H1	1.68	0.42
50:A:1140:C:H2'	50:A:1141:C:H6	1.84	0.42
50:A:1401:G:C6	50:A:1402:C:C2	3.08	0.42
50:A:1452:C:O2	50:A:1453:G:N1	2.53	0.42
50:A:1499:A:OP2	50:A:1500:A:OP2	2.38	0.42
50:A:184:G:C4'	50:A:185:U:OP1	2.68	0.42
50:A:190:A:H2'	50:A:191:G:O4'	2.20	0.42
50:A:572:A:H5'	50:A:573:A:OP2	2.20	0.42
50:A:640:A:N6	50:A:641:U:O4	2.50	0.42
50:A:836:G:H1	50:A:850:U:H3	1.68	0.42
4:E:107:GLY:HA3	50:A:8:A:H1'	2.02	0.42
1:B:166:ASP:OD1	1:B:190:SER:OG	2.36	0.42
1:B:17:HIS:HE1	1:B:189:ASN:ND2	2.14	0.42
8:I:38:PHE:C	8:I:40:ARG:H	2.23	0.42
15:P:10:GLY:HA3	15:P:15:PRO:CA	2.49	0.42
50:A:1083:U:O2'	50:A:1102:A:OP2	2.38	0.42
50:A:1233:G:OP1	50:A:1342:C:N4	2.53	0.42
50:A:505:G:H8	50:A:505:G:O5'	2.03	0.42
50:A:94:G:H4'	50:A:95:C:O5'	2.20	0.42
5:F:11:HIS:CE1	5:F:13:ASP:HB2	2.54	0.42
8:I:113:LYS:HZ1	8:I:117:LEU:CD2	2.24	0.42
15:P:12:LYS:HE3	50:A:393:A:OP2	2.19	0.42
15:P:15:PRO:HG2	15:P:41:PRO:HG3	2.02	0.42
4:E:131:ASN:ND2	50:A:18:C:OP1	2.53	0.42
50:A:352:C:N3	50:A:356:A:N6	2.68	0.42
50:A:539:A:N6	50:A:540:G:O6	2.53	0.42
50:A:551:U:N3	50:A:552:U:C4	2.88	0.42
50:A:60:A:N1	50:A:107:G:O2'	2.36	0.42
7:H:10:LEU:HD22	7:H:74:ILE:HD11	2.01	0.42
10:K:51:PHE:O	10:K:52:ARG:HD2	2.19	0.42
11:L:32:VAL:O	11:L:54:VAL:HG23	2.20	0.42
13:N:63:CYS:SG	13:N:64:ARG:N	2.92	0.42
15:P:12:LYS:HG3	50:A:392:C:O5'	2.15	0.42
16:Q:18:LYS:HB3	16:Q:46:HIS:CE1	2.55	0.42
17:R:23:LYS:NZ	17:R:61:ALA:HA	2.35	0.42
4:E:51:LYS:NZ	50:A:1080:A:H5''	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:1151:A:O2'	50:A:1152:A:H5''	2.19	0.41
50:A:1300:G:C2	50:A:1334:G:C6	3.08	0.41
50:A:235:C:H2'	50:A:236:A:C8	2.55	0.41
50:A:342:C:H2'	50:A:342:C:OP2	2.20	0.41
1:B:30:ILE:HD11	1:B:38:HIS:CG	2.55	0.41
3:D:104:MET:HG2	3:D:172:VAL:HG22	2.02	0.41
3:D:120:LYS:HB2	3:D:145:ARG:NH1	2.35	0.41
50:A:1415:G:H2'	50:A:1416:G:H8	1.85	0.41
50:A:1430:A:N6	50:A:1431:A:N1	2.68	0.41
50:A:160:A:H2'	50:A:161:A:O4'	2.20	0.41
50:A:248:C:H2'	50:A:249:U:O4'	2.20	0.41
50:A:299:G:H2'	50:A:300:A:H8	1.84	0.41
50:A:459:A:C6	50:A:460:A:C6	3.08	0.41
50:A:498:A:O2'	50:A:499:A:P	2.79	0.41
50:A:769:G:H2'	50:A:770:C:H6	1.85	0.41
1:B:124:THR:H	1:B:136:ARG:NH2	2.18	0.41
3:D:130:ASN:HB2	50:A:619:U:H3	1.85	0.41
3:D:150:LYS:O	3:D:155:LYS:NZ	2.50	0.41
4:E:100:GLU:N	4:E:100:GLU:OE1	2.53	0.41
5:F:32:ALA:O	5:F:34:GLY:N	2.47	0.41
8:I:110:VAL:HB	50:A:1348:U:OP2	2.20	0.41
9:J:10:LEU:O	9:J:71:LEU:HD12	2.19	0.41
14:O:21:THR:HB	50:A:657:U:O2	2.20	0.41
50:A:17:U:O2'	50:A:1079:G:O2'	2.26	0.41
50:A:374:A:H3'	50:A:375:U:C6	2.55	0.41
50:A:700:G:H3'	50:A:701:U:H5''	2.01	0.41
50:A:859:G:H2'	50:A:860:A:H8	1.84	0.41
50:A:988:G:N1	50:A:989:U:C2	2.88	0.41
2:C:185:THR:HG22	2:C:198:LYS:HG2	2.02	0.41
3:D:14:GLU:HB2	3:D:62:ARG:HH21	1.85	0.41
8:I:11:ARG:HA	8:I:105:ARG:HH12	1.84	0.41
11:L:74:GLN:OE1	11:L:76:HIS:HE1	2.04	0.41
13:N:1:ALA:N	13:N:66:THR:O	2.53	0.41
15:P:20:VAL:HG22	15:P:32:PHE:HB2	2.01	0.41
50:A:1067:A:N1	50:A:1108:G:O2'	2.52	0.41
50:A:1242:G:C5	50:A:1243:C:C4	3.09	0.41
50:A:1310:G:H2'	50:A:1311:A:O4'	2.20	0.41
50:A:196:A:OP2	50:A:196:A:C8	2.73	0.41
50:A:246:A:O2'	50:A:279:A:N6	2.53	0.41
50:A:448:A:C5	50:A:487:A:C6	3.08	0.41
7:H:104:SER:OG	50:A:642:A:N3	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:671:G:N2	50:A:672:U:H1'	2.35	0.41
50:A:68:G:N1	50:A:69:G:H1'	2.36	0.41
50:A:797:C:H2'	50:A:798:U:C6	2.55	0.41
2:C:71:ARG:HA	2:C:72:PRO:HD2	1.87	0.41
4:E:81:GLN:HE22	4:E:149:PRO:HD3	1.85	0.41
7:H:77:VAL:HG12	7:H:84:ILE:HD11	2.01	0.41
8:I:11:ARG:C	8:I:105:ARG:HH22	2.23	0.41
8:I:27:ILE:HG13	8:I:62:LEU:HD12	2.02	0.41
11:L:45:ASN:ND2	50:A:528:C:H41	2.17	0.41
12:M:93:GLY:O	12:M:108:ARG:HB3	2.19	0.41
13:N:5:MET:HB3	13:N:62:ARG:HH12	1.85	0.41
20:U:26:GLY:C	20:U:28:LEU:N	2.73	0.41
50:A:1004:A:H5'	50:A:1024:G:H22	1.85	0.41
50:A:1296:C:N4	50:A:1297:G:O6	2.53	0.41
50:A:1237:C:O2	50:A:1335:U:H5'	2.19	0.41
50:A:1350:A:H5''	50:A:1351:U:OP2	2.20	0.41
50:A:1362:A:H8	50:A:1362:A:OP2	2.04	0.41
50:A:148:G:H1	50:A:174:A:H61	1.68	0.41
50:A:261:U:H2'	50:A:263:A:OP2	2.20	0.41
50:A:402:G:H2'	50:A:403:C:C6	2.55	0.41
50:A:462:G:OP2	50:A:462:G:H2'	2.20	0.41
50:A:586:C:H2'	50:A:587:G:H5''	2.02	0.41
50:A:877:G:H2'	50:A:878:A:C8	2.52	0.41
2:C:35:ASP:O	2:C:38:VAL:HG12	2.20	0.41
7:H:21:LYS:HE2	50:A:827:U:H5''	2.02	0.41
7:H:5:PRO:O	7:H:8:ASP:HB2	2.21	0.41
15:P:70:ARG:O	15:P:70:ARG:HG3	2.20	0.41
18:S:51:HIS:CD2	18:S:53:GLY:H	2.39	0.41
21:O:7:VAL:HG21	21:O:59:ILE:HD11	2.02	0.41
50:A:1377:A:HO2'	50:A:1378:C:P	2.43	0.41
6:G:77:ARG:HB2	50:A:1381:U:C2	2.56	0.41
50:A:318:G:H1	50:A:335:C:H42	1.67	0.41
50:A:373:A:N1	50:A:481:G:H4'	2.35	0.41
50:A:836:G:C6	50:A:837:U:C2	3.09	0.41
1:B:100:LEU:HB2	1:B:174:GLU:CD	2.41	0.41
1:B:14:HIS:O	1:B:202:ASN:HB3	2.20	0.41
3:D:64:TYR:CD2	3:D:93:LEU:HB3	2.55	0.41
8:I:11:ARG:HH21	50:A:1347:G:H1	1.67	0.41
9:J:29:ALA:HB1	9:J:36:VAL:HG11	2.03	0.41
18:S:19:GLU:HA	18:S:22:VAL:HG13	2.02	0.41
20:U:38:GLU:HG3	50:A:1527:U:OP2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:11:VAL:O	22:1:15:ASN:ND2	2.53	0.41
50:A:143:A:H2	50:A:220:G:H1	1.67	0.41
50:A:182:A:H3'	50:A:182:A:OP2	2.21	0.41
50:A:259:G:H2'	50:A:260:G:C8	2.56	0.41
50:A:97:G:H5'	50:A:98:A:OP2	2.21	0.41
1:B:63:LYS:HZ1	1:B:88:GLN:HE22	1.67	0.41
2:C:6:PRO:HB3	2:C:10:ARG:NH1	2.36	0.41
6:G:115:MET:HA	6:G:118:ARG:HB2	2.02	0.41
6:G:75:LYS:HZ2	6:G:77:ARG:HH22	1.68	0.41
7:H:94:VAL:HG11	7:H:127:TYR:CD2	2.55	0.41
10:K:84:MET:HG2	10:K:110:THR:OG1	2.21	0.41
13:N:66:THR:HG23	13:N:68:ARG:H	1.85	0.41
50:A:1157:A:C2	50:A:1181:G:C5	3.08	0.41
50:A:1418:A:H5''	50:A:1419:G:OP2	2.21	0.41
50:A:1421:G:C2	50:A:1480:A:C2	3.08	0.41
50:A:150:U:H3	50:A:171:A:H62	1.69	0.41
50:A:184:G:H1'	50:A:185:U:O5'	2.21	0.41
50:A:299:G:N2	50:A:566:G:O6	2.51	0.41
50:A:946:A:C2	50:A:947:G:C4	3.09	0.41
12:M:102:LYS:HE3	50:A:952:U:O4	2.21	0.41
5:F:44:ARG:HA	5:F:58:HIS:HA	2.03	0.41
8:I:29:ILE:N	8:I:32:ARG:O	2.35	0.41
8:I:11:ARG:NH1	8:I:73:GLY:HA2	2.36	0.41
12:M:85:TYR:OH	12:M:89:ARG:NH2	2.52	0.41
27:7:26:HIS:NE2	27:7:48:ALA:HB2	2.36	0.41
50:A:1302:C:OP2	50:A:1302:C:H4'	2.20	0.41
50:A:218:U:H2'	50:A:219:U:O4'	2.21	0.41
50:A:444:G:C6	50:A:491:G:C2	3.08	0.41
50:A:550:G:H2'	50:A:551:U:C6	2.55	0.41
10:K:21:HIS:CE1	50:A:707:U:H5''	2.56	0.41
50:A:797:C:H2'	50:A:798:U:H6	1.85	0.41
50:A:997:U:O2'	50:A:998:C:P	2.79	0.41
1:B:118:THR:O	1:B:122:ASP:N	2.53	0.41
2:C:79:LYS:HB3	2:C:80:GLY:H	1.69	0.41
2:C:8:GLY:HA2	2:C:11:LEU:HG	2.03	0.41
3:D:74:TYR:CD1	3:D:92:LEU:HB3	2.56	0.41
8:I:70:GLY:HA3	50:A:1371:G:O3'	2.21	0.41
8:I:90:ASP:OD2	8:I:92:SER:HB3	2.21	0.41
10:K:127:ARG:HH22	50:A:1522:U:H5''	1.84	0.41
50:A:11:G:N2	50:A:24:U:O2	2.54	0.41
50:A:341:C:N4	50:A:342:C:H41	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:98:ASP:OD1	3:D:99:ASN:N	2.53	0.41
4:E:12:GLU:HG3	4:E:38:VAL:HG22	2.01	0.41
4:E:146:MET:O	4:E:147:ASN:HB2	2.20	0.41
8:I:35:GLU:OE1	8:I:44:ARG:NH2	2.54	0.41
17:R:54:LEU:HA	17:R:54:LEU:HD23	1.90	0.41
50:A:1157:A:C5	50:A:1180:A:C6	3.08	0.41
50:A:1389:C:H2'	50:A:1390:U:O4'	2.20	0.41
50:A:1510:C:H2'	50:A:1511:G:H8	1.86	0.41
50:A:247:G:H2'	50:A:248:C:C6	2.56	0.41
50:A:254:G:H1	50:A:272:C:H42	1.69	0.41
50:A:577:G:C2	50:A:765:G:C8	3.09	0.41
50:A:602:A:H2'	50:A:603:U:O4'	2.21	0.41
50:A:680:C:H2'	50:A:681:A:H8	1.86	0.41
50:A:960:U:O2	50:A:1225:A:N6	2.54	0.41
50:A:998:C:C2'	50:A:998:C:O2	2.70	0.41
3:D:107:GLY:O	3:D:157:ALA:HB1	2.21	0.41
3:D:199:ILE:HG13	3:D:200:VAL:N	2.35	0.41
6:G:55:LYS:HB3	6:G:56:SER:H	1.66	0.41
13:N:5:MET:HG2	13:N:8:ARG:HH21	1.86	0.41
17:R:27:THR:O	17:R:30:ASN:HB2	2.20	0.41
18:S:23:GLU:N	18:S:23:GLU:OE1	2.54	0.41
19:T:80:ALA:O	19:T:84:LYS:HG2	2.21	0.41
10:K:125:LYS:NZ	20:U:32:ARG:NE	2.69	0.41
20:U:44:ARG:HB3	20:U:47:ALA:HB2	2.02	0.41
50:A:1116:U:N3	50:A:1117:A:N7	2.70	0.40
50:A:1440:U:H5'	50:A:1441:A:OP2	2.21	0.40
50:A:35:G:H2'	50:A:36:C:C6	2.56	0.40
50:A:459:A:H2'	50:A:460:A:C8	2.56	0.40
50:A:698:G:C6	50:A:699:C:C4	3.09	0.40
3:D:187:ARG:NH1	3:D:196:GLU:CD	2.73	0.40
15:P:56:ARG:NH1	15:P:59:HIS:CD2	2.90	0.40
50:A:1087:G:N1	50:A:1099:G:N3	2.69	0.40
50:A:1285:A:H4'	50:A:1286:U:O4'	2.22	0.40
50:A:1436:U:OP2	50:A:1436:U:H6	2.04	0.40
50:A:1439:G:N1	50:A:1440:U:O2	2.54	0.40
50:A:174:A:OP1	50:A:175:C:OP2	2.39	0.40
50:A:632:U:H3'	50:A:633:G:O4'	2.21	0.40
50:A:671:G:H21	50:A:672:U:H1'	1.86	0.40
50:A:697:U:H2'	50:A:698:G:H5'	2.02	0.40
50:A:5:U:H5'	50:A:6:G:C4	2.56	0.40
1:B:153:MET:SD	1:B:157:PRO:HD3	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:75:LYS:NZ	6:G:77:ARG:HH22	2.19	0.40
8:I:78:ILE:O	8:I:82:ILE:HG12	2.21	0.40
15:P:5:ARG:HH12	15:P:24:SER:HA	1.87	0.40
11:L:4:ASN:ND2	16:Q:35:LYS:HE2	2.30	0.40
18:S:45:GLY:N	18:S:61:VAL:HG23	2.37	0.40
50:A:102:G:N1	50:A:103:U:C5	3.72	0.40
50:A:1063:C:H42	50:A:1193:G:H1	1.68	0.40
50:A:146:G:N2	50:A:147:G:H1'	2.35	0.40
50:A:345:C:H4'	50:A:346:G:H5''	2.02	0.40
50:A:427:U:C4	50:A:428:G:N7	2.89	0.40
50:A:859:G:OP2	50:A:869:G:C2	2.74	0.40
50:A:995:C:H2'	50:A:996:A:H5''	2.02	0.40
50:A:997:U:C2'	50:A:997:U:O2	2.69	0.40
1:B:18:GLN:HB2	1:B:21:TYR:CD2	2.55	0.40
1:B:68:PHE:CD2	1:B:83:ALA:HB2	2.56	0.40
11:L:44:PRO:O	11:L:45:ASN:ND2	2.54	0.40
17:R:48:ALA:O	17:R:52:ARG:HG2	2.21	0.40
18:S:62:THR:HG22	18:S:63:ASP:N	2.37	0.40
50:A:1095:U:H2'	50:A:1096:C:C6	2.56	0.40
50:A:1347:G:C5'	50:A:1348:U:C6	2.93	0.40
50:A:302:G:H21	50:A:556:C:C4'	2.34	0.40
50:A:869:G:O5'	50:A:869:G:H8	2.04	0.40
1:B:54:ALA:HA	1:B:57:ASN:HB2	2.04	0.40
2:C:25:THR:HG22	2:C:26:LYS:HG3	2.02	0.40
10:K:48:GLY:C	10:K:68:ARG:HH12	2.25	0.40
13:N:6:LYS:O	13:N:9:GLU:HB3	2.21	0.40
50:A:100:G:C2	50:A:101:A:H1'	3.03	0.40
50:A:1065:U:C1'	50:A:1066:C:OP2	2.70	0.40
50:A:1339:A:OP2	50:A:1339:A:C8	2.74	0.40
50:A:22:G:H5''	50:A:561:U:C4	2.57	0.40
1:B:145:ASN:OD1	1:B:146:SER:N	2.54	0.40
4:E:20:VAL:O	4:E:30:PHE:HA	2.21	0.40
8:I:126:PHE:HB3	50:A:1342:C:P	2.61	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	
1	B	216/241 (90%)	186 (86%)	22 (10%)	8 (4%)	4	40
2	C	204/233 (88%)	173 (85%)	22 (11%)	9 (4%)	3	34
3	D	203/206 (98%)	179 (88%)	19 (9%)	5 (2%)	7	49
4	E	148/167 (89%)	125 (84%)	18 (12%)	5 (3%)	5	43
5	F	98/131 (75%)	82 (84%)	12 (12%)	4 (4%)	3	37
6	G	148/156 (95%)	128 (86%)	15 (10%)	5 (3%)	5	43
7	H	127/130 (98%)	111 (87%)	12 (9%)	4 (3%)	5	46
8	I	125/130 (96%)	99 (79%)	20 (16%)	6 (5%)	3	32
9	J	96/103 (93%)	77 (80%)	11 (12%)	8 (8%)	1	16
10	K	115/129 (89%)	101 (88%)	13 (11%)	1 (1%)	21	68
11	L	121/124 (98%)	100 (83%)	16 (13%)	5 (4%)	3	37
12	M	111/118 (94%)	100 (90%)	9 (8%)	2 (2%)	11	56
13	N	92/101 (91%)	78 (85%)	7 (8%)	7 (8%)	1	19
14	O	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	8	52
15	P	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	9
16	Q	78/84 (93%)	67 (86%)	9 (12%)	2 (3%)	7	48
17	R	53/75 (71%)	49 (92%)	4 (8%)	0	100	100
18	S	77/92 (84%)	66 (86%)	9 (12%)	2 (3%)	7	48
19	T	83/87 (95%)	78 (94%)	3 (4%)	2 (2%)	7	51
20	U	49/71 (69%)	39 (80%)	6 (12%)	4 (8%)	1	17
21	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
22	1	60/63 (95%)	51 (85%)	7 (12%)	2 (3%)	5	44
23	2	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	11	56
24	3	54/57 (95%)	49 (91%)	3 (6%)	2 (4%)	4	40
25	4	48/55 (87%)	41 (85%)	7 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	6	44/46 (96%)	41 (93%)	1 (2%)	2 (4%)	3	34
27	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
28	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
29	c	269/273 (98%)	252 (94%)	16 (6%)	1 (0%)	39	80
30	d	207/209 (99%)	195 (94%)	10 (5%)	2 (1%)	19	66
31	e	199/201 (99%)	186 (94%)	5 (2%)	8 (4%)	4	37
32	f	175/179 (98%)	154 (88%)	15 (9%)	6 (3%)	5	43
33	g	174/177 (98%)	139 (80%)	30 (17%)	5 (3%)	6	47
34	h	147/149 (99%)	120 (82%)	19 (13%)	8 (5%)	2	29
35	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	14	60
36	k	120/123 (98%)	112 (93%)	6 (5%)	2 (2%)	11	57
37	l	142/144 (99%)	128 (90%)	9 (6%)	5 (4%)	4	43
38	m	131/136 (96%)	125 (95%)	5 (4%)	1 (1%)	24	70
39	n	118/127 (93%)	111 (94%)	4 (3%)	3 (2%)	7	49
40	o	114/117 (97%)	107 (94%)	2 (2%)	5 (4%)	3	34
41	p	112/115 (97%)	106 (95%)	5 (4%)	1 (1%)	21	68
42	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
43	r	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	19	66
44	s	108/110 (98%)	103 (95%)	2 (2%)	3 (3%)	6	47
45	t	91/100 (91%)	82 (90%)	6 (7%)	3 (3%)	5	44
46	u	100/104 (96%)	82 (82%)	12 (12%)	6 (6%)	2	26
47	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
48	y	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
49	z	24/87 (28%)	21 (88%)	3 (12%)	0	100	100
All	All	5497/5903 (93%)	4898 (89%)	440 (8%)	159 (3%)	9	47

All (159) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	76	SER
2	C	7	ASN
2	C	61	LYS
4	E	99	SER
4	E	146	MET

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Mol	Chain	Res	Type
5	F	98	GLU
8	I	127	SER
9	J	58	ASN
13	N	80	ARG
15	P	11	ALA
15	P	80	LYS
18	S	4	LEU
19	T	44	ALA
22	1	3	ALA
24	3	56	ALA
26	6	44	VAL
30	d	152	PRO
31	e	61	ARG
31	e	153	LEU
32	f	62	GLY
32	f	123	ASP
33	g	119	ALA
34	h	41	LYS
35	j	81	ILE
37	l	111	ILE
39	n	70	THR
39	n	119	SER
44	s	65	ASP
46	u	7	ARG
2	C	63	ILE
3	D	125	ASN
5	F	94	HIS
7	H	44	PHE
7	H	46	GLU
8	I	8	THR
8	I	27	ILE
9	J	17	LEU
9	J	57	VAL
9	J	67	ILE
9	J	94	ALA
11	L	24	GLU
11	L	88	ASP
12	M	3	ILE
13	N	52	ARG
13	N	66	THR
14	O	21	THR
15	P	10	GLY

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Mol	Chain	Res	Type
15	P	16	PHE
15	P	36	VAL
16	Q	71	SER
18	S	5	LYS
19	T	67	HIS
20	U	32	ARG
24	3	55	ILE
29	c	253	LYS
33	g	92	VAL
34	h	68	ARG
34	h	119	ASN
34	h	123	ARG
35	j	25	LEU
36	k	35	VAL
37	l	29	LYS
37	l	115	GLU
40	o	59	ALA
41	p	114	LEU
44	s	62	ASP
44	s	63	GLY
45	t	38	ALA
46	u	19	LYS
46	u	99	ASN
1	B	22	TRP
1	B	63	LYS
1	B	123	GLY
2	C	106	ARG
2	C	111	ASP
2	C	145	ALA
3	D	194	ILE
4	E	142	GLY
5	F	85	ILE
6	G	4	ARG
6	G	15	PRO
6	G	113	LYS
7	H	88	LYS
10	K	88	PRO
13	N	21	ALA
13	N	50	LEU
15	P	49	GLY
15	P	78	VAL
20	U	24	LYS

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Mol	Chain	Res	Type
32	f	121	SER
32	f	175	PHE
34	h	15	LEU
36	k	108	ARG
37	l	82	LEU
37	l	86	GLU
40	o	66	GLY
45	t	17	SER
1	B	204	ASP
2	C	129	PHE
3	D	47	LEU
4	E	103	GLY
4	E	147	ASN
5	F	48	ALA
6	G	114	SER
9	J	75	ASP
11	L	46	SER
11	L	60	PHE
12	M	23	GLY
13	N	62	ARG
14	O	20	ASP
20	U	29	ALA
22	1	37	LEU
23	2	4	THR
26	6	45	SER
31	e	80	SER
31	e	127	GLU
32	f	174	ASP
38	m	69	PRO
39	n	118	ARG
40	o	57	ALA
40	o	100	HIS
46	u	75	ALA
46	u	98	SER
1	B	53	LEU
3	D	119	HIS
7	H	87	ARG
9	J	78	GLU
9	J	92	LEU
11	L	76	HIS
31	e	42	GLY
31	e	60	TRP

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Mol	Chain	Res	Type
33	g	118	PRO
33	g	175	LYS
34	h	56	ALA
43	r	53	PHE
1	B	166	ASP
3	D	4	LEU
8	I	12	LYS
13	N	34	ASN
31	e	82	GLY
34	h	29	PHE
45	t	18	GLU
2	C	154	GLY
8	I	57	VAL
15	P	42	ILE
30	d	104	VAL
32	f	149	VAL
8	I	9	GLY
20	U	27	VAL
31	e	83	VAL
33	g	28	GLY
1	B	30	ILE
2	C	107	LYS
6	G	54	GLY
16	Q	4	ILE
15	P	15	PRO
34	h	88	GLY
40	o	101	GLY
46	u	55	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	180/199 (90%)	180 (100%)	0	100	100
2	C	170/190 (90%)	170 (100%)	0	100	100
3	D	172/173 (99%)	172 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	113/126 (90%)	113 (100%)	0	100	100
5	F	87/112 (78%)	87 (100%)	0	100	100
6	G	123/129 (95%)	123 (100%)	0	100	100
7	H	104/105 (99%)	104 (100%)	0	100	100
8	I	105/107 (98%)	104 (99%)	1 (1%)	82	92
9	J	86/90 (96%)	86 (100%)	0	100	100
10	K	90/99 (91%)	90 (100%)	0	100	100
11	L	103/104 (99%)	103 (100%)	0	100	100
12	M	91/96 (95%)	91 (100%)	0	100	100
13	N	79/84 (94%)	79 (100%)	0	100	100
14	O	76/77 (99%)	76 (100%)	0	100	100
15	P	65/65 (100%)	57 (88%)	8 (12%)	6	34
16	Q	74/78 (95%)	74 (100%)	0	100	100
17	R	48/65 (74%)	48 (100%)	0	100	100
18	S	70/79 (89%)	70 (100%)	0	100	100
19	T	65/66 (98%)	65 (100%)	0	100	100
20	U	44/61 (72%)	44 (100%)	0	100	100
21	0	67/68 (98%)	64 (96%)	3 (4%)	34	73
22	1	54/55 (98%)	52 (96%)	2 (4%)	41	77
23	2	48/49 (98%)	47 (98%)	1 (2%)	61	86
24	3	47/48 (98%)	46 (98%)	1 (2%)	61	86
25	4	45/49 (92%)	43 (96%)	2 (4%)	35	74
26	6	38/38 (100%)	35 (92%)	3 (8%)	15	55
27	7	51/52 (98%)	49 (96%)	2 (4%)	39	76
28	8	34/34 (100%)	34 (100%)	0	100	100
29	c	216/218 (99%)	210 (97%)	6 (3%)	51	82
30	d	164/164 (100%)	157 (96%)	7 (4%)	35	74
31	e	165/165 (100%)	158 (96%)	7 (4%)	36	75
32	f	148/150 (99%)	141 (95%)	7 (5%)	32	72
33	g	137/138 (99%)	134 (98%)	3 (2%)	60	85
34	h	114/114 (100%)	112 (98%)	2 (2%)	66	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	j	116/116 (100%)	113 (97%)	3 (3%)	54	83
36	k	103/104 (99%)	101 (98%)	2 (2%)	65	87
37	l	103/103 (100%)	100 (97%)	3 (3%)	50	81
38	m	108/109 (99%)	107 (99%)	1 (1%)	84	93
39	n	100/103 (97%)	97 (97%)	3 (3%)	48	81
40	o	86/87 (99%)	83 (96%)	3 (4%)	43	79
41	p	99/100 (99%)	95 (96%)	4 (4%)	38	76
42	q	89/90 (99%)	88 (99%)	1 (1%)	80	92
43	r	84/84 (100%)	81 (96%)	3 (4%)	42	78
44	s	93/93 (100%)	92 (99%)	1 (1%)	80	92
45	t	80/84 (95%)	80 (100%)	0	100	100
46	u	83/85 (98%)	79 (95%)	4 (5%)	31	72
47	w	78/78 (100%)	74 (95%)	4 (5%)	29	70
48	y	56/63 (89%)	56 (100%)	0	100	100
49	z	21/62 (34%)	9 (43%)	12 (57%)	0	0
All	All	4572/4808 (95%)	4473 (98%)	99 (2%)	63	85

All (99) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	I	105	ARG
15	P	6	LEU
15	P	19	VAL
15	P	33	ILE
15	P	46	LYS
15	P	55	ASP
15	P	63	GLN
15	P	68	SER
15	P	77	GLU
21	0	17	ASN
21	0	22	LEU
21	0	48	THR
22	1	21	LEU
22	1	38	GLN
23	2	10	THR
24	3	29	SER
25	4	8	LYS

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Mol	Chain	Res	Type
25	4	47	VAL
26	6	1	MET
26	6	22	MET
26	6	42	LEU
27	7	31	HIS
27	7	47	LYS
29	c	52	ARG
29	c	187	ASP
29	c	213	TRP
29	c	252	THR
29	c	267	ILE
29	c	269	ARG
30	d	4	LEU
30	d	32	ASN
30	d	51	THR
30	d	91	THR
30	d	150	GLN
30	d	157	LYS
30	d	177	VAL
31	e	60	TRP
31	e	61	ARG
31	e	78	TRP
31	e	93	SER
31	e	116	ASP
31	e	126	VAL
31	e	187	VAL
32	f	5	HIS
32	f	7	TYR
32	f	19	GLU
32	f	83	TYR
32	f	94	GLU
32	f	117	LEU
32	f	174	ASP
33	g	27	LYS
33	g	80	THR
33	g	92	VAL
34	h	42	LYS
34	h	43	ASN
35	j	30	THR
35	j	131	ASN
35	j	142	ILE
36	k	92	GLU

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Mol	Chain	Res	Type
36	k	105	ARG
37	l	48	ARG
37	l	91	ASP
37	l	94	THR
38	m	13	HIS
39	n	95	THR
39	n	116	VAL
39	n	118	ARG
40	o	5	SER
40	o	31	THR
40	o	103	VAL
41	p	19	SER
41	p	26	VAL
41	p	37	LYS
41	p	80	VAL
42	q	16	LYS
43	r	46	GLU
43	r	58	VAL
43	r	102	SER
44	s	73	LYS
46	u	35	ILE
46	u	41	LEU
46	u	55	PRO
46	u	68	SER
47	w	20	LEU
47	w	29	ILE
47	w	53	LYS
47	w	76	ASP
49	z	4	GLN
49	z	6	LEU
49	z	7	ILE
49	z	8	SER
49	z	9	GLU
49	z	12	LEU
49	z	13	PHE
49	z	18	TRP
49	z	21	GLN
49	z	23	GLN
49	z	25	ILE
49	z	26	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (58) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	17	HIS
1	B	167	HIS
1	B	176	ASN
2	C	68	HIS
2	C	175	HIS
3	D	115	GLN
4	E	82	HIS
4	E	88	HIS
4	E	121	ASN
5	F	37	HIS
5	F	68	GLN
5	F	81	ASN
7	H	3	GLN
8	I	30	ASN
8	I	74	GLN
8	I	125	GLN
9	J	70	HIS
10	K	27	ASN
10	K	28	ASN
10	K	39	ASN
11	L	4	ASN
11	L	45	ASN
11	L	58	ASN
11	L	76	HIS
12	M	90	HIS
13	N	34	ASN
14	O	45	HIS
14	O	50	HIS
15	P	26	ASN
15	P	29	ASN
15	P	59	HIS
15	P	63	GLN
16	Q	44	HIS
16	Q	49	ASN
16	Q	50	ASN
18	S	56	HIS
19	T	69	ASN
21	0	16	ASN
22	1	41	HIS
22	1	45	GLN
27	7	31	HIS
28	8	37	GLN
31	e	46	GLN

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Mol	Chain	Res	Type
31	e	115	GLN
32	f	127	ASN
33	g	22	GLN
33	g	38	ASN
34	h	20	ASN
34	h	28	ASN
34	h	43	ASN
39	n	3	HIS
39	n	73	ASN
42	q	37	GLN
44	s	7	HIS
44	s	15	GLN
44	s	61	ASN
46	u	74	ASN
48	y	57	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	A	1530/1542 (99%)	427 (27%)	36 (2%)
51	X	11/11 (100%)	7 (63%)	2 (18%)
52	a	116/120 (96%)	40 (34%)	0
53	b	2902/2904 (99%)	1211 (41%)	0
54	v	75/76 (98%)	27 (36%)	0
All	All	4634/4653 (99%)	1712 (36%)	38 (0%)

All (1712) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	A	6	G
50	A	7	A
50	A	8	A
50	A	9	G
50	A	11	G
50	A	13	U
50	A	29	U
50	A	31	G
50	A	32	A
50	A	39	G
50	A	47	C
50	A	48	C

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Mol	Chain	Res	Type
50	A	51	A
50	A	52	C
50	A	54	C
50	A	57	G
50	A	65	A
50	A	70	U
50	A	71	A
50	A	75	G
50	A	79	G
50	A	81	A
50	A	82	G
50	A	83	C
50	A	84	U
50	A	85	U
50	A	86	G
50	A	87	C
50	A	90	C
50	A	95	C
50	A	97	G
50	A	98	A
50	A	108	G
50	A	116	A
50	A	119	A
50	A	122	G
50	A	126	G
50	A	127	G
50	A	128	G
50	A	130	A
50	A	131	A
50	A	133	U
50	A	137	U
50	A	142	G
50	A	149	A
50	A	157	U
50	A	160	A
50	A	166	U
50	A	177	G
50	A	182	A
50	A	183	C
50	A	184	G
50	A	185	U
50	A	186	C

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Mol	Chain	Res	Type
50	A	196	A
50	A	197	A
50	A	210	C
50	A	211	G
50	A	217	C
50	A	219	U
50	A	229	U
50	A	230	G
50	A	231	U
50	A	239	U
50	A	240	G
50	A	243	A
50	A	244	U
50	A	245	U
50	A	247	G
50	A	251	G
50	A	252	U
50	A	256	U
50	A	264	C
50	A	266	G
50	A	267	C
50	A	275	G
50	A	276	G
50	A	278	G
50	A	280	C
50	A	281	G
50	A	289	G
50	A	302	G
50	A	303	A
50	A	314	C
50	A	324	G
50	A	326	G
50	A	328	C
50	A	330	C
50	A	332	G
50	A	339	C
50	A	342	C
50	A	343	U
50	A	352	C
50	A	354	G
50	A	366	A
50	A	367	U

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Mol	Chain	Res	Type
50	A	368	U
50	A	369	G
50	A	371	A
50	A	372	C
50	A	373	A
50	A	374	A
50	A	376	G
50	A	377	G
50	A	381	C
50	A	385	C
50	A	388	G
50	A	389	A
50	A	390	U
50	A	391	G
50	A	397	A
50	A	398	U
50	A	399	G
50	A	406	G
50	A	411	A
50	A	412	A
50	A	413	G
50	A	414	A
50	A	415	A
50	A	417	G
50	A	422	C
50	A	424	G
50	A	429	U
50	A	435	A
50	A	440	C
50	A	449	G
50	A	451	A
50	A	457	G
50	A	459	A
50	A	461	A
50	A	462	G
50	A	466	A
50	A	468	A
50	A	471	U
50	A	476	U
50	A	477	C
50	A	479	U
50	A	481	G

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Mol	Chain	Res	Type
50	A	484	G
50	A	485	U
50	A	486	U
50	A	496	A
50	A	498	A
50	A	499	A
50	A	508	U
50	A	511	C
50	A	518	C
50	A	521	G
50	A	525	C
50	A	527	G
50	A	531	U
50	A	532	A
50	A	533	A
50	A	543	U
50	A	545	C
50	A	547	A
50	A	548	G
50	A	549	C
50	A	562	U
50	A	563	A
50	A	564	C
50	A	565	U
50	A	566	G
50	A	572	A
50	A	575	G
50	A	576	C
50	A	577	G
50	A	578	C
50	A	579	A
50	A	588	G
50	A	589	U
50	A	591	U
50	A	607	A
50	A	614	C
50	A	618	C
50	A	619	U
50	A	620	C
50	A	621	A
50	A	623	C
50	A	632	U

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Mol	Chain	Res	Type
50	A	633	G
50	A	636	U
50	A	637	C
50	A	652	U
50	A	653	U
50	A	665	A
50	A	687	A
50	A	688	G
50	A	691	G
50	A	693	G
50	A	695	A
50	A	696	A
50	A	697	U
50	A	700	G
50	A	701	U
50	A	702	A
50	A	703	G
50	A	704	A
50	A	710	G
50	A	718	A
50	A	720	C
50	A	721	G
50	A	722	G
50	A	723	U
50	A	724	G
50	A	729	A
50	A	731	G
50	A	734	G
50	A	747	A
50	A	748	G
50	A	753	A
50	A	755	G
50	A	764	C
50	A	779	C
50	A	781	A
50	A	790	A
50	A	793	U
50	A	794	A
50	A	802	A
50	A	812	G
50	A	815	A
50	A	817	C

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Mol	Chain	Res	Type
50	A	818	G
50	A	819	A
50	A	820	U
50	A	821	G
50	A	822	U
50	A	826	C
50	A	828	U
50	A	829	G
50	A	832	G
50	A	841	C
50	A	842	U
50	A	843	U
50	A	845	A
50	A	846	G
50	A	847	G
50	A	849	G
50	A	851	G
50	A	853	C
50	A	857	C
50	A	860	A
50	A	869	G
50	A	871	U
50	A	873	A
50	A	882	C
50	A	887	G
50	A	889	A
50	A	890	G
50	A	891	U
50	A	902	G
50	A	914	A
50	A	922	G
50	A	927	G
50	A	931	C
50	A	932	C
50	A	934	C
50	A	935	A
50	A	945	G
50	A	948	C
50	A	954	G
50	A	958	A
50	A	960	U
50	A	961	U

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Mol	Chain	Res	Type
50	A	969	A
50	A	971	G
50	A	974	A
50	A	975	A
50	A	976	G
50	A	977	A
50	A	982	U
50	A	983	A
50	A	985	C
50	A	987	G
50	A	992	U
50	A	993	G
50	A	996	A
50	A	997	U
50	A	998	C
50	A	999	C
50	A	1004	A
50	A	1010	U
50	A	1018	G
50	A	1020	G
50	A	1022	A
50	A	1028	C
50	A	1030	U
50	A	1031	C
50	A	1034	G
50	A	1046	A
50	A	1053	G
50	A	1056	U
50	A	1057	G
50	A	1064	G
50	A	1065	U
50	A	1066	C
50	A	1070	U
50	A	1071	C
50	A	1085	U
50	A	1091	U
50	A	1093	A
50	A	1094	G
50	A	1095	U
50	A	1101	A
50	A	1102	A
50	A	1103	C

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Mol	Chain	Res	Type
50	A	1108	G
50	A	1112	C
50	A	1125	U
50	A	1130	A
50	A	1131	G
50	A	1132	C
50	A	1135	U
50	A	1136	C
50	A	1138	G
50	A	1139	G
50	A	1140	C
50	A	1143	G
50	A	1152	A
50	A	1157	A
50	A	1159	U
50	A	1160	G
50	A	1164	G
50	A	1168	U
50	A	1169	A
50	A	1184	G
50	A	1186	G
50	A	1189	U
50	A	1192	C
50	A	1193	G
50	A	1196	A
50	A	1197	A
50	A	1201	A
50	A	1202	U
50	A	1210	C
50	A	1212	U
50	A	1213	A
50	A	1215	G
50	A	1225	A
50	A	1226	C
50	A	1227	A
50	A	1228	C
50	A	1233	G
50	A	1234	C
50	A	1238	A
50	A	1240	U
50	A	1241	G
50	A	1246	A

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Mol	Chain	Res	Type
50	A	1256	A
50	A	1258	G
50	A	1261	A
50	A	1270	G
50	A	1272	G
50	A	1279	G
50	A	1280	A
50	A	1285	A
50	A	1286	U
50	A	1287	A
50	A	1292	G
50	A	1298	U
50	A	1300	G
50	A	1301	U
50	A	1302	C
50	A	1303	C
50	A	1305	G
50	A	1312	G
50	A	1316	G
50	A	1319	A
50	A	1320	C
50	A	1322	C
50	A	1323	G
50	A	1324	A
50	A	1331	G
50	A	1333	A
50	A	1336	C
50	A	1338	G
50	A	1339	A
50	A	1340	A
50	A	1342	C
50	A	1343	G
50	A	1346	A
50	A	1347	G
50	A	1348	U
50	A	1349	A
50	A	1350	A
50	A	1353	G
50	A	1358	U
50	A	1362	A
50	A	1363	A
50	A	1364	U

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Mol	Chain	Res	Type
50	A	1365	G
50	A	1378	C
50	A	1398	A
50	A	1399	C
50	A	1401	G
50	A	1402	C
50	A	1403	C
50	A	1419	G
50	A	1432	G
50	A	1436	U
50	A	1440	U
50	A	1441	A
50	A	1443	C
50	A	1446	A
50	A	1448	C
50	A	1449	C
50	A	1452	C
50	A	1454	G
50	A	1469	C
50	A	1477	U
50	A	1484	C
50	A	1493	A
50	A	1494	G
50	A	1497	G
50	A	1499	A
50	A	1503	A
50	A	1505	G
50	A	1506	U
50	A	1508	A
50	A	1514	G
50	A	1517	G
50	A	1519	A
50	A	1520	C
50	A	1528	U
50	A	1529	G
50	A	1530	G
50	A	1534	A
51	X	13	C
51	X	14	U
51	X	15	G
51	X	17	C
51	X	18	C

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Mol	Chain	Res	Type
51	X	19	C
51	X	20	U
52	a	3	C
52	a	4	C
52	a	8	C
52	a	9	G
52	a	12	C
52	a	13	G
52	a	15	A
52	a	16	G
52	a	18	G
52	a	21	G
52	a	24	G
52	a	25	U
52	a	26	C
52	a	30	C
52	a	35	C
52	a	37	C
52	a	42	C
52	a	43	C
52	a	44	G
52	a	50	A
52	a	51	G
52	a	52	A
52	a	53	A
52	a	54	G
52	a	57	A
52	a	59	A
52	a	67	G
52	a	84	G
52	a	85	G
52	a	86	G
52	a	88	C
52	a	89	U
52	a	90	C
52	a	91	C
52	a	96	G
52	a	99	A
52	a	100	G
52	a	106	G
52	a	109	A
52	a	115	A

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Mol	Chain	Res	Type
53	b	4	U
53	b	10	A
53	b	11	C
53	b	13	A
53	b	14	A
53	b	15	G
53	b	20	C
53	b	23	G
53	b	24	G
53	b	27	G
53	b	28	A
53	b	29	U
53	b	34	U
53	b	35	G
53	b	39	G
53	b	45	G
53	b	46	G
53	b	49	A
53	b	51	G
53	b	55	G
53	b	62	U
53	b	63	A
53	b	71	A
53	b	73	A
53	b	74	A
53	b	75	G
53	b	76	C
53	b	77	G
53	b	80	G
53	b	82	U
53	b	83	A
53	b	84	A
53	b	85	G
53	b	88	G
53	b	91	A
53	b	100	U
53	b	101	A
53	b	102	U
53	b	103	A
53	b	109	C
53	b	111	A
53	b	114	U

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Mol	Chain	Res	Type
53	b	116	C
53	b	118	A
53	b	119	A
53	b	120	U
53	b	126	A
53	b	127	A
53	b	136	G
53	b	140	C
53	b	143	C
53	b	144	A
53	b	147	C
53	b	149	A
53	b	159	G
53	b	160	A
53	b	162	U
53	b	163	C
53	b	164	C
53	b	165	A
53	b	172	A
53	b	176	A
53	b	181	A
53	b	186	G
53	b	196	A
53	b	197	A
53	b	202	U
53	b	204	A
53	b	205	G
53	b	210	C
53	b	212	G
53	b	215	G
53	b	216	A
53	b	221	A
53	b	222	A
53	b	223	A
53	b	225	C
53	b	226	A
53	b	228	C
53	b	229	C
53	b	231	A
53	b	233	A
53	b	234	U
53	b	235	U

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Mol	Chain	Res	Type
53	b	239	C
53	b	240	C
53	b	241	A
53	b	245	G
53	b	248	G
53	b	249	C
53	b	250	G
53	b	251	A
53	b	252	G
53	b	254	G
53	b	255	A
53	b	264	C
53	b	265	A
53	b	266	G
53	b	267	C
53	b	270	A
53	b	271	G
53	b	272	A
53	b	273	G
53	b	277	G
53	b	278	A
53	b	279	A
53	b	280	U
53	b	281	C
53	b	282	A
53	b	289	G
53	b	294	A
53	b	298	G
53	b	299	A
53	b	300	A
53	b	307	G
53	b	309	A
53	b	310	A
53	b	311	A
53	b	322	A
53	b	323	C
53	b	324	A
53	b	326	G
53	b	329	G
53	b	330	A
53	b	331	C
53	b	332	A

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Mol	Chain	Res	Type
53	b	333	G
53	b	338	G
53	b	344	A
53	b	345	A
53	b	346	A
53	b	349	U
53	b	353	C
53	b	355	U
53	b	356	G
53	b	358	U
53	b	359	G
53	b	361	G
53	b	362	A
53	b	364	C
53	b	366	C
53	b	368	A
53	b	369	U
53	b	370	G
53	b	371	A
53	b	372	G
53	b	373	U
53	b	374	A
53	b	375	G
53	b	385	C
53	b	386	G
53	b	387	U
53	b	388	G
53	b	391	A
53	b	392	U
53	b	396	G
53	b	400	G
53	b	401	A
53	b	402	A
53	b	403	U
53	b	405	U
53	b	406	G
53	b	409	G
53	b	411	G
53	b	412	A
53	b	413	C
53	b	418	C
53	b	419	U

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Mol	Chain	Res	Type
53	b	421	C
53	b	422	A
53	b	424	G
53	b	425	G
53	b	431	U
53	b	434	U
53	b	435	C
53	b	436	C
53	b	442	G
53	b	443	A
53	b	446	G
53	b	447	A
53	b	448	U
53	b	449	A
53	b	451	U
53	b	452	G
53	b	454	A
53	b	455	C
53	b	456	C
53	b	457	A
53	b	461	C
53	b	465	G
53	b	466	A
53	b	475	C
53	b	477	A
53	b	479	A
53	b	480	A
53	b	481	G
53	b	483	A
53	b	489	G
53	b	490	C
53	b	491	G
53	b	492	A
53	b	502	A
53	b	503	A
53	b	504	A
53	b	505	A
53	b	508	A
53	b	509	C
53	b	510	C
53	b	518	G
53	b	519	U

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Mol	Chain	Res	Type
53	b	521	U
53	b	526	A
53	b	527	C
53	b	529	A
53	b	530	G
53	b	531	C
53	b	532	A
53	b	538	A
53	b	544	C
53	b	545	U
53	b	546	U
53	b	547	A
53	b	548	G
53	b	549	G
53	b	550	C
53	b	559	G
53	b	560	C
53	b	563	A
53	b	568	U
53	b	569	U
53	b	572	A
53	b	573	U
53	b	574	A
53	b	575	A
53	b	584	C
53	b	586	A
53	b	587	C
53	b	588	U
53	b	603	A
53	b	604	G
53	b	607	U
53	b	608	A
53	b	612	G
53	b	613	A
53	b	614	A
53	b	615	U
53	b	617	G
53	b	618	G
53	b	621	A
53	b	622	G
53	b	625	G
53	b	627	A

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Mol	Chain	Res	Type
53	b	628	G
53	b	631	A
53	b	632	A
53	b	636	G
53	b	637	A
53	b	642	U
53	b	644	A
53	b	646	U
53	b	647	G
53	b	651	G
53	b	652	U
53	b	653	U
53	b	654	A
53	b	655	A
53	b	656	G
53	b	657	U
53	b	659	G
53	b	662	G
53	b	664	G
53	b	668	A
53	b	670	A
53	b	671	C
53	b	672	C
53	b	675	A
53	b	686	U
53	b	696	G
53	b	701	G
53	b	704	G
53	b	705	A
53	b	707	G
53	b	711	G
53	b	713	G
53	b	715	A
53	b	716	A
53	b	717	C
53	b	718	A
53	b	719	C
53	b	720	U
53	b	723	C
53	b	727	A
53	b	730	A
53	b	733	G

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Mol	Chain	Res	Type
53	b	734	A
53	b	738	G
53	b	745	G
53	b	746	U
53	b	747	U
53	b	748	G
53	b	749	A
53	b	750	A
53	b	752	A
53	b	753	A
53	b	757	G
53	b	758	C
53	b	763	G
53	b	764	A
53	b	765	C
53	b	766	U
53	b	770	G
53	b	775	G
53	b	776	G
53	b	777	G
53	b	781	A
53	b	782	A
53	b	783	A
53	b	784	G
53	b	785	G
53	b	788	A
53	b	789	A
53	b	790	U
53	b	791	C
53	b	792	A
53	b	794	A
53	b	798	G
53	b	799	G
53	b	800	A
53	b	801	G
53	b	805	G
53	b	812	C
53	b	819	A
53	b	822	G
53	b	827	U
53	b	828	U
53	b	836	G

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Mol	Chain	Res	Type
53	b	844	A
53	b	845	A
53	b	846	U
53	b	847	U
53	b	848	C
53	b	856	G
53	b	858	G
53	b	859	G
53	b	866	A
53	b	867	C
53	b	869	G
53	b	872	U
53	b	873	C
53	b	874	G
53	b	876	C
53	b	877	A
53	b	878	A
53	b	879	G
53	b	880	G
53	b	881	G
53	b	882	G
53	b	883	G
53	b	887	U
53	b	888	C
53	b	889	C
53	b	893	C
53	b	895	U
53	b	896	A
53	b	897	C
53	b	899	A
53	b	900	A
53	b	902	C
53	b	910	A
53	b	911	A
53	b	912	C
53	b	914	G
53	b	915	C
53	b	919	U
53	b	931	U
53	b	932	U
53	b	934	U
53	b	938	G

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Mol	Chain	Res	Type
53	b	941	A
53	b	945	A
53	b	946	C
53	b	948	C
53	b	951	C
53	b	957	C
53	b	958	U
53	b	959	A
53	b	961	C
53	b	962	G
53	b	964	C
53	b	965	C
53	b	968	C
53	b	969	G
53	b	972	A
53	b	973	A
53	b	974	G
53	b	975	A
53	b	979	A
53	b	980	A
53	b	981	A
53	b	983	A
53	b	984	A
53	b	985	C
53	b	986	C
53	b	995	C
53	b	996	A
53	b	1003	G
53	b	1005	C
53	b	1006	C
53	b	1010	A
53	b	1011	G
53	b	1012	U
53	b	1013	C
53	b	1018	U
53	b	1019	U
53	b	1022	G
53	b	1023	U
53	b	1025	G
53	b	1026	G
53	b	1027	A
53	b	1028	A

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Mol	Chain	Res	Type
53	b	1032	A
53	b	1033	U
53	b	1034	G
53	b	1036	G
53	b	1037	G
53	b	1038	G
53	b	1039	A
53	b	1044	C
53	b	1047	G
53	b	1048	A
53	b	1049	C
53	b	1051	G
53	b	1052	C
53	b	1053	C
53	b	1054	A
53	b	1055	G
53	b	1056	G
53	b	1057	A
53	b	1058	U
53	b	1059	G
53	b	1061	U
53	b	1062	G
53	b	1063	G
53	b	1064	C
53	b	1065	U
53	b	1067	A
53	b	1068	G
53	b	1069	A
53	b	1070	A
53	b	1071	G
53	b	1072	C
53	b	1073	A
53	b	1074	G
53	b	1078	U
53	b	1079	C
53	b	1080	A
53	b	1081	U
53	b	1084	A
53	b	1085	A
53	b	1086	A
53	b	1087	G
53	b	1088	A

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Mol	Chain	Res	Type
53	b	1089	A
53	b	1090	A
53	b	1091	G
53	b	1092	C
53	b	1093	G
53	b	1095	A
53	b	1096	A
53	b	1097	U
53	b	1098	A
53	b	1099	G
53	b	1100	C
53	b	1102	C
53	b	1103	A
53	b	1104	C
53	b	1105	U
53	b	1106	G
53	b	1107	G
53	b	1109	C
53	b	1110	G
53	b	1111	A
53	b	1112	G
53	b	1115	G
53	b	1116	G
53	b	1117	C
53	b	1121	C
53	b	1122	G
53	b	1126	A
53	b	1130	U
53	b	1132	U
53	b	1133	A
53	b	1134	A
53	b	1135	C
53	b	1136	G
53	b	1138	G
53	b	1139	G
53	b	1141	U
53	b	1142	A
53	b	1143	A
53	b	1144	A
53	b	1145	C
53	b	1148	U
53	b	1156	A

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Mol	Chain	Res	Type
53	b	1157	G
53	b	1163	G
53	b	1165	A
53	b	1169	A
53	b	1171	G
53	b	1172	C
53	b	1173	U
53	b	1174	U
53	b	1175	A
53	b	1176	U
53	b	1178	C
53	b	1179	G
53	b	1184	U
53	b	1185	G
53	b	1187	G
53	b	1188	U
53	b	1195	G
53	b	1200	C
53	b	1203	U
53	b	1204	A
53	b	1205	A
53	b	1206	G
53	b	1207	C
53	b	1208	C
53	b	1209	U
53	b	1210	G
53	b	1211	C
53	b	1218	G
53	b	1221	C
53	b	1222	U
53	b	1223	G
53	b	1224	U
53	b	1225	G
53	b	1227	G
53	b	1231	U
53	b	1232	G
53	b	1234	U
53	b	1236	G
53	b	1237	A
53	b	1238	G
53	b	1240	U
53	b	1241	A

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Mol	Chain	Res	Type
53	b	1247	A
53	b	1248	G
53	b	1249	U
53	b	1251	C
53	b	1253	A
53	b	1254	A
53	b	1255	U
53	b	1256	G
53	b	1258	U
53	b	1260	A
53	b	1265	A
53	b	1266	G
53	b	1267	U
53	b	1268	A
53	b	1269	A
53	b	1272	A
53	b	1273	U
53	b	1274	A
53	b	1275	A
53	b	1276	A
53	b	1288	G
53	b	1289	C
53	b	1294	U
53	b	1296	G
53	b	1300	G
53	b	1301	A
53	b	1302	A
53	b	1306	C
53	b	1307	A
53	b	1311	G
53	b	1312	U
53	b	1314	C
53	b	1316	U
53	b	1318	U
53	b	1319	C
53	b	1320	C
53	b	1322	A
53	b	1323	C
53	b	1326	U
53	b	1327	A
53	b	1329	U
53	b	1330	C

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Mol	Chain	Res	Type
53	b	1332	G
53	b	1337	G
53	b	1338	G
53	b	1341	G
53	b	1342	A
53	b	1343	G
53	b	1344	U
53	b	1347	A
53	b	1348	C
53	b	1349	C
53	b	1352	U
53	b	1355	G
53	b	1358	G
53	b	1365	A
53	b	1368	G
53	b	1369	G
53	b	1373	A
53	b	1374	G
53	b	1378	A
53	b	1379	U
53	b	1382	G
53	b	1383	A
53	b	1384	A
53	b	1390	U
53	b	1392	A
53	b	1393	A
53	b	1394	U
53	b	1395	A
53	b	1396	U
53	b	1397	U
53	b	1398	C
53	b	1400	U
53	b	1401	G
53	b	1403	A
53	b	1408	G
53	b	1416	G
53	b	1419	A
53	b	1420	A
53	b	1421	G
53	b	1422	G
53	b	1424	G
53	b	1426	G

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Mol	Chain	Res	Type
53	b	1427	A
53	b	1428	C
53	b	1429	G
53	b	1435	G
53	b	1438	U
53	b	1451	C
53	b	1452	G
53	b	1453	A
53	b	1454	C
53	b	1458	U
53	b	1459	G
53	b	1460	U
53	b	1461	C
53	b	1467	U
53	b	1471	G
53	b	1476	U
53	b	1477	A
53	b	1478	G
53	b	1481	U
53	b	1482	G
53	b	1483	G
53	b	1487	U
53	b	1494	A
53	b	1495	A
53	b	1496	A
53	b	1497	U
53	b	1498	C
53	b	1500	G
53	b	1503	A
53	b	1507	C
53	b	1508	A
53	b	1509	A
53	b	1510	G
53	b	1517	G
53	b	1522	A
53	b	1523	U
53	b	1524	G
53	b	1526	C
53	b	1529	G
53	b	1530	G
53	b	1534	U
53	b	1535	A

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Mol	Chain	Res	Type
53	b	1536	C
53	b	1537	G
53	b	1539	U
53	b	1540	G
53	b	1542	U
53	b	1552	A
53	b	1554	U
53	b	1556	C
53	b	1558	C
53	b	1562	U
53	b	1566	A
53	b	1568	G
53	b	1569	A
53	b	1570	A
53	b	1572	A
53	b	1576	U
53	b	1578	U
53	b	1583	A
53	b	1584	U
53	b	1585	C
53	b	1592	C
53	b	1595	C
53	b	1598	A
53	b	1600	C
53	b	1602	U
53	b	1603	A
53	b	1606	C
53	b	1607	C
53	b	1608	A
53	b	1609	A
53	b	1610	A
53	b	1612	C
53	b	1615	C
53	b	1616	A
53	b	1617	C
53	b	1618	A
53	b	1624	U
53	b	1631	G
53	b	1632	A
53	b	1633	G
53	b	1634	A
53	b	1635	A

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Mol	Chain	Res	Type
53	b	1643	G
53	b	1644	C
53	b	1646	C
53	b	1647	U
53	b	1648	U
53	b	1649	G
53	b	1653	G
53	b	1654	A
53	b	1656	C
53	b	1658	C
53	b	1660	G
53	b	1663	G
53	b	1667	G
53	b	1668	A
53	b	1669	A
53	b	1674	G
53	b	1681	G
53	b	1682	G
53	b	1683	U
53	b	1687	G
53	b	1693	U
53	b	1694	C
53	b	1695	G
53	b	1697	G
53	b	1698	A
53	b	1699	G
53	b	1700	A
53	b	1703	G
53	b	1705	A
53	b	1706	C
53	b	1707	G
53	b	1710	G
53	b	1713	A
53	b	1714	U
53	b	1715	G
53	b	1731	G
53	b	1732	C
53	b	1733	G
53	b	1738	G
53	b	1739	A
53	b	1746	A
53	b	1750	G

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Mol	Chain	Res	Type
53	b	1755	A
53	b	1757	A
53	b	1758	U
53	b	1761	C
53	b	1763	G
53	b	1764	C
53	b	1766	G
53	b	1773	A
53	b	1774	C
53	b	1775	U
53	b	1776	G
53	b	1783	A
53	b	1785	A
53	b	1786	A
53	b	1787	A
53	b	1792	G
53	b	1794	A
53	b	1800	C
53	b	1801	A
53	b	1802	A
53	b	1807	G
53	b	1808	A
53	b	1809	A
53	b	1811	G
53	b	1815	A
53	b	1816	C
53	b	1817	G
53	b	1823	G
53	b	1825	U
53	b	1826	G
53	b	1829	A
53	b	1833	C
53	b	1839	G
53	b	1840	G
53	b	1843	C
53	b	1846	G
53	b	1848	A
53	b	1849	G
53	b	1858	A
53	b	1860	G
53	b	1862	G
53	b	1865	U

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Mol	Chain	Res	Type
53	b	1866	A
53	b	1867	G
53	b	1868	C
53	b	1870	C
53	b	1871	A
53	b	1872	A
53	b	1873	G
53	b	1890	A
53	b	1897	G
53	b	1905	C
53	b	1906	G
53	b	1907	G
53	b	1908	C
53	b	1913	A
53	b	1915	U
53	b	1917	U
53	b	1918	A
53	b	1919	A
53	b	1924	C
53	b	1928	A
53	b	1929	G
53	b	1930	G
53	b	1931	U
53	b	1932	A
53	b	1936	A
53	b	1937	A
53	b	1938	A
53	b	1940	U
53	b	1941	C
53	b	1943	U
53	b	1944	U
53	b	1951	U
53	b	1952	A
53	b	1954	G
53	b	1955	U
53	b	1963	U
53	b	1964	G
53	b	1966	A
53	b	1967	C
53	b	1969	A
53	b	1970	A
53	b	1971	U

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Mol	Chain	Res	Type
53	b	1972	G
53	b	1975	G
53	b	1980	G
53	b	1981	A
53	b	1982	U
53	b	1991	U
53	b	1993	U
53	b	1997	C
53	b	1999	C
53	b	2007	U
53	b	2014	A
53	b	2016	U
53	b	2019	A
53	b	2020	A
53	b	2021	C
53	b	2022	U
53	b	2023	C
53	b	2030	A
53	b	2031	A
53	b	2032	G
53	b	2033	A
53	b	2035	G
53	b	2036	C
53	b	2043	C
53	b	2046	G
53	b	2051	A
53	b	2052	A
53	b	2054	A
53	b	2055	C
53	b	2056	G
53	b	2060	A
53	b	2061	G
53	b	2063	C
53	b	2065	C
53	b	2066	C
53	b	2068	U
53	b	2069	G
53	b	2077	A
53	b	2080	A
53	b	2083	G
53	b	2087	G
53	b	2088	A

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Mol	Chain	Res	Type
53	b	2092	U
53	b	2093	G
53	b	2094	A
53	b	2102	G
53	b	2104	C
53	b	2105	U
53	b	2107	G
53	b	2109	U
53	b	2110	G
53	b	2111	U
53	b	2112	G
53	b	2113	U
53	b	2114	A
53	b	2115	G
53	b	2116	G
53	b	2117	A
53	b	2118	U
53	b	2119	A
53	b	2120	G
53	b	2123	G
53	b	2124	G
53	b	2125	G
53	b	2127	G
53	b	2128	G
53	b	2129	C
53	b	2130	U
53	b	2131	U
53	b	2132	U
53	b	2133	G
53	b	2135	A
53	b	2138	G
53	b	2144	G
53	b	2145	C
53	b	2146	C
53	b	2147	A
53	b	2149	U
53	b	2150	C
53	b	2153	C
53	b	2156	G
53	b	2158	A
53	b	2159	G
53	b	2160	C

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Mol	Chain	Res	Type
53	b	2161	C
53	b	2162	G
53	b	2163	A
53	b	2164	C
53	b	2165	C
53	b	2166	U
53	b	2168	G
53	b	2169	A
53	b	2170	A
53	b	2171	A
53	b	2172	U
53	b	2173	A
53	b	2174	C
53	b	2175	C
53	b	2176	A
53	b	2177	C
53	b	2178	C
53	b	2179	C
53	b	2182	U
53	b	2185	U
53	b	2193	G
53	b	2198	A
53	b	2199	A
53	b	2202	U
53	b	2203	U
53	b	2204	G
53	b	2206	C
53	b	2207	C
53	b	2210	U
53	b	2211	A
53	b	2212	A
53	b	2213	U
53	b	2214	C
53	b	2215	C
53	b	2225	A
53	b	2230	G
53	b	2238	G
53	b	2239	G
53	b	2243	U
53	b	2249	U
53	b	2250	G
53	b	2255	G

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Mol	Chain	Res	Type
53	b	2257	U
53	b	2258	C
53	b	2259	U
53	b	2265	U
53	b	2266	A
53	b	2267	A
53	b	2268	A
53	b	2273	A
53	b	2274	A
53	b	2275	C
53	b	2276	G
53	b	2279	G
53	b	2282	G
53	b	2283	C
53	b	2286	G
53	b	2287	A
53	b	2288	A
53	b	2289	G
53	b	2297	A
53	b	2304	G
53	b	2305	U
53	b	2308	G
53	b	2309	A
53	b	2319	G
53	b	2320	U
53	b	2321	U
53	b	2322	A
53	b	2324	U
53	b	2331	G
53	b	2333	A
53	b	2334	U
53	b	2335	A
53	b	2336	A
53	b	2339	C
53	b	2340	A
53	b	2344	U
53	b	2345	G
53	b	2347	C
53	b	2350	C
53	b	2351	G
53	b	2361	G
53	b	2366	A

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Mol	Chain	Res	Type
53	b	2371	G
53	b	2377	A
53	b	2379	G
53	b	2382	G
53	b	2383	G
53	b	2385	C
53	b	2388	A
53	b	2396	G
53	b	2398	U
53	b	2400	G
53	b	2402	U
53	b	2403	C
53	b	2406	A
53	b	2407	A
53	b	2410	G
53	b	2411	A
53	b	2420	C
53	b	2423	U
53	b	2425	A
53	b	2427	C
53	b	2428	G
53	b	2429	G
53	b	2430	A
53	b	2434	A
53	b	2439	A
53	b	2440	C
53	b	2441	U
53	b	2445	G
53	b	2448	A
53	b	2449	U
53	b	2450	A
53	b	2453	A
53	b	2458	G
53	b	2459	A
53	b	2460	U
53	b	2465	C
53	b	2472	G
53	b	2475	C
53	b	2476	A
53	b	2478	A
53	b	2481	G
53	b	2484	G

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Mol	Chain	Res	Type
53	b	2490	G
53	b	2491	U
53	b	2492	U
53	b	2498	C
53	b	2502	G
53	b	2505	G
53	b	2509	G
53	b	2510	C
53	b	2513	A
53	b	2517	C
53	b	2518	A
53	b	2519	U
53	b	2525	G
53	b	2527	C
53	b	2529	G
53	b	2530	A
53	b	2534	A
53	b	2535	G
53	b	2536	G
53	b	2542	A
53	b	2544	G
53	b	2547	A
53	b	2554	U
53	b	2556	C
53	b	2562	U
53	b	2564	A
53	b	2565	A
53	b	2566	A
53	b	2567	G
53	b	2572	A
53	b	2573	C
53	b	2576	G
53	b	2578	G
53	b	2581	G
53	b	2582	G
53	b	2584	U
53	b	2585	U
53	b	2586	U
53	b	2587	A
53	b	2588	G
53	b	2590	A
53	b	2593	U

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Mol	Chain	Res	Type
53	b	2595	G
53	b	2596	U
53	b	2598	A
53	b	2599	G
53	b	2600	A
53	b	2601	C
53	b	2602	A
53	b	2603	G
53	b	2606	C
53	b	2608	G
53	b	2609	U
53	b	2613	U
53	b	2614	A
53	b	2615	U
53	b	2621	G
53	b	2625	G
53	b	2629	U
53	b	2632	A
53	b	2634	A
53	b	2638	G
53	b	2639	A
53	b	2641	G
53	b	2645	G
53	b	2646	C
53	b	2655	G
53	b	2657	A
53	b	2658	C
53	b	2659	G
53	b	2660	A
53	b	2661	G
53	b	2663	G
53	b	2673	G
53	b	2677	G
53	b	2685	G
53	b	2688	G
53	b	2689	U
53	b	2690	U
53	b	2691	C
53	b	2699	C
53	b	2702	G
53	b	2703	C
53	b	2707	U

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Mol	Chain	Res	Type
53	b	2712	C
53	b	2713	U
53	b	2714	G
53	b	2716	C
53	b	2718	G
53	b	2719	G
53	b	2722	G
53	b	2727	A
53	b	2729	G
53	b	2733	A
53	b	2735	G
53	b	2736	A
53	b	2738	A
53	b	2744	G
53	b	2746	U
53	b	2747	G
53	b	2750	A
53	b	2751	G
53	b	2752	C
53	b	2753	A
53	b	2755	C
53	b	2757	A
53	b	2758	A
53	b	2761	A
53	b	2765	A
53	b	2766	A
53	b	2773	C
53	b	2776	A
53	b	2778	A
53	b	2779	U
53	b	2781	A
53	b	2782	G
53	b	2790	U
53	b	2791	G
53	b	2792	A
53	b	2793	C
53	b	2795	C
53	b	2797	U
53	b	2798	U
53	b	2799	A
53	b	2800	A
53	b	2807	U

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Mol	Chain	Res	Type
53	b	2808	G
53	b	2812	G
53	b	2818	U
53	b	2820	A
53	b	2821	A
53	b	2823	A
53	b	2824	C
53	b	2826	A
53	b	2833	U
53	b	2837	A
53	b	2847	U
53	b	2849	U
53	b	2858	C
53	b	2859	G
53	b	2861	U
53	b	2866	U
53	b	2867	G
53	b	2868	A
53	b	2872	A
53	b	2873	A
53	b	2874	C
53	b	2876	G
53	b	2880	C
53	b	2883	A
53	b	2884	U
53	b	2885	G
53	b	2886	A
53	b	2887	A
53	b	2891	U
53	b	2893	A
53	b	2894	G
53	b	2898	U
53	b	2900	A
53	b	2902	C
53	b	2903	U
54	v	5	A
54	v	6	C
54	v	7	G
54	v	9	A
54	v	16	C
54	v	17	C
54	v	18	G

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Mol	Chain	Res	Type
54	v	19	G
54	v	20	U
54	v	21	A
54	v	28	C
54	v	31	C
54	v	34	G
54	v	36	C
54	v	39	G
54	v	40	U
54	v	41	C
54	v	46	G
54	v	47	U
54	v	48	C
54	v	49	G
54	v	50	G
54	v	52	G
54	v	60	U
54	v	64	C
54	v	72	G
54	v	76	A

All (38) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	A	5	U
50	A	14	U
50	A	30	U
50	A	51	A
50	A	64	G
50	A	66	A
50	A	94	G
50	A	132	C
50	A	184	G
50	A	243	A
50	A	279	A
50	A	301	G
50	A	372	C
50	A	484	G
50	A	497	G
50	A	695	A
50	A	701	U
50	A	702	A

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Mol	Chain	Res	Type
50	A	703	G
50	A	811	C
50	A	840	C
50	A	997	U
50	A	998	C
50	A	1065	U
50	A	1129	C
50	A	1135	U
50	A	1201	A
50	A	1300	G
50	A	1302	C
50	A	1332	A
50	A	1346	A
50	A	1347	G
50	A	1348	U
50	A	1377	A
50	A	1493	A
50	A	1527	U
51	X	12	G
51	X	14	U

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

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

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

There are no carbohydrates in this entry.

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

There are no ligands in this entry.

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	b	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	1087:G	O3'	1088:A	P	1.81
1	b	2055:C	O3'	2056:G	P	1.80