



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:35 AM UTC

PDB ID : 6VZJ / pdb_00006vzj
EMDB ID : EMD-21494
Title : Escherichia coli transcription-translation complex A1 (TTC-A1) containing mRNA with a 15 nt long spacer, fMet-tRNAs at E-site and P-site, and lacking transcription factor NusG
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-28
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

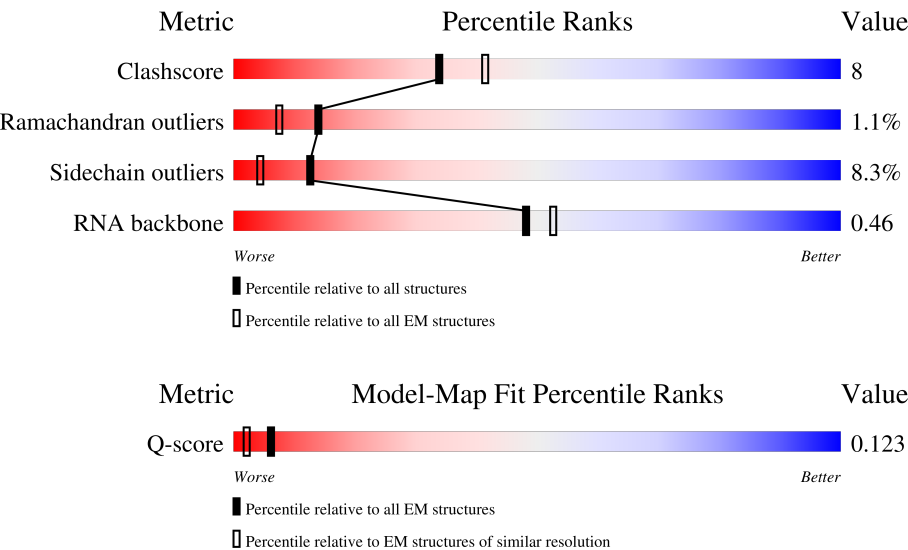
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	100	

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Mol	Chain	Length	Quality of chain
4	3	104	76% 84% 14% ..
5	4	94	77% 97% .
6	5	36	64% 25% 36% . 36%
7	6	36	75% 39% 36% 25%
8	7	32	100% . 47% 47% .
9	9	165	88% 27% 36% 24% . 10%
10	A	76	95% 12% 47% 36% 5%
10	B	76	99% 12% 46% 37% 5%
11	AA	1342	99% 69% 22% 6% ..
12	AC	329	70% 50% 16% . 30%
12	AD	329	69% 52% 17% . 31%
13	AE	1407	95% 67% 24% . 5%
14	C	75	67% 72% 15% . 12%
15	D	1542	27% 71% 24% ..
16	E	87	76% 87% 11% .
17	F	71	82% 87% 10% ..
18	G	241	72% 79% 13% . 7%
19	H	557	46% 25% 16% . 54%
20	I	233	76% 79% 9% . 11%
21	J	205	84% 90% 9%
22	K	167	50% 76% 14% .. 7%
23	L	135	67% 67% 10% 23%
24	M	151	83% 84% 14% ..
25	N	129	69% 91% 9%
26	O	127	84% 81% 18% .

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Mol	Chain	Length	Quality of chain
27	P	99	
28	Q	117	
29	R	123	
30	S	101	
31	T	89	
32	U	82	
33	V	84	
34	W	83	
35	X	116	
36	Y	141	
37	Z	121	
38	a	2904	
39	b	76	
40	c	78	
41	d	120	
42	e	62	
43	f	58	
44	g	66	
45	h	271	
46	i	56	
47	j	209	
48	k	55	
49	l	201	
50	m	46	
51	n	177	

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Mol	Chain	Length	Quality of chain
52	o	64	81% 89% 6% 5%
53	p	175	87% 91% 9%
54	q	38	71% 87% 11%
55	r	149	95% 88% 9%
56	s	142	62% 81% 18%
57	t	123	53% 80% 18%
58	u	144	71% 88% 12%
59	v	136	67% 91% 8%
60	w	119	56% 82% 18%
61	x	116	83% 83% 16%
62	y	114	81% 89% 11%
63	z	117	43% 84% 15%

2 Entry composition [i](#)

There are 65 unique types of molecules in this entry. The entry contains 299095 atoms, of which 123940 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 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	32	Total	C	H	N	O	P	0	0
			769	300	97	100	240	32		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	U	deletion	GB 1848959854
B	?	-	U	deletion	GB 1848959854

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AA	1322	Total	C	H	N	O	S	0	0
			20851	6539	10426	1817	2026	43		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
12	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

- Molecule 14 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 15 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 16 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 17 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 18 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 19 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 20 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 21 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 22 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 23 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 24 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 25 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 26 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 27 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 28 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 29 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 31 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 32 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 33 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 34 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 35 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 36 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 37 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 38 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 40 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 41 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 44 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 45 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 47 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 49 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 53 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 55 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 56 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 57 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 58 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 59 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 60 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 61 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 62 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 63 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 64 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	AE	1	Total	Mg	0
			1	1	

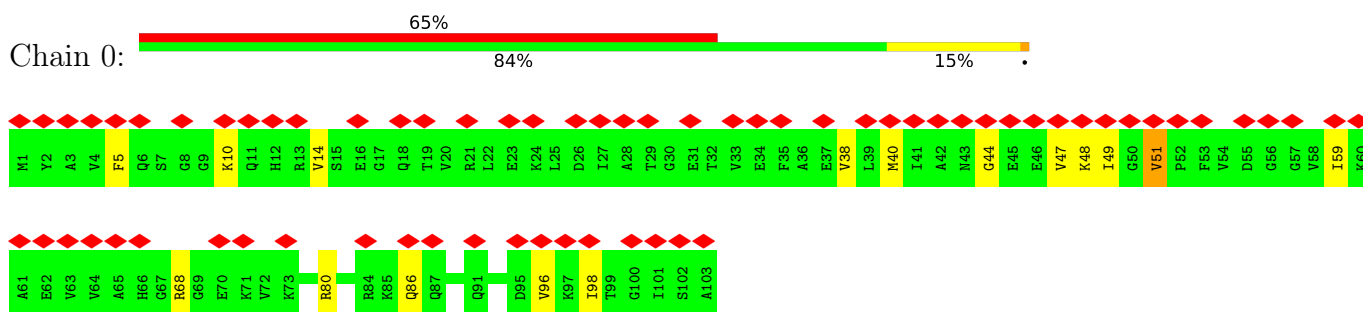
- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	AE	2	Total	Zn	0
			2	2	

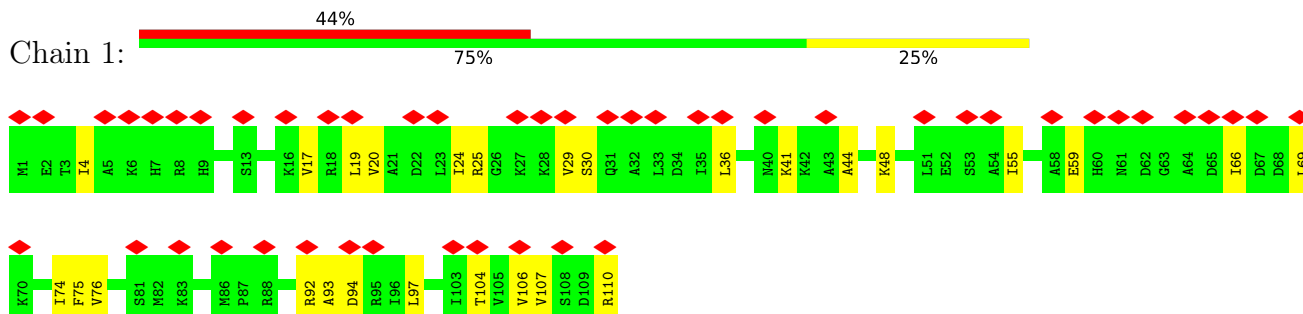
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

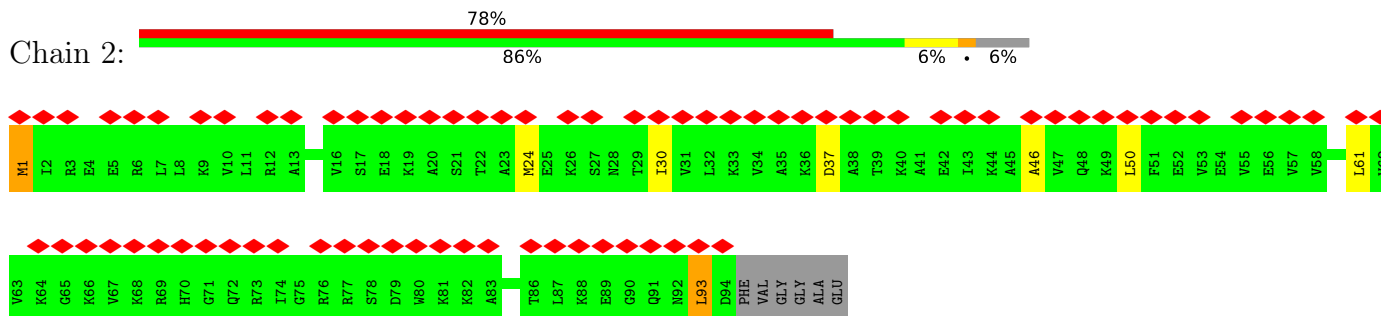
- Molecule 1: 50S ribosomal protein L21



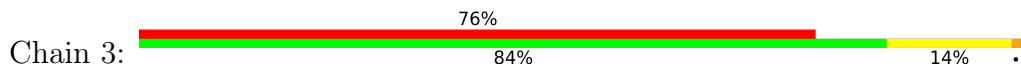
- Molecule 2: 50S ribosomal protein L22

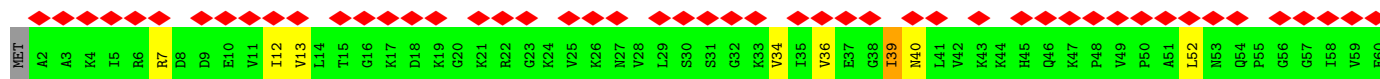


- Molecule 3: 50S ribosomal protein L23

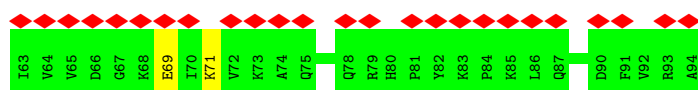
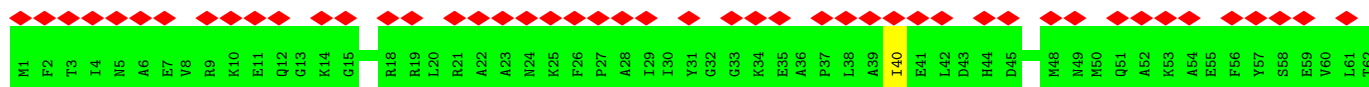
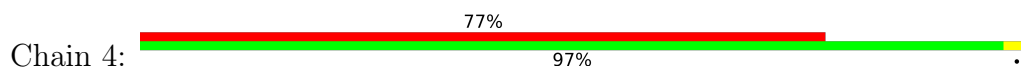


- Molecule 4: 50S ribosomal protein L24

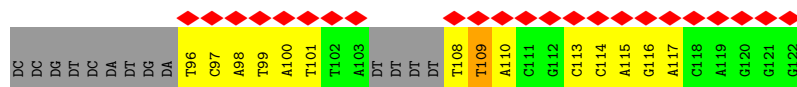
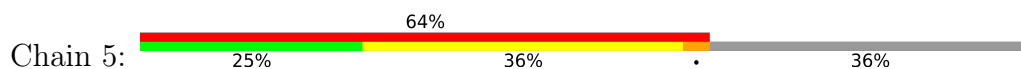




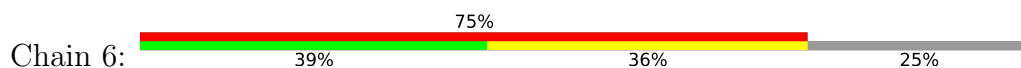
• Molecule 5: 50S ribosomal protein L25



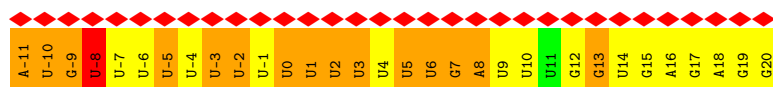
• Molecule 6: NT DNA



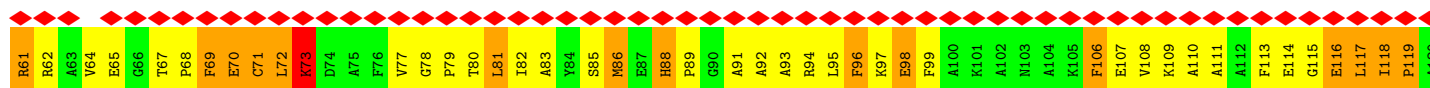
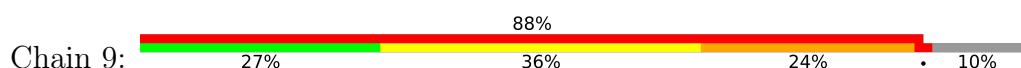
• Molecule 7: T DNA

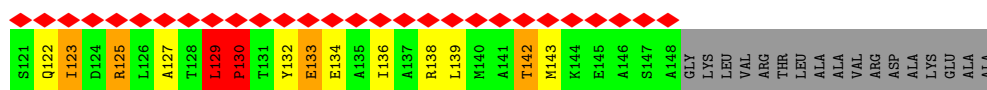


• Molecule 8: mRNA with 27 nt long spacer



• Molecule 9: 50S ribosomal protein L10

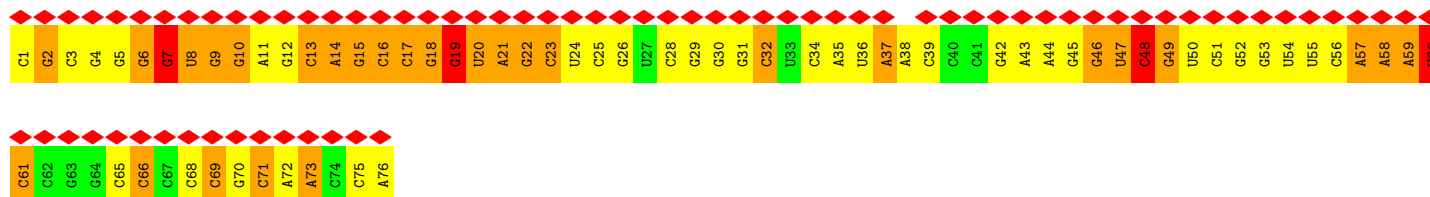




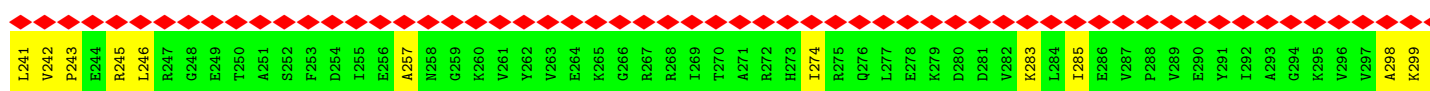
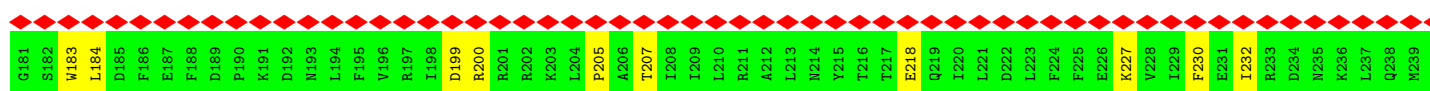
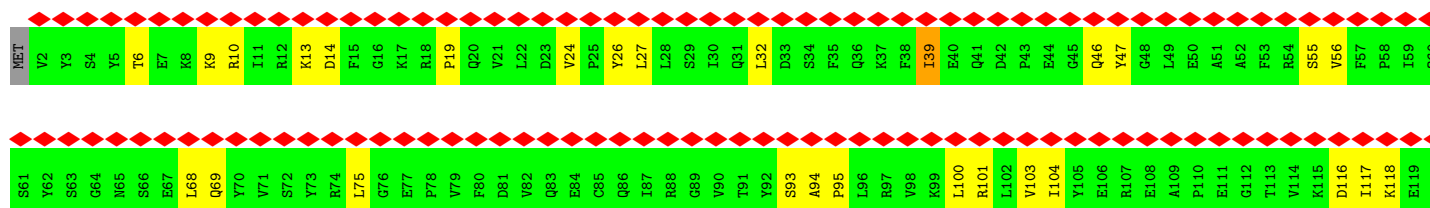
• Molecule 10: E-site and P-site tRNA (fMet)



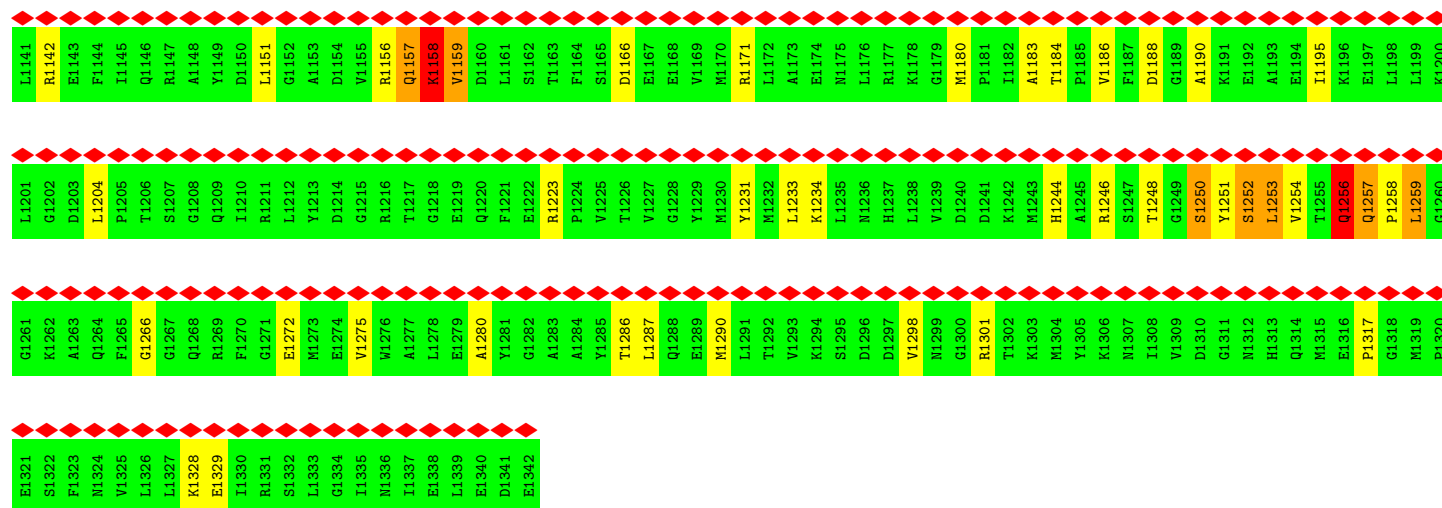
• Molecule 10: E-site and P-site tRNA (fMet)



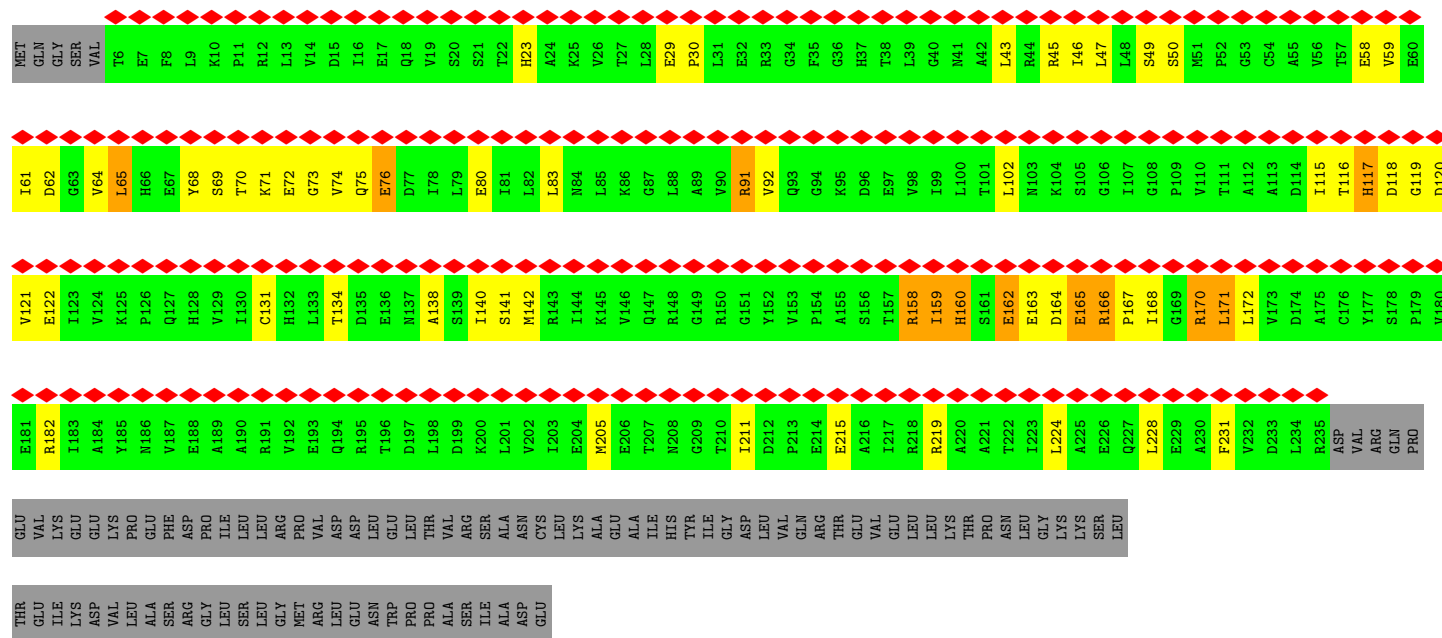
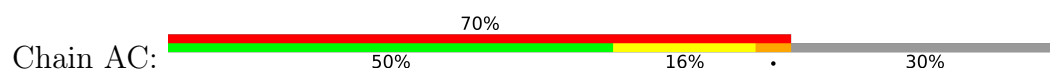
• Molecule 11: DNA-directed RNA polymerase subunit beta



P1081	L1021	S961	R841	D781	G721	V661	D601	E541	L481	S421	S361
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E1083	H1023	E963	T843	L783	V723	V663	I603	A543	D483	D423	L363
D1084	E1024	L964	K844	A784	V724	G664	H604	G544	L484	D424	V364
M1085	F1025	Q965	L845	D785	Q725	A665	Y605	F545	T485	I425	E365
P1086	E1026	I966	G846	G786	Q726	S666	L606	E546	T486	I426	I366
Y1087	K1027	L967	P847	P787	V727	L667	S607	V547	L487	D427	Y367
L1088	K1028	E968	E848	S788	D728	I668	A608	R548	M488	V428	R368
A1089	L1029	A969	E849	T789	A729	P669	I609	D549	P489	M429	M369
N1090	E1030	G970	T850	D790	S730	F670	E510	V550	Q490	K430	M370
G1091	A1031	L971	T851	L791	R731	L671	E511	H551	D491	K431	R371
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P1093	R1033	D853	D853	E793	V733	H673	N613	T553	I493	I434	G373
V1094	R1034	T854	T854	L794	I734	D674	Y614	H554	A494	D434	E374
D1095	K1035	P855	P855	A795	K735	D675	V615	Y555	A495	I435	P375
I1096	I1036	N856	N856	L796	K736	A676	I616	G556	K496	R436	P376
Y1097	T1037	H857	H857	G797	M737	N677	A617	R557	P497	N437	T377
L1098	Q1038	G858	G858	Q798	E738	R678	Q618	R558	I498	G438	R378
N1099	G1039	E859	E859	N799	D739	A679	A619	C559	S499	K439	E379
P1100	D1040	A860	A860	M800	E740	L680	N620	P560	A500	G440	A380
L1101	D1041	A861	A861	R801	M741	M681	S621	I561	A501	E441	A381
V1103	L1042	L862	L862	V802	V742	G682	N622	E562	V502	V442	E382
P1104	A1043	S863	S863	A803	F743	A683	L623	T563	K503	D443	S383
P1105	P1044	K864	K864	F804	G744	N684	D624	P564	E504	D444	L384
S1106	G1045	L865	L865	M805	E745	M685	E625	E565	F505	I445	F385
R1106	G1046	D866	D866	P806	A746	Q686	E626	G566	F506	D446	F386
M1107	L1047	E867	E867	M807	G747	R687	G627	P567	G507	H447	N387
N1108	K1048	S868	S868	N808	I748	Q688	H628	N568	S508	L448	L388
I1109	I1049	G869	G869	G809	D749	A889	F629	I569	S509	G449	F389
G1110	V1050	D990	D990	Y810	I750	V690	V630	G570	Q510	N450	F390
Q1111	K1051	R991	R991	H811	Y751	P691	E631	L571	L511	R451	S391
I1112	V1052	L992	L992	F812	N752	T692	D632	I572	S512	R452	E392
L1113	Y1053	P993	P993	E813	L753	L693	L633	N573	Q513	I453	D393
E1114	L1054	R994	R994	D814	T754	R694	V634	S574	F514	R454	R394
T1115	A1055	D995	D995	S815	K755	A695	T635	L575	M515	S455	Y395
H1116	V1056	R996	R996	I816	Y756	D696	C636	S576	D516	V456	D396
L1117	K1057	E997	E997	L817	T757	K697	R637	V577	Q517	G457	L397
G1118	L1058	T878	T878	V818	F758	P698	S638	Y578	N518	E458	S398
M1119	R1059	G879	G879	S819	S759	L699	K639	A579	N519	M459	A399
A1120	I1060	C880	C880	E820	N760	V700	G640	Q580	P520	A460	V400
A1121	Q1061	D881	D881	R821	Q761	G701	E641	T581	L521	E461	G401
K1122	P1062	T882	T882	V822	N762	T702	S642	N582	S522	E462	R402
G1123	G1063	L883	L883	E823	T763	G703	S643	E583	E523	Q463	M403
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G1125	K1065	G885	G885	E825	I765	E705	F645	G585	T525	R465	F405
D1126	M1066	X886	X886	D826	T766	R706	S646	F586	H526	V466	N406
K1127	A1067	V887	V887	R827	Q767	A707	R647	L587	K527	G467	R407
I1128	G1068	T888	T888	F828	M768	V708	D648	E588	R528	V468	S408
N1129	N1069	P889	P889	T829	P769	A709	Q649	T589	E529	V469	L409
A1130	H1070	K890	K890	T830	G770	V710	V650	I630	R470	L410	L409
M1131	G1071	G891	G891	L831	V771	D711	D651	S531	V471	E472	R411
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K1133	Q1073	Q955	Q955	I633	L773	G713	M653	K593	L533	R474	E413
Y1134	G1074	A956	A956	Q834	G774	V714	D654	V594	G534	A474	I414
Q1135	V1075	K957	K957	E835	E775	T715	V655	T595	P535	V475	E415
Q1136	I1076	THR	THR	L836	P776	A716	S656	D596	K476	K476	G416
E1137	I1077	PRD	PRD	A837	P777	V717	G567	G597	E477	E477	S417
V1138	K1078	GLU	GLU	C838	E778	A718	T657	V598	L538	R478	G418
A1139	I1079	LYS	LYS	V839	R779	K719	Q658	V599	T539	L479	I419
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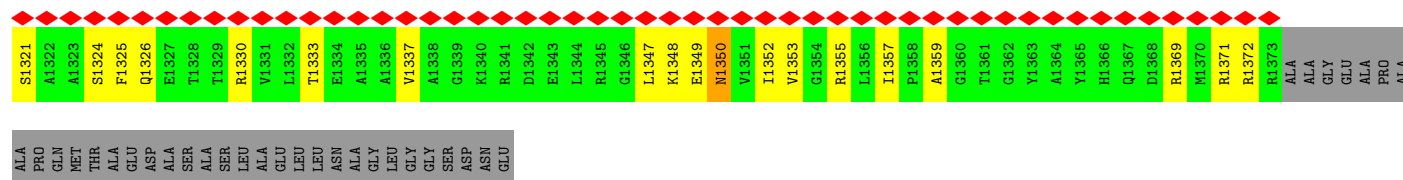
• Molecule 12: DNA-directed RNA polymerase subunit alpha



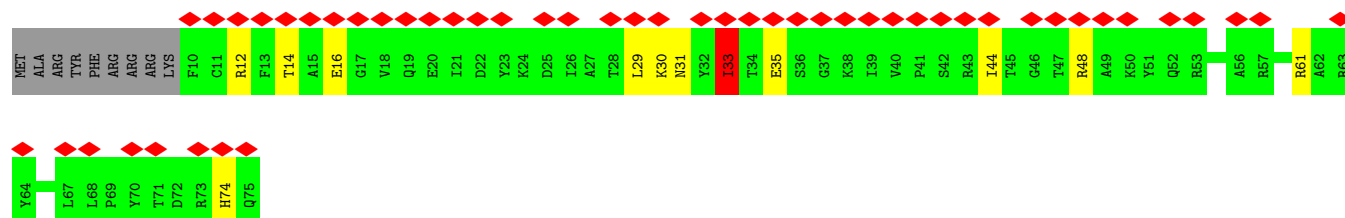
• Molecule 12: DNA-directed RNA polymerase subunit alpha



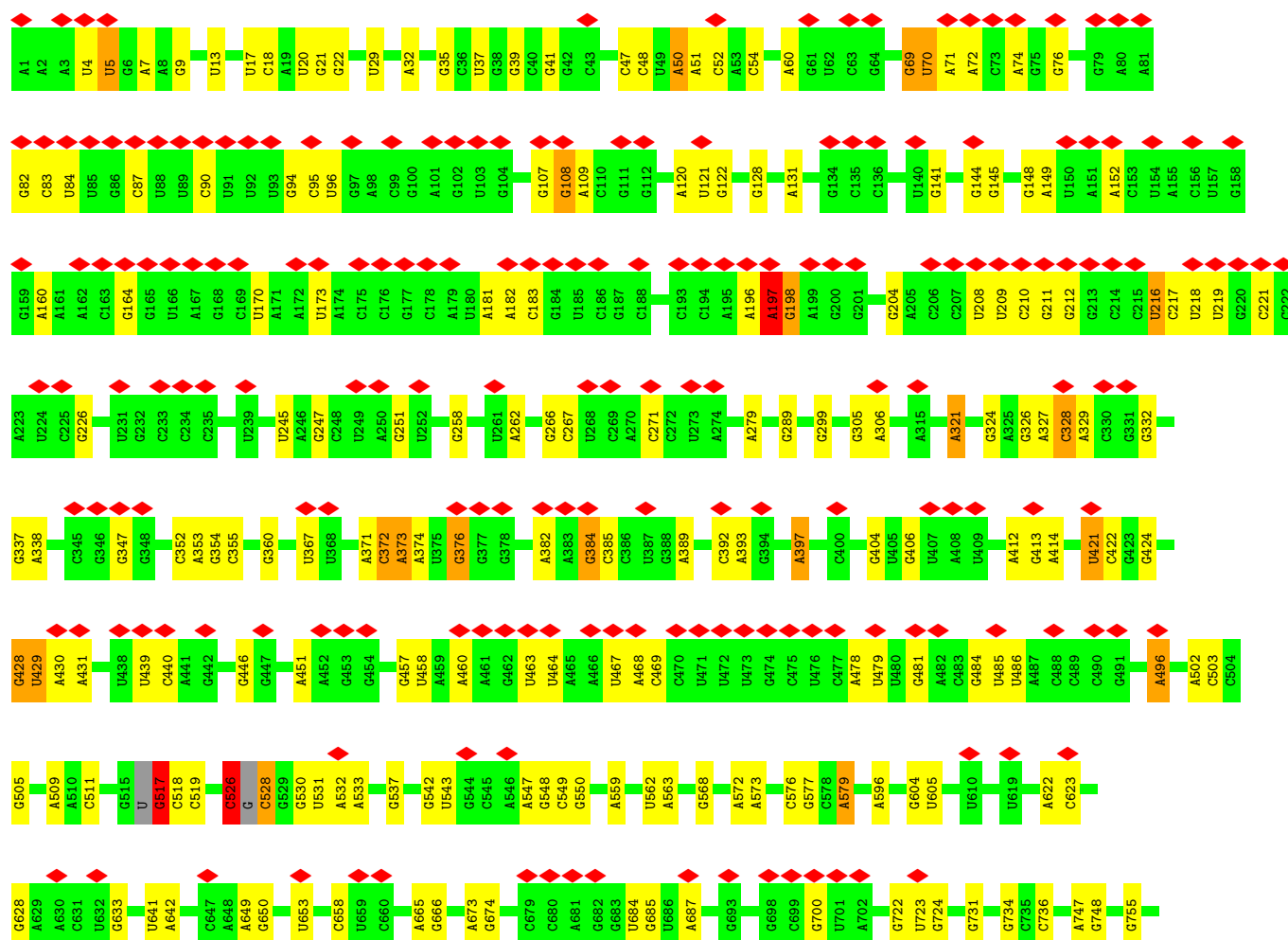
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K1263	R1203	D1143	A1083	H1023	V963	A904	T844	L783	Y723	E663	K603	S543
A1264	V1204	L1144	Q1084	T1024	K964	L904	V844	A784	M724	I664	M604	L544
T1265	E1205	F1145	G1085	M1025	S965	R905	A845	D785	M725	Q665	L605	H545
L1266	R1206	E1146	N1086	P1026	V966	G906	E846	T786	A726	E666	N606	A546
V1267	G1207	A1147	D1087	V1027	V967	H907	D847	A787	T727	Q667	T607	R547
N1268	D1208	R1148	V1088	I1028	N968	I908	V848	L788	S728	F668	C608	V548
A1269	V1209	R1149	L1089	T1029	S969	I909	L849	K789	G729	Q669	Y609	K549
G1270	I1210	P1150	I1090	E1030	S970	N910	K850	T790	A730	S670	R610	V550
S1271	S1211	K1151	P1091	S1031	G971	K911	P851	A791	R731	G671	I611	R551
S1272	D1212	E1152	G1092	S1032	K972	G912	G852	N792	G732	L672	L612	I552
D1273	G1213	P1153	T1093	G1033	L973	E913	T853	S793	S733	V673	G613	T553
F1274	P1214	A1154	D1094	F1034	V974	A914	A854	G794	A734	T674	L614	E554
L1275	E1215	I1155	M1095	V1035	I975	I915	D855	Y795	A735	A675	K615	Y555
E1276	A1216	L1156	P1096	R1036	T976	G916	I856	L796	Q736	G676	P616	E556
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E1281	L1221	G1161	L1101	I1041	E981	Q921	N861	V801	A741	K681	A621	G561
Y1282	R1222	I1162	P1102	D1042	L982	S922	T862	D802	G742	V682	D622	E562
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G1296	E1236	V1176	S1116	L1056	K996	HIS	S876	T816	E756	A696	G636	G575
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A1300	V1240	V1180	T1120	V1060	G1000	ALA	V880	I820	T760	N700	G640	M580
Y1241	Y1241	D1181	L1121	V1061	G1001	ALA	K881	M821	A761	L701	I641	M681
R1242	R1242	G1182	A1122	L1062	V1002	ALA	V882	M822	N762	Q702	D642	I582
L1243	L1243	S1183	R1123	D1063	L1003	ALA	R883	T823	F763	T703	D643	V583
Q1244	Q1244	D1184	T1124	S1064	A1004	GLU	S884	P824	R764	E704	M644	P584
D1305	G1245	P1185	P1125	A1065	K1005	S948	V885	V825	E765	T705	V645	K585
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L1307	K1247	E1187	GLU	R1067	D1007	I950	S887	E827	L767	I707	P647	L587
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A1312	H1252	K1192	ASP	K1072	E1012	K955	F892	K832	Y772	Q712	E652	V592
S1313	I1253	W1193	ILE	D1073	G1013	G956	G893	E833	F773	E713	I653	N593
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E1317	V1257	M1197	P1139	A1077	V1017	L960	H897	D837	H777	V717	A657	G597
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F1319	I1259	F1199	K1079	N1019	N1019		Y899	V839	A779	N720	A659	K599
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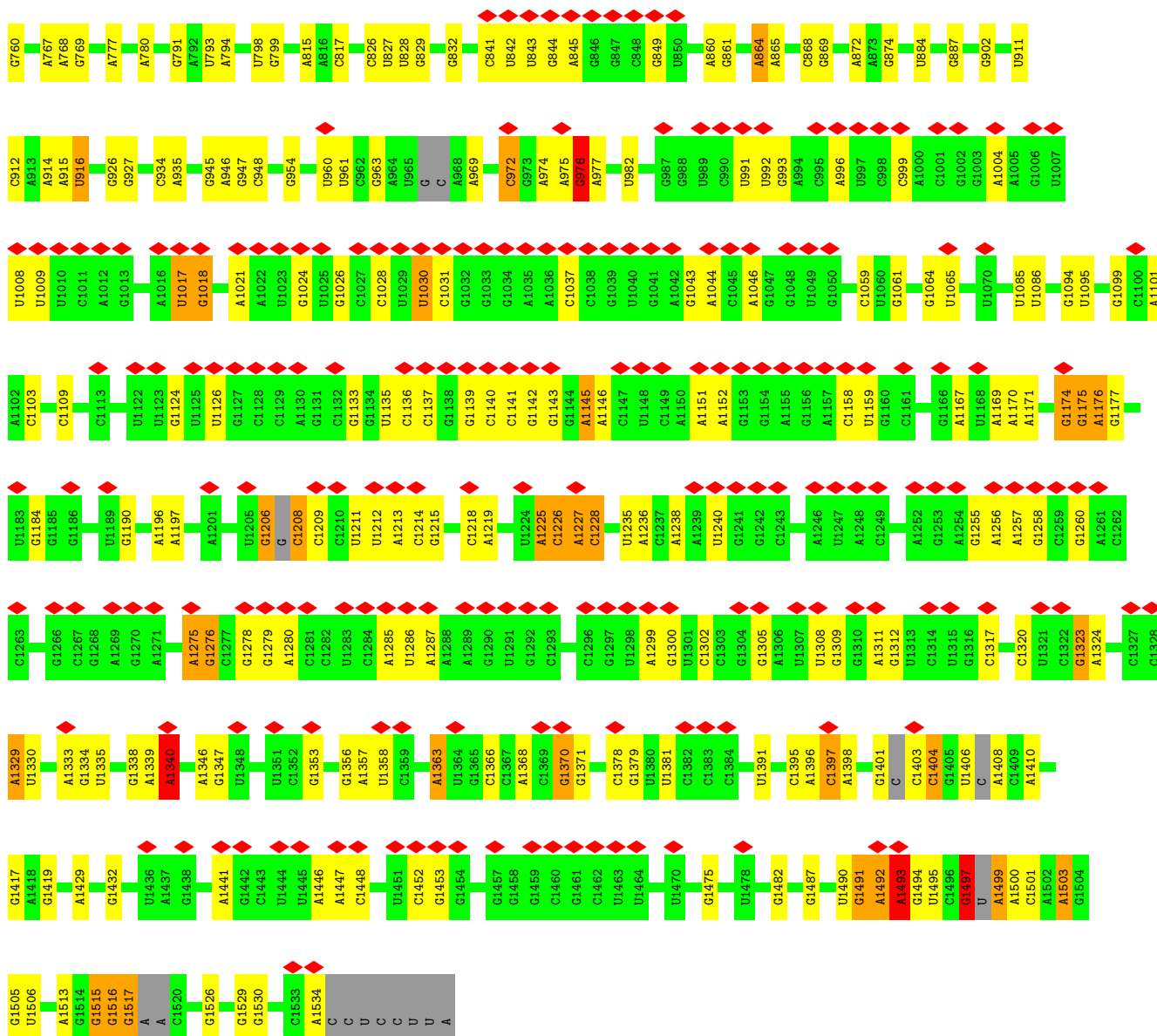


• Molecule 14: 30S ribosomal protein S18

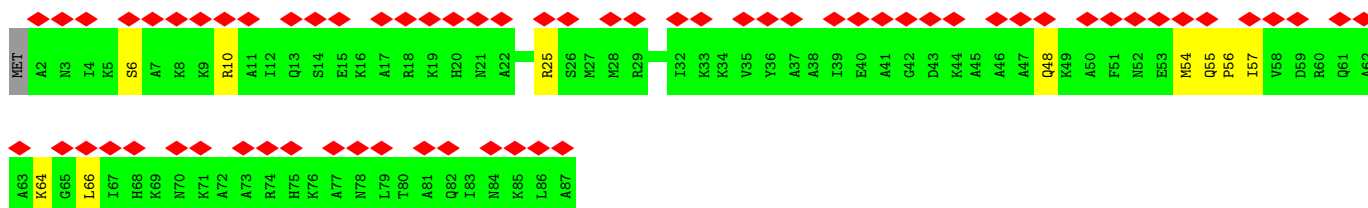
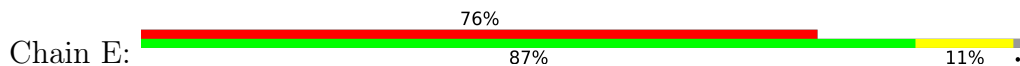


• Molecule 15: 16S rRNA

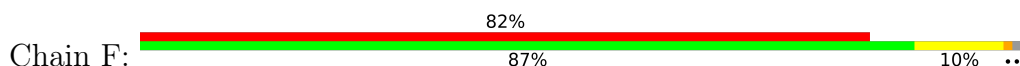




- Molecule 16: 30S ribosomal protein S20

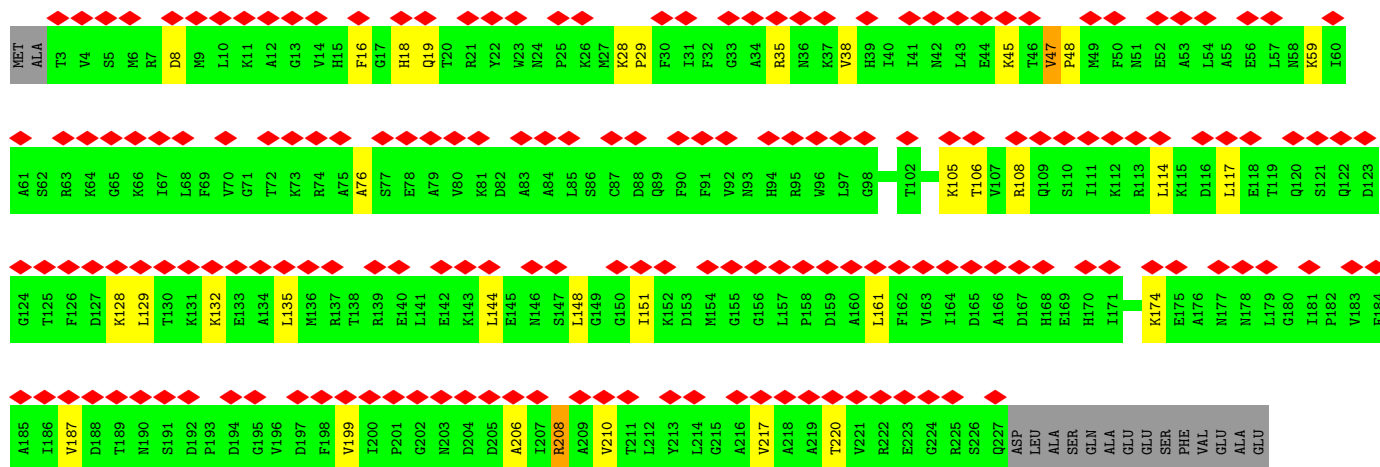
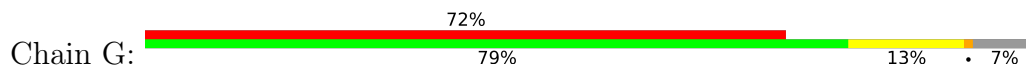


- Molecule 17: 30S ribosomal protein S21

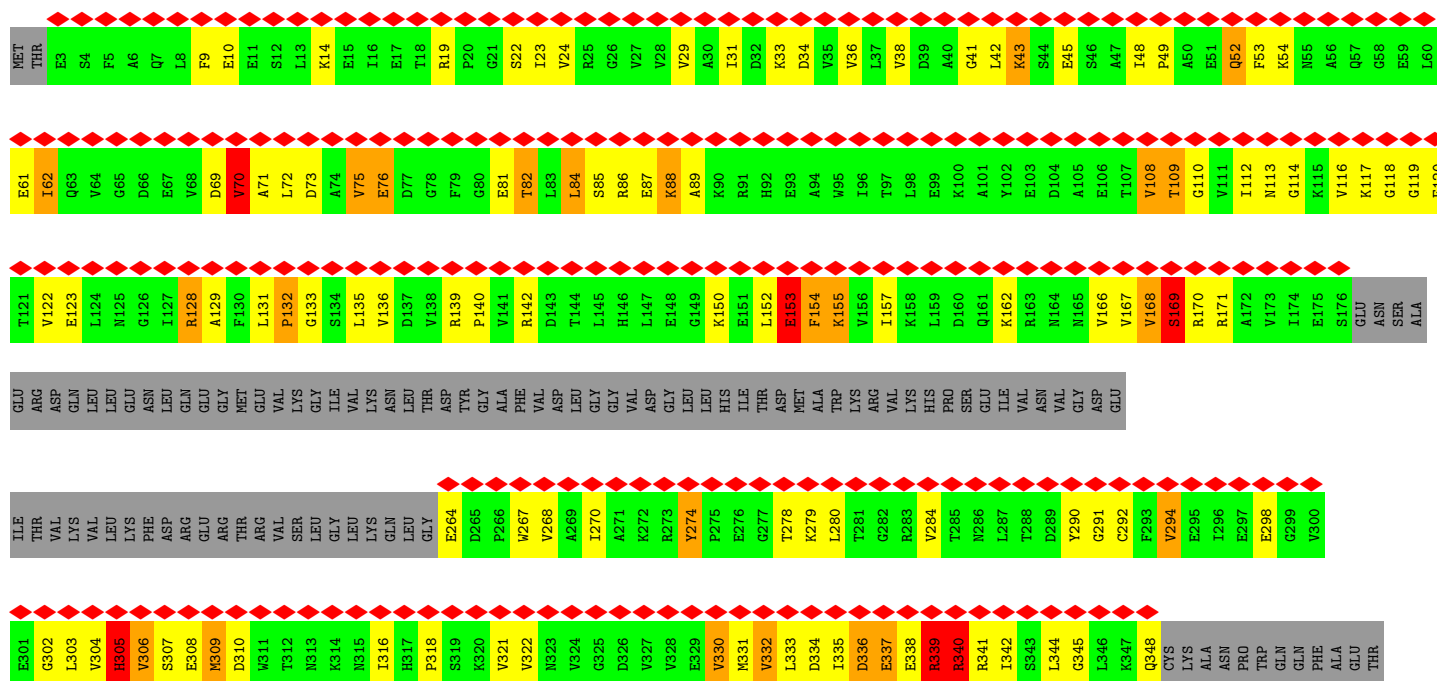
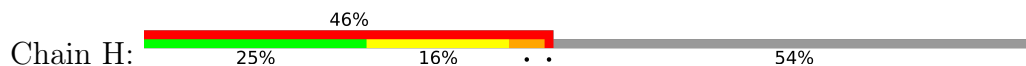


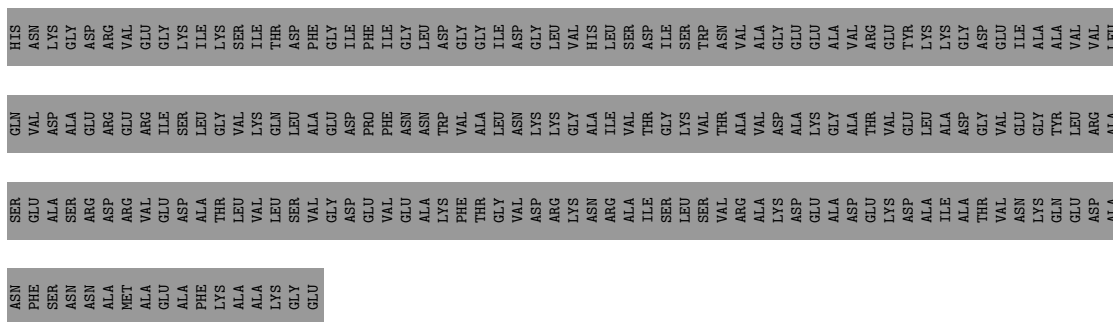


• Molecule 18: 30S ribosomal protein S2

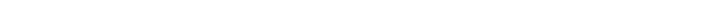


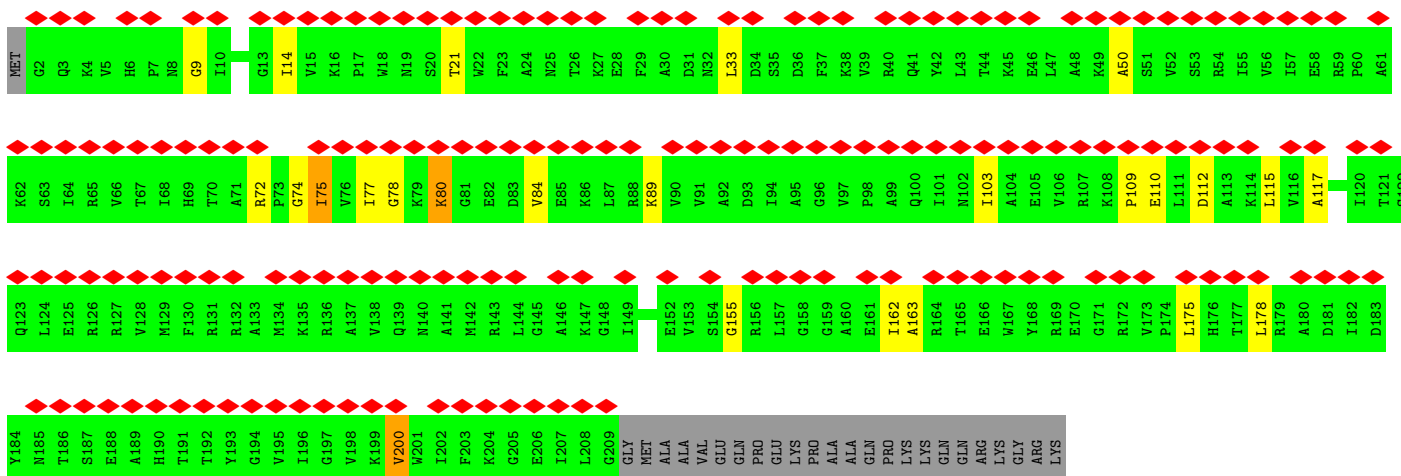
• Molecule 19: 30S ribosomal protein S1



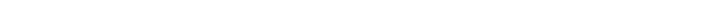


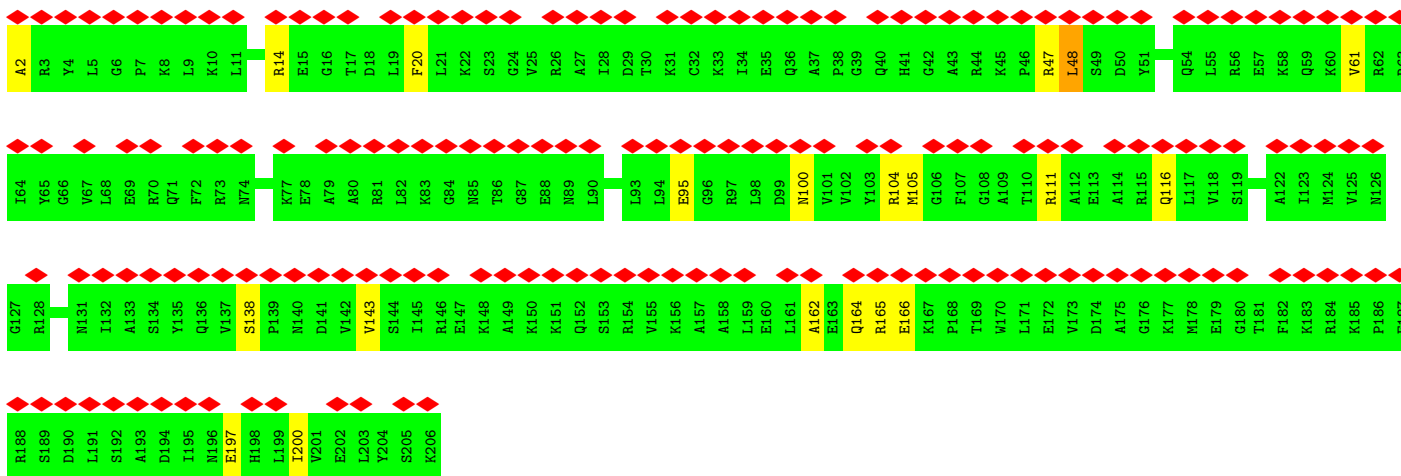
- Molecule 20: 30S ribosomal protein S3

Chain I:  76% 79% 9% 11%

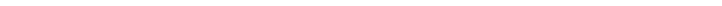


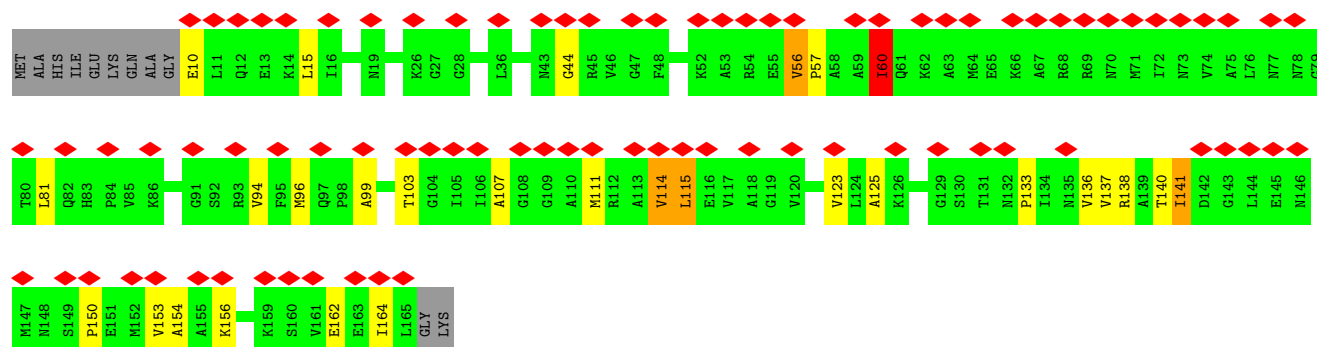
- Molecule 21: 30S ribosomal protein S4

Chain J:  84% 90% 9%

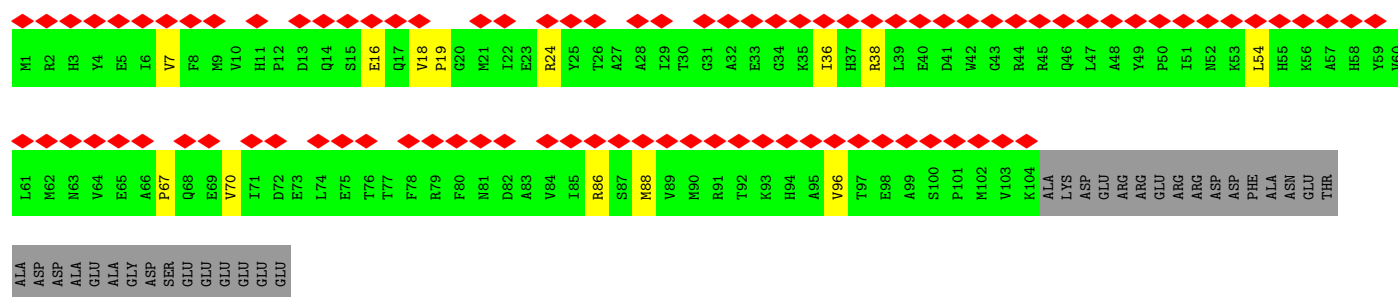


- Molecule 22: 30S ribosomal protein S5

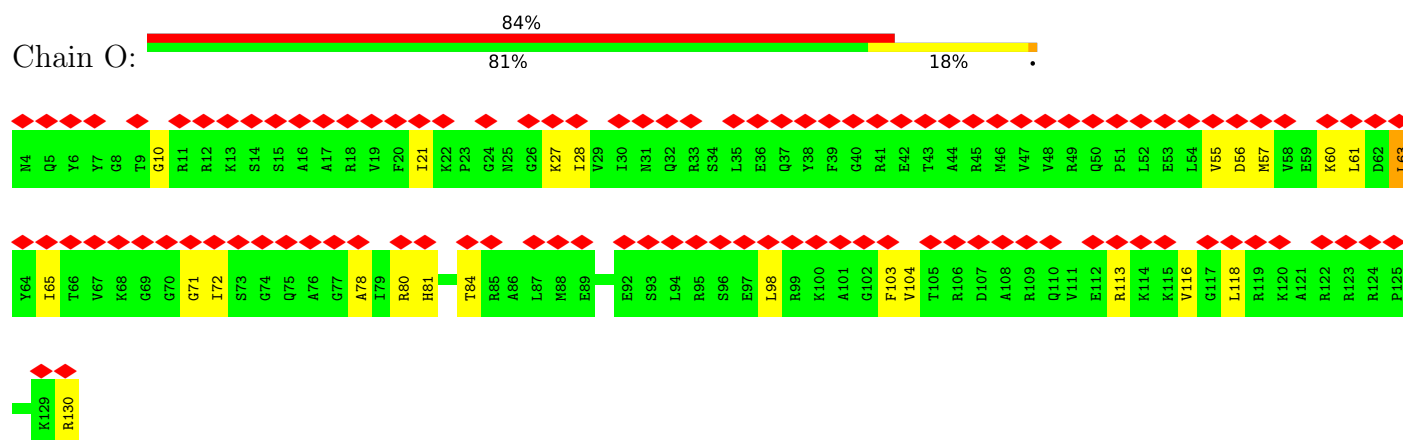
Chain K:  50% 76% 14% 7%



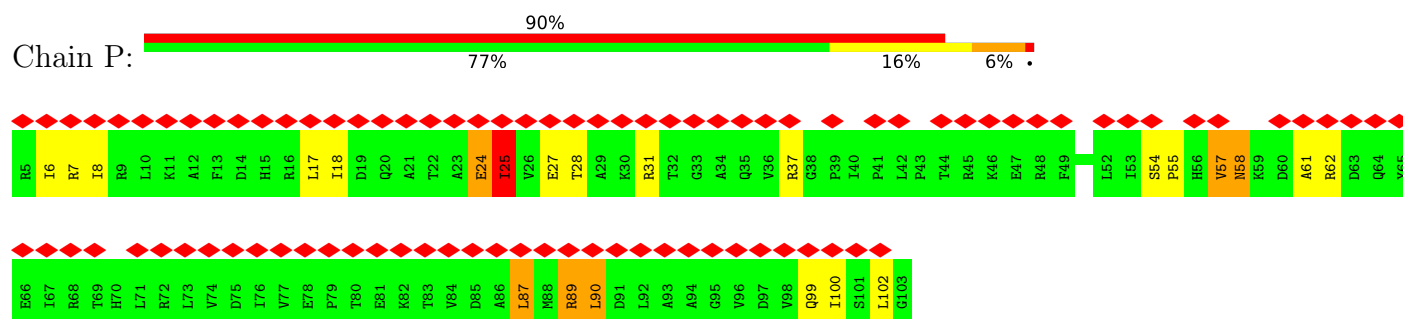
• Molecule 23: 30S ribosomal protein S6



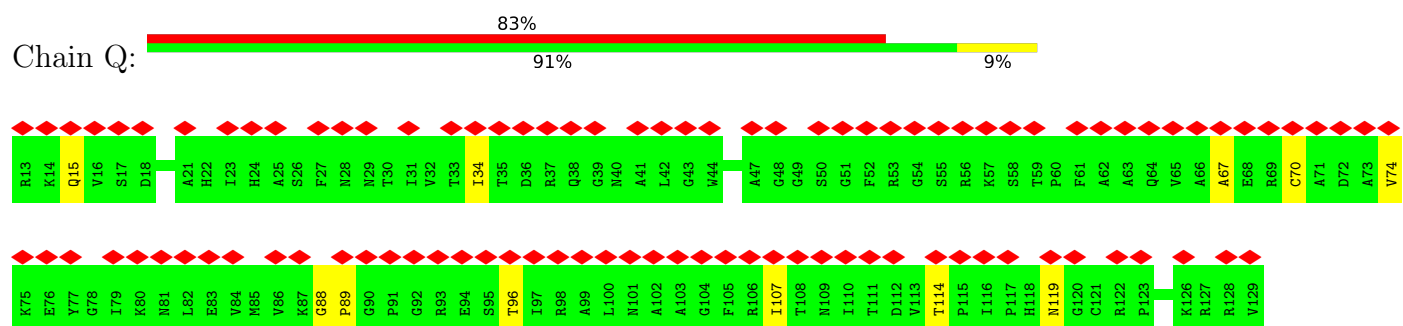
- Molecule 26: 30S ribosomal protein S9



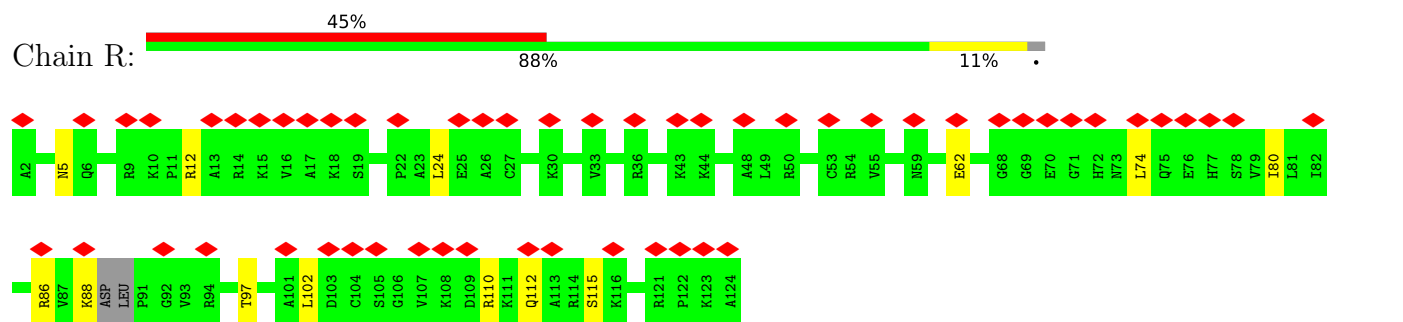
- Molecule 27: 30S ribosomal protein S10



- Molecule 28: 30S ribosomal protein S11

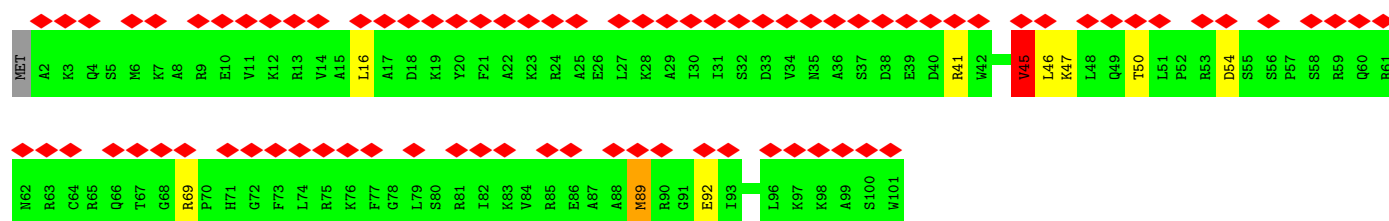


- Molecule 29: 30S ribosomal protein S12



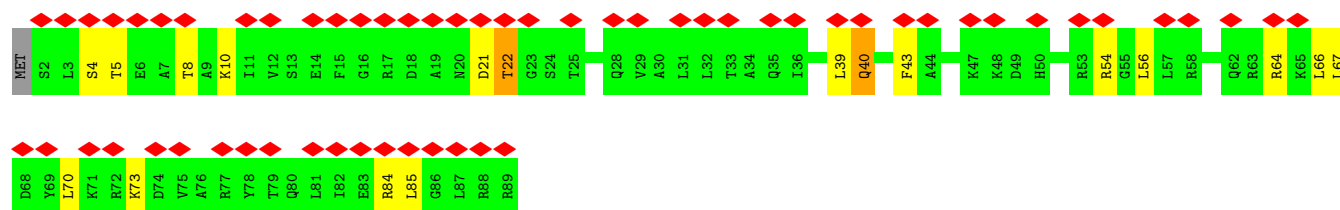
- Molecule 30: 30S ribosomal protein S14

Chain S: 



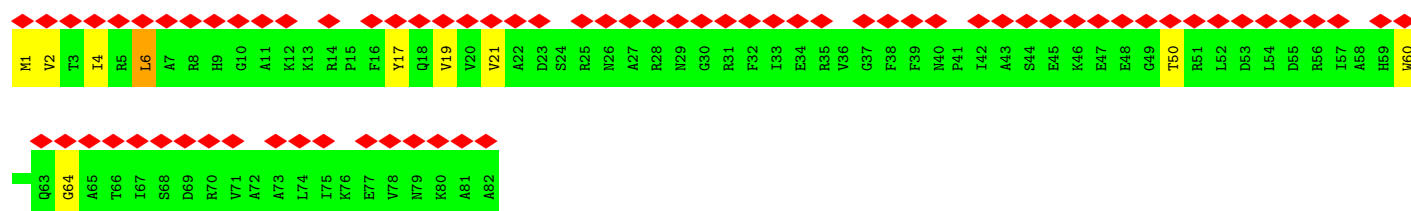
- Molecule 31: 30S ribosomal protein S15

Chain T: 



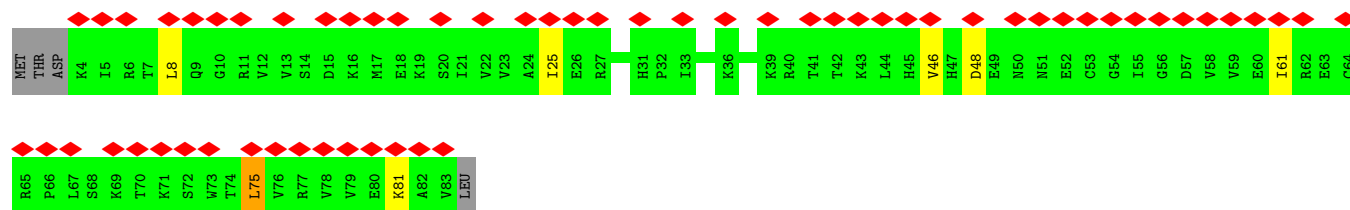
- Molecule 32: 30S ribosomal protein S16

Chain U: 

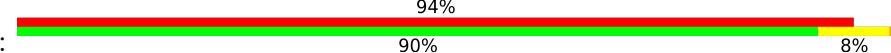


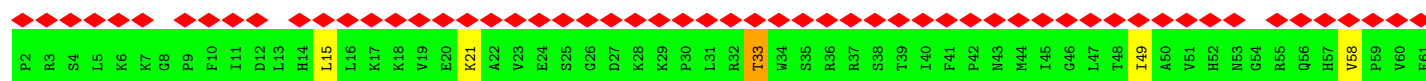
- Molecule 33: 30S ribosomal protein S17

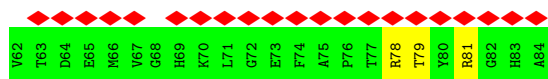
Chain V: 



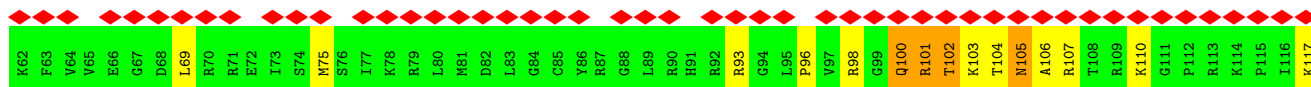
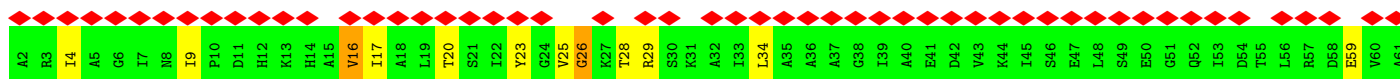
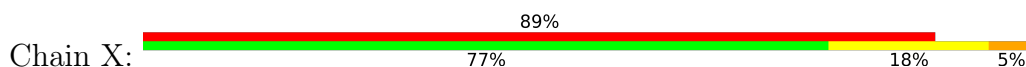
- Molecule 34: 30S ribosomal protein S19

Chain W: 

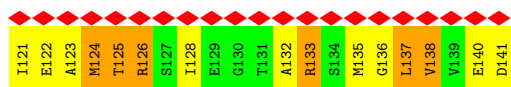
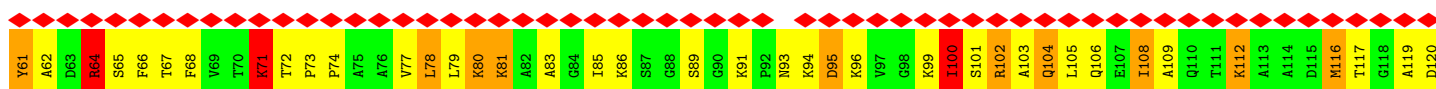




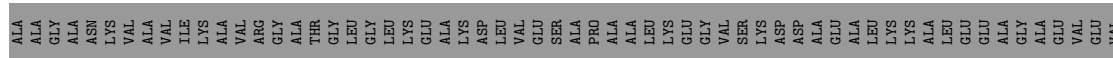
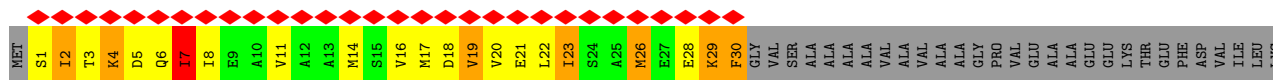
• Molecule 35: 30S ribosomal protein S13



• Molecule 36: 50S ribosomal protein L11

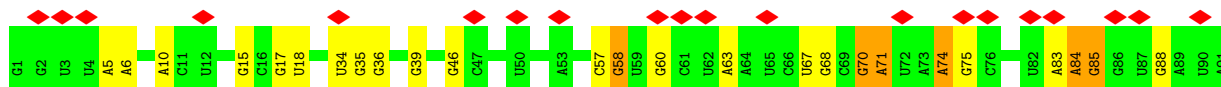


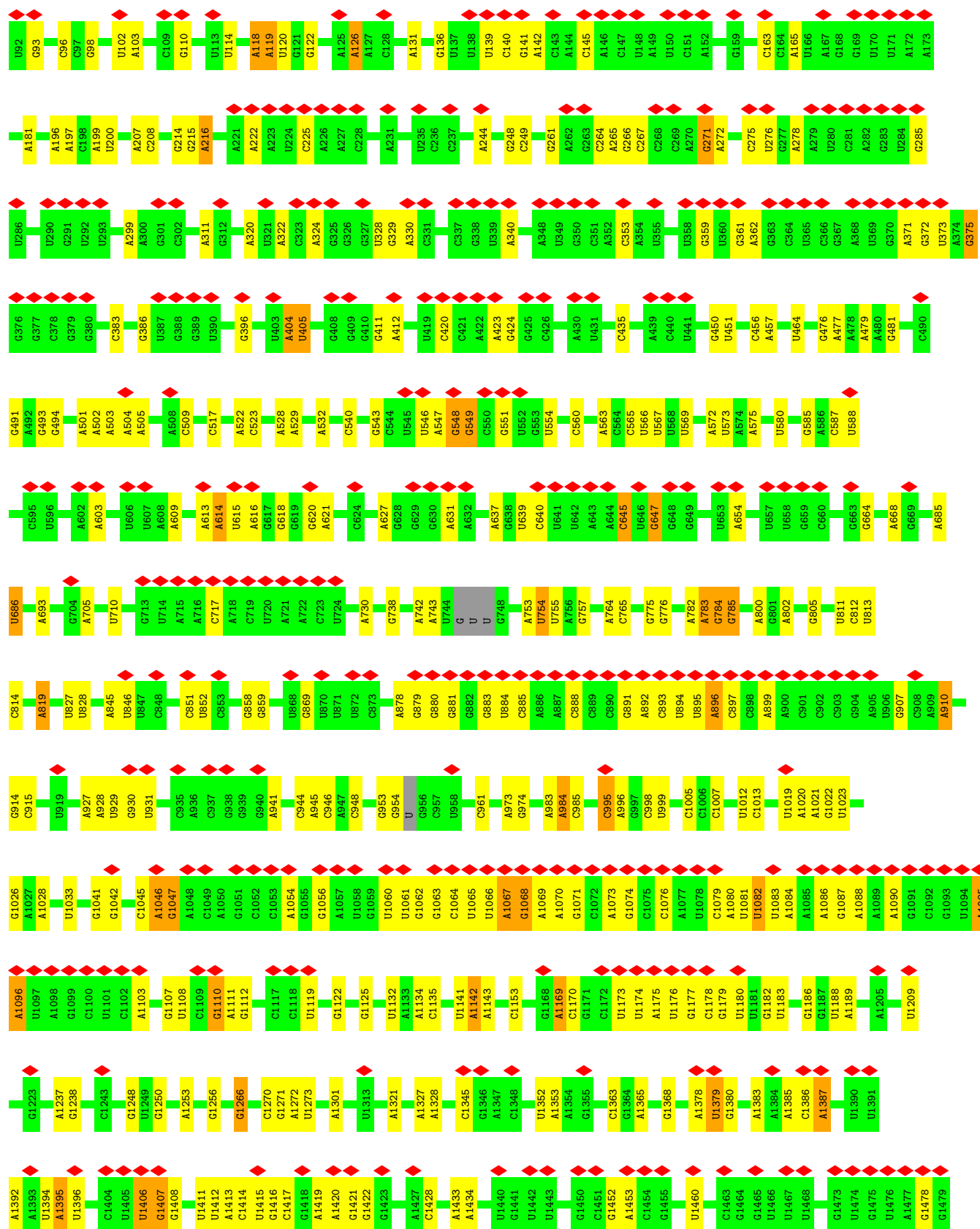
• Molecule 37: 50S ribosomal protein L7/L12

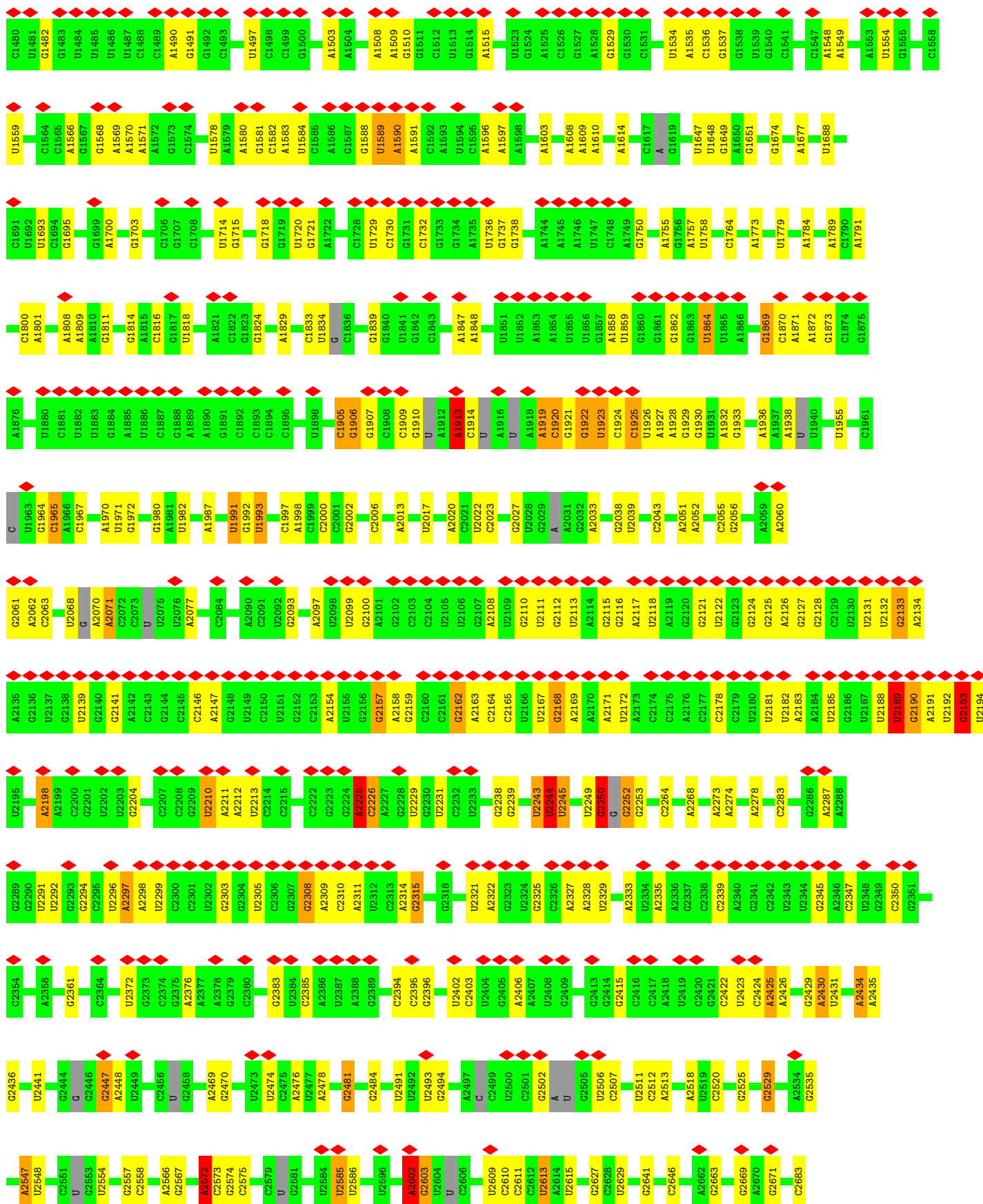


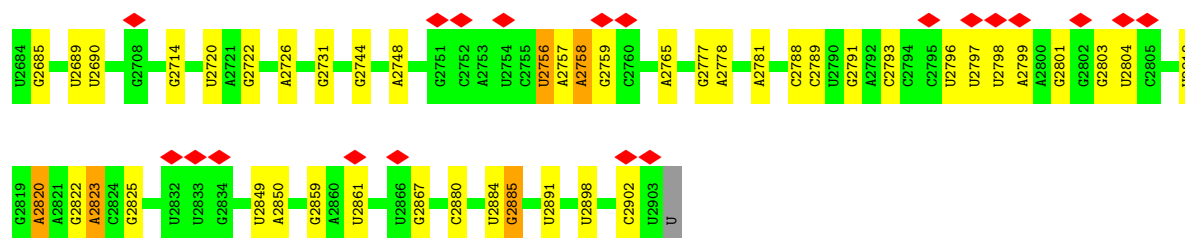
LYS

• Molecule 38: 23S rRNA

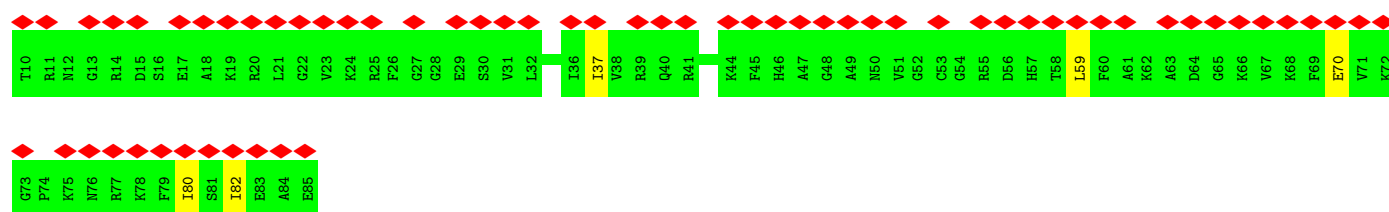
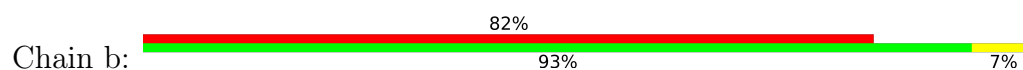




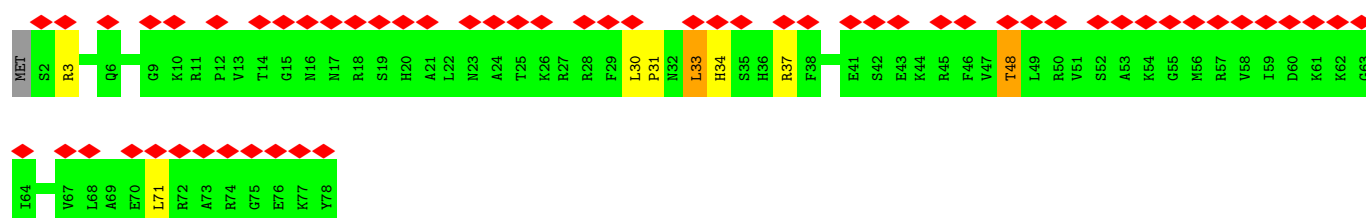
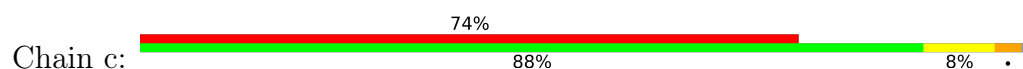




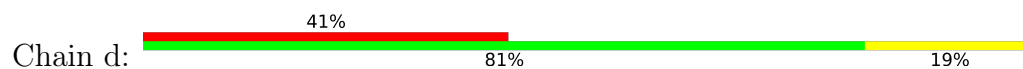
• Molecule 39: 50S ribosomal protein L27



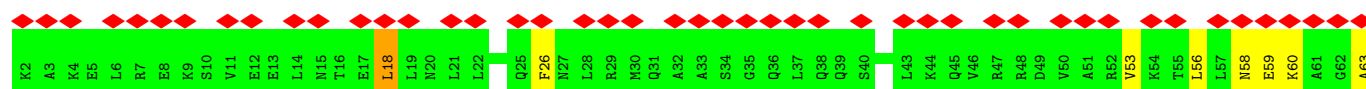
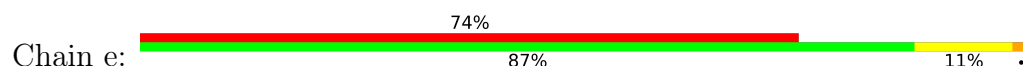
• Molecule 40: 50S ribosomal protein L28



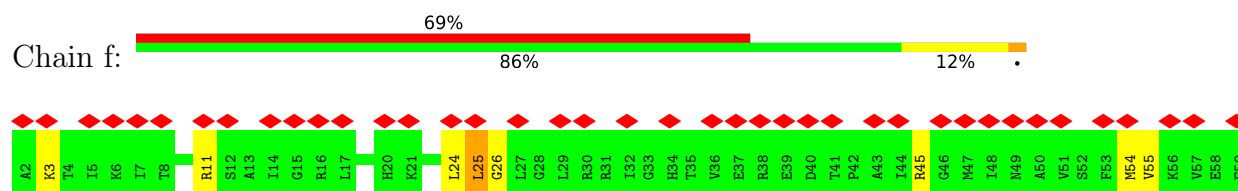
• Molecule 41: 5S rRNA



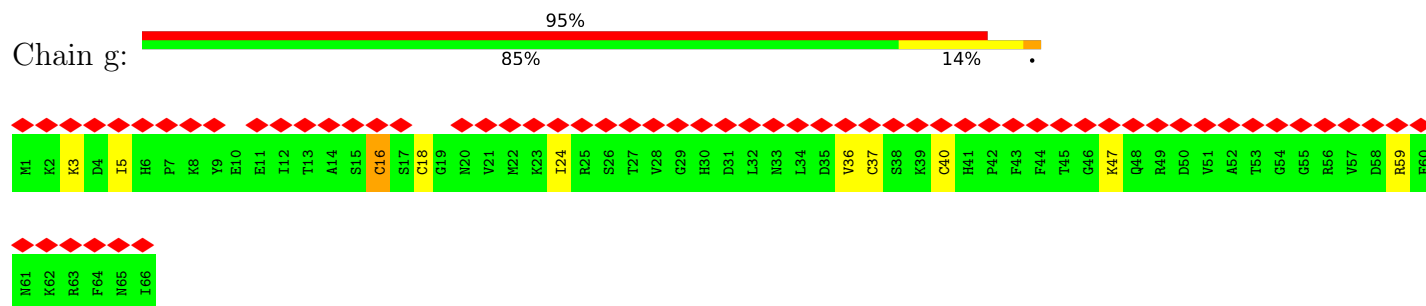
• Molecule 42: 50S ribosomal protein L29



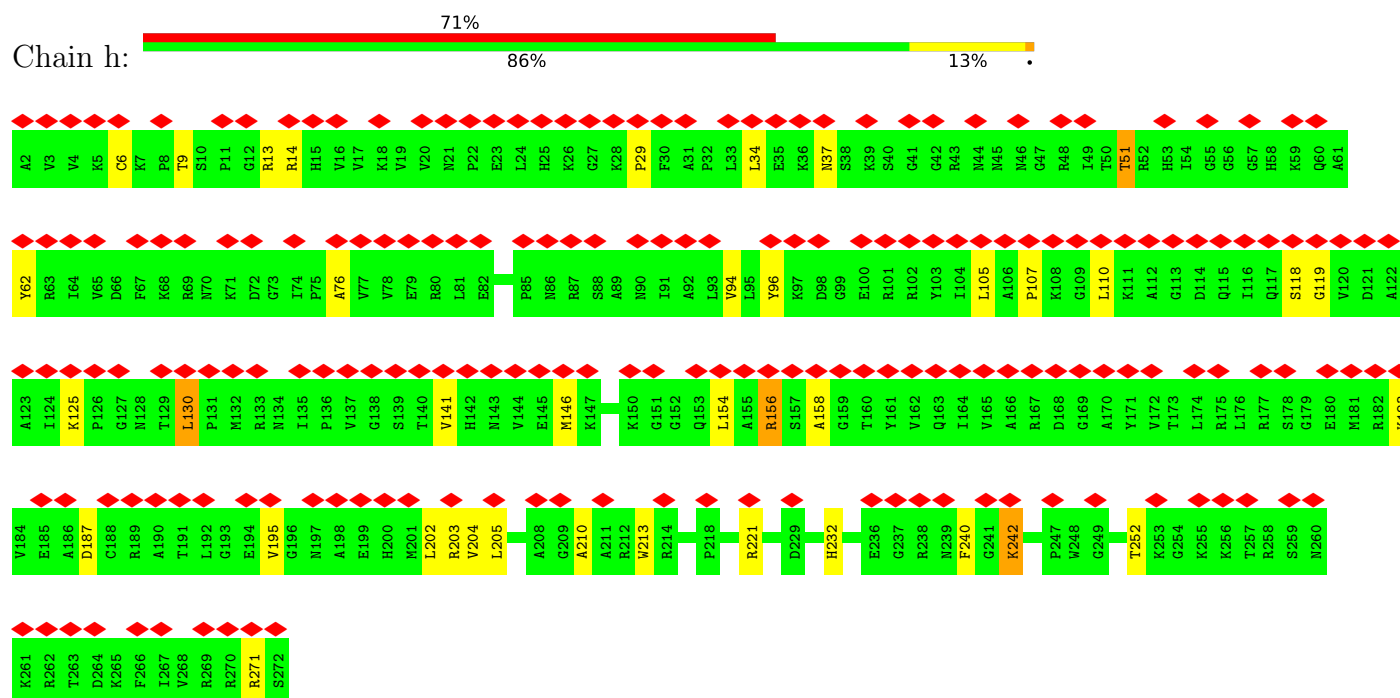
• Molecule 43: 50S ribosomal protein L30



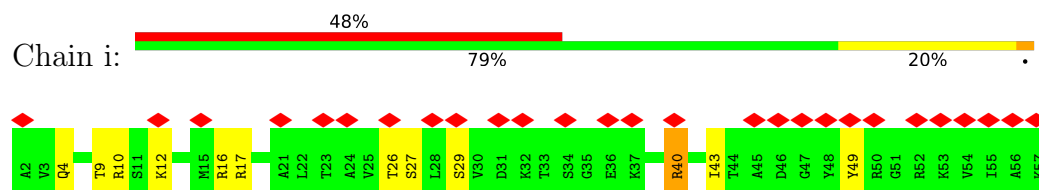
- Molecule 44: 50S ribosomal protein L31



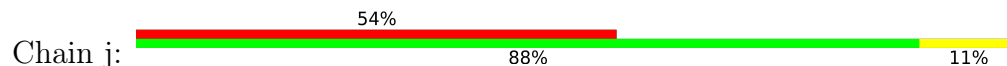
- Molecule 45: 50S ribosomal protein L2

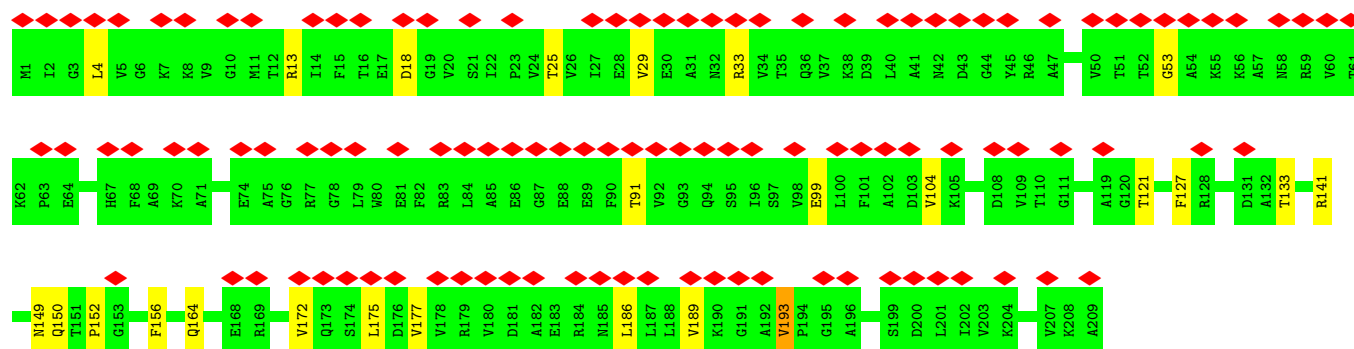


- Molecule 46: 50S ribosomal protein L32

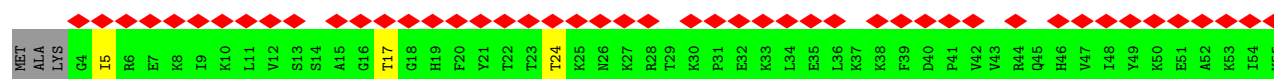
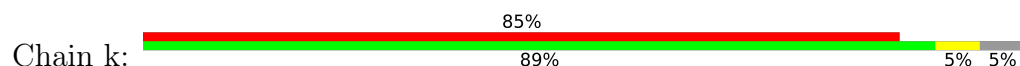


- Molecule 47: 50S ribosomal protein L3

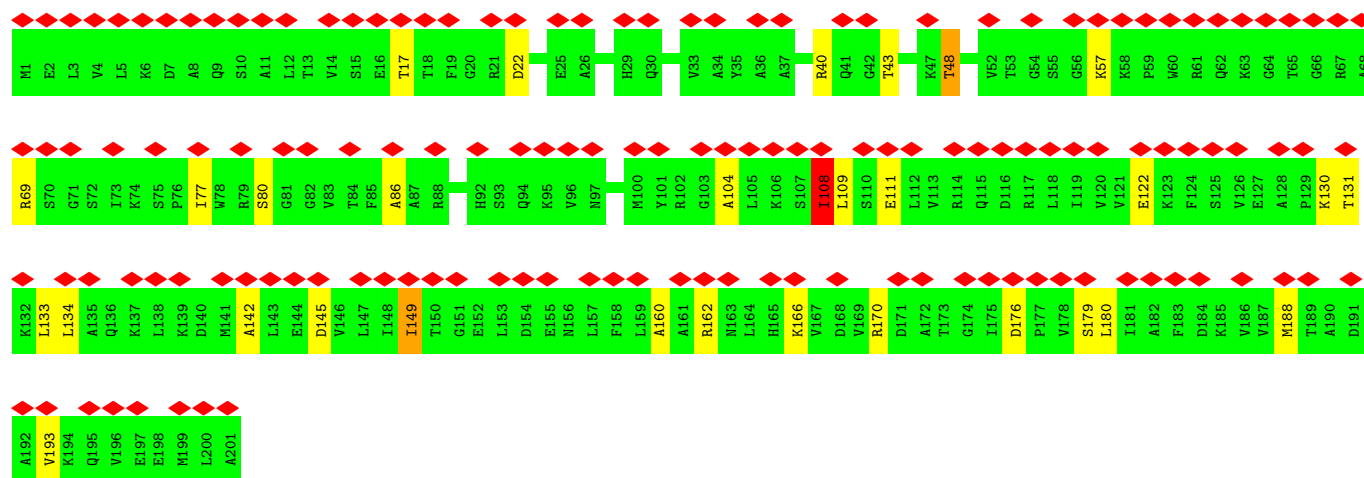
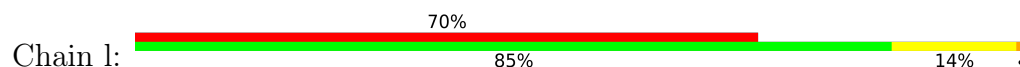




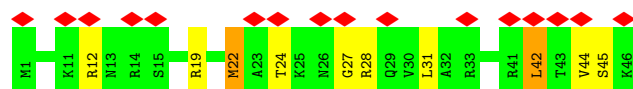
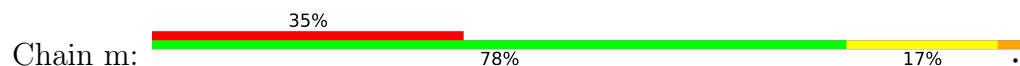
• Molecule 48: 50S ribosomal protein L33



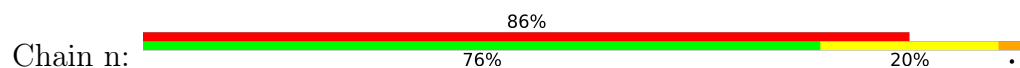
• Molecule 49: 50S ribosomal protein L4



• Molecule 50: 50S ribosomal protein L34

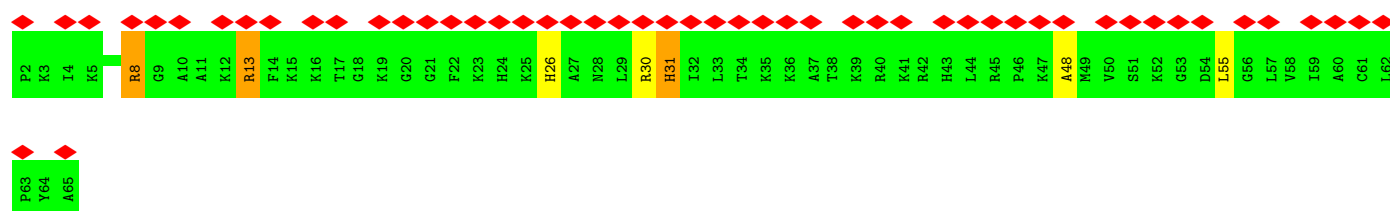
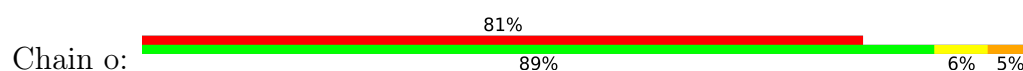


• Molecule 51: 50S ribosomal protein L5

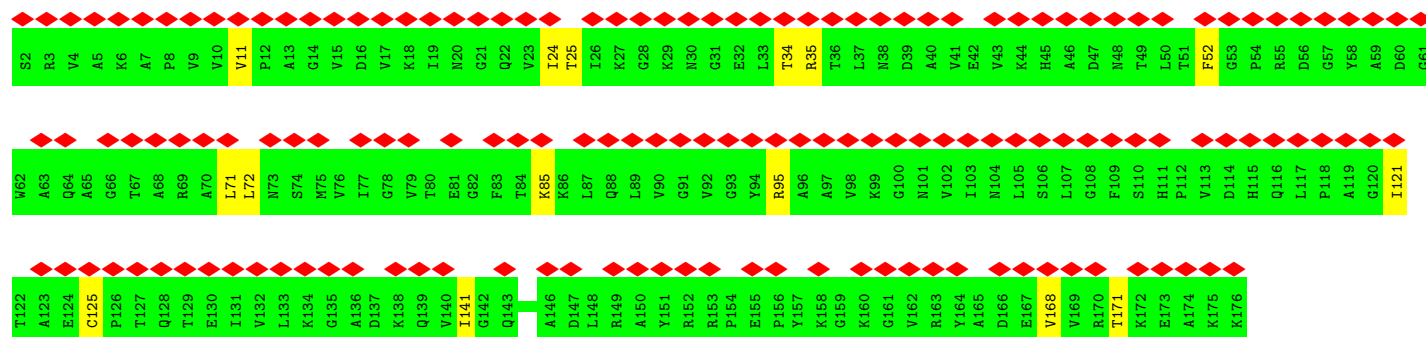
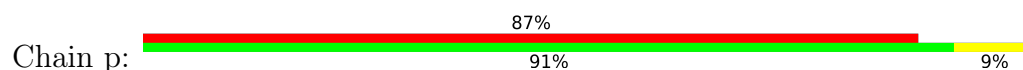




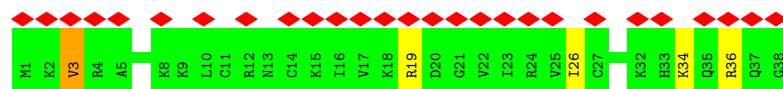
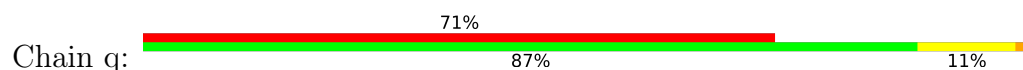
• Molecule 52: 50S ribosomal protein L35



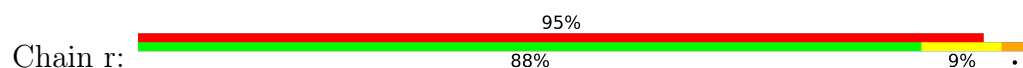
• Molecule 53: 50S ribosomal protein L6

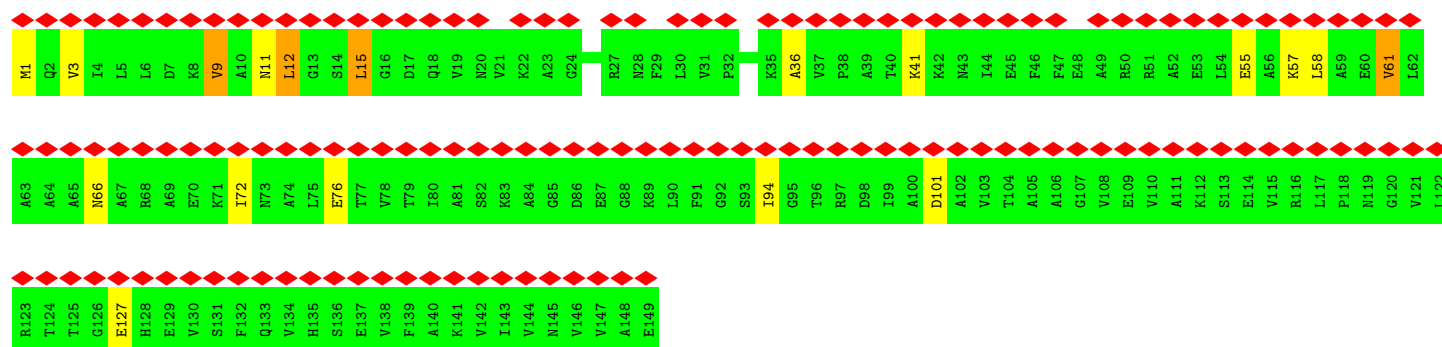


• Molecule 54: 50S ribosomal protein L36



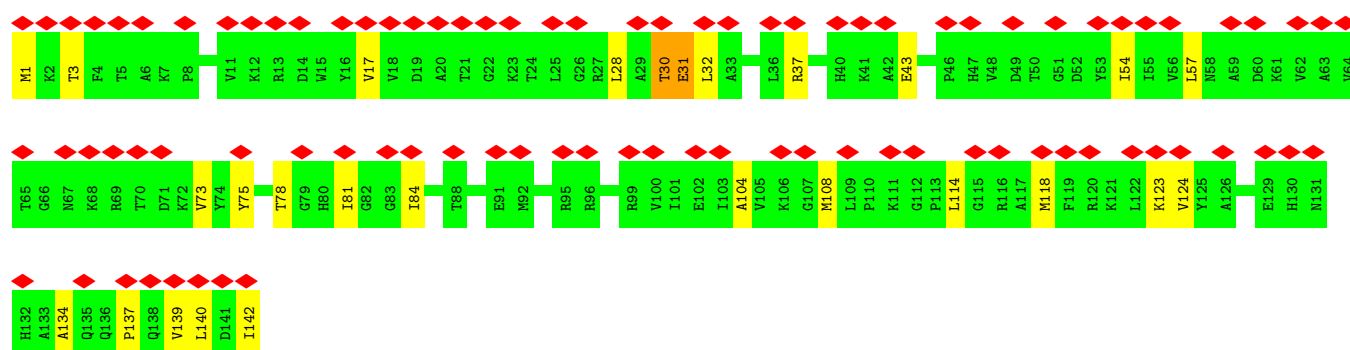
• Molecule 55: 50S ribosomal protein L9





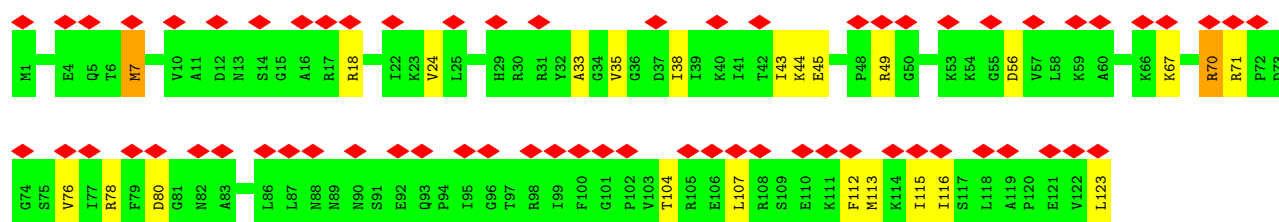
• Molecule 56: 50S ribosomal protein L13

Chain s: .



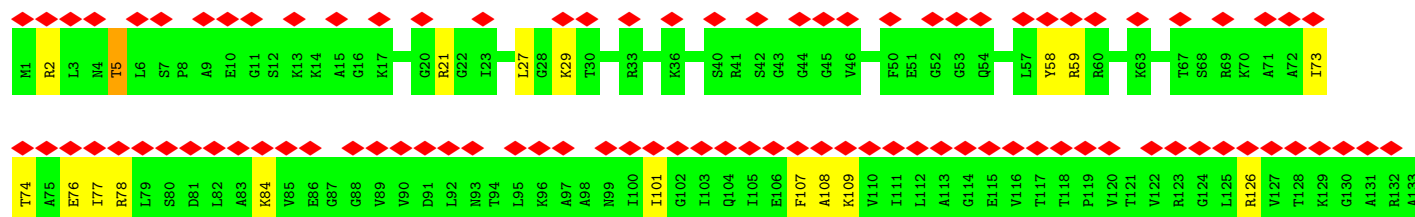
• Molecule 57: 50S ribosomal protein L14

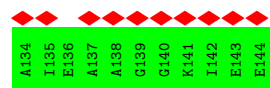
Chain t: .



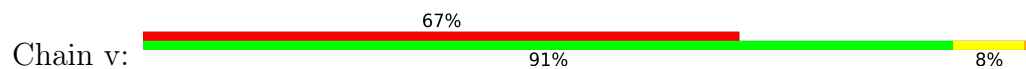
• Molecule 58: 50S ribosomal protein L15

Chain u: .

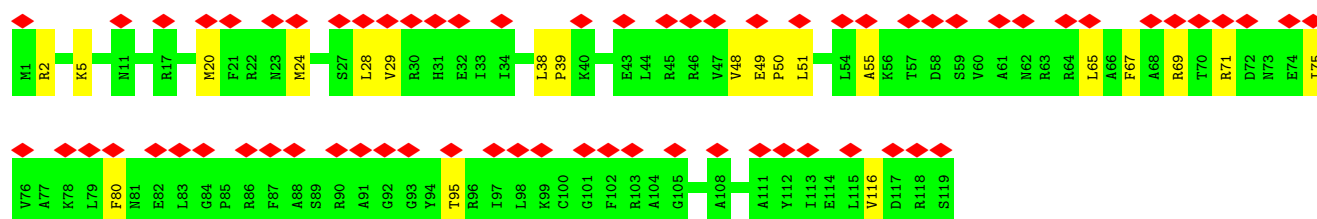
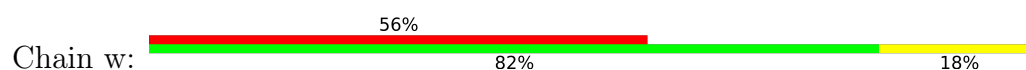




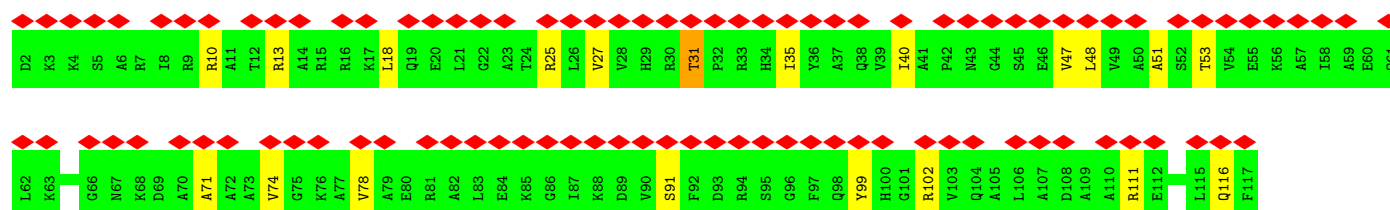
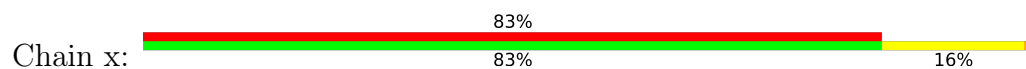
• Molecule 59: 50S ribosomal protein L16



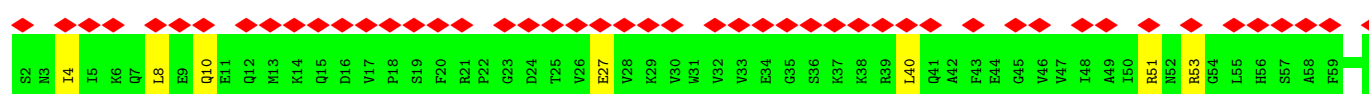
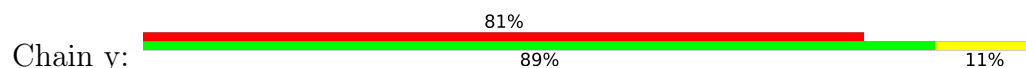
• Molecule 60: 50S ribosomal protein L17

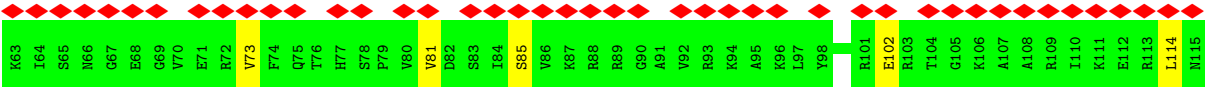


• Molecule 61: 50S ribosomal protein L18

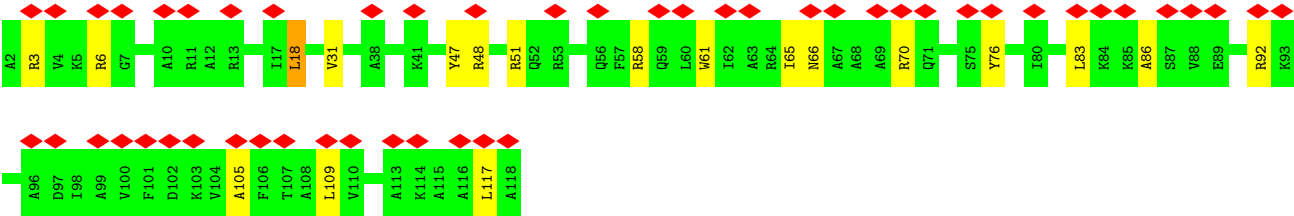
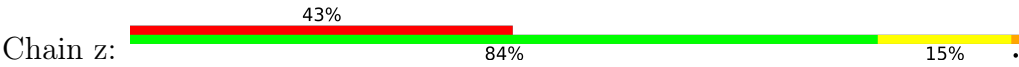


• Molecule 62: 50S ribosomal protein L19





• Molecule 63: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27650	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.067	Depositor
Minimum map value	-0.032	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.56	2/747 (0.3%)	0.81	2/1160 (0.2%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.67	12/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AC	0.60	3/1808 (0.2%)	0.73	9/2450 (0.4%)
12	AD	0.39	0/1789	0.56	0/2425
13	AE	0.54	9/10545 (0.1%)	0.74	23/14236 (0.2%)
14	C	0.66	0/553	1.15	2/743 (0.3%)
15	D	0.40	9/36610 (0.0%)	0.75	39/57091 (0.1%)
16	E	0.76	0/675	1.32	0/895
17	F	0.71	0/597	1.20	0/792
18	G	0.65	0/1791	1.08	1/2413 (0.0%)
19	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
20	I	0.58	0/1663	0.98	0/2241
21	J	0.63	0/1665	1.08	0/2227
22	K	0.63	1/1165 (0.1%)	1.06	2/1568 (0.1%)
23	L	0.58	0/867	0.94	0/1171
24	M	0.68	0/1195	1.19	3/1602 (0.2%)
25	N	0.55	0/989	0.91	0/1326
26	O	0.58	0/1034	1.02	1/1375 (0.1%)
27	P	0.60	0/800	1.11	4/1082 (0.4%)
28	Q	0.55	0/893	0.91	0/1205
29	R	0.49	0/952	0.81	0/1274
30	S	0.64	0/817	1.11	1/1088 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	T	0.69	0/722	1.21	0/964
32	U	0.58	0/659	0.99	0/884
33	V	0.46	0/657	0.73	0/881
34	W	0.51	0/680	0.83	0/915
35	X	0.67	0/909	1.21	3/1215 (0.2%)
36	Y	1.03	0/1046	1.08	0/1410
37	Z	1.03	0/227	1.13	0/304
38	a	0.40	3/69247 (0.0%)	0.75	57/107985 (0.1%)
39	b	0.50	0/589	0.76	0/779
40	c	0.63	0/635	0.97	0/848
41	d	0.37	0/2872	0.69	0/4478
42	e	0.69	0/502	1.19	0/667
43	f	0.62	0/452	1.02	0/605
44	g	0.55	0/531	0.99	1/709 (0.1%)
45	h	0.54	0/2121	0.85	0/2852
46	i	0.52	0/450	0.94	0/599
47	j	0.59	0/1586	0.87	0/2134
48	k	0.47	0/433	0.80	0/576
49	l	0.61	0/1571	1.03	1/2113 (0.0%)
50	m	0.68	0/380	1.22	0/498
51	n	0.62	0/1434	1.18	10/1926 (0.5%)
52	o	0.63	0/513	1.10	1/676 (0.1%)
53	p	0.58	0/1333	0.89	0/1805
54	q	0.50	0/303	0.88	0/397
55	r	0.63	0/1122	0.97	1/1515 (0.1%)
56	s	0.68	0/1152	1.02	2/1551 (0.1%)
57	t	0.57	0/955	0.88	0/1279
58	u	0.54	0/1062	0.95	1/1413 (0.1%)
59	v	0.59	0/1093	0.97	0/1460
60	w	0.67	0/964	1.13	0/1289
61	x	0.61	0/902	1.09	0/1209
62	y	0.52	0/929	0.79	0/1242
63	z	0.80	0/960	1.25	0/1278
All	All	0.50	48/188372 (0.0%)	0.84	267/277748 (0.1%)

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
10	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
13	AE	0	5
19	H	0	3
35	X	0	1
All	All	0	23

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.18	1.70	1.47
11	AA	374	GLU	C-N	17.55	1.54	1.33
11	AA	850	ILE	N-CA	-13.11	1.29	1.46
13	AE	93	THR	CA-C	12.23	1.69	1.52
19	H	169	SER	N-CA	11.75	1.61	1.46
15	D	1516	G	O3'-P	-10.73	1.45	1.61
13	AE	70	CYS	CA-CB	-8.66	1.41	1.53
15	D	1339	A	O3'-P	8.47	1.73	1.61
8	7	19	G	C1'-N9	-7.45	1.36	1.48
8	7	-10	U	C1'-N1	7.17	1.59	1.48
19	H	88	LYS	N-CA	7.05	1.55	1.46
6	5	109	DT	O3'-P	6.97	1.71	1.61
12	AC	76	GLU	N-CA	-6.92	1.37	1.46
15	D	145	G	O3'-P	6.74	1.71	1.61
15	D	196	A	O3'-P	6.65	1.71	1.61
19	H	168	VAL	C-N	6.47	1.42	1.33
15	D	1275	A	O3'-P	6.21	1.70	1.61
12	AC	75	GLN	CA-C	-6.16	1.45	1.53
38	a	2434	A	O3'-P	5.98	1.70	1.61
15	D	1515	G	O3'-P	-5.83	1.52	1.61
19	H	88	LYS	CA-C	5.79	1.60	1.52
13	AE	90	VAL	CA-C	5.76	1.60	1.52
15	D	1395	C	O3'-P	5.74	1.69	1.61
11	AA	885	GLY	C-O	-5.66	1.16	1.23
15	D	1490	U	O3'-P	5.45	1.69	1.61
7	6	10	DG	C1'-N9	-5.39	1.35	1.46
11	AA	604	HIS	ND1-CE1	5.32	1.37	1.32
15	D	1492	A	O3'-P	5.28	1.69	1.61
38	a	1905	C	O3'-P	5.27	1.69	1.61
11	AA	996	ARG	N-CA	-5.26	1.38	1.45
38	a	2167	U	O3'-P	5.25	1.69	1.61
13	AE	1350	ASN	CG-ND2	-5.24	1.22	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	AC	160	HIS	CD2-NE2	-5.23	1.32	1.37
11	AA	1116	HIS	ND1-CE1	5.21	1.37	1.32
13	AE	777	HIS	ND1-CE1	5.15	1.37	1.32
9	9	129	LEU	C-N	5.13	1.45	1.33
11	AA	1257	GLN	CD-OE1	5.12	1.33	1.23
11	AA	1157	GLN	CD-NE2	-5.11	1.22	1.33
13	AE	424	ASN	CG-ND2	-5.10	1.22	1.33
13	AE	450	HIS	CD2-NE2	-5.10	1.32	1.37
13	AE	1108	GLN	CD-OE1	5.10	1.33	1.23
22	K	56	VAL	CA-CB	5.08	1.57	1.54
9	9	116	GLU	N-CA	5.08	1.49	1.46
11	AA	604	HIS	CD2-NE2	-5.08	1.32	1.37
11	AA	1116	HIS	CD2-NE2	-5.08	1.32	1.37
11	AA	1256	GLN	CD-OE1	5.05	1.33	1.23
11	AA	760	ASN	CG-ND2	-5.05	1.22	1.33
13	AE	1268	ASN	CG-OD1	5.05	1.33	1.23

All (267) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	1516	G	O3'-P-O5'	17.49	130.24	104.00
11	AA	727	VAL	N-CA-C	-17.26	95.03	110.74
19	H	88	LYS	CA-C-N	16.90	143.53	120.38
19	H	88	LYS	C-N-CA	16.90	143.53	120.38
10	B	29	G	C3'-C2'-O2'	15.98	134.67	110.70
9	9	129	LEU	CA-C-N	15.88	139.69	119.84
9	9	129	LEU	C-N-CA	15.88	139.69	119.84
15	D	1516	G	P-O3'-C3'	-15.53	96.91	120.20
11	AA	374	GLU	CA-C-N	15.03	135.86	120.38
11	AA	374	GLU	C-N-CA	15.03	135.86	120.38
11	AA	1250	SER	CA-C-N	14.91	149.56	123.01
11	AA	1250	SER	C-N-CA	14.91	149.56	123.01
19	H	332	VAL	N-CA-C	13.64	124.53	110.62
19	H	169	SER	N-CA-C	12.73	137.93	110.80
19	H	330	VAL	N-CA-C	12.18	126.93	109.51
19	H	305	HIS	N-CA-C	11.96	131.09	111.37
13	AE	90	VAL	N-CA-C	9.89	122.19	107.75
11	AA	995	ASP	O-C-N	-9.83	109.52	122.59
38	a	2244	U	C1'-C2'-O2'	-9.79	93.71	108.40
11	AA	375	PRO	CA-N-CD	-9.68	98.45	112.00
51	n	73	SER	N-CA-CB	-9.56	94.61	110.47
15	D	1206	G	C4'-C3'-O3'	9.52	127.27	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AA	935	THR	CA-CB-OG1	-9.43	95.46	109.60
27	P	54	SER	CA-C-N	9.35	129.04	118.85
27	P	54	SER	C-N-CA	9.35	129.04	118.85
38	a	2250	G	C4'-C3'-O3'	-9.25	95.53	109.40
11	AA	376	PRO	N-CA-CB	-9.11	93.69	103.25
11	AA	943	LYS	CA-C-O	-9.00	107.64	120.51
15	D	1401	G	C4'-C3'-O3'	8.85	126.27	113.00
15	D	428	G	C4'-C3'-O3'	8.72	122.47	109.40
9	9	130	PRO	CA-N-CD	-8.61	99.95	112.00
8	7	-11	A	O3'-P-O5'	-8.60	91.11	104.00
19	H	339	ARG	CA-C-N	8.54	137.84	121.54
19	H	339	ARG	C-N-CA	8.54	137.84	121.54
15	D	1515	G	O3'-P-O5'	-8.44	91.34	104.00
30	S	45	VAL	N-CA-CB	8.44	120.42	110.55
38	a	2296	U	C4'-C3'-O3'	8.43	122.05	109.40
11	AA	375	PRO	N-CA-C	8.42	120.97	110.70
38	a	404	A	C2'-C3'-O3'	8.36	122.04	109.50
11	AA	849	GLU	CA-C-N	8.31	136.93	121.97
11	AA	849	GLU	C-N-CA	8.31	136.93	121.97
8	7	-8	U	C2'-C3'-O3'	8.29	121.93	109.50
27	P	57	VAL	N-CA-C	8.28	120.03	107.77
15	D	197	A	C2'-C3'-O3'	8.20	121.80	109.50
38	a	2252	G	N9-C1'-C2'	-8.14	99.80	112.00
11	AA	1048	LYS	CA-C-N	-7.94	115.42	122.96
11	AA	1048	LYS	C-N-CA	-7.94	115.42	122.96
15	D	1401	G	N9-C1'-C2'	-7.92	100.12	112.00
38	a	2425	A	C2'-C3'-O3'	7.84	121.26	109.50
11	AA	855	PRO	N-CA-CB	-7.82	95.04	103.25
19	H	155	LYS	CA-C-N	-7.75	110.97	121.66
19	H	155	LYS	C-N-CA	-7.75	110.97	121.66
38	a	2071	A	C4'-C3'-O3'	-7.73	101.41	113.00
19	H	168	VAL	CA-C-N	7.70	136.25	121.54
19	H	168	VAL	C-N-CA	7.70	136.25	121.54
15	D	1493	A	C2'-C3'-O3'	7.65	125.18	113.70
19	H	52	GLN	N-CA-C	-7.62	104.12	113.50
51	n	75	ALA	CA-C-N	7.61	129.65	120.14
51	n	75	ALA	C-N-CA	7.61	129.65	120.14
19	H	84	LEU	N-CA-C	7.60	120.96	110.24
13	AE	903	LEU	CA-C-N	7.58	136.02	121.54
13	AE	903	LEU	C-N-CA	7.58	136.02	121.54
15	D	1499	A	N9-C1'-C2'	-7.58	100.63	112.00
15	D	1339	A	P-O3'-C3'	7.56	131.54	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	X	102	THR	CB-CA-C	7.55	123.37	110.84
22	K	60	ILE	N-CA-CB	7.54	119.37	110.55
15	D	528	C	N1-C1'-C2'	-7.53	100.71	112.00
11	AA	864	LYS	N-CA-C	-7.48	102.39	112.26
19	H	336	ASP	CB-CA-C	-7.47	98.61	110.79
51	n	73	SER	CB-CA-C	7.42	122.88	110.79
22	K	56	VAL	O-C-N	7.41	125.16	120.42
10	B	28	C	P-O3'-C3'	7.38	131.26	120.20
51	n	108	VAL	O-C-N	7.36	125.30	120.07
38	a	2602	A	C4'-C3'-O3'	7.30	120.36	109.40
38	a	783	A	C4'-C3'-O3'	7.29	123.94	113.00
11	AA	751	TYR	CA-C-N	7.23	132.20	121.72
11	AA	751	TYR	C-N-CA	7.23	132.20	121.72
18	G	47	VAL	O-C-N	7.17	125.01	120.42
15	D	1497	G	C1'-C2'-O2'	-7.16	97.66	108.40
10	B	29	G	N9-C1'-C2'	-7.15	101.28	112.00
15	D	196	A	P-O3'-C3'	7.10	130.85	120.20
38	a	2162	G	C4'-C3'-O3'	7.09	120.04	109.40
11	AA	375	PRO	CB-CA-C	-7.09	102.27	110.92
38	a	896	A	C4'-C3'-O3'	7.04	119.95	109.40
38	a	2225	A	C4'-C3'-O3'	6.99	119.88	109.40
38	a	1379	U	C2'-C3'-O3'	6.97	124.16	113.70
24	M	27	VAL	N-CA-CB	6.95	118.68	110.55
38	a	2244	U	C4'-C3'-O3'	6.88	123.33	113.00
19	H	140	PRO	N-CA-CB	6.87	110.47	103.25
11	AA	728	ASP	N-CA-C	6.82	125.31	110.80
11	AA	604	HIS	CB-CG-CD2	-6.81	122.34	131.20
38	a	2252	G	C4'-C3'-O3'	6.79	123.19	113.00
19	H	340	ARG	CA-C-N	-6.79	112.56	123.23
19	H	340	ARG	C-N-CA	-6.79	112.56	123.23
51	n	71	ARG	CA-C-N	6.75	133.98	122.37
51	n	71	ARG	C-N-CA	6.75	133.98	122.37
12	AC	160	HIS	CB-CG-CD2	-6.74	122.44	131.20
11	AA	855	PRO	CB-CA-C	-6.68	100.54	111.56
38	a	2243	U	C4'-C3'-O3'	6.66	123.00	113.00
19	H	170	ARG	N-CA-C	6.64	119.60	110.24
15	D	517	G	C5'-C4'-C3'	6.63	125.14	115.20
38	a	2189	U	C1'-C2'-O2'	-6.60	101.89	111.80
11	AA	1116	HIS	CB-CG-CD2	-6.60	122.62	131.20
12	AC	117	HIS	CB-CA-C	-6.59	97.97	109.64
19	H	303	LEU	N-CA-C	6.59	121.16	112.13
19	H	87	GLU	N-CA-C	-6.58	104.11	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	H	132	PRO	N-CA-CB	6.57	110.28	103.38
38	a	2167	U	P-O3'-C3'	6.56	130.04	120.20
19	H	112	ILE	N-CA-C	6.53	117.10	106.72
19	H	155	LYS	N-CA-C	-6.52	98.27	108.90
51	n	127	ASN	CB-CA-C	6.52	121.66	110.77
15	D	526	C	C4'-C3'-O3'	6.51	122.77	113.00
26	O	72	ILE	N-CA-C	-6.51	105.36	111.48
38	a	894	U	C2'-C3'-O3'	6.51	119.26	109.50
15	D	526	C	N1-C1'-C2'	-6.50	102.26	112.00
55	r	61	VAL	N-CA-CB	6.47	118.12	110.55
15	D	1340	A	C1'-C2'-O2'	6.45	118.07	108.40
52	o	13	ARG	N-CA-C	6.45	120.98	113.18
12	AC	23	HIS	CB-CG-CD2	-6.43	122.84	131.20
51	n	127	ASN	CA-CB-CG	-6.43	106.17	112.60
38	a	754	U	N1-C1'-C2'	6.41	121.62	112.00
13	AE	450	HIS	CB-CG-CD2	-6.37	122.91	131.20
13	AE	93	THR	CA-C-N	6.37	133.03	121.06
13	AE	93	THR	C-N-CA	6.37	133.03	121.06
15	D	69	G	C4'-C3'-O3'	-6.36	103.46	113.00
13	AE	61	ILE	CA-C-N	-6.35	114.02	121.64
13	AE	61	ILE	C-N-CA	-6.35	114.02	121.64
11	AA	150	HIS	CB-CG-CD2	-6.28	123.04	131.20
15	D	1208	C	N1-C1'-C2'	-6.28	102.58	112.00
14	C	33	ILE	CA-C-O	-6.27	114.91	121.93
19	H	153	GLU	N-CA-C	-6.27	97.45	110.80
13	AE	777	HIS	CB-CG-CD2	-6.26	123.06	131.20
38	a	2434	A	P-O3'-C3'	6.26	129.59	120.20
11	AA	888	THR	CB-CA-C	-6.24	99.37	108.91
10	B	28	C	O3'-P-O5'	-6.22	94.67	104.00
11	AA	850	ILE	N-CA-CB	6.21	121.48	111.23
38	a	2425	A	C4'-C3'-O3'	6.20	118.69	109.40
19	H	113	ASN	N-CA-C	6.16	118.08	111.36
13	AE	70	CYS	CB-CA-C	6.14	120.35	110.29
15	D	1206	G	N9-C1'-C2'	-6.13	102.80	112.00
11	AA	861	ALA	CA-C-N	6.12	133.24	121.54
11	AA	861	ALA	C-N-CA	6.12	133.24	121.54
11	AA	869	GLY	CA-C-O	-6.09	117.71	122.52
15	D	1516	G	OP1-P-O3'	-6.05	89.85	108.00
38	a	271	G	C4'-C3'-O3'	6.03	118.44	109.40
11	AA	1004	ASP	CB-CA-C	6.02	122.40	110.42
15	D	1408	A	C4'-C3'-O3'	6.01	122.01	113.00
38	a	2820	A	C4'-C3'-O3'	-6.01	103.99	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	550	G	C3'-C2'-O2'	6.00	119.71	110.70
38	a	2210	U	C4'-C3'-O3'	6.00	118.41	109.40
12	AC	74	VAL	N-CA-C	5.99	117.46	108.96
38	a	1913	A	C2'-C3'-O3'	5.98	118.47	109.50
13	AE	90	VAL	CA-C-O	-5.95	114.21	120.39
24	M	92	ARG	CA-C-N	5.91	125.39	119.24
24	M	92	ARG	C-N-CA	5.91	125.39	119.24
12	AC	75	GLN	N-CA-CB	5.90	119.34	110.19
11	AA	604	HIS	CB-CG-ND1	5.89	131.53	122.70
38	a	2308	G	C2'-C3'-O3'	-5.88	104.88	113.70
49	l	108	ILE	N-CA-CB	5.86	118.51	110.54
38	a	2756	U	C4'-C3'-O3'	5.85	118.18	109.40
19	H	150	LYS	N-CA-C	5.85	118.25	110.53
19	H	109	THR	N-CA-C	-5.85	99.12	109.06
11	AA	1116	HIS	CB-CG-ND1	5.84	131.45	122.70
19	H	75	VAL	N-CA-C	5.82	116.50	108.12
51	n	72	LYS	N-CA-C	-5.81	99.18	109.06
35	X	26	GLY	N-CA-C	-5.81	104.34	112.13
11	AA	936	ARG	CA-C-O	-5.81	114.02	120.70
11	AA	732	ILE	CB-CA-C	-5.80	103.61	111.15
15	D	1275	A	P-O3'-C3'	5.80	128.90	120.20
12	AC	76	GLU	N-CA-C	-5.79	101.71	110.28
10	B	29	G	O5'-C5'-C4'	-5.79	102.81	111.50
38	a	70	G	C4'-C3'-O3'	5.79	118.08	109.40
38	a	1905	C	P-O3'-C3'	5.79	128.88	120.20
13	AE	91	GLU	N-CA-C	5.75	123.04	110.80
10	B	48	C	N1-C1'-C2'	5.73	120.59	112.00
10	A	48	C	N1-C1'-C2'	5.71	120.57	112.00
12	AC	160	HIS	CB-CG-ND1	5.71	131.26	122.70
15	D	1490	U	P-O3'-C3'	5.71	128.76	120.20
15	D	1492	A	P-O3'-C3'	5.71	128.76	120.20
38	a	2168	G	C4'-C3'-O3'	-5.71	104.44	113.00
15	D	1406	U	N1-C1'-C2'	-5.70	103.46	112.00
15	D	976	G	C4'-C3'-O3'	-5.68	104.48	113.00
15	D	1340	A	C5'-C4'-C3'	5.67	124.50	116.00
38	a	1757	A	C4'-C3'-O3'	-5.66	104.51	113.00
11	AA	996	ARG	N-CA-C	-5.64	101.23	109.63
19	H	114	GLY	N-CA-C	5.61	121.24	111.14
38	a	2017	U	C2'-C3'-O3'	-5.59	105.32	113.70
12	AC	23	HIS	CB-CG-ND1	5.55	131.03	122.70
15	D	780	A	C4'-C3'-O3'	-5.54	104.68	113.00
11	AA	942	ASP	N-CA-C	-5.54	106.69	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	AE	450	HIS	CB-CG-ND1	5.53	130.99	122.70
11	AA	853	ASP	CA-C-N	5.52	130.31	120.70
11	AA	853	ASP	C-N-CA	5.52	130.31	120.70
38	a	1568	G	C4'-C3'-O3'	-5.52	104.72	113.00
38	a	2731	G	C4'-C3'-O3'	-5.51	104.73	113.00
38	a	2447	G	C2'-C3'-O3'	-5.51	101.23	109.50
11	AA	940	GLU	CA-C-O	-5.51	112.63	120.51
11	AA	150	HIS	CB-CG-ND1	5.44	130.86	122.70
13	AE	69	GLU	CA-C-N	-5.44	113.83	121.72
13	AE	69	GLU	C-N-CA	-5.44	113.83	121.72
11	AA	872	TYR	CA-C-N	5.42	131.72	121.97
11	AA	872	TYR	C-N-CA	5.42	131.72	121.97
11	AA	375	PRO	N-CA-CB	5.41	108.33	103.08
13	AE	93	THR	CB-CA-C	5.41	121.19	110.42
38	a	2068	U	C4'-C3'-O3'	-5.41	104.89	113.00
15	D	864	A	N9-C1'-C2'	5.40	120.10	112.00
38	a	2572	A	C4'-C3'-O3'	-5.39	101.32	109.40
38	a	944	C	C4'-C3'-O3'	-5.39	104.92	113.00
15	D	1145	A	C4'-C3'-O3'	-5.37	104.94	113.00
15	D	1499	A	C4'-C3'-O3'	5.37	121.05	113.00
38	a	2481	G	C4'-C3'-O3'	-5.37	104.95	113.00
15	D	517	G	C4'-C3'-O3'	-5.35	101.37	109.40
10	B	35	A	P-O3'-C3'	5.35	128.22	120.20
38	a	375	G	C2'-C3'-O3'	5.35	121.72	113.70
38	a	1270	C	C2'-C3'-O3'	-5.33	105.71	113.70
13	AE	70	CYS	N-CA-C	-5.33	101.10	109.25
13	AE	777	HIS	CB-CG-ND1	5.31	130.67	122.70
35	X	102	THR	CA-C-O	-5.31	114.81	121.02
44	g	5	ILE	N-CA-C	5.30	117.68	111.05
11	AA	1158	LYS	CA-C-N	5.30	131.51	121.97
11	AA	1158	LYS	C-N-CA	5.30	131.51	121.97
38	a	2231	U	C1'-C2'-O2'	5.30	116.35	108.40
15	D	145	G	P-O3'-C3'	5.30	128.15	120.20
38	a	2020	A	C4'-C3'-O3'	-5.29	105.06	113.00
11	AA	732	ILE	N-CA-CB	5.28	116.28	110.53
13	AE	73	GLY	N-CA-C	5.26	125.65	113.18
38	a	2529	G	C4'-C3'-O3'	-5.26	105.11	113.00
13	AE	90	VAL	O-C-N	-5.26	117.63	123.20
11	AA	1030	GLU	N-CA-C	-5.25	105.23	111.69
13	AE	88	CYS	N-CA-C	5.22	120.31	113.88
11	AA	870	ILE	CA-C-N	5.22	128.31	120.69
11	AA	870	ILE	C-N-CA	5.22	128.31	120.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	1395	C	P-O3'-C3'	5.22	128.03	120.20
11	AA	934	PHE	N-CA-C	-5.21	103.79	111.81
10	B	60	U	C2'-C3'-O3'	5.19	117.28	109.50
38	a	423	A	C2'-C3'-O3'	-5.18	105.94	113.70
10	A	60	U	C2'-C3'-O3'	5.17	117.26	109.50
38	a	2245	U	N1-C1'-C2'	-5.17	104.25	112.00
19	H	128	ARG	CA-C-N	-5.17	114.13	122.81
19	H	128	ARG	C-N-CA	-5.17	114.13	122.81
15	D	1335	U	C4'-C3'-O3'	-5.14	105.29	113.00
19	H	154	PHE	N-CA-C	-5.13	100.34	109.06
38	a	528	A	C4'-C3'-O3'	-5.13	105.31	113.00
58	u	101	ILE	N-CA-C	5.12	116.42	112.12
38	a	1834	U	C4'-C3'-O3'	-5.12	105.31	113.00
38	a	126	A	C4'-C3'-O3'	-5.10	105.36	113.00
38	a	328	U	C4'-C3'-O3'	-5.10	105.35	113.00
13	AE	61	ILE	CA-C-O	-5.09	115.65	120.95
38	a	479	A	C4'-C3'-O3'	5.08	117.02	109.40
9	9	115	GLY	CA-C-O	-5.08	118.17	122.29
14	C	35	GLU	N-CA-C	-5.08	105.93	111.82
27	P	25	ILE	N-CA-CB	5.08	117.44	110.54
12	AC	117	HIS	N-CA-C	5.07	116.83	110.24
38	a	1864	U	C4'-C3'-O3'	-5.06	105.41	113.00
13	AE	1184	ASP	N-CA-C	5.05	120.98	109.81
38	a	614	A	C2'-C3'-O3'	5.05	117.08	109.50
38	a	2193	G	C2'-C3'-O3'	5.05	121.28	113.70
11	AA	943	LYS	N-CA-C	5.04	121.52	110.80
11	AA	377	THR	CA-C-N	5.03	126.98	120.44
11	AA	377	THR	C-N-CA	5.03	126.98	120.44
19	H	108	VAL	N-CA-C	-5.03	98.87	109.34
56	s	28	LEU	CA-C-N	5.03	126.97	120.44
56	s	28	LEU	C-N-CA	5.03	126.97	120.44
10	B	19	G	N9-C1'-C2'	5.02	119.52	112.00
38	a	1991	U	C3'-C2'-O2'	5.01	118.22	110.70
38	a	2335	A	C4'-C3'-O3'	-5.00	105.49	113.00
15	D	70	U	C2'-C3'-O3'	5.00	117.00	109.50

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain

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Mol	Chain	Res	Type	Group
11	AA	1134	GLN	Peptide
11	AA	1157	GLN	Peptide
11	AA	1158	LYS	Peptide
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide
11	AA	595	THR	Peptide
11	AA	596	ASP	Mainchain
11	AA	696	ASP	Peptide
11	AA	746	ALA	Peptide
11	AA	853	ASP	Mainchain
13	AE	1184	ASP	Peptide
13	AE	1326	GLN	Peptide
13	AE	313	GLY	Peptide
13	AE	416	ILE	Peptide
13	AE	804	ALA	Peptide
10	B	19	G	Sidechain
10	B	7	G	Sidechain
19	H	274	TYR	Peptide
19	H	81	GLU	Peptide
19	H	82	THR	Peptide
35	X	100	GLN	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	261	24	0
7	6	542	305	306	26	0
8	7	672	97	332	80	0
9	9	1117	0	1153	164	0
10	A	1620	826	826	175	0
10	B	1620	813	827	137	0
11	AA	10425	10426	10428	390	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	AC	1786	1813	1813	87	0
12	AD	1767	1789	1789	48	0
13	AE	10388	10612	10611	364	0
14	C	544	559	560	23	0
15	D	32703	16423	16459	225	0
16	E	669	719	719	3	0
17	F	589	629	629	8	0
18	G	1760	1785	1785	47	0
19	H	1730	1454	1454	211	0
20	I	1636	1710	1710	41	0
21	J	1643	1707	1707	30	0
22	K	1152	1196	1196	22	0
23	L	848	846	846	3	0
24	M	1181	1235	1235	34	0
25	N	979	1031	1031	5	0
26	O	1022	1070	1070	13	0
27	P	790	831	831	45	0
28	Q	877	887	887	4	0
29	R	939	1001	1001	7	0
30	S	805	844	844	5	0
31	T	714	734	734	8	0
32	U	649	666	666	3	0
33	V	648	691	691	4	0
34	W	663	688	688	2	0
35	X	900	964	964	57	0
36	Y	1032	0	1088	85	0
37	Z	227	0	237	18	0
38	a	61841	31077	31123	302	0
39	b	582	599	599	3	0
40	c	625	652	652	4	0
41	d	2569	1301	1301	3	0
42	e	501	531	531	5	0
43	f	448	488	488	5	0
44	g	522	520	520	11	0
45	h	2082	2154	2154	19	0
46	i	444	459	458	6	0
47	j	1565	1617	1616	15	0
48	k	426	464	464	0	0
49	l	1552	1619	1619	14	0
50	m	377	418	418	10	0
51	n	1410	1443	1444	28	0
52	o	504	572	572	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	p	1313	1358	1358	7	0
54	q	302	343	343	2	0
55	r	1111	1148	1148	6	0
56	s	1129	1162	1162	15	0
57	t	946	1023	1023	12	0
58	u	1053	1129	1129	9	0
59	v	1074	1157	1157	5	0
60	w	951	994	994	8	0
61	x	892	923	923	9	0
62	y	917	962	962	4	0
63	z	947	1020	1019	14	0
64	AE	1	0	0	0	0
65	AE	2	0	0	0	0
All	All	175155	123940	126751	2450	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 8.

All (2450) 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)
14:C:12:ARG:HG3	19:H:264:GLU:CB	1.30	1.58
19:H:131:LEU:CB	19:H:167:VAL:CA	1.78	1.57
19:H:131:LEU:CB	19:H:167:VAL:HA	1.03	1.48
12:AC:117:HIS:O	27:P:89:ARG:CB	1.64	1.46
9:9:31:ARG:NE	38:a:1054:A:H5'	1.31	1.43
9:9:130:PRO:N	9:9:130:PRO:CA	1.70	1.39
11:AA:1026:GLU:HG3	15:D:1030:U:C2	1.54	1.39
19:H:71:ALA:C	19:H:72:LEU:HD12	1.49	1.35
9:9:57:ASN:OD1	9:9:62:ARG:CG	1.75	1.34
19:H:118:GLY:O	19:H:133:GLY:CA	1.74	1.34
38:a:1839:G:H1'	38:a:1927:A:C8	1.62	1.34
15:D:1358:U:O4	15:D:1363:A:N1	1.60	1.33
38:a:1021:A:N1	38:a:1141:U:O4	1.63	1.30
15:D:1308:U:H2'	35:X:98:ARG:NH2	1.48	1.27
15:D:948:C:OP2	35:X:105:ASN:OD1	1.53	1.26
8:7:17:G:OP2	11:AA:540:ARG:NH1	1.68	1.26
10:A:32:C:O4'	24:M:144:MET:HE1	1.09	1.25
9:9:31:ARG:CZ	38:a:1054:A:H5'	1.63	1.25
14:C:12:ARG:CG	19:H:264:GLU:CB	2.15	1.25
13:AE:87:LYS:HG3	21:J:20:PHE:CE1	1.73	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:18:G:N7	10:A:57:A:N6	1.87	1.23
15:D:563:A:N1	15:D:884:U:O4	1.73	1.21
10:B:18:G:N7	10:B:57:A:N6	1.87	1.21
19:H:118:GLY:O	19:H:133:GLY:HA3	1.27	1.20
9:9:88:HIS:HB3	9:9:89:PRO:CD	1.70	1.20
15:D:1308:U:C2'	35:X:98:ARG:NH2	2.03	1.19
19:H:267:TRP:CZ2	19:H:340:ARG:HG2	1.75	1.19
15:D:1227:A:OP2	35:X:110:LYS:HE3	1.35	1.19
12:AC:117:HIS:O	27:P:89:ARG:HB3	1.03	1.18
15:D:1308:U:H3'	35:X:98:ARG:CZ	1.43	1.17
14:C:44:ILE:HD13	19:H:339:ARG:HG2	1.18	1.17
9:9:31:ARG:NE	38:a:1054:A:C5'	2.07	1.16
14:C:44:ILE:HD13	19:H:339:ARG:CG	1.78	1.13
8:7:-9:G:H5''	15:D:1500:A:N6	1.61	1.12
19:H:135:LEU:CB	19:H:167:VAL:CB	2.27	1.12
13:AE:86:GLU:HA	21:J:166:GLU:CB	1.79	1.12
13:AE:53:ARG:NH2	21:J:164:GLN:O	1.83	1.11
19:H:267:TRP:CE2	19:H:340:ARG:HG2	1.84	1.11
12:AC:65:LEU:HB3	20:I:80:LYS:HB2	1.17	1.11
12:AC:118:ASP:HA	27:P:89:ARG:HB2	1.32	1.11
15:D:1329:A:OP1	35:X:28:THR:HB	1.47	1.11
10:A:32:C:O4'	24:M:144:MET:CE	1.97	1.10
12:AC:65:LEU:HA	20:I:80:LYS:HB3	1.26	1.10
15:D:1308:U:C2'	35:X:98:ARG:HH21	1.63	1.10
9:9:50:VAL:HG22	36:Y:119:ALA:CB	1.82	1.10
11:AA:1026:GLU:HG3	15:D:1030:U:N1	1.65	1.09
38:a:1839:G:C8	38:a:1927:A:H1'	1.87	1.09
10:B:70:G:H2'	10:B:71:C:H5''	1.23	1.09
15:D:1308:U:C3'	35:X:98:ARG:CZ	2.31	1.09
15:D:1308:U:C3'	35:X:98:ARG:NH2	2.16	1.08
18:G:19:GLN:CD	19:H:76:GLU:HB3	1.67	1.08
13:AE:24:LEU:HG	13:AE:232:ASN:HD21	1.17	1.08
19:H:119:GLY:HA2	19:H:133:GLY:HA2	1.14	1.08
19:H:267:TRP:CH2	19:H:340:ARG:HG2	1.86	1.08
13:AE:86:GLU:HA	21:J:166:GLU:HB3	1.35	1.08
9:9:57:ASN:OD1	9:9:62:ARG:HG3	1.44	1.08
9:9:88:HIS:CB	9:9:89:PRO:HD3	1.83	1.08
10:A:70:G:H2'	10:A:71:C:H5''	1.22	1.08
9:9:129:LEU:N	9:9:130:PRO:HD3	1.66	1.07
21:J:162:ALA:HA	21:J:165:ARG:CZ	1.83	1.07
9:9:142:THR:HG21	37:Z:7:ILE:HG12	1.21	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:G:19:GLN:CD	19:H:76:GLU:CB	2.19	1.07
18:G:19:GLN:CG	19:H:75:VAL:HG22	1.84	1.07
12:AC:119:GLY:H	27:P:90:LEU:HD23	1.01	1.06
19:H:71:ALA:O	19:H:72:LEU:HD12	1.54	1.05
19:H:162:LYS:CB	19:H:298:GLU:CD	2.30	1.05
10:A:56:C:H2'	10:A:57:A:H5''	1.38	1.04
10:B:56:C:O4'	51:n:80:ARG:NH2	1.91	1.04
9:9:129:LEU:H	9:9:130:PRO:HD3	0.90	1.04
15:D:1308:U:H2'	35:X:98:ARG:HH21	1.06	1.04
10:A:18:G:N2	10:A:55:U:O2	1.90	1.03
10:B:56:C:H2'	10:B:57:A:H5''	1.39	1.03
10:B:70:G:C2'	10:B:71:C:H5''	1.89	1.03
10:B:18:G:N2	10:B:55:U:O2	1.90	1.03
12:AC:119:GLY:N	27:P:90:LEU:HD23	1.72	1.03
12:AC:167:PRO:HB3	20:I:103:ILE:O	1.59	1.03
19:H:290:TYR:O	19:H:305:HIS:O	1.77	1.02
10:B:56:C:H5'	51:n:80:ARG:CZ	1.89	1.02
8:7:-9:G:C5'	15:D:1500:A:H62	1.73	1.02
8:7:2:U:O2'	22:K:57:PRO:HB3	1.58	1.02
8:7:-10:U:P	15:D:1505:G:H8	1.83	1.02
8:7:-8:U:O2'	15:D:1403:C:O2	1.78	1.02
10:A:70:G:C2'	10:A:71:C:H5''	1.89	1.02
18:G:19:GLN:HG3	19:H:75:VAL:HG22	1.38	1.01
19:H:19:ARG:O	19:H:72:LEU:HB2	1.58	1.01
15:D:1227:A:OP2	35:X:110:LYS:CE	2.06	1.01
18:G:38:VAL:CG2	19:H:75:VAL:HG21	1.90	1.01
15:D:1329:A:OP1	35:X:28:THR:CB	2.07	1.01
11:AA:992:LEU:HD22	11:AA:992:LEU:H	1.21	1.01
15:D:13:U:N3	15:D:915:A:C6	2.29	1.00
15:D:1308:U:H3'	35:X:98:ARG:NH2	1.76	1.00
15:D:13:U:O4	15:D:20:U:O4	1.79	1.00
38:a:2297:A:N1	38:a:2321:U:C4	2.29	0.99
13:AE:111:THR:HG23	13:AE:300:GLN:CD	1.86	0.99
19:H:131:LEU:CB	19:H:167:VAL:CB	2.40	0.99
9:9:93:ALA:O	9:9:129:LEU:HD12	1.60	0.98
18:G:38:VAL:HG22	19:H:75:VAL:HG21	1.44	0.98
38:a:1839:G:C1'	38:a:1927:A:C8	2.46	0.98
10:A:32:C:C4'	24:M:144:MET:HE1	1.93	0.97
9:9:129:LEU:H	9:9:130:PRO:CD	1.77	0.97
10:A:32:C:O2'	24:M:86:GLN:CG	2.12	0.97
19:H:118:GLY:O	19:H:133:GLY:HA2	1.63	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:31:ARG:CD	38:a:1054:A:H5'	1.94	0.96
19:H:119:GLY:CA	19:H:133:GLY:HA2	1.95	0.96
9:9:142:THR:HG21	37:Z:7:ILE:CG1	1.95	0.96
38:a:1839:G:O4'	38:a:1927:A:O4'	1.82	0.96
11:AA:1026:GLU:CG	15:D:1030:U:C2	2.50	0.95
7:6:15:DC:N4	7:6:16:DC:N4	2.15	0.95
8:7:-10:U:OP2	15:D:1505:G:C8	2.20	0.95
10:A:72:A:H2'	10:A:73:A:H5''	1.49	0.95
13:AE:68:TYR:O	13:AE:75:TYR:CE2	2.20	0.94
38:a:67:U:N3	38:a:74:A:C6	2.36	0.94
12:AC:118:ASP:HB3	27:P:90:LEU:HD22	1.50	0.94
38:a:1839:G:O4'	38:a:1927:A:C1'	2.15	0.94
10:A:32:C:O2'	24:M:86:GLN:HG3	1.68	0.94
11:AA:878:THR:O	11:AA:920:VAL:HG11	1.68	0.94
19:H:119:GLY:HA3	19:H:131:LEU:O	1.68	0.94
19:H:135:LEU:HA	19:H:157:ILE:CB	1.98	0.94
15:D:13:U:N3	15:D:915:A:N6	2.16	0.93
15:D:13:U:C4	15:D:915:A:N6	2.36	0.93
8:7:-9:G:C5'	15:D:1500:A:N6	2.31	0.93
9:9:88:HIS:CB	9:9:89:PRO:CD	2.41	0.93
10:B:75:C:OP1	38:a:2602:A:C8	2.22	0.93
12:AC:118:ASP:HB3	27:P:90:LEU:CD2	1.99	0.92
9:9:57:ASN:OD1	9:9:62:ARG:HG2	1.64	0.92
10:A:68:C:H2'	10:A:69:C:H5''	1.51	0.92
9:9:50:VAL:HG22	36:Y:119:ALA:HB1	1.50	0.92
9:9:88:HIS:HB3	9:9:89:PRO:HD3	0.93	0.92
11:AA:768:MET:CE	12:AC:80:GLU:OE1	2.17	0.92
12:AC:158:ARG:HB3	12:AC:158:ARG:HH11	1.32	0.92
13:AE:202:ARG:HG2	13:AE:202:ARG:HH11	1.35	0.92
10:B:68:C:H2'	10:B:69:C:H5''	1.50	0.92
10:B:72:A:H2'	10:B:73:A:H5''	1.49	0.92
13:AE:86:GLU:CA	21:J:166:GLU:HB3	2.00	0.92
10:A:56:C:H1'	38:a:2112:G:C6	2.06	0.91
15:D:13:U:C4	15:D:20:U:O4	2.23	0.91
38:a:1406:U:O2'	38:a:1407:G:C5'	2.19	0.91
8:7:-10:U:P	15:D:1505:G:C8	2.62	0.91
11:AA:1030:GLU:CD	15:D:1030:U:O4	2.14	0.91
19:H:71:ALA:C	19:H:72:LEU:CD1	2.42	0.91
11:AA:868:SER:OG	11:AA:941:LYS:HG2	1.69	0.91
9:9:93:ALA:O	9:9:129:LEU:CD1	2.19	0.91
10:A:18:G:N2	10:A:58:A:N7	2.19	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:136:GLU:OE1	13:AE:312:ARG:NH1	2.04	0.90
11:AA:728:ASP:OD1	11:AA:769:PRO:HG2	1.71	0.90
10:B:18:G:N2	10:B:58:A:N7	2.19	0.90
6:5:109:DT:H2''	11:AA:200:ARG:HG3	1.53	0.90
19:H:279:LYS:HA	19:H:331:MET:HB3	1.54	0.89
8:7:1:U:H5'	22:K:56:VAL:HG21	1.52	0.89
13:AE:68:TYR:C	13:AE:75:TYR:HE2	1.80	0.89
38:a:2013:A:N6	38:a:2613:U:H3	1.68	0.89
36:Y:104:GLN:HG2	36:Y:108:ILE:HD11	1.53	0.89
38:a:2314:A:H1'	51:n:155:THR:HG21	1.54	0.89
6:5:113:DC:OP2	11:AA:163:LYS:HD3	1.71	0.89
18:G:18:HIS:HA	19:H:43:LYS:HD2	1.55	0.89
9:9:31:ARG:CZ	38:a:1054:A:C5'	2.49	0.88
6:5:114:DC:H5''	13:AE:1148:ARG:NH2	1.87	0.88
19:H:162:LYS:N	19:H:298:GLU:OE2	2.06	0.88
12:AC:65:LEU:HA	20:I:80:LYS:CB	2.02	0.88
13:AE:24:LEU:HB2	13:AE:232:ASN:OD1	1.72	0.88
19:H:119:GLY:HA2	19:H:133:GLY:CA	2.01	0.88
9:9:142:THR:CG2	37:Z:7:ILE:HG12	2.02	0.88
10:A:33:U:H5''	24:M:84:THR:HG21	1.55	0.88
13:AE:86:GLU:HA	21:J:166:GLU:HB2	1.54	0.88
36:Y:21:PRO:HB2	36:Y:22:PRO:HD3	1.54	0.88
38:a:783:A:N3	38:a:783:A:H2'	1.89	0.88
12:AC:91:ARG:NE	12:AC:122:GLU:OE2	2.07	0.88
8:7:17:G:OP2	11:AA:540:ARG:CZ	2.21	0.88
19:H:131:LEU:CB	19:H:167:VAL:N	2.37	0.88
12:AC:65:LEU:CB	20:I:80:LYS:HB2	2.02	0.87
14:C:31:ASN:OD1	19:H:268:VAL:HG22	1.74	0.87
36:Y:81:LYS:O	36:Y:81:LYS:HE3	1.75	0.87
9:9:50:VAL:CG2	36:Y:119:ALA:HB3	2.04	0.87
21:J:162:ALA:HB2	21:J:165:ARG:NH2	1.90	0.86
11:AA:1026:GLU:CG	15:D:1030:U:N1	2.38	0.86
8:7:-3:U:C5	15:D:528:C:P	2.69	0.86
19:H:348:GLN:N	19:H:348:GLN:OE1	2.08	0.86
6:5:110:DA:N7	11:AA:183:TRP:CH2	2.43	0.86
11:AA:980:VAL:HA	11:AA:984:VAL:HB	1.58	0.86
9:9:31:ARG:HH11	9:9:31:ARG:HG3	1.41	0.86
11:AA:1008:GLN:NE2	11:AA:1008:GLN:O	2.07	0.86
44:g:16:CYS:CB	44:g:37:CYS:HB3	2.05	0.86
11:AA:975:ILE:HG13	11:AA:1014:LEU:HD23	1.57	0.86
11:AA:1090:ASN:O	12:AC:182:ARG:NH1	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:967:LEU:O	11:AA:967:LEU:HD12	1.76	0.85
19:H:267:TRP:CZ3	19:H:340:ARG:HG2	2.11	0.85
9:9:129:LEU:N	9:9:130:PRO:CD	2.34	0.85
12:AC:167:PRO:CB	20:I:103:ILE:O	2.24	0.85
13:AE:24:LEU:HG	13:AE:232:ASN:ND2	1.90	0.85
10:A:16:C:O2	38:a:2181:U:H5'	1.76	0.85
15:D:197:A:C6	15:D:221:C:H4'	2.11	0.85
36:Y:60:VAL:HG13	36:Y:66:PHE:HB3	1.58	0.85
9:9:31:ARG:CD	38:a:1054:A:H4'	2.06	0.85
9:9:52:MET:C	9:9:52:MET:HE3	2.00	0.85
10:A:18:G:N7	10:A:57:A:C6	2.44	0.85
21:J:61:VAL:HG21	21:J:200:ILE:HD11	1.57	0.85
12:AC:65:LEU:HB3	20:I:80:LYS:CB	2.06	0.85
19:H:332:VAL:HG11	19:H:335:ILE:HG13	1.57	0.85
11:AA:883:LEU:HD11	11:AA:920:VAL:HG22	1.59	0.84
13:AE:68:TYR:HB3	13:AE:75:TYR:OH	1.76	0.84
13:AE:425:ARG:NH1	13:AE:458:ASN:O	2.09	0.84
19:H:135:LEU:CB	19:H:167:VAL:C	2.50	0.84
9:9:125:ARG:NH1	9:9:125:ARG:HA	1.92	0.84
36:Y:20:SER:HB3	36:Y:21:PRO:HD3	1.59	0.84
7:6:21:DA:N1	8:7:15:G:N2	2.26	0.84
13:AE:68:TYR:O	13:AE:75:TYR:HE2	1.58	0.84
13:AE:26:SER:HB2	13:AE:236:TRP:CZ2	2.12	0.84
19:H:131:LEU:CB	19:H:166:VAL:O	2.26	0.84
10:B:18:G:N7	10:B:57:A:C6	2.44	0.84
18:G:16:PHE:HB3	19:H:43:LYS:HA	1.60	0.84
19:H:162:LYS:CA	19:H:298:GLU:OE2	2.17	0.84
19:H:267:TRP:CD2	19:H:340:ARG:HG2	2.11	0.84
10:B:56:C:H5'	51:n:80:ARG:NE	1.93	0.84
11:AA:981:ALA:HB3	11:AA:1008:GLN:HG3	1.57	0.84
38:a:2303:G:C2	38:a:2314:A:C2	2.66	0.84
10:B:68:C:C2'	10:B:69:C:H5''	2.08	0.83
15:D:1227:A:H5'	35:X:110:LYS:NZ	1.93	0.83
11:AA:953:LEU:HA	11:AA:1036:ILE:HD13	1.59	0.83
14:C:12:ARG:HH22	19:H:268:VAL:CG2	1.90	0.83
38:a:67:U:N3	38:a:74:A:N6	2.25	0.83
9:9:50:VAL:HG22	36:Y:119:ALA:HB3	1.60	0.83
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.58	0.83
7:6:18:DC:H42	8:7:17:G:H1	1.27	0.83
9:9:31:ARG:CD	38:a:1054:A:C4'	2.56	0.83
10:B:72:A:C2'	10:B:73:A:H5''	2.09	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:72:A:C2'	10:A:73:A:H5''	2.08	0.83
19:H:267:TRP:CH2	19:H:340:ARG:CG	2.60	0.83
38:a:1021:A:N6	38:a:1141:U:H3	1.77	0.83
10:A:68:C:C2'	10:A:69:C:H5''	2.08	0.82
9:9:3:LEU:HD13	9:9:5:LEU:HG	1.61	0.82
10:B:54:U:H3	10:B:58:A:N6	1.78	0.82
10:A:54:U:H3	10:A:58:A:N6	1.78	0.82
12:AC:119:GLY:H	27:P:90:LEU:CD2	1.89	0.82
19:H:267:TRP:CZ3	19:H:340:ARG:CG	2.63	0.82
22:K:111:MET:HE2	22:K:125:ALA:HB1	1.59	0.82
11:AA:1043:ALA:HB1	11:AA:1044:PRO:HD2	1.61	0.82
13:AE:141:PHE:HE2	13:AE:296:LYS:HB2	1.44	0.82
11:AA:1026:GLU:HG3	15:D:1030:U:N3	1.94	0.82
18:G:19:GLN:OE1	19:H:75:VAL:O	1.85	0.82
9:9:57:ASN:OD1	9:9:62:ARG:CD	2.27	0.82
11:AA:724:VAL:CG1	11:AA:774:GLY:H	1.93	0.82
19:H:122:VAL:O	19:H:129:ALA:N	2.13	0.82
9:9:28:ALA:H	9:9:110:ALA:HA	1.44	0.82
19:H:305:HIS:CD2	19:H:306:VAL:H	1.98	0.82
38:a:1019:U:H3	38:a:1142:A:N6	1.77	0.82
21:J:162:ALA:HA	21:J:165:ARG:NH2	1.95	0.82
12:AC:118:ASP:CA	27:P:89:ARG:HB2	2.09	0.81
12:AD:86:LYS:CE	13:AE:528:THR:HB	2.09	0.81
9:9:43:LYS:HD2	9:9:43:LYS:C	2.05	0.81
13:AE:1169:THR:OG1	13:AE:1192:LYS:NZ	2.13	0.81
36:Y:102:ARG:HB3	36:Y:141:ASP:HA	1.61	0.81
9:9:62:ARG:HG2	9:9:62:ARG:HH21	1.44	0.81
11:AA:886:LYS:HE3	11:AA:886:LYS:O	1.80	0.81
19:H:155:LYS:CB	19:H:169:SER:CB	2.58	0.81
36:Y:72:THR:OG1	36:Y:73:PRO:HD2	1.81	0.81
13:AE:141:PHE:CE2	13:AE:296:LYS:HB2	2.15	0.81
15:D:972:C:O2'	27:P:57:VAL:CG2	2.29	0.81
13:AE:144:TYR:HE1	13:AE:162:GLU:OE2	1.64	0.81
15:D:37:U:N3	15:D:397:A:N6	2.28	0.81
15:D:1227:A:H5'	35:X:110:LYS:HZ1	1.45	0.81
36:Y:27:LEU:HD12	36:Y:27:LEU:O	1.81	0.81
9:9:31:ARG:HD2	38:a:1054:A:H4'	1.62	0.81
10:A:22:G:H2'	10:A:23:C:C6	2.16	0.81
38:a:1021:A:H61	38:a:1141:U:H3	1.29	0.81
38:a:585:G:N7	63:z:6:ARG:NH1	2.29	0.81
7:6:21:DA:N1	8:7:15:G:C2	2.49	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:76:A:H1'	38:a:2494:G:P	2.20	0.81
11:AA:118:LYS:NZ	11:AA:487:LEU:O	2.14	0.80
19:H:123:GLU:HA	19:H:128:ARG:HA	1.63	0.80
38:a:1406:U:O2'	38:a:1407:G:H5''	1.79	0.80
10:A:56:C:C2'	10:A:57:A:H5''	2.10	0.80
12:AC:117:HIS:O	27:P:89:ARG:HB2	1.75	0.80
13:AE:111:THR:HG23	13:AE:300:GLN:OE1	1.81	0.80
11:AA:611:GLU:OE2	11:AA:637:ARG:NH2	2.13	0.80
21:J:162:ALA:CA	21:J:165:ARG:NH2	2.44	0.80
38:a:1839:G:C1'	38:a:1927:A:N9	2.43	0.80
15:D:1397:C:OP1	15:D:1397:C:H2'	1.80	0.80
10:B:22:G:H2'	10:B:23:C:C6	2.16	0.80
38:a:2298:A:C4	38:a:2321:U:C5	2.70	0.80
44:g:16:CYS:HB2	44:g:37:CYS:HB3	1.63	0.80
13:AE:87:LYS:HA	13:AE:87:LYS:HE3	1.64	0.80
15:D:1329:A:P	35:X:28:THR:HB	2.22	0.80
21:J:162:ALA:CB	21:J:165:ARG:NH2	2.44	0.80
6:5:110:DA:N7	11:AA:183:TRP:HH2	1.77	0.80
10:B:18:G:N2	10:B:58:A:C5	2.50	0.80
14:C:12:ARG:CB	19:H:264:GLU:CB	2.59	0.80
51:n:125:ARG:O	51:n:127:ASN:ND2	2.14	0.80
9:9:3:LEU:H	9:9:3:LEU:HD12	1.47	0.79
9:9:78:GLY:N	9:9:79:PRO:HD2	1.97	0.79
38:a:1019:U:H3	38:a:1142:A:H61	1.28	0.79
13:AE:186:GLN:HG3	13:AE:238:ILE:HG13	1.65	0.79
10:B:7:G:H4'	10:B:8:U:OP1	1.81	0.79
21:J:162:ALA:HB2	21:J:165:ARG:HH22	1.47	0.79
10:A:18:G:N2	10:A:58:A:C5	2.50	0.79
10:B:58:A:O2'	10:B:59:A:H3'	1.82	0.79
11:AA:1007:LYS:O	11:AA:1007:LYS:HD2	1.83	0.79
13:AE:37:GLU:O	13:AE:61:ILE:HD11	1.81	0.79
38:a:2297:A:N1	38:a:2321:U:O4	2.14	0.79
44:g:18:CYS:HB3	44:g:40:CYS:CB	2.12	0.79
9:9:39:THR:HA	9:9:42:ARG:HD2	1.64	0.79
19:H:270:ILE:CG2	19:H:337:GLU:HB3	2.12	0.79
38:a:2189:U:OP1	38:a:2189:U:O4'	2.00	0.78
11:AA:1257:GLN:OE1	13:AE:345:LYS:CG	2.32	0.78
10:B:56:C:C2'	10:B:57:A:H5''	2.11	0.78
38:a:1406:U:O2'	38:a:1407:G:P	2.41	0.78
10:A:5:G:H2'	10:A:6:G:H5'	1.66	0.78
10:A:58:A:O2'	10:A:59:A:H3'	1.81	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:955:GLN:OE1	11:AA:955:GLN:HA	1.83	0.78
12:AC:167:PRO:HB3	20:I:103:ILE:C	2.09	0.78
10:B:5:G:H2'	10:B:6:G:H5'	1.66	0.78
47:j:4:LEU:HD23	47:j:29:VAL:HG11	1.65	0.78
10:A:7:G:H4'	10:A:8:U:OP1	1.81	0.78
13:AE:1075:ARG:NH2	13:AE:1168:GLU:OE2	2.17	0.78
10:A:18:G:C5	10:A:57:A:C6	2.72	0.78
9:9:31:ARG:CD	38:a:1054:A:C5'	2.58	0.78
38:a:1406:U:O2'	38:a:1407:G:O5'	2.01	0.78
8:7:-3:U:C5	15:D:528:C:OP2	2.37	0.77
13:AE:90:VAL:HG13	13:AE:90:VAL:O	1.82	0.77
9:9:11:ILE:HD11	9:9:62:ARG:HA	1.66	0.77
10:B:18:G:C5	10:B:57:A:C6	2.72	0.77
18:G:16:PHE:CZ	19:H:41:GLY:O	2.36	0.77
19:H:305:HIS:CD2	19:H:306:VAL:N	2.53	0.77
7:6:15:DC:C4	7:6:16:DC:N4	2.53	0.77
10:A:15:G:N1	10:A:20:U:O2	2.17	0.77
10:A:70:G:H2'	10:A:71:C:C5'	2.11	0.77
36:Y:74:PRO:HG2	36:Y:77:VAL:HB	1.67	0.77
10:A:33:U:O3'	24:M:84:THR:OG1	2.02	0.77
11:AA:1257:GLN:HE22	13:AE:345:LYS:HA	1.48	0.77
12:AC:76:GLU:CD	12:AC:131:CYS:HA	2.09	0.77
10:B:15:G:N1	10:B:20:U:O2	2.17	0.77
36:Y:32:VAL:HG13	36:Y:60:VAL:HG21	1.66	0.77
11:AA:1024:GLU:HA	11:AA:1027:LYS:HE3	1.66	0.77
14:C:44:ILE:CD1	19:H:339:ARG:CG	2.62	0.77
9:9:27:VAL:HG23	9:9:83:ALA:HB3	1.67	0.77
11:AA:1026:GLU:CG	15:D:1030:U:C6	2.65	0.77
19:H:19:ARG:HD3	19:H:73:ASP:CG	2.09	0.77
38:a:2756:U:N3	38:a:2758:A:C6	2.53	0.77
38:a:2756:U:N3	38:a:2758:A:N6	2.32	0.77
10:A:76:A:H2'	38:a:2394:C:H42	1.48	0.77
10:B:70:G:H2'	10:B:71:C:C5'	2.11	0.77
11:AA:1026:GLU:HA	11:AA:1026:GLU:OE2	1.84	0.76
6:5:108:DT:H72	11:AA:199:ASP:HB3	1.67	0.76
18:G:35:ARG:HD2	19:H:14:LYS:HD3	1.65	0.76
8:7:-3:U:C6	15:D:528:C:OP1	2.38	0.76
11:AA:964:LEU:HD12	11:AA:964:LEU:O	1.84	0.76
13:AE:202:ARG:HG2	13:AE:202:ARG:NH1	1.99	0.76
9:9:31:ARG:NE	38:a:1054:A:C4'	2.48	0.76
12:AC:120:ASP:HA	27:P:31:ARG:NH2	2.01	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:52:MET:HG3	9:9:95:LEU:HD11	1.68	0.76
11:AA:871:VAL:N	11:AA:883:LEU:O	2.18	0.76
22:K:137:VAL:O	22:K:140:THR:OG1	2.04	0.76
11:AA:985:GLU:HG2	11:AA:988:LYS:HE3	1.68	0.76
11:AA:1246:ARG:HH11	11:AA:1266:GLY:HA2	1.50	0.76
10:B:68:C:C3'	10:B:69:C:H5''	2.15	0.75
38:a:2298:A:C4	38:a:2321:U:H5	2.05	0.75
4:3:36:VAL:HG11	4:3:39:ILE:HD12	1.68	0.75
8:7:-3:U:C5	15:D:528:C:OP1	2.39	0.75
13:AE:123:ARG:HG3	13:AE:1337:VAL:HG11	1.67	0.75
18:G:35:ARG:HG3	19:H:10:GLU:OE2	1.87	0.75
9:9:60:LEU:HD23	9:9:64:VAL:HG21	1.67	0.75
10:A:68:C:C3'	10:A:69:C:H5''	2.15	0.75
11:AA:1272:GLU:OE2	13:AE:798:ARG:NH1	2.19	0.75
13:AE:87:LYS:CG	21:J:20:PHE:CE1	2.65	0.75
44:g:18:CYS:CB	44:g:40:CYS:HB3	2.16	0.75
10:A:41:C:O4'	24:M:143:ARG:NH1	2.20	0.75
12:AC:118:ASP:HA	27:P:89:ARG:CB	2.16	0.75
19:H:109:THR:HA	19:H:153:GLU:HA	1.68	0.75
10:A:41:C:H1'	24:M:143:ARG:HH12	1.52	0.75
13:AE:86:GLU:CB	21:J:166:GLU:HB3	2.15	0.75
15:D:197:A:N6	15:D:221:C:H4'	2.01	0.75
19:H:131:LEU:CB	19:H:166:VAL:C	2.60	0.74
11:AA:1034:ARG:HG2	11:AA:1034:ARG:HH11	1.52	0.74
9:9:78:GLY:N	9:9:79:PRO:CD	2.51	0.74
13:AE:44:ILE:HD12	13:AE:252:LEU:CD2	2.18	0.74
27:P:24:GLU:OE2	27:P:90:LEU:HD11	1.87	0.74
9:9:97:LYS:HD3	9:9:127:ALA:HA	1.68	0.74
15:D:1358:U:C4	15:D:1363:A:N1	2.53	0.74
10:A:32:C:C1'	24:M:144:MET:HE1	2.16	0.74
19:H:110:GLY:CA	19:H:153:GLU:O	2.36	0.74
61:x:31:THR:O	61:x:102:ARG:NH1	2.19	0.74
8:7:14:U:H4'	13:AE:322:ARG:CD	2.18	0.74
12:AD:196:THR:HB	13:AE:443:GLU:HG3	1.68	0.74
13:AE:110:PRO:HG2	13:AE:183:GLU:HG3	1.68	0.74
19:H:109:THR:CA	19:H:153:GLU:HA	2.18	0.74
11:AA:998:LEU:HD13	11:AA:998:LEU:C	2.13	0.74
10:B:18:G:H1'	10:B:58:A:C2	2.23	0.74
15:D:1228:C:OP1	35:X:107:ARG:NH1	2.21	0.74
7:6:18:DC:N3	8:7:17:G:N2	2.31	0.74
10:A:18:G:O2'	10:A:60:U:C2	2.41	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:G:19:GLN:CG	19:H:76:GLU:HB2	2.18	0.74
19:H:304:VAL:HG12	19:H:309:MET:SD	2.28	0.74
13:AE:68:TYR:C	13:AE:75:TYR:CE2	2.65	0.73
6:5:115:DA:OP1	13:AE:1148:ARG:NE	2.21	0.73
8:7:-9:G:C3'	15:D:1500:A:N6	2.51	0.73
9:9:50:VAL:CG2	36:Y:119:ALA:CB	2.59	0.73
13:AE:107:LEU:HD11	13:AE:242:LEU:HB2	1.70	0.73
10:B:6:G:O2'	10:B:7:G:O5'	2.05	0.73
36:Y:85:ILE:H	36:Y:85:ILE:HD12	1.52	0.73
10:A:70:G:C3'	10:A:71:C:H5''	2.18	0.73
11:AA:979:LEU:HD21	11:AA:998:LEU:HD23	1.70	0.73
10:B:76:A:H2'	10:B:76:A:N3	2.03	0.73
11:AA:956:ALA:HB1	11:AA:1032:LYS:HG3	1.70	0.73
11:AA:1026:GLU:HG3	15:D:1030:U:C6	2.17	0.73
13:AE:1143:ASP:OD1	13:AE:1148:ARG:NH1	2.21	0.73
10:A:33:U:H5''	24:M:84:THR:CG2	2.19	0.73
11:AA:991:LYS:HD2	11:AA:991:LYS:N	2.03	0.73
10:B:76:A:H1'	38:a:2494:G:OP1	1.88	0.73
38:a:1913:A:OP2	38:a:1913:A:H3'	1.89	0.73
8:7:-10:U:OP1	15:D:1505:G:C8	2.41	0.73
11:AA:972:PHE:HA	11:AA:975:ILE:HD12	1.71	0.73
10:B:70:G:C3'	10:B:71:C:H5''	2.17	0.73
10:A:6:G:O2'	10:A:7:G:O5'	2.05	0.73
8:7:-9:G:C4'	15:D:1500:A:H62	2.02	0.73
11:AA:1047:LEU:O	11:AA:1049:ILE:HD12	1.89	0.73
12:AC:158:ARG:HB3	12:AC:158:ARG:NH1	2.02	0.73
19:H:267:TRP:CE3	19:H:340:ARG:CG	2.72	0.73
11:AA:964:LEU:HD12	11:AA:964:LEU:C	2.13	0.72
11:AA:1253:LEU:HD12	13:AE:253:VAL:CG1	2.19	0.72
10:B:18:G:O2'	10:B:60:U:C2	2.41	0.72
26:O:84:THR:HG21	26:O:103:PHE:HB3	1.71	0.72
38:a:67:U:C4	38:a:74:A:N6	2.57	0.72
10:A:18:G:H1'	10:A:58:A:C2	2.23	0.72
13:AE:211:GLU:HG2	13:AE:215:LYS:HE3	1.70	0.72
15:D:827:U:H3	15:D:872:A:N6	1.87	0.72
19:H:19:ARG:HB2	19:H:73:ASP:OD2	1.88	0.72
19:H:70:VAL:HA	19:H:85:SER:CB	2.20	0.72
8:7:2:U:O2'	22:K:57:PRO:CB	2.37	0.72
15:D:517:G:O2'	15:D:530:G:H4'	1.88	0.72
38:a:1839:G:H8	38:a:1927:A:H1'	1.54	0.72
7:6:21:DA:C6	8:7:15:G:N2	2.57	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-9:G:H5''	15:D:1500:A:H62	1.33	0.72
12:AC:117:HIS:O	27:P:89:ARG:CG	2.35	0.72
13:AE:120:LEU:O	13:AE:1330:ARG:NH1	2.21	0.72
13:AE:142:GLU:HG3	13:AE:142:GLU:O	1.89	0.72
11:AA:954:LYS:HZ2	11:AA:954:LYS:C	1.96	0.72
11:AA:1257:GLN:OE1	13:AE:345:LYS:HD3	1.89	0.72
11:AA:1043:ALA:HB1	11:AA:1044:PRO:CD	2.19	0.72
10:B:72:A:C3'	10:B:73:A:H5''	2.20	0.72
12:AC:61:ILE:HB	12:AC:64:VAL:HG21	1.71	0.72
10:A:46:G:H1'	10:A:47:U:C5	2.25	0.72
29:R:86:ARG:HG3	29:R:86:ARG:O	1.89	0.72
13:AE:220:ARG:HG2	13:AE:220:ARG:HH11	1.55	0.72
38:a:1839:G:C1'	38:a:1927:A:C1'	2.67	0.72
10:A:34:C:P	24:M:84:THR:HG1	2.12	0.71
13:AE:105:ILE:HD12	13:AE:242:LEU:HD22	1.71	0.71
10:A:72:A:C3'	10:A:73:A:H5''	2.20	0.71
11:AA:870:ILE:HG12	11:AA:884:VAL:HG12	1.71	0.71
10:B:46:G:H1'	10:B:47:U:C5	2.25	0.71
15:D:1308:U:O5'	35:X:98:ARG:HG3	1.91	0.71
18:G:16:PHE:CB	19:H:43:LYS:HA	2.20	0.71
38:a:1021:A:N1	38:a:1141:U:C4	2.55	0.71
9:9:77:VAL:HG12	9:9:82:ILE:HG21	1.71	0.71
19:H:267:TRP:CE3	19:H:340:ARG:HG2	2.25	0.71
10:A:18:G:C5	10:A:57:A:N6	2.59	0.71
10:A:32:C:C4'	24:M:144:MET:CE	2.66	0.71
10:B:18:G:C5	10:B:57:A:N6	2.59	0.71
8:7:-9:G:H3'	15:D:1500:A:N6	2.04	0.71
14:C:12:ARG:HB2	19:H:264:GLU:CB	2.20	0.71
19:H:86:ARG:O	19:H:89:ALA:HB3	1.91	0.71
35:X:96:PRO:HG2	35:X:102:THR:CG2	2.21	0.71
11:AA:839:VAL:O	11:AA:886:LYS:HD3	1.90	0.71
13:AE:44:ILE:HD12	13:AE:252:LEU:HD21	1.71	0.71
13:AE:157:GLN:OE1	13:AE:157:GLN:HA	1.88	0.71
13:AE:210:SER:HB3	13:AE:213:LYS:HB2	1.71	0.71
36:Y:36:GLU:OE1	36:Y:36:GLU:HA	1.88	0.71
8:7:-10:U:OP2	15:D:1505:G:H8	1.67	0.71
11:AA:839:VAL:HA	11:AA:1048:LYS:O	1.91	0.71
9:9:18:VAL:HA	9:9:86:MET:HE2	1.71	0.70
11:AA:19:PRO:HA	11:AA:1156:ARG:HD3	1.73	0.70
11:AA:207:THR:OG1	11:AA:354:ASP:OD2	2.09	0.70
8:7:-10:U:OP1	15:D:1505:G:H8	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:742:A:H2'	38:a:743:A:C8	2.26	0.70
10:A:32:C:C1'	24:M:144:MET:CE	2.69	0.70
44:g:18:CYS:CB	44:g:40:CYS:CB	2.68	0.70
11:AA:878:THR:O	11:AA:920:VAL:CG1	2.40	0.70
11:AA:878:THR:HA	11:AA:925:SER:HA	1.73	0.70
13:AE:128:LEU:HD11	13:AE:189:LEU:HG	1.73	0.70
9:9:3:LEU:HD12	9:9:3:LEU:N	2.05	0.70
11:AA:1009:ASN:O	11:AA:1009:ASN:ND2	2.24	0.70
15:D:972:C:O2'	27:P:57:VAL:HG23	1.92	0.70
15:D:1309:G:H8	35:X:98:ARG:NH2	1.89	0.70
38:a:2314:A:C1'	51:n:155:THR:HG21	2.21	0.70
11:AA:1005:GLU:OE1	11:AA:1005:GLU:HA	1.92	0.70
13:AE:54:ASP:OD1	13:AE:54:ASP:N	2.24	0.70
8:7:-2:U:O4	15:D:1397:C:C5	2.45	0.70
12:AD:86:LYS:HE3	13:AE:528:THR:HB	1.72	0.70
15:D:1308:U:C3'	35:X:98:ARG:HH21	1.92	0.70
38:a:2310:C:O2'	51:n:74:VAL:CG1	2.40	0.70
9:9:50:VAL:HG13	36:Y:119:ALA:CB	2.22	0.70
10:A:15:G:H2'	10:A:15:G:N3	2.06	0.70
11:AA:883:LEU:HD11	11:AA:920:VAL:CG2	2.22	0.70
19:H:19:ARG:HD3	19:H:73:ASP:OD1	1.92	0.70
36:Y:21:PRO:CB	36:Y:22:PRO:HD3	2.22	0.70
10:B:76:A:H2'	38:a:2493:U:H5''	1.72	0.70
15:D:37:U:H3	15:D:397:A:N6	1.90	0.70
19:H:19:ARG:HD3	19:H:73:ASP:OD2	1.92	0.70
19:H:267:TRP:CZ2	19:H:340:ARG:CG	2.68	0.70
8:7:16:A:P	11:AA:540:ARG:HH21	2.15	0.69
9:9:31:ARG:HD2	38:a:1054:A:C5'	2.22	0.69
10:A:11:A:H2'	10:A:12:G:O4'	1.92	0.69
15:D:915:A:N6	15:D:916:U:C4	2.60	0.69
45:h:146:MET:HE3	45:h:154:LEU:HD21	1.74	0.69
11:AA:935:THR:HA	11:AA:1049:ILE:HD12	1.74	0.69
12:AC:76:GLU:OE1	12:AC:131:CYS:HA	1.92	0.69
8:7:14:U:H4'	13:AE:322:ARG:HD2	1.73	0.69
19:H:70:VAL:HA	19:H:85:SER:CA	2.22	0.69
10:A:41:C:C1'	24:M:143:ARG:NH1	2.55	0.69
38:a:1021:A:H3'	38:a:1021:A:N3	2.07	0.69
38:a:1839:G:C4	38:a:1927:A:C4	2.81	0.69
11:AA:1047:LEU:O	11:AA:1049:ILE:CD1	2.40	0.69
14:C:44:ILE:HD13	19:H:339:ARG:HG3	1.69	0.69
18:G:19:GLN:CD	19:H:76:GLU:HB2	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:58:THR:HG21	9:9:81:LEU:HG	1.74	0.69
38:a:1596:A:H2'	38:a:1597:A:C8	2.28	0.69
11:AA:728:ASP:OD1	11:AA:769:PRO:CG	2.41	0.69
10:A:16:C:O2	38:a:2181:U:C5'	2.40	0.69
11:AA:872:TYR:HD2	20:I:78:GLY:O	1.75	0.69
35:X:96:PRO:CG	35:X:102:THR:CG2	2.71	0.69
38:a:2013:A:N6	38:a:2613:U:N3	2.33	0.69
1:0:80:ARG:NH2	38:a:572:A:OP2	2.26	0.68
12:AC:167:PRO:HA	20:I:103:ILE:O	1.93	0.68
10:B:11:A:H2'	10:B:12:G:O4'	1.92	0.68
11:AA:802:VAL:HA	11:AA:1096:ILE:O	1.93	0.68
12:AC:65:LEU:CA	20:I:80:LYS:HB3	2.15	0.68
7:6:8:DC:C2'	7:6:9:DT:H71	2.24	0.68
10:B:15:G:H2'	10:B:15:G:N3	2.06	0.68
15:D:13:U:O4	15:D:21:G:C2	2.46	0.68
12:AC:167:PRO:CA	20:I:103:ILE:O	2.41	0.68
13:AE:832:LYS:C	13:AE:1242:ARG:HH12	2.01	0.68
19:H:117:LYS:CB	19:H:279:LYS:O	2.41	0.68
38:a:927:A:H2'	38:a:928:A:C8	2.28	0.68
13:AE:94:GLN:HB2	13:AE:97:VAL:HG23	1.76	0.68
10:A:19:G:N2	38:a:2112:G:C8	2.62	0.68
11:AA:868:SER:OG	11:AA:941:LYS:CG	2.41	0.68
13:AE:117:LEU:HD12	13:AE:117:LEU:O	1.94	0.68
38:a:2310:C:O2'	51:n:74:VAL:HG12	1.94	0.68
13:AE:141:PHE:CD2	13:AE:293:ARG:O	2.47	0.68
15:D:563:A:N1	15:D:884:U:C4	2.60	0.68
13:AE:39:LYS:O	13:AE:273:ILE:CG2	2.41	0.68
13:AE:161:THR:HG22	13:AE:164:GLN:HB2	1.76	0.68
38:a:1153:C:OP1	63:z:92:ARG:NH1	2.27	0.68
38:a:1920:C:O5'	38:a:1920:C:H6	1.77	0.68
19:H:267:TRP:CD2	19:H:340:ARG:CG	2.76	0.67
7:6:16:DC:H1'	13:AE:426:ALA:HB1	1.77	0.67
9:9:11:ILE:CD1	9:9:62:ARG:HD3	2.24	0.67
36:Y:14:ALA:HB2	36:Y:54:ILE:HD12	1.76	0.67
19:H:70:VAL:HA	19:H:85:SER:HA	1.77	0.67
36:Y:116:MET:HB3	36:Y:124:MET:HG2	1.76	0.67
38:a:2756:U:C4	38:a:2758:A:N6	2.62	0.67
9:9:67:THR:N	9:9:68:PRO:CD	2.58	0.67
11:AA:768:MET:HE3	12:AC:80:GLU:OE1	1.95	0.67
12:AC:76:GLU:OE2	12:AC:131:CYS:HA	1.95	0.67
13:AE:984:LEU:HB3	13:AE:993:GLU:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:X:96:PRO:CG	35:X:102:THR:HG22	2.25	0.67
7:6:21:DA:C2	8:7:15:G:N2	2.62	0.67
11:AA:339:ASN:HB3	11:AA:343:HIS:H	1.58	0.67
11:AA:768:MET:HE1	12:AC:80:GLU:OE1	1.94	0.67
11:AA:958:LYS:HB3	11:AA:958:LYS:NZ	2.08	0.67
13:AE:108:ALA:HB3	13:AE:279:LEU:HD22	1.77	0.67
10:B:66:C:H5'	10:B:66:C:H6	1.60	0.67
36:Y:58:ILE:HD13	36:Y:58:ILE:N	2.09	0.67
19:H:110:GLY:HA3	19:H:153:GLU:O	1.93	0.67
13:AE:108:ALA:CB	13:AE:279:LEU:HD22	2.25	0.67
13:AE:1355:ARG:NH1	13:AE:1369:ARG:HH12	1.93	0.67
10:B:21:A:H4'	10:B:21:A:OP1	1.95	0.67
9:9:43:LYS:HD2	9:9:43:LYS:O	1.94	0.67
10:A:5:G:H2'	10:A:6:G:C5'	2.24	0.67
11:AA:768:MET:HE1	12:AC:80:GLU:CD	2.19	0.67
11:AA:852:ALA:O	11:AA:854:ILE:N	2.28	0.67
10:B:5:G:H2'	10:B:6:G:C5'	2.24	0.67
8:7:-9:G:C4'	15:D:1500:A:N6	2.57	0.67
20:I:75:ILE:O	20:I:75:ILE:HD13	1.95	0.67
12:AC:65:LEU:CA	20:I:80:LYS:CB	2.72	0.66
35:X:96:PRO:HG3	35:X:102:THR:HG22	1.78	0.66
38:a:1839:G:C8	38:a:1927:A:C1'	2.74	0.66
9:9:60:LEU:HA	9:9:64:VAL:HB	1.77	0.66
9:9:73:LYS:HB2	9:9:117:LEU:HD21	1.75	0.66
10:A:66:C:H6	10:A:66:C:H5'	1.60	0.66
12:AD:102:LEU:HB2	12:AD:115:ILE:HG13	1.77	0.66
9:9:118:ILE:HB	9:9:119:PRO:HD3	1.76	0.66
11:AA:1251:TYR:C	11:AA:1259:LEU:CD1	2.69	0.66
19:H:110:GLY:N	19:H:153:GLU:C	2.53	0.66
10:A:56:C:C5	38:a:2168:G:C6	2.83	0.66
19:H:19:ARG:O	19:H:72:LEU:CB	2.41	0.66
33:V:25:ILE:HD11	33:V:61:ILE:HD11	1.77	0.66
38:a:1779:U:H5	38:a:1784:A:N7	1.93	0.66
38:a:1923:U:H2'	38:a:1923:U:OP2	1.96	0.66
12:AC:118:ASP:HB3	27:P:90:LEU:HD23	1.78	0.66
15:D:1227:A:OP2	35:X:110:LYS:NZ	2.29	0.66
11:AA:992:LEU:HD22	11:AA:992:LEU:N	2.04	0.66
15:D:1308:U:H5''	35:X:98:ARG:HG2	1.78	0.66
11:AA:1257:GLN:OE1	13:AE:345:LYS:HG2	1.96	0.66
9:9:61:ARG:NH1	38:a:1047:G:N7	2.44	0.65
11:AA:964:LEU:HD21	11:AA:1022:LYS:HD2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:11:ILE:HG13	9:9:65:GLU:HB3	1.79	0.65
11:AA:962:GLU:OE1	11:AA:962:GLU:HA	1.97	0.65
11:AA:963:GLU:HA	11:AA:966:ILE:HD12	1.77	0.65
12:AD:86:LYS:HE3	13:AE:528:THR:CG2	2.26	0.65
13:AE:978:ARG:HG2	13:AE:1197:ASN:HD21	1.60	0.65
11:AA:9:LYS:HG2	11:AA:1171:ARG:NH1	2.11	0.65
11:AA:839:VAL:O	11:AA:886:LYS:CD	2.44	0.65
11:AA:960:LEU:HD13	11:AA:1029:LEU:HB2	1.77	0.65
9:9:29:ASP:HB2	9:9:56:ARG:HD3	1.79	0.65
9:9:50:VAL:CG1	36:Y:119:ALA:HB3	2.26	0.65
11:AA:9:LYS:HG2	11:AA:1171:ARG:HH12	1.61	0.65
11:AA:978:VAL:HG21	11:AA:1010:GLN:HG3	1.79	0.65
13:AE:67:ASP:OD1	13:AE:95:THR:OG1	2.15	0.65
13:AE:975:ILE:HG22	13:AE:977:SER:H	1.62	0.65
10:B:56:C:H5'	51:n:80:ARG:NH2	2.10	0.65
19:H:270:ILE:HG23	19:H:337:GLU:HB3	1.78	0.65
36:Y:116:MET:HE2	36:Y:116:MET:HA	1.79	0.65
10:A:21:A:H4'	10:A:21:A:OP1	1.95	0.65
13:AE:68:TYR:HB3	13:AE:75:TYR:CE2	2.32	0.65
13:AE:84:ILE:O	13:AE:84:ILE:HG13	1.96	0.65
13:AE:1037:PHE:HB3	13:AE:1040:MET:HB2	1.78	0.65
38:a:1839:G:H1'	38:a:1927:A:N9	2.03	0.65
56:s:114:LEU:HG	56:s:118:MET:HE3	1.78	0.65
9:9:142:THR:HG21	37:Z:7:ILE:CD1	2.26	0.65
10:B:22:G:H2'	10:B:23:C:H6	1.62	0.65
19:H:110:GLY:H	19:H:153:GLU:CA	2.08	0.65
19:H:162:LYS:CB	19:H:298:GLU:OE1	2.44	0.65
11:AA:858:GLY:C	11:AA:860:ALA:H	2.03	0.65
19:H:52:GLN:O	19:H:53:PHE:CD1	2.50	0.65
13:AE:111:THR:CG2	13:AE:300:GLN:CD	2.66	0.65
52:o:26:HIS:CE1	52:o:48:ALA:HB2	2.32	0.65
53:p:24:ILE:HD13	53:p:72:LEU:HD21	1.77	0.65
53:p:121:ILE:HD12	53:p:141:ILE:HG22	1.79	0.65
11:AA:529:ARG:HH11	11:AA:572:ILE:HG22	1.62	0.65
19:H:118:GLY:C	19:H:133:GLY:CA	2.67	0.65
38:a:1839:G:O4'	38:a:1927:A:H1'	1.97	0.65
38:a:1082:U:N3	38:a:1086:A:N6	2.45	0.64
11:AA:1253:LEU:HD12	13:AE:253:VAL:HG11	1.77	0.64
11:AA:1257:GLN:OE1	13:AE:345:LYS:CD	2.44	0.64
15:D:1308:U:O5'	35:X:98:ARG:CG	2.45	0.64
18:G:18:HIS:HA	19:H:43:LYS:CD	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1909:C:O5'	38:a:1909:C:H6	1.81	0.64
13:AE:245:LEU:HG	13:AE:246:PRO:HD2	1.80	0.64
10:B:18:G:C8	10:B:57:A:C6	2.85	0.64
18:G:16:PHE:HZ	19:H:41:GLY:O	1.77	0.64
18:G:35:ARG:HH21	19:H:10:GLU:HG2	1.62	0.64
18:G:38:VAL:HG22	19:H:75:VAL:CG2	2.24	0.64
38:a:2303:G:N3	38:a:2314:A:C2	2.66	0.64
11:AA:872:TYR:CD2	20:I:78:GLY:O	2.51	0.64
11:AA:988:LYS:NZ	11:AA:988:LYS:HB3	2.13	0.64
13:AE:141:PHE:HD2	13:AE:293:ARG:O	1.80	0.64
13:AE:193:ASP:HB3	13:AE:196:GLN:HB2	1.78	0.64
15:D:1358:U:H3	15:D:1363:A:N6	1.96	0.64
10:B:50:U:H2'	10:B:51:C:C6	2.33	0.64
10:A:18:G:C8	10:A:57:A:C6	2.85	0.64
10:B:37:A:H3'	10:B:37:A:OP2	1.96	0.64
19:H:85:SER:O	19:H:88:LYS:CB	2.45	0.64
10:A:50:U:H2'	10:A:51:C:C6	2.33	0.64
11:AA:1257:GLN:HE22	13:AE:345:LYS:CA	2.09	0.64
12:AC:71:LYS:HZ1	12:AC:140:ILE:HB	1.63	0.64
10:A:41:C:C4'	24:M:143:ARG:NH1	2.60	0.64
13:AE:162:GLU:OE1	13:AE:162:GLU:HA	1.97	0.64
19:H:162:LYS:CB	19:H:298:GLU:OE2	2.45	0.64
10:B:76:A:H1'	38:a:2493:U:O3'	1.96	0.64
2:1:36:LEU:HD13	2:1:48:LYS:HA	1.80	0.63
10:A:31:G:O2'	24:M:144:MET:SD	2.56	0.63
13:AE:44:ILE:CD1	13:AE:252:LEU:HD21	2.29	0.63
19:H:135:LEU:CA	19:H:157:ILE:CB	2.74	0.63
11:AA:1251:TYR:C	11:AA:1259:LEU:HD13	2.24	0.63
19:H:267:TRP:CE3	19:H:340:ARG:HG3	2.32	0.63
19:H:270:ILE:HG21	19:H:337:GLU:HB3	1.80	0.63
30:S:47:LYS:O	30:S:50:THR:OG1	2.12	0.63
7:6:15:DC:N4	7:6:16:DC:H41	1.96	0.63
9:9:31:ARG:HD2	38:a:1054:A:H5'	1.80	0.63
19:H:49:PRO:CD	19:H:84:LEU:HD11	2.29	0.63
19:H:72:LEU:HD12	19:H:72:LEU:N	2.11	0.63
19:H:332:VAL:HG12	19:H:334:ASP:H	1.62	0.63
10:A:41:C:C1'	24:M:143:ARG:HH12	2.12	0.63
11:AA:118:LYS:NZ	11:AA:485:ASP:OD1	2.25	0.63
11:AA:867:GLU:HB3	20:I:75:ILE:HG13	1.81	0.63
38:a:2885:G:N7	46:i:40:ARG:NH2	2.46	0.63
9:9:11:ILE:HD12	9:9:62:ARG:HD3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:23:LEU:HB3	9:9:92:ALA:HA	1.81	0.63
11:AA:995:ASP:OD1	11:AA:995:ASP:N	2.29	0.63
9:9:78:GLY:H	9:9:79:PRO:CD	2.10	0.63
10:A:3:C:H2'	10:A:4:G:H8	1.62	0.63
15:D:1329:A:P	35:X:28:THR:CB	2.83	0.63
21:J:162:ALA:CB	21:J:165:ARG:HH22	2.08	0.63
38:a:2189:U:O4'	38:a:2189:U:P	2.57	0.63
13:AE:92:VAL:O	13:AE:92:VAL:HG12	1.99	0.63
15:D:1358:U:N3	15:D:1363:A:N6	2.46	0.63
18:G:19:GLN:CG	19:H:76:GLU:CB	2.76	0.63
13:AE:136:GLU:CD	13:AE:312:ARG:HH22	2.06	0.63
10:B:3:C:H2'	10:B:4:G:H8	1.62	0.63
15:D:197:A:C6	15:D:221:C:C4'	2.80	0.63
15:D:1309:G:C8	35:X:98:ARG:NH2	2.66	0.63
18:G:19:GLN:CG	19:H:75:VAL:CG2	2.70	0.63
10:A:56:C:O2	38:a:2112:G:C4	2.52	0.62
12:AD:176:CYS:SG	13:AE:535:ARG:NH2	2.72	0.62
10:B:75:C:OP1	38:a:2602:A:N9	2.30	0.62
6:5:101:DT:OP2	13:AE:275:ARG:NH2	2.31	0.62
15:D:37:U:O2	15:D:548:G:C2	2.52	0.62
15:D:1358:U:O4	15:D:1363:A:C2	2.47	0.62
19:H:280:LEU:N	19:H:330:VAL:O	2.32	0.62
38:a:1789:A:OP2	45:h:221:ARG:NH1	2.32	0.62
38:a:1998:A:OP2	47:j:141:ARG:NH2	2.32	0.62
36:Y:32:VAL:HA	36:Y:60:VAL:HG11	1.81	0.62
1:0:40:MET:HE1	63:z:105:ALA:HB1	1.80	0.62
3:2:50:LEU:HD23	42:e:26:PHE:CE1	2.35	0.62
6:5:98:DA:C2'	6:5:99:DT:H72	2.28	0.62
9:9:18:VAL:HG13	9:9:71:CYS:HB2	1.81	0.62
13:AE:144:TYR:CE1	13:AE:162:GLU:OE2	2.51	0.62
15:D:13:U:O4	15:D:20:U:C4	2.52	0.62
18:G:19:GLN:CD	19:H:75:VAL:HG22	2.25	0.62
19:H:270:ILE:CG2	19:H:337:GLU:CB	2.77	0.62
38:a:1839:G:N9	38:a:1927:A:N9	2.48	0.62
8:7:16:A:P	11:AA:540:ARG:NH2	2.72	0.62
10:A:69:C:H2'	10:A:70:G:O4'	1.99	0.62
11:AA:868:SER:CB	11:AA:941:LYS:HG2	2.29	0.62
11:AA:978:VAL:HG11	11:AA:1010:GLN:HB3	1.82	0.62
10:B:42:G:H2'	10:B:43:A:H8	1.65	0.62
15:D:1059:C:O2	27:P:55:PRO:HG3	1.99	0.62
19:H:110:GLY:N	19:H:153:GLU:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:H:304:VAL:HG12	19:H:304:VAL:O	1.99	0.62
11:AA:13:LYS:HB2	11:AA:1180:MET:HE2	1.81	0.62
11:AA:992:LEU:N	11:AA:992:LEU:HD13	2.14	0.62
38:a:2297:A:C2	38:a:2321:U:C4	2.86	0.62
11:AA:1328:LYS:HD2	13:AE:102:MET:SD	2.40	0.62
14:C:44:ILE:CD1	19:H:339:ARG:HG3	2.28	0.62
38:a:84:A:N1	38:a:98:G:O2'	2.33	0.62
9:9:92:ALA:HB3	9:9:129:LEU:HB2	1.82	0.62
11:AA:724:VAL:HG23	11:AA:734:ILE:HD13	1.80	0.62
11:AA:850:ILE:O	11:AA:850:ILE:HG22	1.98	0.62
13:AE:111:THR:CG2	13:AE:300:GLN:NE2	2.63	0.62
13:AE:201:LEU:HB2	13:AE:221:ILE:HD13	1.80	0.62
10:B:69:C:H2'	10:B:70:G:O4'	1.99	0.62
14:C:29:LEU:O	14:C:33:ILE:HG23	2.00	0.62
19:H:267:TRP:CE2	19:H:340:ARG:CG	2.73	0.62
8:7:2:U:H4'	22:K:57:PRO:CD	2.18	0.62
8:7:5:U:H1'	8:7:6:U:H2'	1.82	0.62
10:A:37:A:O2'	10:A:38:A:H5'	1.99	0.62
15:D:13:U:C5	15:D:20:U:O4	2.53	0.62
27:P:57:VAL:O	27:P:58:ASN:CG	2.43	0.62
13:AE:68:TYR:HB3	13:AE:75:TYR:CZ	2.35	0.61
13:AE:90:VAL:O	13:AE:90:VAL:CG1	2.48	0.61
7:6:15:DC:C4	7:6:16:DC:C4	2.88	0.61
9:9:57:ASN:CG	9:9:62:ARG:HG2	2.24	0.61
10:A:3:C:H2'	10:A:4:G:C8	2.36	0.61
13:AE:128:LEU:HA	13:AE:192:MET:HE1	1.81	0.61
10:B:54:U:N3	10:B:58:A:N6	2.47	0.61
9:9:31:ARG:HD2	38:a:1054:A:C4'	2.29	0.61
9:9:57:ASN:OD1	9:9:62:ARG:HD2	1.98	0.61
11:AA:1223:ARG:NH2	13:AE:721:SER:OG	2.34	0.61
13:AE:395:LYS:HZ2	13:AE:399:LYS:CD	2.12	0.61
13:AE:1161:GLY:HA3	13:AE:1179:PRO:HA	1.83	0.61
13:AE:1355:ARG:NH1	13:AE:1369:ARG:NH1	2.47	0.61
18:G:19:GLN:HG3	19:H:76:GLU:HB2	1.82	0.61
22:K:107:ALA:HB2	22:K:125:ALA:HB3	1.82	0.61
37:Z:7:ILE:HG23	37:Z:7:ILE:O	2.01	0.61
38:a:754:U:H2'	38:a:755:U:C6	2.35	0.61
11:AA:840:SER:O	11:AA:840:SER:OG	2.19	0.61
24:M:23:LEU:O	24:M:27:VAL:HG13	1.99	0.61
10:B:3:C:H2'	10:B:4:G:C8	2.36	0.61
19:H:305:HIS:O	19:H:306:VAL:HB	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:981:ALA:HB3	11:AA:1008:GLN:CG	2.28	0.61
6:5:108:DT:O4	11:AA:199:ASP:OD2	2.18	0.61
8:7:-5:U:H6	8:7:-5:U:H5''	1.65	0.61
9:9:57:ASN:CG	9:9:62:ARG:CG	2.68	0.61
9:9:77:VAL:HG12	9:9:77:VAL:O	2.01	0.61
11:AA:660:VAL:HG13	11:AA:661:VAL:HG13	1.82	0.61
13:AE:87:LYS:HG3	21:J:20:PHE:CD1	2.34	0.61
24:M:69:VAL:HG23	24:M:100:ALA:HB1	1.83	0.61
32:U:21:VAL:HG21	32:U:60:TRP:CD1	2.36	0.61
11:AA:478:ARG:NH1	11:AA:491:ASP:O	2.34	0.61
13:AE:395:LYS:NZ	13:AE:399:LYS:HD3	2.15	0.61
10:A:54:U:N3	10:A:58:A:N6	2.48	0.60
9:9:47:GLU:HG3	9:9:95:LEU:HD21	1.83	0.60
10:B:56:C:C4'	51:n:80:ARG:NH2	2.63	0.60
19:H:305:HIS:CD2	19:H:307:SER:H	2.20	0.60
36:Y:54:ILE:O	36:Y:54:ILE:HG22	2.00	0.60
10:A:41:C:H4'	24:M:143:ARG:CZ	2.31	0.60
11:AA:374:GLU:HG3	11:AA:374:GLU:O	2.01	0.60
11:AA:376:PRO:O	11:AA:376:PRO:HG2	2.02	0.60
9:9:6:GLN:OE1	9:9:6:GLN:HA	2.00	0.60
11:AA:872:TYR:CD2	20:I:74:GLY:HA2	2.37	0.60
11:AA:954:LYS:O	11:AA:954:LYS:NZ	2.33	0.60
10:B:65:C:H2'	10:B:66:C:H5'	1.82	0.60
32:U:4:ILE:HG12	32:U:21:VAL:HG22	1.84	0.60
10:A:34:C:P	24:M:84:THR:OG1	2.59	0.60
12:AD:81:ILE:HD13	12:AD:131:CYS:HB2	1.83	0.60
13:AE:416:ILE:HG13	13:AE:441:LEU:HD11	1.83	0.60
13:AE:951:GLN:NE2	13:AE:1014:GLY:O	2.35	0.60
15:D:658:C:H1'	31:T:22:THR:HG21	1.83	0.60
15:D:827:U:N3	15:D:872:A:N6	2.45	0.60
15:D:1218:C:H2'	15:D:1219:A:C8	2.36	0.60
18:G:19:GLN:HG3	19:H:75:VAL:CG2	2.23	0.60
11:AA:861:ALA:HA	11:AA:882:ILE:HD13	1.83	0.60
11:AA:979:LEU:HD11	11:AA:998:LEU:HD23	1.83	0.60
19:H:84:LEU:HD22	19:H:84:LEU:N	2.16	0.60
19:H:331:MET:N	19:H:331:MET:SD	2.75	0.60
11:AA:1030:GLU:OE1	15:D:1030:U:O4	2.20	0.60
13:AE:223:LEU:HG	13:AE:223:LEU:O	2.00	0.60
35:X:101:ARG:O	35:X:101:ARG:HD3	2.00	0.60
9:9:19:ALA:HA	9:9:70:GLU:HG2	1.84	0.60
10:A:42:G:H2'	10:A:43:A:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:H:117:LYS:CB	19:H:278:THR:HG23	2.32	0.60
50:m:31:LEU:HD22	50:m:42:LEU:HD13	1.84	0.60
10:A:22:G:H2'	10:A:23:C:H6	1.62	0.60
13:AE:67:ASP:OD1	13:AE:67:ASP:N	2.34	0.60
37:Z:20:VAL:O	37:Z:20:VAL:HG12	2.02	0.60
9:9:136:ILE:HD12	9:9:139:LEU:HD12	1.83	0.59
13:AE:395:LYS:HZ2	13:AE:399:LYS:HD3	1.67	0.59
19:H:71:ALA:O	19:H:72:LEU:CD1	2.42	0.59
38:a:2297:A:C2	38:a:2321:U:C5	2.89	0.59
19:H:284:VAL:HG12	19:H:294:VAL:HB	1.84	0.59
38:a:1590:A:H2'	38:a:1591:A:C8	2.38	0.59
10:A:6:G:HO2'	10:A:7:G:H8	1.49	0.59
13:AE:514:THR:HG21	13:AE:596:LEU:HD12	1.84	0.59
19:H:36:VAL:HB	19:H:48:ILE:HB	1.84	0.59
13:AE:342:LEU:HD23	13:AE:1352:ILE:HG23	1.83	0.59
10:B:47:U:O2'	10:B:50:U:P	2.60	0.59
18:G:217:VAL:O	18:G:220:THR:HG22	2.02	0.59
38:a:2720:U:OP1	62:y:53:ARG:NH2	2.34	0.59
10:A:65:C:H2'	10:A:66:C:H5'	1.82	0.59
12:AD:86:LYS:HE3	13:AE:528:THR:CB	2.32	0.59
13:AE:201:LEU:HD11	13:AE:220:ARG:HH11	1.67	0.59
15:D:1308:U:C5'	35:X:98:ARG:HG2	2.32	0.59
4:3:36:VAL:CG1	4:3:39:ILE:HD12	2.32	0.59
12:AC:76:GLU:OE1	12:AC:131:CYS:CA	2.51	0.59
13:AE:99:ARG:HG3	13:AE:99:ARG:NH1	2.18	0.59
15:D:1225:A:H4'	34:W:78:ARG:NH1	2.18	0.59
11:AA:858:GLY:O	11:AA:860:ALA:N	2.17	0.59
11:AA:859:GLU:HB3	20:I:109:PRO:CG	2.33	0.59
13:AE:412:LEU:HD22	13:AE:441:LEU:HD21	1.84	0.59
10:A:33:U:H4'	24:M:84:THR:HB	1.82	0.59
10:A:47:U:O2'	10:A:50:U:P	2.61	0.59
11:AA:888:THR:OG1	11:AA:889:PRO:HD2	2.02	0.59
13:AE:97:VAL:HG11	13:AE:101:ARG:NH2	2.18	0.59
13:AE:118:LYS:HD2	13:AE:312:ARG:NH2	2.17	0.59
10:B:58:A:H1'	10:B:60:U:C5	2.38	0.59
19:H:119:GLY:CA	19:H:131:LEU:O	2.46	0.59
19:H:270:ILE:HG21	19:H:337:GLU:CB	2.32	0.59
38:a:1921:G:O5'	38:a:1921:G:H8	1.84	0.59
43:f:24:LEU:HD11	43:f:54:MET:HE2	1.84	0.59
8:7:-3:U:C4	15:D:528:C:OP2	2.56	0.59
11:AA:528:ARG:NH2	11:AA:576:SER:O	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:967:LEU:HD12	11:AA:967:LEU:C	2.25	0.59
13:AE:154:LEU:HD21	13:AE:160:LEU:HD21	1.83	0.59
11:AA:974:ARG:HD2	11:AA:1014:LEU:HD11	1.85	0.58
11:AA:981:ALA:CB	11:AA:1008:GLN:HG3	2.31	0.58
11:AA:1184:THR:HG23	11:AA:1190:ALA:H	1.67	0.58
13:AE:275:ARG:NH1	13:AE:278:ARG:NH1	2.51	0.58
38:a:2572:A:C8	47:j:149:ASN:OD1	2.56	0.58
9:9:61:ARG:CZ	38:a:1047:G:N7	2.66	0.58
11:AA:963:GLU:HA	11:AA:963:GLU:OE1	2.01	0.58
13:AE:438:GLU:HG3	13:AE:485:MET:HE1	1.85	0.58
15:D:13:U:C2	15:D:915:A:N6	2.70	0.58
17:F:4:ILE:CD1	17:F:19:PHE:HA	2.33	0.58
19:H:118:GLY:C	19:H:133:GLY:HA2	2.27	0.58
19:H:119:GLY:HA3	19:H:132:PRO:C	2.28	0.58
38:a:2683:C:OP1	62:y:51:ARG:NH2	2.32	0.58
11:AA:10:ARG:NH1	11:AA:697:LYS:HD3	2.19	0.58
13:AE:370:LYS:HG2	13:AE:441:LEU:HD23	1.84	0.58
15:D:1308:U:H2'	35:X:98:ARG:HH22	1.61	0.58
6:5:99:DT:H2''	6:5:100:DA:H5''	1.86	0.58
11:AA:979:LEU:HD13	11:AA:1011:LEU:HD21	1.84	0.58
13:AE:124:ILE:HG22	13:AE:124:ILE:O	2.04	0.58
15:D:563:A:N6	15:D:884:U:N3	2.51	0.58
38:a:70:G:H4'	38:a:71:A:OP1	2.02	0.58
9:9:52:MET:HE3	9:9:52:MET:O	2.03	0.58
11:AA:1256:GLN:OE1	11:AA:1256:GLN:HA	2.03	0.58
13:AE:86:GLU:CA	21:J:166:GLU:CB	2.64	0.58
18:G:35:ARG:HD2	19:H:14:LYS:CD	2.32	0.58
19:H:305:HIS:HD2	19:H:306:VAL:H	1.49	0.58
36:Y:78:LEU:HD13	36:Y:108:ILE:HG22	1.85	0.58
15:D:404:G:N7	21:J:2:ALA:HB3	2.17	0.58
15:D:439:U:O2	15:D:440:C:C6	2.56	0.58
35:X:104:THR:O	35:X:104:THR:HG22	2.03	0.58
11:AA:914:LYS:H	11:AA:914:LYS:HD3	1.68	0.58
13:AE:24:LEU:CG	13:AE:232:ASN:ND2	2.63	0.58
9:9:31:ARG:HG3	9:9:31:ARG:NH1	2.16	0.58
10:A:35:A:H2'	10:A:36:U:C6	2.38	0.58
11:AA:870:ILE:HG12	11:AA:884:VAL:CG1	2.33	0.58
15:D:1329:A:P	35:X:28:THR:OG1	2.62	0.58
19:H:291:GLY:HA2	19:H:305:HIS:HA	1.86	0.58
10:A:60:U:P	10:A:61:C:H41	2.27	0.58
15:D:496:A:N3	15:D:496:A:H2'	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:862:LEU:HD12	20:I:72:ARG:NH2	2.19	0.58
11:AA:1142:ARG:NH2	11:AA:1166:ASP:OD1	2.36	0.58
13:AE:241:VAL:HG12	13:AE:241:VAL:O	2.04	0.58
13:AE:491:LEU:HB2	13:AE:904:ALA:HA	1.86	0.58
47:j:33:ARG:NH1	47:j:53:GLY:O	2.36	0.58
11:AA:1008:GLN:C	11:AA:1010:GLN:H	2.12	0.57
11:AA:1072:ASN:ND2	11:AA:1111:GLN:OE1	2.37	0.57
12:AC:118:ASP:CB	27:P:90:LEU:CD2	2.80	0.57
13:AE:37:GLU:O	13:AE:61:ILE:CD1	2.52	0.57
10:B:56:C:C5'	51:n:80:ARG:NH2	2.67	0.57
8:7:-5:U:H5''	8:7:-5:U:C6	2.39	0.57
8:7:-2:U:O4	15:D:1397:C:C4	2.57	0.57
13:AE:926:PRO:HG2	13:AE:1248:ILE:HD11	1.84	0.57
10:B:11:A:H2'	10:B:12:G:C8	2.40	0.57
15:D:1526:G:OP2	17:F:42:THR:HG23	2.04	0.57
18:G:148:LEU:HD22	18:G:151:ILE:HD11	1.86	0.57
22:K:56:VAL:O	22:K:60:ILE:HG23	2.04	0.57
38:a:1406:U:HO2'	38:a:1407:G:C5'	2.12	0.57
38:a:1839:G:N9	38:a:1927:A:C4	2.72	0.57
11:AA:818:VAL:HG22	11:AA:1096:ILE:HG12	1.87	0.57
11:AA:976:ARG:HG3	11:AA:989:LEU:HD13	1.85	0.57
11:AA:1069:ARG:NH2	11:AA:1114:GLU:OE2	2.30	0.57
10:B:50:U:H2'	10:B:51:C:H6	1.69	0.57
18:G:18:HIS:CA	19:H:43:LYS:HD2	2.29	0.57
19:H:110:GLY:H	19:H:153:GLU:C	2.12	0.57
10:A:58:A:H1'	10:A:60:U:C5	2.38	0.57
13:AE:53:ARG:NH2	21:J:164:GLN:C	2.61	0.57
10:B:56:C:C5'	51:n:80:ARG:CZ	2.76	0.57
16:E:25:ARG:HA	16:E:66:LEU:HD21	1.85	0.57
19:H:330:VAL:HB	19:H:344:LEU:HD23	1.86	0.57
10:A:50:U:H2'	10:A:51:C:H6	1.69	0.57
11:AA:400:VAL:HG11	11:AA:452:ARG:HD2	1.86	0.57
13:AE:903:LEU:HD21	13:AE:1249:ASN:HD22	1.70	0.57
10:B:60:U:P	10:B:61:C:H41	2.27	0.57
19:H:267:TRP:CH2	19:H:340:ARG:CB	2.86	0.57
27:P:6:ILE:HG23	27:P:100:ILE:HG23	1.87	0.57
28:Q:67:ALA:HB2	28:Q:96:THR:HG23	1.86	0.57
44:g:16:CYS:HB3	44:g:37:CYS:HB3	1.86	0.57
10:A:11:A:H2'	10:A:12:G:C8	2.40	0.57
11:AA:218:GLU:OE2	11:AA:300:ASP:N	2.28	0.57
13:AE:1046:ILE:HD12	13:AE:1059:LEU:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:G:19:GLN:NE2	19:H:75:VAL:HG22	2.19	0.57
8:7:-9:G:H5''	15:D:1501:C:N4	2.19	0.57
9:9:34:THR:HG22	9:9:38:MET:HE3	1.85	0.57
11:AA:1008:GLN:C	11:AA:1008:GLN:HE21	2.11	0.57
11:AA:1014:LEU:HA	11:AA:1017:GLN:HG2	1.85	0.57
13:AE:161:THR:HG23	13:AE:164:GLN:H	1.68	0.57
19:H:49:PRO:HD3	19:H:84:LEU:HD11	1.87	0.57
11:AA:1034:ARG:NH1	11:AA:1034:ARG:O	2.37	0.57
13:AE:198:CYS:HA	13:AE:221:ILE:HD11	1.86	0.57
38:a:2314:A:O2'	51:n:155:THR:CG2	2.52	0.57
15:D:321:A:N7	15:D:328:C:O2'	2.34	0.57
19:H:110:GLY:N	19:H:153:GLU:CA	2.67	0.57
19:H:332:VAL:CG1	19:H:335:ILE:HG13	2.33	0.57
11:AA:1006:GLU:OE1	11:AA:1006:GLU:HA	2.04	0.57
13:AE:102:MET:HG2	13:AE:246:PRO:HG3	1.87	0.57
13:AE:130:MET:HE2	13:AE:135:ILE:HG12	1.87	0.57
25:N:10:MET:HE3	25:N:61:LEU:HD11	1.87	0.57
9:9:54:VAL:O	9:9:54:VAL:HG22	2.03	0.56
11:AA:859:GLU:CB	20:I:109:PRO:HG2	2.35	0.56
13:AE:343:LEU:HD11	13:AE:1324:SER:HB3	1.87	0.56
13:AE:510:LEU:HD22	13:AE:601:ILE:HD12	1.86	0.56
36:Y:21:PRO:HB2	36:Y:22:PRO:CD	2.30	0.56
38:a:2245:U:O2'	38:a:2436:G:OP2	2.22	0.56
40:c:31:PRO:HG2	40:c:33:LEU:HD13	1.87	0.56
2:1:20:VAL:HG11	2:1:44:ALA:HA	1.86	0.56
2:1:93:ALA:HB2	38:a:1614:A:C2	2.40	0.56
10:A:76:A:H2'	38:a:2394:C:N4	2.11	0.56
11:AA:801:ARG:HG2	11:AA:1094:VAL:HG23	1.87	0.56
6:5:115:DA:OP2	13:AE:1148:ARG:HG3	2.04	0.56
8:7:8:A:H8	8:7:8:A:O5'	1.88	0.56
11:AA:449:GLY:HA3	11:AA:609:ILE:HG23	1.87	0.56
11:AA:855:PRO:CB	11:AA:913:VAL:HG21	2.36	0.56
12:AC:117:HIS:O	27:P:89:ARG:HD3	2.05	0.56
12:AD:15:ASP:HB3	12:AD:27:THR:HB	1.86	0.56
13:AE:74:LYS:HD2	13:AE:85:CYS:SG	2.45	0.56
13:AE:638:SER:OG	13:AE:639:VAL:N	2.36	0.56
36:Y:59:THR:HG22	36:Y:61:TYR:HE1	1.69	0.56
38:a:1021:A:C2	38:a:1141:U:O4	2.51	0.56
38:a:1818:U:OP2	45:h:156:ARG:NH1	2.38	0.56
7:6:8:DC:H2'	7:6:9:DT:H71	1.86	0.56
11:AA:1257:GLN:OE1	13:AE:345:LYS:HB3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:35:VAL:HA	9:9:38:MET:HB2	1.88	0.56
15:D:528:C:H6	15:D:528:C:H5''	1.71	0.56
58:u:77:ILE:HD11	58:u:108:ALA:HB1	1.87	0.56
11:AA:859:GLU:HB3	20:I:109:PRO:HG3	1.87	0.56
11:AA:1046:VAL:HG22	11:AA:1049:ILE:HG13	1.88	0.56
12:AC:120:ASP:CA	27:P:31:ARG:NH2	2.68	0.56
13:AE:160:LEU:HD22	13:AE:164:GLN:HB3	1.86	0.56
36:Y:137:LEU:N	36:Y:137:LEU:HD23	2.19	0.56
9:9:17:GLU:HB3	9:9:86:MET:HB2	1.87	0.56
9:9:50:VAL:HG13	36:Y:119:ALA:HB3	1.88	0.56
10:A:56:C:C6	38:a:2168:G:C6	2.94	0.56
10:A:76:A:C2'	38:a:2394:C:H42	2.16	0.56
11:AA:174:ALA:HB2	11:AA:432:LEU:HD13	1.88	0.56
15:D:927:G:O2'	15:D:1503:A:N7	2.36	0.56
36:Y:7:TYR:HB2	36:Y:57:VAL:HG22	1.86	0.56
11:AA:855:PRO:O	11:AA:855:PRO:HG2	2.04	0.56
11:AA:1246:ARG:NH1	11:AA:1266:GLY:HA2	2.20	0.56
12:AC:69:SER:OG	12:AC:70:THR:N	2.38	0.56
13:AE:39:LYS:O	13:AE:273:ILE:HG21	2.06	0.56
15:D:769:G:H4'	15:D:1513:A:H4'	1.88	0.56
15:D:1227:A:P	35:X:110:LYS:HZ1	2.28	0.56
19:H:267:TRP:CH2	19:H:340:ARG:HB3	2.41	0.56
38:a:580:U:O3'	63:z:31:VAL:HG13	2.05	0.56
1:0:51:VAL:HG23	63:z:86:ALA:O	2.05	0.56
7:6:18:DC:N4	8:7:17:G:H1	1.99	0.56
18:G:38:VAL:CG2	19:H:75:VAL:CG2	2.77	0.56
31:T:5:THR:O	31:T:8:THR:OG1	2.18	0.56
11:AA:1070:HIS:NE2	11:AA:1114:GLU:OE1	2.36	0.55
13:AE:99:ARG:HH11	13:AE:99:ARG:CG	2.18	0.55
34:W:15:LEU:HD13	34:W:33:THR:HG21	1.88	0.55
36:Y:77:VAL:O	36:Y:77:VAL:HG12	2.05	0.55
8:7:-2:U:H5''	8:7:-2:U:O2	2.07	0.55
10:A:38:A:H2'	10:A:39:C:H5'	1.88	0.55
13:AE:247:PRO:HA	13:AE:250:ARG:HG3	1.87	0.55
13:AE:741:ALA:O	13:AE:762:ASN:ND2	2.38	0.55
38:a:2303:G:C4	38:a:2314:A:C2	2.95	0.55
8:7:-11:A:H2'	8:7:-10:U:H6	1.70	0.55
11:AA:227:LYS:NZ	11:AA:298:ALA:HB1	2.21	0.55
10:B:6:G:HO2'	10:B:7:G:H8	1.54	0.55
11:AA:241:LEU:HD21	11:AA:246:LEU:HD11	1.88	0.55
11:AA:699:LEU:HG	11:AA:799:ASN:HD22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:991:LYS:HB2	11:AA:992:LEU:HD22	1.88	0.55
13:AE:171:GLU:HA	13:AE:171:GLU:OE1	2.05	0.55
10:B:32:C:OP2	26:O:130:ARG:NH2	2.38	0.55
14:C:44:ILE:CD1	19:H:339:ARG:HG2	2.12	0.55
36:Y:116:MET:HG3	36:Y:124:MET:HB3	1.89	0.55
59:v:66:ARG:NH1	59:v:104:GLU:OE1	2.39	0.55
7:6:21:DA:N6	8:7:15:G:H1	2.04	0.55
11:AA:880:GLY:O	11:AA:919:ARG:HD3	2.06	0.55
12:AD:81:ILE:HD11	12:AD:130:ILE:HG22	1.87	0.55
19:H:279:LYS:HA	19:H:331:MET:CB	2.33	0.55
38:a:2249:U:H3'	38:a:2250:G:C5'	2.36	0.55
11:AA:1257:GLN:NE2	13:AE:346:ARG:H	2.04	0.55
12:AD:196:THR:HB	13:AE:443:GLU:CG	2.36	0.55
38:a:811:U:H2'	58:u:21:ARG:HA	1.89	0.55
49:l:104:ALA:O	49:l:108:ILE:HG23	2.05	0.55
13:AE:87:LYS:HG3	21:J:20:PHE:HE1	1.56	0.55
19:H:154:PHE:CB	19:H:168:VAL:CB	2.85	0.55
38:a:404:A:O2'	38:a:405:U:OP2	2.22	0.55
11:AA:1246:ARG:NH1	11:AA:1258:PRO:HB3	2.22	0.55
13:AE:144:TYR:HE1	13:AE:162:GLU:CD	2.14	0.55
10:B:56:C:H2'	10:B:57:A:C5'	2.27	0.55
38:a:2314:A:O2'	51:n:155:THR:HG21	2.06	0.55
49:l:108:ILE:HD11	49:l:180:LEU:HD13	1.89	0.55
10:A:11:A:O5'	10:A:11:A:H8	1.89	0.55
12:AD:215:GLU:OE1	12:AD:218:ARG:NH1	2.40	0.55
13:AE:1166:GLY:HA3	13:AE:1174:ARG:HB2	1.88	0.55
10:B:11:A:H8	10:B:11:A:O5'	1.89	0.55
15:D:13:U:C2	15:D:915:A:C6	2.95	0.55
8:7:3:U:O2	8:7:3:U:H2'	2.06	0.55
15:D:961:U:O4	15:D:974:A:N1	2.40	0.55
22:K:99:ALA:HB1	22:K:103:THR:HG21	1.89	0.55
36:Y:96:LYS:HE3	36:Y:136:GLY:HA3	1.87	0.55
38:a:2000:C:OP1	60:w:5:LYS:NZ	2.36	0.55
8:7:-11:A:C4	8:7:-10:U:C5	2.95	0.54
11:AA:39:ILE:HD12	11:AA:75:LEU:HD22	1.88	0.54
11:AA:1252:SER:N	11:AA:1259:LEU:CD1	2.70	0.54
13:AE:136:GLU:OE1	13:AE:312:ARG:CZ	2.55	0.54
10:B:60:U:O2'	10:B:61:C:OP1	2.23	0.54
19:H:45:GLU:OE1	19:H:45:GLU:N	2.40	0.54
36:Y:57:VAL:O	36:Y:57:VAL:HG12	2.07	0.54
36:Y:112:LYS:HZ2	36:Y:112:LYS:HB3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AD:142:MET:N	12:AD:142:MET:SD	2.80	0.54
19:H:22:SER:N	19:H:69:ASP:OD2	2.40	0.54
19:H:52:GLN:OE1	19:H:86:ARG:CB	2.55	0.54
27:P:8:ILE:HD12	27:P:25:ILE:HD11	1.89	0.54
49:I:130:LYS:HB2	49:I:133:LEU:HD12	1.89	0.54
9:9:51:TYR:CD1	9:9:51:TYR:C	2.85	0.54
11:AA:738:GLU:HA	11:AA:741:MET:HE2	1.90	0.54
11:AA:1084:ASP:OD1	12:AC:45:ARG:NH1	2.32	0.54
12:AC:65:LEU:CB	20:I:80:LYS:CB	2.76	0.54
13:AE:46:TYR:CD1	13:AE:46:TYR:C	2.85	0.54
15:D:563:A:N6	15:D:884:U:H3	2.05	0.54
19:H:290:TYR:C	19:H:305:HIS:O	2.47	0.54
13:AE:124:ILE:HG23	13:AE:128:LEU:HD12	1.89	0.54
13:AE:205:LEU:HG	13:AE:217:LEU:HB3	1.90	0.54
15:D:945:G:C2	15:D:946:A:C8	2.96	0.54
39:b:37:ILE:HD11	39:b:82:ILE:HD11	1.90	0.54
49:I:131:THR:HG22	49:I:160:ALA:O	2.08	0.54
10:A:12:G:H2'	10:A:13:C:OP1	2.08	0.54
11:AA:976:ARG:HG3	11:AA:976:ARG:HH11	1.71	0.54
10:B:12:G:H2'	10:B:13:C:OP1	2.08	0.54
38:a:2192:U:H2'	38:a:2193:G:C8	2.43	0.54
7:6:26:DT:H2''	7:6:27:DG:H5'	1.89	0.54
8:7:15:G:H2'	8:7:16:A:C8	2.43	0.54
9:9:125:ARG:HA	9:9:125:ARG:CZ	2.38	0.54
12:AC:162:GLU:HG2	12:AC:162:GLU:O	2.04	0.54
15:D:439:U:O2	15:D:440:C:C5	2.61	0.54
61:x:27:VAL:HG21	61:x:40:ILE:HD12	1.89	0.54
9:9:43:LYS:HG2	9:9:98:GLU:HG2	1.90	0.54
12:AC:65:LEU:HD22	20:I:80:LYS:O	2.08	0.54
13:AE:26:SER:HB2	13:AE:236:TRP:CE2	2.42	0.54
13:AE:833:GLU:HB2	13:AE:1242:ARG:NH1	2.22	0.54
19:H:84:LEU:HD22	19:H:84:LEU:H	1.72	0.54
19:H:84:LEU:H	19:H:84:LEU:CD2	2.21	0.54
37:Z:2:ILE:HB	37:Z:5:ASP:HB3	1.89	0.54
10:A:18:G:C2	10:A:58:A:C5	2.96	0.54
13:AE:30:ILE:HG21	13:AE:241:VAL:O	2.08	0.54
15:D:1515:G:H2'	15:D:1516:G:H8	1.72	0.54
19:H:116:VAL:C	19:H:279:LYS:HB2	2.33	0.54
9:9:58:THR:HG21	9:9:81:LEU:HA	1.90	0.54
11:AA:724:VAL:HG12	11:AA:774:GLY:H	1.72	0.54
13:AE:58:CYS:SG	13:AE:59:ALA:N	2.80	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:111:THR:HG22	13:AE:300:GLN:NE2	2.23	0.54
13:AE:814:CYS:SG	13:AE:883:ARG:NH2	2.81	0.54
10:B:17:C:O2	10:B:17:C:H2'	2.08	0.54
7:6:2:DC:H2''	7:6:3:DC:C5	2.43	0.53
9:9:71:CYS:HA	9:9:117:LEU:HD13	1.90	0.53
11:AA:452:ARG:HH12	11:AA:458:GLU:CD	2.15	0.53
11:AA:859:GLU:HB2	20:I:110:GLU:OE1	2.08	0.53
11:AA:1251:TYR:C	11:AA:1259:LEU:HD11	2.31	0.53
13:AE:78:LEU:O	13:AE:78:LEU:HD13	2.08	0.53
19:H:332:VAL:O	19:H:334:ASP:N	2.40	0.53
36:Y:109:ALA:HB2	36:Y:128:ILE:HG13	1.89	0.53
10:A:17:C:O2	10:A:17:C:H2'	2.08	0.53
11:AA:1275:VAL:HG13	11:AA:1287:LEU:HD11	1.90	0.53
12:AC:215:GLU:OE2	12:AC:219:ARG:NH2	2.41	0.53
13:AE:145:VAL:HG23	13:AE:159:ILE:HG22	1.89	0.53
13:AE:1175:LEU:HD22	13:AE:1190:ILE:HD11	1.88	0.53
15:D:1228:C:OP2	35:X:110:LYS:NZ	2.41	0.53
15:D:1329:A:OP1	35:X:28:THR:N	2.42	0.53
19:H:19:ARG:O	19:H:72:LEU:HD22	2.09	0.53
36:Y:12:VAL:HG12	36:Y:23:VAL:HG21	1.90	0.53
3:2:50:LEU:HD23	42:e:26:PHE:CZ	2.42	0.53
11:AA:1287:LEU:HD13	13:AE:1357:ILE:HD11	1.89	0.53
13:AE:56:LEU:CD1	13:AE:273:ILE:HD12	2.39	0.53
10:B:76:A:N3	38:a:2493:U:H4'	2.24	0.53
8:7:20:G:O2'	13:AE:425:ARG:NH2	2.40	0.53
13:AE:99:ARG:HG3	13:AE:99:ARG:HH11	1.74	0.53
19:H:267:TRP:CZ3	19:H:340:ARG:HG3	2.43	0.53
19:H:321:VAL:HG13	19:H:322:VAL:HG23	1.90	0.53
2:1:59:GLU:CG	2:1:66:ILE:HD11	2.38	0.53
10:A:56:C:C2	38:a:2112:G:C8	2.96	0.53
11:AA:870:ILE:HG23	11:AA:884:VAL:HG13	1.90	0.53
12:AC:91:ARG:HD2	12:AC:122:GLU:HB3	1.88	0.53
12:AC:140:ILE:HD11	12:AC:142:MET:HE3	1.89	0.53
36:Y:116:MET:HE2	36:Y:117:THR:H	1.74	0.53
55:r:58:LEU:O	55:r:61:VAL:HG22	2.08	0.53
4:3:13:VAL:CG2	4:3:39:ILE:HD13	2.39	0.53
9:9:78:GLY:H	9:9:79:PRO:HD2	1.68	0.53
10:A:18:G:C8	10:A:57:A:N6	2.69	0.53
13:AE:975:ILE:HD11	13:AE:1003:LEU:HD11	1.90	0.53
10:B:18:G:C2	10:B:58:A:C5	2.97	0.53
15:D:767:A:H2'	15:D:768:A:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1056:G:O2'	38:a:1103:A:N6	2.41	0.53
11:AA:985:GLU:HB2	11:AA:988:LYS:HB2	1.90	0.53
12:AD:33:ARG:HD3	12:AD:197:ASP:HB2	1.91	0.53
13:AE:39:LYS:O	13:AE:273:ILE:HG23	2.08	0.53
13:AE:209:ASN:HA	13:AE:214:ARG:HH21	1.74	0.53
15:D:13:U:C4	15:D:21:G:C2	2.96	0.53
27:P:24:GLU:OE2	27:P:90:LEU:CD1	2.56	0.53
29:R:80:ILE:HD12	29:R:97:THR:HG22	1.89	0.53
38:a:2298:A:C5	38:a:2321:U:O4	2.62	0.53
11:AA:726:TYR:HD2	11:AA:726:TYR:O	1.92	0.53
11:AA:808:ASN:H	13:AE:633:ALA:HB2	1.74	0.53
36:Y:138:VAL:HG12	36:Y:138:VAL:O	2.08	0.53
38:a:523:C:O2	38:a:554:U:O2'	2.25	0.53
10:A:16:C:O2	10:A:16:C:H2'	2.08	0.53
11:AA:840:SER:HA	11:AA:886:LYS:HD2	1.89	0.53
11:AA:1257:GLN:OE1	13:AE:345:LYS:CB	2.57	0.53
13:AE:201:LEU:HD12	13:AE:224:LEU:HD12	1.91	0.53
13:AE:832:LYS:HB3	13:AE:1242:ARG:NH1	2.24	0.53
13:AE:1155:ILE:HG13	13:AE:1210:ILE:HB	1.89	0.53
10:B:12:G:C2'	10:B:13:C:OP1	2.57	0.53
19:H:24:VAL:HG12	19:H:69:ASP:H	1.74	0.53
38:a:1906:G:H5''	38:a:1906:G:H8	1.73	0.53
9:9:139:LEU:HD11	37:Z:11:VAL:HG13	1.90	0.53
11:AA:813:GLU:HB2	13:AE:461:PHE:HD2	1.74	0.53
10:B:6:G:O2'	10:B:7:G:H8	1.92	0.53
10:B:16:C:O2	10:B:16:C:H2'	2.08	0.53
19:H:49:PRO:HD2	19:H:84:LEU:CD1	2.39	0.53
36:Y:37:PHE:CZ	36:Y:56:VAL:HG11	2.44	0.53
11:AA:835:GLU:OE2	11:AA:1051:LYS:HD3	2.08	0.52
11:AA:884:VAL:HG11	11:AA:1050:VAL:HG11	1.90	0.52
12:AD:22:THR:OG1	12:AD:207:THR:O	2.26	0.52
13:AE:785:ASP:O	13:AE:789:LYS:HB2	2.08	0.52
36:Y:19:PRO:HG2	36:Y:24:GLY:H	1.73	0.52
36:Y:33:ASN:H	36:Y:66:PHE:HE1	1.56	0.52
38:a:2315:G:O2'	51:n:125:ARG:HD3	2.09	0.52
38:a:2328:A:H2'	38:a:2329:U:C6	2.44	0.52
44:g:18:CYS:HB3	44:g:40:CYS:HB2	1.88	0.52
11:AA:994:ARG:HD2	11:AA:994:ARG:O	2.09	0.52
12:AC:171:LEU:HD23	12:AC:171:LEU:N	2.24	0.52
12:AD:95:LYS:O	12:AD:148:ARG:NH2	2.42	0.52
13:AE:68:TYR:CA	13:AE:75:TYR:HE2	2.21	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:759:ILE:HG23	13:AE:771:GLN:HB3	1.89	0.52
10:B:18:G:C8	10:B:57:A:N6	2.70	0.52
36:Y:59:THR:HG22	36:Y:61:TYR:CE1	2.45	0.52
9:9:57:ASN:CG	9:9:62:ARG:HG3	2.30	0.52
9:9:93:ALA:O	9:9:129:LEU:HD13	2.06	0.52
10:A:6:G:O2'	10:A:7:G:H8	1.92	0.52
11:AA:862:LEU:HD23	11:AA:862:LEU:H	1.75	0.52
11:AA:953:LEU:HD13	11:AA:1036:ILE:HG21	1.91	0.52
13:AE:746:LEU:HG	13:AE:758:PRO:HG3	1.90	0.52
19:H:135:LEU:CB	19:H:167:VAL:CA	2.86	0.52
22:K:94:VAL:HG13	22:K:111:MET:HE1	1.91	0.52
61:x:35:ILE:HG21	61:x:71:ALA:HA	1.89	0.52
8:7:15:G:H2'	8:7:16:A:H8	1.75	0.52
8:7:17:G:H2'	8:7:18:A:C8	2.44	0.52
9:9:123:ILE:O	9:9:123:ILE:HG12	2.08	0.52
13:AE:802:ASP:OD1	13:AE:1348:LYS:NZ	2.31	0.52
14:C:30:LYS:HA	14:C:33:ILE:HD13	1.91	0.52
19:H:135:LEU:CB	19:H:157:ILE:CB	2.87	0.52
10:A:22:G:O2'	10:A:23:C:P	2.68	0.52
10:A:60:U:O2'	10:A:61:C:OP1	2.23	0.52
11:AA:958:LYS:HB3	11:AA:958:LYS:HZ1	1.74	0.52
12:AD:182:ARG:CD	13:AE:581:MET:HE1	2.39	0.52
10:B:22:G:O2'	10:B:23:C:P	2.67	0.52
38:a:1266:G:OP2	46:i:17:ARG:NE	2.43	0.52
57:t:7:MET:HE1	57:t:44:LYS:HD2	1.91	0.52
63:z:58:ARG:HA	63:z:61:TRP:CE3	2.45	0.52
9:9:11:ILE:CD1	9:9:11:ILE:N	2.73	0.52
11:AA:242:VAL:HB	11:AA:245:ARG:NH1	2.24	0.52
11:AA:724:VAL:CG1	11:AA:774:GLY:N	2.68	0.52
11:AA:1244:HIS:NE2	11:AA:1266:GLY:O	2.34	0.52
13:AE:88:CYS:HB3	13:AE:90:VAL:HG12	1.92	0.52
13:AE:850:LYS:HB2	13:AE:857:LEU:HB2	1.91	0.52
14:C:61:ARG:NH2	15:D:736:C:OP1	2.43	0.52
20:I:77:ILE:HA	20:I:84:VAL:HG23	1.91	0.52
38:a:639:U:H2'	38:a:640:C:C6	2.45	0.52
47:j:4:LEU:HD23	47:j:29:VAL:CG1	2.39	0.52
10:A:56:C:H2'	10:A:57:A:C5'	2.27	0.52
11:AA:628:HIS:HB3	11:AA:647:ARG:HH21	1.74	0.52
13:AE:144:TYR:CE1	13:AE:162:GLU:CD	2.88	0.52
15:D:864:A:C2	15:D:865:A:C2	2.98	0.52
22:K:81:LEU:HD13	22:K:123:VAL:HG12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:94:ARG:HB3	4:3:103:ILE:HD12	1.91	0.52
7:6:8:DC:H2''	7:6:9:DT:H71	1.91	0.52
8:7:7:G:C2'	8:7:7:G:N3	2.73	0.52
10:A:12:G:C2'	10:A:13:C:OP1	2.58	0.52
10:A:38:A:C2'	10:A:39:C:H5'	2.39	0.52
11:AA:946:LEU:HD23	11:AA:946:LEU:N	2.23	0.52
13:AE:390:LEU:N	13:AE:390:LEU:CD1	2.73	0.52
15:D:673:A:H2'	15:D:674:G:C8	2.44	0.52
19:H:119:GLY:CA	19:H:133:GLY:CA	2.74	0.52
38:a:523:C:H4'	38:a:540:C:O2	2.10	0.52
51:n:8:TYR:HA	51:n:12:VAL:HB	1.91	0.52
8:7:16:A:H2'	8:7:17:G:C8	2.45	0.52
11:AA:984:VAL:O	11:AA:984:VAL:HG22	2.10	0.52
41:d:106:G:H2'	41:d:107:G:O4'	2.10	0.52
60:w:38:LEU:N	60:w:39:PRO:CD	2.73	0.52
2:1:93:ALA:HB2	38:a:1614:A:N1	2.25	0.51
8:7:-10:U:H2'	8:7:-9:G:C8	2.45	0.51
19:H:332:VAL:C	19:H:334:ASP:H	2.18	0.51
38:a:1980:G:O2'	38:a:1982:U:OP2	2.28	0.51
10:A:56:C:C3'	10:A:57:A:H5''	2.40	0.51
11:AA:817:LEU:HD12	11:AA:1078:LYS:HB3	1.93	0.51
12:AD:109:PRO:HA	12:AD:132:HIS:HA	1.91	0.51
13:AE:215:LYS:HA	13:AE:218:THR:HG22	1.91	0.51
13:AE:1167:LYS:HZ2	13:AE:1170:LYS:HB2	1.74	0.51
26:O:98:LEU:HB3	26:O:104:VAL:HG13	1.92	0.51
38:a:929:U:H1'	43:f:26:GLY:O	2.10	0.51
44:g:16:CYS:CB	44:g:37:CYS:CB	2.82	0.51
50:m:31:LEU:HD22	50:m:42:LEU:CD1	2.40	0.51
10:A:56:C:H1'	38:a:2112:G:C5	2.46	0.51
11:AA:998:LEU:HD21	11:AA:1011:LEU:HD13	1.90	0.51
36:Y:112:LYS:NZ	36:Y:112:LYS:CB	2.73	0.51
38:a:118:A:C8	38:a:119:A:C8	2.99	0.51
2:1:59:GLU:HG3	2:1:66:ILE:HD11	1.92	0.51
9:9:125:ARG:O	9:9:125:ARG:HG3	2.10	0.51
11:AA:657:THR:HG21	11:AA:1188:ASP:HB2	1.92	0.51
11:AA:880:GLY:C	11:AA:919:ARG:HD3	2.36	0.51
11:AA:1045:GLY:O	11:AA:1047:LEU:HD13	2.10	0.51
10:B:56:C:C3'	10:B:57:A:H5''	2.40	0.51
56:s:17:VAL:HG23	56:s:137:PRO:HB2	1.93	0.51
10:A:48:C:H2'	10:A:48:C:O2	2.11	0.51
11:AA:524:ILE:HG21	11:AA:708:VAL:HG13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:689:ALA:HB2	11:AA:1233:LEU:HD23	1.93	0.51
11:AA:862:LEU:HD23	11:AA:862:LEU:N	2.25	0.51
11:AA:960:LEU:HB3	11:AA:1025:PHE:CE1	2.45	0.51
12:AD:182:ARG:HD3	13:AE:581:MET:HE1	1.91	0.51
13:AE:112:ALA:HA	13:AE:238:ILE:HA	1.91	0.51
10:B:15:G:N3	10:B:15:G:C2'	2.73	0.51
15:D:1228:C:OP1	35:X:107:ARG:CZ	2.58	0.51
31:T:40:GLN:CA	31:T:40:GLN:HE21	2.23	0.51
38:a:1839:G:N9	38:a:1927:A:H1'	2.23	0.51
11:AA:1253:LEU:HD12	13:AE:253:VAL:HG13	1.90	0.51
10:B:24:U:O2'	38:a:1922:G:O3'	2.29	0.51
36:Y:100:ILE:HB	36:Y:105:LEU:HD11	1.92	0.51
6:5:101:DT:H72	13:AE:271:ARG:CZ	2.41	0.51
13:AE:804:ALA:O	13:AE:806:ASP:N	2.41	0.51
13:AE:972:LYS:HD2	13:AE:1004:ALA:HA	1.93	0.51
38:a:1910:G:O5'	38:a:1910:G:H8	1.93	0.51
57:t:71:ARG:NH2	57:t:123:LEU:O	2.42	0.51
11:AA:1007:LYS:HD2	11:AA:1007:LYS:C	2.35	0.51
13:AE:24:LEU:CB	13:AE:232:ASN:OD1	2.54	0.51
15:D:5:U:O2	15:D:5:U:O4'	2.29	0.51
15:D:1276:G:O5'	15:D:1276:G:H8	1.93	0.51
10:A:41:C:H4'	24:M:143:ARG:NH1	2.25	0.51
11:AA:1252:SER:HA	11:AA:1259:LEU:HD11	1.93	0.51
10:B:34:C:O2	10:B:34:C:H2'	2.11	0.51
15:D:1410:A:C2	15:D:1491:G:C2	2.99	0.51
38:a:783:A:N3	38:a:783:A:C2'	2.70	0.51
6:5:96:DT:H2''	6:5:97:DC:C5	2.46	0.51
9:9:3:LEU:HD13	9:9:5:LEU:H	1.75	0.51
9:9:41:LEU:HD12	36:Y:117:THR:HG22	1.92	0.51
11:AA:988:LYS:HB3	11:AA:988:LYS:HZ1	1.74	0.51
13:AE:99:ARG:HA	13:AE:248:ASP:HB2	1.92	0.51
15:D:1308:U:P	35:X:98:ARG:HG3	2.50	0.51
15:D:1366:C:O2'	27:P:62:ARG:NH2	2.44	0.51
19:H:49:PRO:HD2	19:H:84:LEU:HD11	1.92	0.51
21:J:61:VAL:HG21	21:J:200:ILE:CD1	2.35	0.51
38:a:587:C:OP2	58:u:21:ARG:NH1	2.43	0.51
38:a:1693:U:O2'	45:h:14:ARG:NH2	2.43	0.51
11:AA:958:LYS:NZ	11:AA:958:LYS:CB	2.73	0.50
11:AA:1252:SER:CA	11:AA:1259:LEU:HD11	2.41	0.50
10:B:18:G:C2	10:B:58:A:C6	2.99	0.50
10:B:47:U:H2'	10:B:48:C:H4'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:13:U:C4	15:D:915:A:C6	2.92	0.50
19:H:308:GLU:O	19:H:310:ASP:N	2.43	0.50
27:P:57:VAL:O	27:P:57:VAL:HG13	2.11	0.50
36:Y:27:LEU:HD12	36:Y:27:LEU:C	2.35	0.50
10:A:18:G:C2	10:A:58:A:C6	2.98	0.50
10:A:72:A:H2'	10:A:73:A:C5'	2.32	0.50
11:AA:876:GLU:HG2	12:AC:159:ILE:HD11	1.92	0.50
15:D:1404:C:H2'	15:D:1404:C:O2	2.10	0.50
15:D:1499:A:O2'	15:D:1500:A:H5'	2.10	0.50
38:a:2243:U:H2'	38:a:2244:U:C6	2.46	0.50
11:AA:876:GLU:HA	11:AA:876:GLU:OE2	2.11	0.50
15:D:108:G:H5''	15:D:108:G:N3	2.27	0.50
17:F:4:ILE:HD12	17:F:19:PHE:HA	1.93	0.50
38:a:1406:U:H3	38:a:1596:A:H2	1.59	0.50
38:a:1814:G:H4'	45:h:51:THR:HG21	1.92	0.50
38:a:2557:G:H2'	38:a:2558:C:C6	2.47	0.50
11:AA:1034:ARG:HH11	11:AA:1034:ARG:CG	2.20	0.50
13:AE:1371:ARG:HE	13:AE:1372:ARG:NH1	2.10	0.50
10:B:15:G:H22	10:B:20:U:H3	1.59	0.50
38:a:1824:G:O2'	45:h:252:THR:HG21	2.11	0.50
56:s:30:THR:HG22	56:s:31:GLU:N	2.27	0.50
4:3:12:ILE:HG21	4:3:80:ALA:HB2	1.92	0.50
9:9:44:ALA:HB1	9:9:52:MET:HB3	1.93	0.50
10:A:28:C:H2'	10:A:29:G:H8	1.76	0.50
10:A:76:A:O2'	38:a:2395:C:C2	2.64	0.50
11:AA:859:GLU:HG3	20:I:109:PRO:HG2	1.94	0.50
26:O:81:HIS:O	26:O:84:THR:OG1	2.23	0.50
38:a:1964:G:H4'	38:a:1965:C:OP2	2.11	0.50
38:a:2298:A:N3	38:a:2321:U:C5	2.80	0.50
60:w:55:ALA:HA	60:w:80:PHE:CE1	2.47	0.50
2:1:24:ILE:HD13	2:1:36:LEU:HD11	1.93	0.50
11:AA:988:LYS:NZ	11:AA:988:LYS:CB	2.73	0.50
13:AE:683:ILE:HD12	13:AE:754:ILE:HG21	1.93	0.50
38:a:1141:U:O2	38:a:1142:A:N6	2.44	0.50
38:a:2297:A:C6	38:a:2321:U:O4	2.65	0.50
10:A:15:G:N3	10:A:15:G:C2'	2.73	0.50
11:AA:728:ASP:HA	11:AA:731:ARG:O	2.12	0.50
9:9:23:LEU:HA	9:9:118:ILE:HG13	1.93	0.50
10:A:56:C:C5	38:a:2168:G:O6	2.64	0.50
11:AA:227:LYS:HZ3	11:AA:298:ALA:HB1	1.75	0.50
12:AC:118:ASP:CB	27:P:90:LEU:HD23	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:5:G:C2'	10:B:6:G:H5'	2.40	0.50
15:D:1227:A:H5'	35:X:110:LYS:HZ3	1.74	0.50
18:G:35:ARG:NH2	19:H:10:GLU:HG2	2.25	0.50
19:H:117:LYS:CB	19:H:278:THR:CG2	2.90	0.50
31:T:4:SER:O	31:T:8:THR:HG23	2.12	0.50
41:d:5:U:OP1	41:d:61:G:O2'	2.26	0.50
6:5:98:DA:N9	6:5:99:DT:H72	2.26	0.50
9:9:62:ARG:CG	9:9:62:ARG:NH2	2.73	0.50
10:A:59:A:H2'	10:A:60:U:H5'	1.94	0.50
13:AE:201:LEU:HD11	13:AE:220:ARG:HG2	1.94	0.50
15:D:1208:C:H2'	15:D:1209:C:C6	2.47	0.50
15:D:1499:A:H3'	15:D:1499:A:OP2	2.12	0.50
51:n:127:ASN:ND2	51:n:127:ASN:N	2.60	0.50
10:B:48:C:O2	10:B:48:C:H2'	2.11	0.49
25:N:3:MET:HA	25:N:3:MET:HE3	1.94	0.49
31:T:21:ASP:O	31:T:22:THR:HG22	2.12	0.49
44:g:37:CYS:N	44:g:40:CYS:SG	2.78	0.49
56:s:32:LEU:CD2	56:s:54:ILE:HG21	2.42	0.49
63:z:47:TYR:CD1	63:z:47:TYR:C	2.90	0.49
8:7:0:U:H5''	8:7:0:U:O2	2.11	0.49
9:9:52:MET:HE3	9:9:52:MET:CA	2.42	0.49
11:AA:733:VAL:HG22	11:AA:750:ILE:HG12	1.93	0.49
13:AE:799:ARG:HG2	13:AE:1325:PHE:HZ	1.78	0.49
10:B:25:C:H2'	10:B:26:G:H5'	1.94	0.49
15:D:872:A:H2'	15:D:872:A:N3	2.27	0.49
15:D:1356:G:H2'	15:D:1357:A:C8	2.47	0.49
38:a:464:U:O3'	50:m:12:ARG:NH2	2.45	0.49
53:p:121:ILE:HD12	53:p:141:ILE:CG2	2.41	0.49
57:t:113:MET:O	57:t:116:ILE:HG13	2.11	0.49
13:AE:145:VAL:HG12	13:AE:184:ALA:HB1	1.94	0.49
13:AE:421:VAL:O	13:AE:436:ALA:HA	2.11	0.49
13:AE:749:LYS:HB3	13:AE:755:ILE:HD11	1.94	0.49
10:B:22:G:HO2'	10:B:23:C:P	2.34	0.49
10:B:72:A:H2'	10:B:73:A:C5'	2.33	0.49
19:H:120:PHE:CB	19:H:136:VAL:CB	2.91	0.49
10:A:76:A:C2'	38:a:2394:C:N4	2.75	0.49
11:AA:694:ARG:NH2	12:AC:83:LEU:HD13	2.26	0.49
13:AE:437:PHE:HZ	13:AE:453:VAL:HG11	1.76	0.49
15:D:1311:A:OP1	44:g:59:ARG:NH1	2.46	0.49
36:Y:80:LYS:HG3	36:Y:86:LYS:HA	1.93	0.49
38:a:1869:G:N2	38:a:1871:A:O2'	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:2646:C:O5'	38:a:2646:C:H6	1.95	0.49
47:j:25:THR:HG21	47:j:193:VAL:HG22	1.94	0.49
11:AA:103:VAL:HG12	11:AA:117:ILE:HG22	1.94	0.49
12:AC:117:HIS:O	27:P:89:ARG:CD	2.60	0.49
13:AE:395:LYS:NZ	13:AE:399:LYS:CD	2.74	0.49
10:B:18:G:C5	10:B:57:A:C5	3.01	0.49
10:B:39:C:O5'	10:B:39:C:H6	1.95	0.49
10:B:59:A:H2'	10:B:60:U:H5'	1.94	0.49
11:AA:232:ILE:HD12	11:AA:331:LYS:HA	1.94	0.49
23:L:18:VAL:N	23:L:19:PRO:CD	2.76	0.49
38:a:1433:A:H2'	38:a:1434:A:O4'	2.13	0.49
39:b:37:ILE:HG21	39:b:80:ILE:HG21	1.95	0.49
57:t:43:ILE:HD12	57:t:56:ASP:HB2	1.93	0.49
10:A:19:G:C5	38:a:2112:G:H4'	2.44	0.49
11:AA:14:ASP:HA	11:AA:1183:ALA:HB3	1.93	0.49
13:AE:220:ARG:HG2	13:AE:220:ARG:NH1	2.26	0.49
43:f:24:LEU:HD11	43:f:54:MET:CE	2.42	0.49
9:9:43:LYS:HZ1	9:9:95:LEU:HD13	1.78	0.49
11:AA:991:LYS:HA	11:AA:991:LYS:HE3	1.95	0.49
11:AA:1008:GLN:C	11:AA:1010:GLN:N	2.70	0.49
11:AA:1034:ARG:HG2	11:AA:1034:ARG:NH1	2.25	0.49
12:AC:71:LYS:NZ	12:AC:140:ILE:HB	2.27	0.49
12:AD:100:LEU:O	12:AD:144:ILE:N	2.39	0.49
22:K:114:VAL:HG21	22:K:141:ILE:HD12	1.94	0.49
38:a:2038:G:H2'	38:a:2039:U:O4'	2.13	0.49
47:j:156:PHE:CE1	56:s:81:ILE:HD13	2.48	0.49
60:w:67:PHE:O	60:w:71:ARG:N	2.45	0.49
10:A:11:A:H2'	10:A:12:G:C1'	2.42	0.49
10:A:49:G:H8	10:A:49:G:O5'	1.96	0.49
11:AA:1013:GLN:N	11:AA:1013:GLN:NE2	2.60	0.49
12:AC:158:ARG:NH1	12:AC:158:ARG:CB	2.73	0.49
12:AD:20:SER:OG	12:AD:21:SER:N	2.46	0.49
13:AE:550:VAL:O	13:AE:569:LEU:HA	2.13	0.49
13:AE:1321:SER:OG	13:AE:1349:GLU:OE2	2.21	0.49
10:B:49:G:O5'	10:B:49:G:H8	1.96	0.49
15:D:13:U:O4	15:D:21:G:N3	2.46	0.49
22:K:99:ALA:CB	22:K:103:THR:HG21	2.43	0.49
45:h:107:PRO:HD2	45:h:110:LEU:HD22	1.94	0.49
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.94	0.49
2:1:55:ILE:HG23	2:1:66:ILE:HD12	1.93	0.49
9:9:31:ARG:NH1	9:9:31:ARG:CG	2.73	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:76:A:N6	38:a:2422:C:O4'	2.46	0.49
13:AE:102:MET:HG2	13:AE:246:PRO:HD3	1.95	0.49
13:AE:152:THR:HB	13:AE:172:PHE:CZ	2.48	0.49
15:D:1169:A:H2'	15:D:1170:A:C8	2.48	0.49
19:H:132:PRO:N	19:H:167:VAL:CB	2.75	0.49
27:P:6:ILE:CG2	27:P:100:ILE:HG23	2.43	0.49
38:a:742:A:C2	38:a:743:A:C6	3.00	0.49
53:p:35:ARG:HD3	53:p:71:LEU:HD13	1.94	0.49
2:1:25:ARG:NH1	2:1:74:ILE:O	2.46	0.48
4:3:7:ARG:HB2	38:a:85:G:OP2	2.13	0.48
10:A:47:U:H2'	10:A:48:C:H4'	1.94	0.48
11:AA:1101:LEU:HD21	13:AE:508:LEU:HD22	1.95	0.48
13:AE:141:PHE:HE2	13:AE:296:LYS:CB	2.22	0.48
15:D:974:A:OP1	30:S:69:ARG:NH1	2.46	0.48
38:a:565:C:H2'	38:a:566:U:O4'	2.13	0.48
38:a:995:C:O2	56:s:3:THR:OG1	2.24	0.48
38:a:1067:A:O2'	38:a:1068:G:O4'	2.31	0.48
9:9:8:LYS:NZ	38:a:1046:A:H61	2.11	0.48
10:A:15:G:C2	10:A:20:U:O2	2.66	0.48
11:AA:991:LYS:N	11:AA:991:LYS:CD	2.73	0.48
13:AE:1027:VAL:HB	13:AE:1121:LEU:HB2	1.96	0.48
10:B:11:A:H2'	10:B:12:G:C1'	2.43	0.48
15:D:50:A:O2'	15:D:360:G:N2	2.45	0.48
15:D:1017:U:O2'	15:D:1018:G:O4'	2.31	0.48
15:D:1329:A:OP1	35:X:28:THR:OG1	2.31	0.48
38:a:2898:U:O2'	56:s:134:ALA:O	2.28	0.48
10:A:37:A:H2'	10:A:38:A:H8	1.77	0.48
11:AA:857:VAL:CG1	11:AA:861:ALA:HB2	2.43	0.48
11:AA:935:THR:HA	11:AA:1049:ILE:CD1	2.41	0.48
13:AE:1261:LEU:HD12	13:AE:1304:ARG:HH21	1.79	0.48
25:N:102:ALA:HB3	25:N:113:ASP:HB3	1.96	0.48
38:a:1412:U:C4	38:a:1413:A:N7	2.81	0.48
61:x:51:ALA:HB3	61:x:78:VAL:HB	1.94	0.48
1:0:14:VAL:CG2	1:0:98:ILE:HG13	2.43	0.48
2:1:4:ILE:HG12	2:1:106:VAL:HG22	1.95	0.48
9:9:51:TYR:CD1	9:9:88:HIS:HB2	2.49	0.48
9:9:51:TYR:CG	9:9:89:PRO:HD2	2.47	0.48
11:AA:125:GLY:HA2	11:AA:499:SER:HB2	1.94	0.48
11:AA:845:LEU:HD23	11:AA:845:LEU:N	2.28	0.48
11:AA:1102:GLY:HA2	11:AA:1106:ARG:NH1	2.28	0.48
13:AE:117:LEU:HG	13:AE:118:LYS:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1588:G:C6	38:a:1589:U:O4	2.67	0.48
38:a:2303:G:C6	38:a:2314:A:N1	2.81	0.48
10:A:42:G:H2'	10:A:43:A:C8	2.47	0.48
11:AA:632:ASP:HA	11:AA:647:ARG:HB2	1.94	0.48
12:AC:71:LYS:NZ	12:AC:140:ILE:CG1	2.76	0.48
12:AC:102:LEU:HB2	12:AC:115:ILE:HG12	1.95	0.48
13:AE:275:ARG:HH12	13:AE:278:ARG:NH1	2.09	0.48
13:AE:968:ASN:HA	13:AE:1117:SER:HB2	1.96	0.48
33:V:75:LEU:C	33:V:75:LEU:HD12	2.38	0.48
36:Y:77:VAL:HG13	36:Y:80:LYS:CE	2.44	0.48
36:Y:77:VAL:HG13	36:Y:80:LYS:HE3	1.95	0.48
38:a:2303:G:C2	38:a:2314:A:N3	2.82	0.48
38:a:2685:G:OP1	57:t:78:ARG:NH2	2.47	0.48
40:c:3:ARG:HD2	40:c:30:LEU:HD22	1.95	0.48
50:m:24:THR:HG23	50:m:27:GLY:H	1.78	0.48
8:7:-10:U:OP1	15:D:1505:G:O5'	2.31	0.48
10:A:18:G:C5	10:A:57:A:C5	3.01	0.48
11:AA:936:ARG:O	11:AA:936:ARG:HD3	2.13	0.48
11:AA:1032:LYS:HZ1	11:AA:1036:ILE:HD11	1.77	0.48
12:AD:191:ARG:NH2	12:AD:193:GLU:O	2.47	0.48
13:AE:47:ARG:CZ	13:AE:47:ARG:HB2	2.44	0.48
13:AE:800:LEU:HB3	13:AE:920:ALA:HB1	1.95	0.48
13:AE:1146:GLU:OE2	13:AE:1310:THR:HG22	2.14	0.48
10:B:68:C:H3'	10:B:69:C:H5''	1.96	0.48
15:D:911:U:H2'	15:D:912:C:C6	2.49	0.48
19:H:33:LYS:HA	19:H:34:ASP:HA	1.61	0.48
38:a:1839:G:N9	38:a:1927:A:C1'	2.77	0.48
53:p:24:ILE:CD1	53:p:72:LEU:HD21	2.44	0.48
10:A:14:A:H2'	10:A:14:A:N3	2.29	0.48
11:AA:992:LEU:H	11:AA:992:LEU:CD2	1.95	0.48
10:B:14:A:N3	10:B:14:A:H2'	2.29	0.48
19:H:23:ILE:N	19:H:69:ASP:OD2	2.47	0.48
19:H:318:PRO:HA	19:H:321:VAL:HG12	1.95	0.48
19:H:330:VAL:HG12	19:H:345:GLY:O	2.14	0.48
50:m:22:MET:O	50:m:28:ARG:NH1	2.45	0.48
13:AE:123:ARG:HD3	13:AE:123:ARG:HA	1.49	0.48
10:B:11:A:C2'	10:B:12:G:O4'	2.60	0.48
10:B:18:G:N3	10:B:58:A:C6	2.82	0.48
38:a:1814:G:C4'	45:h:51:THR:HG21	2.44	0.48
8:7:-6:U:C2	15:D:1493:A:C2	3.02	0.48
11:AA:24:VAL:HG22	11:AA:578:TYR:HE1	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:1029:LEU:C	11:AA:1029:LEU:HD23	2.39	0.48
13:AE:1036:ARG:HE	13:AE:1081:VAL:HG11	1.79	0.48
9:9:23:LEU:HD22	9:9:92:ALA:HB1	1.95	0.48
10:A:5:G:C2'	10:A:6:G:H5'	2.40	0.48
11:AA:985:GLU:OE2	11:AA:1000:LEU:HD11	2.14	0.48
13:AE:103:GLY:H	13:AE:244:VAL:HG22	1.78	0.48
13:AE:115:TRP:O	13:AE:1333:THR:HG21	2.13	0.48
10:B:60:U:H4'	10:B:61:C:OP2	2.14	0.48
7:6:21:DA:N6	8:7:15:G:N1	2.61	0.47
10:A:58:A:OP2	10:A:58:A:C8	2.67	0.47
11:AA:1280:ALA:HB1	13:AE:918:ILE:HG22	1.96	0.47
12:AD:96:ASP:OD1	12:AD:96:ASP:N	2.46	0.47
10:B:15:G:C2	10:B:20:U:O2	2.66	0.47
10:B:68:C:C4	10:B:69:C:C5	3.02	0.47
33:V:48:ASP:HB3	33:V:75:LEU:HD23	1.94	0.47
38:a:2585:U:O2	38:a:2585:U:O4'	2.32	0.47
45:h:210:ALA:HA	45:h:213:TRP:CE3	2.48	0.47
2:1:29:VAL:HB	2:1:55:ILE:HD11	1.95	0.47
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.47
9:9:17:GLU:HG2	9:9:88:HIS:NE2	2.29	0.47
10:A:9:G:H5''	10:A:10:G:OP2	2.14	0.47
11:AA:562:GLU:OE1	11:AA:662:SER:OG	2.31	0.47
12:AD:48:LEU:HD22	13:AE:535:ARG:HG3	1.95	0.47
13:AE:1060:VAL:HG13	13:AE:1106:ILE:HG12	1.96	0.47
10:B:58:A:C8	10:B:58:A:OP2	2.67	0.47
15:D:604:G:H2'	15:D:605:U:O4'	2.14	0.47
36:Y:21:PRO:CB	36:Y:22:PRO:CD	2.90	0.47
36:Y:133:ARG:O	36:Y:133:ARG:HG2	2.14	0.47
55:r:3:VAL:HG22	55:r:36:ALA:HB1	1.95	0.47
56:s:84:ILE:HG23	56:s:84:ILE:O	2.14	0.47
1:0:5:PHE:HB3	1:0:59:ILE:HD12	1.96	0.47
1:0:40:MET:HE3	1:0:49:ILE:CD1	2.43	0.47
11:AA:618:GLN:HG3	13:AE:770:LEU:HD13	1.95	0.47
11:AA:855:PRO:HB3	11:AA:913:VAL:HG21	1.97	0.47
13:AE:395:LYS:NZ	13:AE:399:LYS:CE	2.77	0.47
19:H:316:ILE:HD11	19:H:321:VAL:HG11	1.97	0.47
10:A:37:A:H2'	10:A:38:A:C8	2.48	0.47
11:AA:618:GLN:OE1	11:AA:635:THR:OG1	2.32	0.47
11:AA:1032:LYS:CA	11:AA:1032:LYS:CE	2.92	0.47
12:AC:43:LEU:O	12:AC:47:LEU:HB2	2.14	0.47
42:e:18:LEU:HB2	42:e:53:VAL:HG11	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:x:27:VAL:CG2	61:x:40:ILE:HD12	2.44	0.47
10:A:11:A:C2'	10:A:12:G:O4'	2.60	0.47
10:A:18:G:N3	10:A:58:A:C6	2.82	0.47
10:A:68:C:C4	10:A:69:C:C5	3.02	0.47
11:AA:529:ARG:HH22	11:AA:687:ARG:NH1	2.11	0.47
13:AE:809:VAL:HG21	13:AE:909:ILE:HG12	1.95	0.47
10:B:76:A:N3	10:B:76:A:C2'	2.74	0.47
15:D:1064:G:O2'	15:D:1190:G:N2	2.47	0.47
27:P:6:ILE:HG23	27:P:100:ILE:CG2	2.43	0.47
10:A:33:U:H2'	10:A:35:A:OP2	2.14	0.47
11:AA:957:LYS:HA	11:AA:1029:LEU:HD12	1.97	0.47
11:AA:1034:ARG:NH1	11:AA:1034:ARG:C	2.73	0.47
11:AA:1119:MET:HG3	11:AA:1204:LEU:HD13	1.97	0.47
10:B:18:G:C6	10:B:57:A:N7	2.83	0.47
15:D:1308:U:OP1	35:X:100:GLN:OE1	2.23	0.47
16:E:54:MET:O	16:E:57:ILE:HG22	2.15	0.47
20:I:75:ILE:HD13	20:I:75:ILE:C	2.40	0.47
47:j:121:THR:HB	47:j:127:PHE:CD2	2.49	0.47
9:9:27:VAL:HG22	9:9:99:PHE:HE2	1.80	0.47
10:A:25:C:H2'	10:A:26:G:H5'	1.95	0.47
10:A:41:C:H5'	24:M:143:ARG:HD2	1.95	0.47
10:A:68:C:H3'	10:A:69:C:H5''	1.95	0.47
11:AA:93:SER:HA	11:AA:128:PRO:HA	1.97	0.47
11:AA:735:LYS:HA	11:AA:748:ILE:HG22	1.96	0.47
11:AA:1023:HIS:C	11:AA:1023:HIS:ND1	2.73	0.47
13:AE:526:VAL:HG12	13:AE:549:LYS:HB2	1.96	0.47
13:AE:833:GLU:N	13:AE:1242:ARG:HH12	2.12	0.47
13:AE:1347:LEU:HG	13:AE:1357:ILE:HG23	1.96	0.47
10:B:9:G:H5''	10:B:10:G:OP2	2.14	0.47
14:C:33:ILE:O	14:C:33:ILE:HG12	2.15	0.47
15:D:946:A:H2'	15:D:947:G:C8	2.50	0.47
15:D:1174:G:H2'	15:D:1175:G:H5'	1.95	0.47
19:H:332:VAL:HG11	19:H:335:ILE:CG1	2.38	0.47
38:a:686:U:O4	50:m:12:ARG:HB2	2.14	0.47
38:a:1020:A:C6	38:a:1141:U:O2	2.68	0.47
38:a:2168:G:H8	38:a:2168:G:OP1	1.97	0.47
38:a:2756:U:C4	38:a:2759:G:C6	3.03	0.47
57:t:18:ARG:HB2	57:t:45:GLU:HB3	1.97	0.47
11:AA:841:ARG:HB2	11:AA:841:ARG:NH1	2.30	0.47
11:AA:914:LYS:NZ	11:AA:914:LYS:HB2	2.29	0.47
11:AA:1010:GLN:C	11:AA:1010:GLN:NE2	2.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:1219:ASP:O	13:AE:1223:LEU:HB2	2.15	0.47
15:D:1103:C:O2	18:G:106:THR:HG21	2.15	0.47
15:D:1228:C:P	35:X:107:ARG:HH12	2.38	0.47
37:Z:18:ASP:HB3	37:Z:22:LEU:CD1	2.45	0.47
38:a:299:A:N1	38:a:322:A:O2'	2.47	0.47
8:7:-5:U:C6	8:7:-5:U:C3'	2.97	0.47
8:7:16:A:H2'	8:7:17:G:H8	1.79	0.47
8:7:17:G:H2'	8:7:18:A:H8	1.80	0.47
10:A:15:G:H22	10:A:20:U:H3	1.59	0.47
10:A:29:G:H2'	10:A:30:G:O4'	2.15	0.47
11:AA:588:GLU:HA	11:AA:606:LEU:O	2.15	0.47
12:AC:49:SER:OG	12:AC:50:SER:OG	2.26	0.47
13:AE:114:ILE:HG12	13:AE:311:ARG:HD2	1.95	0.47
15:D:371:A:H2'	15:D:372:C:O4'	2.14	0.47
15:D:1308:U:P	35:X:98:ARG:CG	3.03	0.47
37:Z:4:LYS:O	37:Z:4:LYS:HD2	2.15	0.47
37:Z:29:LYS:HE2	37:Z:29:LYS:HB2	1.45	0.47
1:0:51:VAL:HG22	1:0:51:VAL:O	2.15	0.47
6:5:109:DT:H2''	11:AA:200:ARG:CG	2.37	0.47
9:9:43:LYS:NZ	9:9:95:LEU:HD13	2.30	0.47
9:9:132:TYR:CE1	37:Z:19:VAL:HG22	2.50	0.47
12:AC:166:ARG:HB3	12:AC:166:ARG:NH1	2.30	0.47
13:AE:128:LEU:HD21	13:AE:188:LEU:HB3	1.97	0.47
13:AE:842:ARG:HH22	13:AE:1250:ASP:HB2	1.80	0.47
10:B:18:G:C8	10:B:57:A:N1	2.83	0.47
15:D:13:U:O2	15:D:915:A:N7	2.47	0.47
21:J:162:ALA:O	21:J:165:ARG:O	2.33	0.47
22:K:96:MET:CE	22:K:115:LEU:HD11	2.45	0.47
23:L:67:PRO:O	23:L:70:VAL:HG22	2.15	0.47
10:A:18:G:C8	10:A:57:A:N1	2.83	0.46
11:AA:46:GLN:HA	11:AA:47:TYR:HA	1.77	0.46
11:AA:318:SER:H	11:AA:321:LEU:HD12	1.80	0.46
11:AA:549:ASP:OD2	13:AE:750:PRO:HB3	2.15	0.46
11:AA:756:TYR:CD2	12:AC:68:TYR:O	2.68	0.46
11:AA:1032:LYS:CE	11:AA:1032:LYS:HA	2.45	0.46
12:AD:199:ASP:N	12:AD:199:ASP:OD1	2.47	0.46
13:AE:1150:PRO:HG3	13:AE:1214:PRO:HB2	1.96	0.46
13:AE:1167:LYS:NZ	13:AE:1170:LYS:HB2	2.30	0.46
13:AE:1221:LEU:HD22	13:AE:1306:LEU:HB2	1.97	0.46
15:D:60:A:N1	15:D:107:G:O2'	2.42	0.46
15:D:373:A:C2	15:D:374:A:C8	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:526:C:P	29:R:88:LYS:HE3	2.55	0.46
15:D:915:A:C8	15:D:915:A:H3'	2.51	0.46
15:D:1175:G:N3	15:D:1176:A:C8	2.83	0.46
38:a:742:A:C2	38:a:755:U:N3	2.80	0.46
9:9:50:VAL:CG1	36:Y:119:ALA:CB	2.88	0.46
12:AD:104:LYS:HG2	12:AD:110:VAL:HB	1.97	0.46
15:D:526:C:OP2	29:R:88:LYS:HE3	2.15	0.46
9:9:1:MET:SD	9:9:2:ALA:N	2.88	0.46
9:9:48:ALA:HB3	9:9:51:TYR:CD2	2.50	0.46
12:AD:109:PRO:HB3	12:AD:132:HIS:CD2	2.50	0.46
19:H:72:LEU:CD1	19:H:72:LEU:N	2.73	0.46
33:V:8:LEU:HD23	33:V:25:ILE:HG21	1.97	0.46
38:a:517:C:OP2	46:i:10:ARG:NH2	2.48	0.46
38:a:1363:C:O2'	38:a:1809:A:N3	2.46	0.46
52:o:13:ARG:HD3	58:u:58:TYR:O	2.14	0.46
59:v:96:ILE:HG21	59:v:126:ILE:HD12	1.97	0.46
11:AA:243:PRO:HB2	11:AA:274:ILE:HG23	1.96	0.46
11:AA:948:ILE:HA	11:AA:951:MET:SD	2.55	0.46
11:AA:976:ARG:HG3	11:AA:976:ARG:NH1	2.30	0.46
12:AC:117:HIS:HB2	27:P:89:ARG:HD3	1.98	0.46
13:AE:87:LYS:HE3	13:AE:87:LYS:CA	2.42	0.46
13:AE:891:ASP:OD2	13:AE:1290:ARG:NH2	2.47	0.46
10:B:5:G:C2'	10:B:6:G:C5'	2.93	0.46
15:D:1255:G:O2'	15:D:1258:G:N3	2.47	0.46
35:X:16:VAL:HG23	35:X:17:ILE:HD12	1.97	0.46
35:X:106:ALA:HB3	35:X:110:LYS:HD2	1.98	0.46
10:A:5:G:C2'	10:A:6:G:C5'	2.93	0.46
10:A:18:G:C6	10:A:57:A:N7	2.83	0.46
12:AD:212:ASP:O	12:AD:215:GLU:N	2.48	0.46
15:D:35:G:N3	29:R:115:SER:OG	2.47	0.46
19:H:52:GLN:O	19:H:53:PHE:HD1	1.95	0.46
19:H:309:MET:HE2	19:H:318:PRO:HB3	1.97	0.46
26:O:63:LEU:HD13	26:O:65:ILE:HD11	1.98	0.46
38:a:1993:U:H4'	47:j:133:THR:HG22	1.96	0.46
45:h:76:ALA:HB2	45:h:96:TYR:CD1	2.51	0.46
11:AA:724:VAL:HG13	11:AA:774:GLY:H	1.76	0.46
11:AA:1018:TYR:CD1	11:AA:1018:TYR:C	2.94	0.46
11:AA:1252:SER:N	11:AA:1259:LEU:HD11	2.30	0.46
13:AE:902:ASP:OD2	13:AE:905:ARG:HB2	2.15	0.46
10:B:42:G:H2'	10:B:43:A:C8	2.47	0.46
14:C:61:ARG:HG2	23:L:88:MET:HE1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:94:ARG:CB	4:3:103:ILE:HD12	2.45	0.46
7:6:18:DC:C2	8:7:17:G:N2	2.78	0.46
11:AA:559:CYS:HB2	11:AA:662:SER:HB3	1.97	0.46
11:AA:829:THR:HG23	11:AA:1059:ARG:HA	1.97	0.46
12:AD:96:ASP:HB3	12:AD:148:ARG:HE	1.81	0.46
13:AE:420:PRO:HA	13:AE:437:PHE:O	2.15	0.46
10:B:6:G:O2'	10:B:7:G:C5'	2.64	0.46
15:D:1517:G:H1'	38:a:1919:A:O2'	2.16	0.46
19:H:69:ASP:O	19:H:85:SER:CB	2.63	0.46
19:H:84:LEU:N	19:H:84:LEU:CD2	2.78	0.46
28:Q:34:ILE:HG12	28:Q:70:CYS:SG	2.56	0.46
51:n:36:LEU:HB3	51:n:57:LEU:HD21	1.97	0.46
10:A:6:G:O2'	10:A:7:G:C5'	2.64	0.46
11:AA:685:MET:SD	11:AA:1073:LYS:HG2	2.55	0.46
11:AA:1257:GLN:CD	13:AE:345:LYS:HB3	2.40	0.46
12:AC:117:HIS:CB	27:P:89:ARG:HD3	2.45	0.46
13:AE:198:CYS:HA	13:AE:221:ILE:CD1	2.45	0.46
31:T:21:ASP:OD1	31:T:22:THR:N	2.49	0.46
38:a:930:G:H1'	43:f:25:LEU:HD11	1.98	0.46
38:a:1394:U:H4'	38:a:1603:A:H4'	1.97	0.46
38:a:2298:A:C6	38:a:2299:U:C2	3.04	0.46
3:2:30:ILE:HD13	3:2:93:LEU:HD12	1.97	0.46
9:9:67:THR:H	9:9:68:PRO:HD3	1.80	0.46
9:9:127:ALA:O	9:9:130:PRO:HG2	2.16	0.46
11:AA:978:VAL:HG11	11:AA:1010:GLN:CB	2.45	0.46
12:AC:73:GLY:HA3	12:AC:138:ALA:CB	2.46	0.46
10:B:58:A:C1'	10:B:60:U:C5	2.99	0.46
15:D:429:U:N3	15:D:431:A:N6	2.64	0.46
19:H:291:GLY:HA2	19:H:305:HIS:O	2.15	0.46
38:a:1720:U:H2'	38:a:1721:G:O4'	2.16	0.46
38:a:2315:G:H5'	51:n:157:THR:HG23	1.97	0.46
43:f:25:LEU:C	43:f:25:LEU:HD13	2.41	0.46
7:6:15:DC:N3	7:6:16:DC:C4	2.84	0.46
9:9:58:THR:HB	9:9:82:ILE:H	1.80	0.46
10:A:60:U:H4'	10:A:61:C:OP2	2.14	0.46
11:AA:538:LEU:HD11	11:AA:571:LEU:HD22	1.98	0.46
11:AA:875:ALA:H	20:I:80:LYS:HE3	1.81	0.46
11:AA:933:VAL:O	11:AA:933:VAL:HG12	2.16	0.46
11:AA:994:ARG:C	11:AA:994:ARG:CD	2.89	0.46
12:AC:71:LYS:HZ1	12:AC:140:ILE:HD12	1.81	0.46
12:AC:120:ASP:HB3	27:P:31:ARG:HH21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:105:ILE:HD12	13:AE:242:LEU:CD2	2.44	0.46
14:C:12:ARG:CZ	19:H:264:GLU:HA	2.46	0.46
36:Y:79:LEU:HD13	36:Y:132:ALA:HA	1.97	0.46
36:Y:116:MET:CB	36:Y:124:MET:HG2	2.46	0.46
38:a:2070:A:H2'	38:a:2071:A:O4'	2.16	0.46
6:5:116:DG:OP1	13:AE:1311:LYS:NZ	2.46	0.45
8:7:-11:A:H2'	8:7:-10:U:C6	2.50	0.45
9:9:34:THR:HG22	9:9:38:MET:CE	2.47	0.45
9:9:106:PHE:CG	9:9:106:PHE:O	2.69	0.45
10:A:18:G:O2'	10:A:60:U:N3	2.48	0.45
11:AA:726:TYR:O	11:AA:726:TYR:CD2	2.69	0.45
12:AC:228:LEU:HD11	12:AD:224:LEU:HD23	1.97	0.45
12:AD:60:GLU:OE2	12:AD:170:ARG:NE	2.44	0.45
12:AD:86:LYS:HE3	13:AE:528:THR:HG21	1.97	0.45
12:AD:131:CYS:SG	12:AD:132:HIS:N	2.89	0.45
12:AD:211:ILE:HD11	12:AD:215:GLU:HG3	1.98	0.45
13:AE:43:THR:HG22	13:AE:57:PHE:HE1	1.80	0.45
13:AE:86:GLU:CG	21:J:166:GLU:HB3	2.45	0.45
10:B:48:C:N4	10:B:59:A:C5	2.84	0.45
15:D:1225:A:OP1	35:X:101:ARG:HB2	2.15	0.45
18:G:16:PHE:CD2	19:H:42:LEU:O	2.69	0.45
27:P:99:GLN:O	27:P:99:GLN:HG2	2.16	0.45
38:a:1095:A:O2'	38:a:1096:A:O4'	2.33	0.45
47:j:152:PRO:HG3	47:j:156:PHE:CZ	2.50	0.45
9:9:125:ARG:NH1	9:9:125:ARG:CA	2.73	0.45
9:9:139:LEU:HD21	37:Z:11:VAL:HG22	1.97	0.45
11:AA:446:ASP:HA	11:AA:451:ARG:HH21	1.81	0.45
12:AC:59:VAL:O	12:AC:171:LEU:HG	2.16	0.45
13:AE:395:LYS:NZ	13:AE:399:LYS:HE2	2.32	0.45
15:D:1240:U:OP1	24:M:116:MET:HB2	2.16	0.45
15:D:1308:U:O5'	35:X:98:ARG:HG2	2.16	0.45
15:D:1340:A:H8	15:D:1340:A:O5'	2.00	0.45
17:F:21:ARG:HH22	19:H:341:ARG:HD2	1.82	0.45
19:H:135:LEU:CB	19:H:167:VAL:O	2.63	0.45
20:I:117:ALA:HB2	20:I:200:VAL:CG1	2.46	0.45
24:M:24:ALA:O	24:M:27:VAL:HG22	2.16	0.45
27:P:8:ILE:HD12	27:P:25:ILE:CD1	2.46	0.45
36:Y:42:ASN:HA	36:Y:45:THR:HB	1.98	0.45
9:9:50:VAL:HG22	36:Y:119:ALA:C	2.41	0.45
11:AA:1046:VAL:CG2	11:AA:1049:ILE:HG13	2.46	0.45
11:AA:1047:LEU:O	11:AA:1049:ILE:HD11	2.13	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AC:65:LEU:CD2	20:I:80:LYS:O	2.65	0.45
13:AE:75:TYR:CD2	13:AE:75:TYR:O	2.70	0.45
13:AE:108:ALA:HB1	13:AE:279:LEU:HD22	1.96	0.45
13:AE:506:VAL:HG23	13:AE:628:GLY:HA3	1.98	0.45
38:a:784:G:H5'	38:a:785:G:OP1	2.15	0.45
56:s:30:THR:CG2	56:s:31:GLU:N	2.79	0.45
6:5:113:DC:P	11:AA:163:LYS:HD3	2.55	0.45
10:A:60:U:OP2	10:A:61:C:N4	2.45	0.45
11:AA:850:ILE:HD12	11:AA:1048:LYS:HG2	1.99	0.45
11:AA:965:GLN:HA	11:AA:968:GLU:HB3	1.97	0.45
15:D:1397:C:O5'	15:D:1397:C:C6	2.70	0.45
18:G:114:LEU:HA	18:G:144:LEU:HD13	1.98	0.45
19:H:38:VAL:HG22	19:H:48:ILE:HD11	1.99	0.45
24:M:27:VAL:HG12	24:M:43:VAL:HG11	1.98	0.45
38:a:954:G:OP2	59:v:16:ARG:NH2	2.50	0.45
38:a:2291:U:H2'	38:a:2292:U:C6	2.51	0.45
7:6:15:DC:C4	7:6:16:DC:C5	3.05	0.45
7:6:21:DA:C6	8:7:15:G:C2	3.03	0.45
9:9:39:THR:HA	9:9:42:ARG:HH11	1.81	0.45
9:9:50:VAL:CG2	36:Y:120:ASP:N	2.79	0.45
10:A:14:A:H1'	10:A:22:G:N2	2.31	0.45
13:AE:1158:GLU:HA	13:AE:1223:LEU:HD21	1.99	0.45
10:B:14:A:H1'	10:B:22:G:N2	2.31	0.45
17:F:67:ARG:HD3	17:F:67:ARG:N	2.31	0.45
18:G:114:LEU:HD13	18:G:144:LEU:CB	2.46	0.45
38:a:560:C:O2	63:z:48:ARG:NH1	2.41	0.45
38:a:1007:C:OP1	56:s:37:ARG:NH2	2.50	0.45
38:a:1021:A:N3	38:a:1021:A:C3'	2.78	0.45
49:l:170:ARG:NH2	49:l:176:ASP:OD1	2.49	0.45
51:n:17:MET:HE2	51:n:25:VAL:HA	1.98	0.45
10:A:41:C:C5'	24:M:143:ARG:HD2	2.46	0.45
11:AA:176:ILE:HD12	11:AA:184:LEU:HD23	1.99	0.45
11:AA:914:LYS:HD3	11:AA:914:LYS:N	2.31	0.45
11:AA:974:ARG:HD2	11:AA:1014:LEU:CD1	2.46	0.45
12:AC:117:HIS:C	27:P:89:ARG:HD3	2.42	0.45
13:AE:51:PRO:HB2	13:AE:52:GLU:H	1.65	0.45
19:H:19:ARG:O	19:H:72:LEU:HD13	2.16	0.45
36:Y:125:THR:HA	36:Y:128:ILE:HG12	1.98	0.45
9:9:24:SER:HB2	9:9:116:GLU:HG2	1.98	0.45
9:9:139:LEU:CD2	37:Z:11:VAL:HG22	2.47	0.45
10:A:48:C:C5	10:A:59:A:C8	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:641:GLU:OE2	13:AE:749:LYS:NZ	2.47	0.45
13:AE:109:SER:HB2	13:AE:296:LYS:HG2	1.98	0.45
15:D:17:U:H2'	15:D:18:C:C6	2.52	0.45
15:D:198:G:OP2	15:D:198:G:C8	2.70	0.45
15:D:868:C:H2'	15:D:869:G:O4'	2.16	0.45
18:G:208:ARG:HH12	19:H:29:VAL:HG11	1.82	0.45
38:a:340:A:O2'	49:l:162:ARG:NH1	2.50	0.45
38:a:1209:U:O2'	38:a:1237:A:N1	2.40	0.45
38:a:2547:A:H2'	38:a:2548:U:C6	2.52	0.45
41:d:48:U:H2'	41:d:49:C:C6	2.52	0.45
45:h:6:CYS:SG	45:h:13:ARG:NH1	2.89	0.45
13:AE:395:LYS:HE3	13:AE:395:LYS:HB3	1.45	0.45
15:D:1176:A:H2'	15:D:1177:G:O4'	2.16	0.45
35:X:75:MET:HA	35:X:75:MET:HE3	1.99	0.45
37:Z:26:MET:HE2	37:Z:26:MET:HB2	1.71	0.45
38:a:1906:G:H4'	38:a:1906:G:OP1	2.16	0.45
38:a:2168:G:OP1	38:a:2168:G:C8	2.69	0.45
38:a:2822:G:OP1	47:j:164:GLN:NE2	2.47	0.45
49:l:149:ILE:CD1	49:l:188:MET:HE3	2.46	0.45
4:3:36:VAL:HG11	4:3:39:ILE:CD1	2.44	0.45
11:AA:857:VAL:HG11	11:AA:861:ALA:HB2	1.99	0.45
11:AA:1029:LEU:HA	11:AA:1032:LYS:HB2	1.99	0.45
11:AA:1029:LEU:HD11	11:AA:1033:ARG:HH21	1.82	0.45
12:AC:58:GLU:HB3	12:AC:170:ARG:HG2	1.99	0.45
12:AC:71:LYS:NZ	12:AC:140:ILE:HG13	2.32	0.45
13:AE:385:LEU:HD23	13:AE:390:LEU:HB2	1.98	0.45
13:AE:515:ARG:NH2	13:AE:718:SER:O	2.48	0.45
13:AE:847:ASP:N	13:AE:847:ASP:OD1	2.49	0.45
13:AE:978:ARG:HD3	13:AE:999:TYR:H	1.82	0.45
15:D:376:G:C2	15:D:389:A:C2	3.05	0.45
19:H:290:TYR:O	19:H:305:HIS:C	2.56	0.45
38:a:1385:A:O2'	38:a:1396:U:O2	2.35	0.45
60:w:28:LEU:HD23	60:w:48:VAL:HG21	1.98	0.45
9:9:60:LEU:HB2	9:9:61:ARG:NH2	2.31	0.45
9:9:72:LEU:HD22	9:9:72:LEU:C	2.42	0.45
10:A:48:C:N4	10:A:59:A:C5	2.84	0.45
11:AA:933:VAL:HG22	11:AA:935:THR:CG2	2.47	0.45
12:AD:16:ILE:HD13	12:AD:214:GLU:HG2	1.99	0.45
13:AE:126:LEU:HD12	13:AE:223:LEU:HD22	1.99	0.45
13:AE:161:THR:H	13:AE:164:GLN:HB2	1.82	0.45
13:AE:201:LEU:CD1	13:AE:224:LEU:HD12	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:34:C:O5'	10:B:34:C:C6	2.70	0.45
38:a:39:G:H1'	49:l:43:THR:HG21	1.99	0.45
38:a:68:G:N2	38:a:74:A:OP2	2.49	0.45
38:a:1925:C:C5	38:a:1925:C:OP2	2.70	0.45
9:9:111:ALA:HB3	9:9:114:GLU:HG3	1.98	0.44
10:A:58:A:C1'	10:A:60:U:C5	2.99	0.44
11:AA:1020:GLU:HA	11:AA:1023:HIS:HD2	1.81	0.44
11:AA:1026:GLU:HG3	15:D:1030:U:C4	2.48	0.44
13:AE:76:LYS:HB3	13:AE:76:LYS:NZ	2.32	0.44
13:AE:213:LYS:CA	13:AE:213:LYS:HE3	2.47	0.44
13:AE:1357:ILE:HG22	13:AE:1359:ALA:H	1.82	0.44
10:B:37:A:N3	10:B:37:A:H5''	2.32	0.44
19:H:332:VAL:HG13	19:H:342:ILE:HG23	1.98	0.44
27:P:28:THR:HG21	27:P:87:LEU:CD1	2.46	0.44
36:Y:19:PRO:HG2	36:Y:24:GLY:N	2.32	0.44
38:a:1695:G:N7	45:h:14:ARG:NH2	2.64	0.44
51:n:57:LEU:HD22	51:n:89:VAL:CG2	2.47	0.44
63:z:76:TYR:OH	63:z:92:ARG:NH1	2.51	0.44
9:9:67:THR:H	9:9:68:PRO:CD	2.29	0.44
9:9:71:CYS:CA	9:9:117:LEU:HD13	2.48	0.44
10:A:22:G:H2'	10:A:23:C:C5	2.52	0.44
10:A:25:C:C2'	10:A:26:G:H5'	2.48	0.44
10:A:49:G:C2'	10:A:50:U:H5'	2.47	0.44
11:AA:1010:GLN:C	11:AA:1010:GLN:CD	2.86	0.44
13:AE:53:ARG:HA	13:AE:54:ASP:HA	1.55	0.44
13:AE:115:TRP:HB3	13:AE:1333:THR:CG2	2.47	0.44
13:AE:388:ARG:HG2	13:AE:388:ARG:NH1	2.32	0.44
10:B:34:C:C5	10:B:34:C:OP1	2.70	0.44
15:D:915:A:H8	15:D:915:A:O5'	2.00	0.44
20:I:155:GLY:HA2	20:I:163:ALA:HB1	1.99	0.44
36:Y:7:TYR:CD2	36:Y:7:TYR:O	2.70	0.44
36:Y:37:PHE:CD2	36:Y:37:PHE:O	2.71	0.44
38:a:57:C:H2'	38:a:58:G:O4'	2.18	0.44
38:a:645:C:H2'	38:a:647:G:C8	2.52	0.44
10:A:57:A:O5'	10:A:58:A:P	2.76	0.44
11:AA:685:MET:HE3	11:AA:685:MET:HB2	1.84	0.44
11:AA:976:ARG:NH2	11:AA:989:LEU:HB3	2.32	0.44
11:AA:1032:LYS:CA	11:AA:1032:LYS:HE2	2.47	0.44
13:AE:926:PRO:HB2	13:AE:1241:TYR:HE1	1.82	0.44
15:D:1493:A:C8	15:D:1493:A:OP1	2.70	0.44
16:E:55:GLN:N	16:E:56:PRO:HD2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:37:PHE:CE1	36:Y:56:VAL:HG11	2.51	0.44
47:j:186:LEU:HD21	62:y:4:ILE:HG21	1.98	0.44
6:5:115:DA:P	13:AE:1148:ARG:HG3	2.58	0.44
8:7:14:U:H2'	8:7:15:G:C8	2.52	0.44
9:9:106:PHE:C	9:9:106:PHE:CD2	2.95	0.44
10:A:56:C:OP1	38:a:2168:G:C4	2.71	0.44
12:AD:64:VAL:HG11	12:AD:78:ILE:HG21	1.99	0.44
13:AE:128:LEU:CD2	13:AE:188:LEU:HB3	2.47	0.44
13:AE:209:ASN:HA	13:AE:214:ARG:NH2	2.31	0.44
21:J:165:ARG:NH1	21:J:165:ARG:HB2	2.32	0.44
26:O:84:THR:HG21	26:O:103:PHE:CB	2.45	0.44
27:P:28:THR:HG21	27:P:87:LEU:HD12	1.99	0.44
36:Y:95:ASP:OD2	36:Y:95:ASP:N	2.50	0.44
2:1:17:VAL:HG12	2:1:76:VAL:HG21	1.98	0.44
11:AA:844:LYS:HD3	11:AA:844:LYS:HA	1.48	0.44
13:AE:111:THR:HG21	13:AE:303:VAL:HB	2.00	0.44
13:AE:1033:GLY:HA3	13:AE:1081:VAL:O	2.18	0.44
13:AE:1108:GLN:HG3	13:AE:1109:LEU:HD12	1.99	0.44
15:D:337:G:H2'	15:D:338:A:C8	2.52	0.44
36:Y:123:ALA:HA	36:Y:126:ARG:HG3	2.00	0.44
38:a:1266:G:OP1	46:i:16:ARG:NE	2.45	0.44
6:5:98:DA:C2'	6:5:99:DT:C7	2.96	0.44
10:A:76:A:C2	52:o:31:HIS:NE2	2.85	0.44
11:AA:967:LEU:HD23	11:AA:1021:LEU:HD21	1.98	0.44
12:AC:92:VAL:HG12	12:AC:121:VAL:HG12	1.98	0.44
12:AD:57:THR:HG21	12:AD:147:GLN:HB2	1.99	0.44
13:AE:850:LYS:HB3	13:AE:855:ASP:HB2	2.00	0.44
10:B:1:C:C5	10:B:2:G:N7	2.86	0.44
10:B:48:C:C5	10:B:59:A:C8	3.05	0.44
15:D:1515:G:H2'	15:D:1516:G:C8	2.52	0.44
18:G:76:ALA:CB	18:G:210:VAL:HG11	2.47	0.44
36:Y:140:GLU:OE1	36:Y:140:GLU:N	2.50	0.44
38:a:1327:A:H2'	38:a:1328:A:O4'	2.17	0.44
6:5:114:DC:H5''	13:AE:1148:ARG:CZ	2.46	0.44
9:9:31:ARG:HE	38:a:1054:A:C5'	2.18	0.44
9:9:62:ARG:HG2	9:9:62:ARG:NH2	2.20	0.44
11:AA:596:ASP:N	11:AA:596:ASP:OD1	2.49	0.44
13:AE:201:LEU:HD11	13:AE:220:ARG:NH1	2.31	0.44
10:B:9:G:O2'	10:B:45:G:H2'	2.18	0.44
10:B:25:C:C2'	10:B:26:G:H5'	2.47	0.44
10:B:57:A:O5'	10:B:58:A:P	2.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:12:ARG:HD3	14:C:16:GLU:OE1	2.18	0.44
18:G:16:PHE:CG	19:H:43:LYS:HA	2.53	0.44
18:G:114:LEU:HD13	18:G:144:LEU:HB3	1.99	0.44
18:G:206:ALA:O	18:G:210:VAL:HG23	2.18	0.44
22:K:111:MET:CE	22:K:125:ALA:HB1	2.39	0.44
26:O:80:ARG:O	26:O:84:THR:HG23	2.17	0.44
38:a:2133:G:O2'	38:a:2157:G:N2	2.51	0.44
9:9:31:ARG:NE	38:a:1054:A:O4'	2.46	0.44
10:A:49:G:O5'	10:A:49:G:C8	2.71	0.44
11:AA:800:MET:HE3	11:AA:800:MET:HB2	1.60	0.44
11:AA:939:VAL:HG12	11:AA:939:VAL:O	2.17	0.44
11:AA:1008:GLN:HE22	11:AA:1011:LEU:HG	1.82	0.44
11:AA:1117:LEU:HD12	11:AA:1195:ILE:HG12	2.00	0.44
13:AE:394:ILE:O	13:AE:394:ILE:HG13	2.18	0.44
13:AE:515:ARG:HH12	13:AE:724:MET:HG2	1.83	0.44
15:D:397:A:H3'	15:D:397:A:N3	2.33	0.44
36:Y:121:ILE:HA	36:Y:124:MET:SD	2.58	0.44
38:a:631:A:N3	38:a:2415:G:O2'	2.48	0.44
38:a:1589:U:C2	38:a:1590:A:C8	3.06	0.44
55:r:55:GLU:HA	55:r:58:LEU:HD12	1.99	0.44
11:AA:717:VAL:HG22	11:AA:782:VAL:HG12	2.00	0.44
12:AC:118:ASP:HA	27:P:89:ARG:C	2.43	0.44
12:AC:141:SER:O	12:AC:141:SER:OG	2.33	0.44
13:AE:1046:ILE:HG22	13:AE:1061:VAL:HA	2.00	0.44
10:B:26:G:N2	10:B:45:G:N2	2.66	0.44
10:B:49:G:O5'	10:B:49:G:C8	2.71	0.44
18:G:35:ARG:CD	19:H:14:LYS:HD3	2.40	0.44
55:r:15:LEU:HD13	55:r:15:LEU:C	2.42	0.44
9:9:52:MET:HE1	9:9:85:SER:HB2	2.00	0.43
10:A:34:C:OP1	24:M:84:THR:OG1	2.35	0.43
11:AA:529:ARG:HH22	11:AA:687:ARG:HH11	1.66	0.43
13:AE:213:LYS:HE3	13:AE:213:LYS:HA	1.99	0.43
10:B:49:G:C2'	10:B:50:U:H5'	2.47	0.43
37:Z:18:ASP:HB3	37:Z:22:LEU:HD12	2.00	0.43
44:g:18:CYS:HB2	44:g:40:CYS:HB3	1.96	0.43
58:u:2:ARG:H	58:u:5:THR:HG1	1.66	0.43
10:A:46:G:O2'	10:A:47:U:H5''	2.19	0.43
11:AA:469:VAL:HA	11:AA:472:GLU:HG2	2.00	0.43
13:AE:120:LEU:HA	13:AE:121:PRO:HA	1.84	0.43
13:AE:211:GLU:CG	13:AE:215:LYS:HE3	2.44	0.43
10:B:18:G:O2'	10:B:60:U:N3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:13:U:C2	15:D:915:A:C5	3.06	0.43
15:D:109:A:C6	15:D:326:G:C6	3.05	0.43
15:D:976:G:C8	15:D:1358:U:O2	2.71	0.43
22:K:156:LYS:HG2	25:N:71:VAL:HG13	2.00	0.43
35:X:106:ALA:HB3	35:X:110:LYS:CD	2.47	0.43
3:2:1:MET:N	38:a:142:A:O2'	2.48	0.43
7:6:12:DC:O5'	7:6:12:DC:H6	2.01	0.43
8:7:-2:U:O2'	20:I:162:ILE:HG13	2.18	0.43
9:9:106:PHE:O	9:9:106:PHE:CD2	2.70	0.43
10:A:1:C:C5	10:A:2:G:N7	2.86	0.43
11:AA:724:VAL:HG12	11:AA:774:GLY:N	2.31	0.43
19:H:294:VAL:HG21	19:H:330:VAL:HG21	1.99	0.43
38:a:705:A:O4'	45:h:9:THR:HG21	2.18	0.43
38:a:813:U:H2'	38:a:814:C:C6	2.53	0.43
38:a:1927:A:C8	38:a:1927:A:O5'	2.71	0.43
60:w:49:GLU:HB2	60:w:50:PRO:HD3	2.01	0.43
10:A:18:G:N3	10:A:58:A:C5	2.87	0.43
11:AA:998:LEU:CD2	11:AA:1011:LEU:HD13	2.49	0.43
11:AA:1253:LEU:CD1	13:AE:253:VAL:CG1	2.95	0.43
12:AC:205:MET:HE3	12:AC:205:MET:HB2	1.87	0.43
12:AD:86:LYS:NZ	13:AE:528:THR:HB	2.33	0.43
13:AE:1024:THR:HG23	13:AE:1123:ARG:HA	2.00	0.43
13:AE:1227:HIS:HA	13:AE:1230:THR:HG22	1.99	0.43
20:I:50:ALA:HB2	20:I:75:ILE:HD12	2.00	0.43
38:a:74:A:N7	38:a:88:G:C5	2.86	0.43
38:a:1095:A:H2'	38:a:1096:A:C8	2.53	0.43
38:a:2252:G:O2'	38:a:2253:G:H5'	2.18	0.43
38:a:2395:C:H2'	38:a:2396:G:O4'	2.18	0.43
42:e:59:GLU:O	42:e:63:ALA:HB3	2.17	0.43
51:n:77:PHE:N	51:n:77:PHE:CD1	2.82	0.43
56:s:73:VAL:HG11	56:s:75:TYR:CZ	2.53	0.43
8:7:-6:U:C2	15:D:1493:A:H2	2.36	0.43
9:9:16:SER:HB2	9:9:20:LYS:NZ	2.33	0.43
10:A:32:C:O2'	24:M:86:GLN:CD	2.31	0.43
11:AA:830:THR:HG22	11:AA:1234:LYS:NZ	2.34	0.43
13:AE:62:PHE:CD1	13:AE:62:PHE:N	2.86	0.43
13:AE:141:PHE:CE2	13:AE:296:LYS:CB	2.94	0.43
15:D:842:U:H3'	15:D:843:U:C5'	2.48	0.43
15:D:1126:U:OP1	27:P:7:ARG:NH2	2.51	0.43
15:D:1499:A:O2'	15:D:1500:A:C5'	2.67	0.43
19:H:61:GLU:HG2	19:H:62:ILE:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1082:U:H3	38:a:1086:A:N6	2.15	0.43
45:h:37:ASN:HB2	45:h:62:TYR:HB2	2.01	0.43
9:9:118:ILE:HB	9:9:119:PRO:CD	2.45	0.43
11:AA:27:LEU:O	11:AA:528:ARG:NH1	2.42	0.43
12:AC:50:SER:HB3	12:AD:8:PHE:HZ	1.84	0.43
13:AE:242:LEU:C	13:AE:242:LEU:HD23	2.44	0.43
15:D:684:U:H2'	15:D:685:G:O4'	2.18	0.43
19:H:119:GLY:O	19:H:120:PHE:C	2.62	0.43
22:K:150:PRO:O	22:K:153:VAL:HG22	2.19	0.43
36:Y:100:ILE:HB	36:Y:101:SER:H	1.71	0.43
42:e:56:LEU:HD23	42:e:56:LEU:HA	1.87	0.43
50:m:12:ARG:HG3	50:m:44:VAL:HG11	2.00	0.43
57:t:24:VAL:HG13	57:t:33:ALA:HB2	2.00	0.43
8:7:7:G:N3	8:7:7:G:H2'	2.33	0.43
9:9:62:ARG:CG	9:9:62:ARG:HH21	2.14	0.43
11:AA:95:PRO:HB3	11:AA:123:TYR:HE1	1.83	0.43
11:AA:960:LEU:HB3	11:AA:1025:PHE:CD1	2.53	0.43
13:AE:107:LEU:HA	13:AE:276:ASN:ND2	2.33	0.43
13:AE:559:ALA:HB3	13:AE:562:GLU:HB3	2.01	0.43
13:AE:568:SER:HB3	13:AE:570:LYS:NZ	2.34	0.43
10:B:53:G:C2	10:B:54:U:C5	3.07	0.43
15:D:1417:G:C6	15:D:1482:G:C6	3.06	0.43
19:H:302:GLY:HA3	19:H:344:LEU:HD13	2.00	0.43
27:P:89:ARG:H	27:P:89:ARG:HG3	1.59	0.43
38:a:998:C:OP2	63:z:58:ARG:NH2	2.49	0.43
51:n:29:PRO:HB2	51:n:169:LEU:HD22	1.99	0.43
10:A:26:G:N2	10:A:45:G:N2	2.66	0.43
11:AA:241:LEU:N	11:AA:283:LYS:O	2.51	0.43
11:AA:623:LEU:HD13	11:AA:627:GLY:HA2	2.01	0.43
11:AA:971:LEU:HG	11:AA:1014:LEU:HG	2.00	0.43
12:AD:207:THR:OG1	12:AD:208:ASN:N	2.52	0.43
13:AE:126:LEU:CD1	13:AE:223:LEU:HD22	2.49	0.43
19:H:280:LEU:HB2	19:H:330:VAL:O	2.18	0.43
21:J:197:GLU:HA	21:J:200:ILE:HD12	1.99	0.43
36:Y:10:LEU:HD13	36:Y:10:LEU:HA	1.79	0.43
36:Y:34:ILE:HG22	36:Y:34:ILE:O	2.18	0.43
38:a:879:G:H2'	38:a:880:G:O4'	2.19	0.43
9:9:72:LEU:HD22	9:9:72:LEU:O	2.19	0.43
10:A:9:G:O2'	10:A:45:G:H2'	2.18	0.43
10:A:36:U:H2'	10:A:37:A:O4'	2.19	0.43
11:AA:803:ALA:HB2	11:AA:1094:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:964:LEU:C	11:AA:964:LEU:CD1	2.85	0.43
12:AD:111:THR:OG1	12:AD:126:PRO:O	2.35	0.43
12:AD:228:LEU:HD23	12:AD:228:LEU:HA	1.89	0.43
13:AE:201:LEU:CB	13:AE:221:ILE:HD13	2.47	0.43
13:AE:220:ARG:NH1	13:AE:220:ARG:CG	2.82	0.43
13:AE:1079:LYS:HD3	13:AE:1098:GLN:HB3	1.99	0.43
10:B:58:A:OP2	10:B:58:A:H8	2.02	0.43
15:D:384:G:H2'	15:D:385:C:C6	2.54	0.43
18:G:47:VAL:N	18:G:48:PRO:HD2	2.34	0.43
19:H:136:VAL:HA	19:H:168:VAL:O	2.18	0.43
35:X:23:TYR:CD2	35:X:69:LEU:HD23	2.53	0.43
38:a:819:A:C4	38:a:1189:A:C2	3.07	0.43
61:x:18:LEU:HD23	61:x:25:ARG:HD2	1.99	0.43
6:5:116:DG:C6	6:5:117:DA:C6	3.06	0.43
11:AA:395:TYR:HE2	11:AA:420:LEU:HG	1.84	0.43
11:AA:524:ILE:HB	11:AA:712:SER:HB2	1.99	0.43
11:AA:666:SER:HB2	11:AA:1186:VAL:HG21	2.01	0.43
11:AA:839:VAL:O	11:AA:886:LYS:HD2	2.19	0.43
11:AA:1043:ALA:CB	11:AA:1044:PRO:CD	2.91	0.43
13:AE:190:LYS:HB2	13:AE:190:LYS:HE3	1.41	0.43
13:AE:245:LEU:CG	13:AE:246:PRO:HD2	2.47	0.43
13:AE:388:ARG:HG2	13:AE:388:ARG:HH11	1.84	0.43
13:AE:450:HIS:HA	13:AE:451:PRO:HD3	1.90	0.43
13:AE:513:MET:HG3	13:AE:544:LEU:HD11	2.01	0.43
10:B:8:U:O2'	10:B:47:U:C4	2.72	0.43
10:B:18:G:N3	10:B:58:A:C5	2.87	0.43
10:B:22:G:O2'	10:B:23:C:O5'	2.36	0.43
14:C:12:ARG:O	14:C:16:GLU:HG3	2.19	0.43
19:H:119:GLY:CA	19:H:132:PRO:C	2.92	0.43
26:O:55:VAL:O	26:O:57:MET:N	2.52	0.43
38:a:1386:C:H2'	38:a:1387:A:C8	2.53	0.43
4:3:39:ILE:HG22	4:3:40:ASN:N	2.34	0.42
11:AA:75:LEU:HD23	11:AA:94:ALA:HB3	2.00	0.42
11:AA:300:ASP:OD1	11:AA:313:ALA:N	2.52	0.42
12:AC:211:ILE:HD12	12:AC:211:ILE:HA	1.92	0.42
13:AE:102:MET:HG2	13:AE:246:PRO:CG	2.49	0.42
10:B:60:U:OP2	10:B:61:C:N4	2.45	0.42
15:D:324:G:N2	15:D:327:A:C8	2.86	0.42
15:D:421:U:O2	15:D:421:U:O4'	2.37	0.42
15:D:1323:G:H2'	15:D:1324:A:C8	2.54	0.42
15:D:1333:A:H2'	15:D:1334:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:H:109:THR:C	19:H:153:GLU:HA	2.43	0.42
28:Q:88:GLY:H	28:Q:114:THR:HG22	1.84	0.42
38:a:126:A:O5'	50:m:19:ARG:HG3	2.19	0.42
38:a:973:A:O4'	38:a:1188:U:C6	2.72	0.42
38:a:2469:A:N6	38:a:2481:G:O2'	2.52	0.42
56:s:114:LEU:HD12	56:s:114:LEU:HA	1.87	0.42
10:A:22:G:O2'	10:A:23:C:O5'	2.36	0.42
13:AE:47:ARG:HA	13:AE:47:ARG:NE	2.35	0.42
13:AE:111:THR:CG2	13:AE:300:GLN:HA	2.48	0.42
13:AE:1026:PRO:HB2	13:AE:1028:ILE:HG23	2.00	0.42
14:C:44:ILE:HG21	19:H:339:ARG:HA	2.01	0.42
19:H:335:ILE:HG12	19:H:342:ILE:HG23	2.00	0.42
20:I:9:GLY:HA3	30:S:89:MET:HE3	2.01	0.42
22:K:153:VAL:HG23	22:K:164:ILE:HD13	2.00	0.42
38:a:1020:A:C2	38:a:1141:U:C2	3.07	0.42
38:a:1028:A:N6	38:a:1125:G:H2'	2.34	0.42
38:a:2252:G:H2'	38:a:2253:G:H8	1.84	0.42
51:n:123:ASP:C	51:n:123:ASP:OD1	2.62	0.42
6:5:108:DT:C7	11:AA:199:ASP:HB3	2.45	0.42
9:9:31:ARG:HE	38:a:1054:A:C4'	2.26	0.42
10:A:53:G:C2	10:A:54:U:C5	3.07	0.42
11:AA:796:LEU:N	11:AA:1231:TYR:OH	2.52	0.42
11:AA:805:MET:HE3	11:AA:805:MET:HB2	1.87	0.42
11:AA:859:GLU:CG	20:I:110:GLU:OE1	2.67	0.42
40:c:37:ARG:HG2	40:c:48:THR:HG23	2.00	0.42
54:q:3:VAL:HA	54:q:36:ARG:O	2.19	0.42
61:x:99:TYR:OH	61:x:111:ARG:NH1	2.53	0.42
8:7:-5:U:H6	8:7:-5:U:H3'	1.83	0.42
10:A:47:U:O2'	10:A:50:U:OP1	2.37	0.42
10:A:56:C:C2	38:a:2112:G:C5	3.07	0.42
11:AA:55:SER:CB	11:AA:465:ARG:HH12	2.32	0.42
11:AA:68:LEU:HD11	11:AA:100:LEU:HB3	2.01	0.42
11:AA:941:LYS:HD3	11:AA:941:LYS:HA	1.78	0.42
11:AA:985:GLU:CG	11:AA:988:LYS:HE3	2.45	0.42
11:AA:1018:TYR:HA	11:AA:1021:LEU:HD12	2.00	0.42
11:AA:1329:GLU:HA	13:AE:245:LEU:HD13	2.01	0.42
12:AC:231:PHE:HE2	12:AD:39:LEU:HD13	1.84	0.42
13:AE:141:PHE:CD2	13:AE:297:ARG:HB2	2.54	0.42
13:AE:839:VAL:HG12	13:AE:864:LEU:HD12	2.02	0.42
10:B:46:G:O2'	10:B:47:U:H5''	2.19	0.42
15:D:37:U:O2	15:D:548:G:N2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:429:U:O2	15:D:430:A:C8	2.72	0.42
15:D:1371:G:O3'	26:O:71:GLY:HA3	2.19	0.42
17:F:32:VAL:HG11	28:Q:89:PRO:HG3	2.01	0.42
19:H:19:ARG:CD	19:H:73:ASP:OD1	2.66	0.42
19:H:76:GLU:HA	19:H:76:GLU:OE2	2.18	0.42
38:a:2093:G:O2'	38:a:2198:A:N1	2.41	0.42
38:a:2511:U:O4	38:a:2575:C:N3	2.52	0.42
45:h:240:PHE:CD2	45:h:240:PHE:O	2.73	0.42
49:l:145:ASP:HA	49:l:166:LYS:HB3	2.01	0.42
56:s:32:LEU:HD23	56:s:54:ILE:HD13	2.01	0.42
59:v:35:ALA:HB2	59:v:102:LEU:HD11	2.00	0.42
10:A:15:G:H1	10:A:20:U:H3	1.68	0.42
11:AA:104:ILE:HD11	11:AA:116:ASP:HB2	2.02	0.42
13:AE:67:ASP:CG	13:AE:95:THR:HG1	2.24	0.42
13:AE:137:ARG:HA	13:AE:142:GLU:HG2	2.02	0.42
15:D:622:A:C8	15:D:623:C:C6	3.08	0.42
19:H:110:GLY:H	19:H:153:GLU:N	2.17	0.42
38:a:1142:A:H2'	38:a:1142:A:N3	2.34	0.42
11:AA:484:LEU:HA	11:AA:485:ASP:HA	1.82	0.42
11:AA:812:PHE:HZ	13:AE:503:SER:HB2	1.85	0.42
11:AA:1034:ARG:NH1	11:AA:1034:ARG:CG	2.77	0.42
13:AE:144:TYR:CE1	13:AE:162:GLU:OE1	2.73	0.42
13:AE:586:GLY:HA3	13:AE:612:LEU:HD11	2.01	0.42
15:D:826:C:O2	25:N:16:ASN:ND2	2.52	0.42
19:H:292:CYS:SG	19:H:304:VAL:HB	2.60	0.42
21:J:48:LEU:HD13	21:J:48:LEU:N	2.33	0.42
30:S:41:ARG:O	30:S:45:VAL:HG12	2.20	0.42
36:Y:112:LYS:HB3	36:Y:112:LYS:NZ	2.34	0.42
38:a:1688:U:O2'	38:a:1700:A:N7	2.49	0.42
38:a:1925:C:OP2	38:a:1925:C:C6	2.73	0.42
38:a:2756:U:C4	38:a:2759:G:O6	2.72	0.42
47:j:172:VAL:HG11	47:j:175:LEU:HD21	2.00	0.42
57:t:38:ILE:HD11	57:t:112:PHE:CZ	2.54	0.42
57:t:113:MET:HE3	57:t:116:ILE:HD11	2.01	0.42
8:7:-9:G:C5'	15:D:1501:C:H41	2.33	0.42
8:7:-8:U:C6	15:D:1403:C:H1'	2.55	0.42
11:AA:230:PHE:HB2	11:AA:333:ILE:HB	2.01	0.42
11:AA:959:ASP:HA	11:AA:962:GLU:HB2	2.01	0.42
13:AE:820:ILE:HD11	13:AE:822:MET:HE2	2.02	0.42
13:AE:824:PRO:HD3	13:AE:835:LEU:HD12	2.00	0.42
13:AE:848:VAL:HB	13:AE:858:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:216:U:H2'	15:D:217:C:C6	2.55	0.42
19:H:274:TYR:HD1	19:H:335:ILE:HD12	1.84	0.42
38:a:567:U:OP2	58:u:29:LYS:NZ	2.53	0.42
38:a:948:C:H1'	38:a:984:A:C8	2.55	0.42
38:a:2803:G:H2'	38:a:2804:U:C5	2.55	0.42
49:l:48:THR:HG23	49:l:86:ALA:HB3	2.02	0.42
57:t:107:LEU:HD21	57:t:115:ILE:HG21	2.01	0.42
4:3:12:ILE:CG2	4:3:80:ALA:HB2	2.49	0.42
9:9:47:GLU:HG3	9:9:95:LEU:CD2	2.49	0.42
11:AA:565:GLU:HA	11:AA:569:ILE:HG12	2.01	0.42
13:AE:24:LEU:CD1	13:AE:232:ASN:ND2	2.82	0.42
13:AE:244:VAL:HA	13:AE:269:TYR:OH	2.19	0.42
13:AE:894:VAL:HG22	13:AE:1258:ARG:HH11	1.83	0.42
13:AE:1289:ASN:O	13:AE:1293:GLU:HB2	2.20	0.42
14:C:14:THR:CG2	14:C:48:ARG:HE	2.33	0.42
15:D:502:A:H2'	15:D:503:C:O4'	2.20	0.42
15:D:1208:C:H2'	15:D:1209:C:H6	1.85	0.42
26:O:28:ILE:HD12	26:O:28:ILE:N	2.35	0.42
36:Y:64:ARG:HE	36:Y:64:ARG:HB2	1.52	0.42
38:a:693:A:O2'	38:a:1353:A:N3	2.48	0.42
38:a:742:A:N1	38:a:755:U:O4	2.53	0.42
38:a:1921:G:C2'	38:a:1922:G:H5'	2.49	0.42
38:a:1932:A:H2'	38:a:1933:G:O4'	2.19	0.42
38:a:2602:A:H5''	38:a:2603:G:C5'	2.49	0.42
38:a:2615:U:C2	46:i:4:GLN:HA	2.55	0.42
57:t:76:VAL:HG12	62:y:73:VAL:HB	2.00	0.42
63:z:65:ILE:CD1	63:z:92:ARG:HB2	2.49	0.42
10:A:65:C:C2'	10:A:66:C:H5'	2.49	0.42
11:AA:257:ALA:HB2	11:AA:285:ILE:HG22	2.02	0.42
11:AA:452:ARG:NH1	11:AA:458:GLU:OE2	2.52	0.42
11:AA:1252:SER:N	11:AA:1259:LEU:HD13	2.35	0.42
12:AC:29:GLU:HA	12:AC:30:PRO:HA	1.84	0.42
13:AE:58:CYS:SG	13:AE:60:ARG:HG2	2.59	0.42
13:AE:609:TYR:HD2	13:AE:610:ARG:NH1	2.17	0.42
15:D:37:U:C4	15:D:397:A:N6	2.86	0.42
35:X:96:PRO:HG2	35:X:102:THR:HG23	1.97	0.42
36:Y:41:PHE:HA	36:Y:68:PHE:CE2	2.54	0.42
11:AA:998:LEU:C	11:AA:998:LEU:CD1	2.85	0.42
13:AE:26:SER:HB2	13:AE:236:TRP:CH2	2.51	0.42
13:AE:1272:SER:OG	13:AE:1273:ASP:N	2.53	0.42
15:D:1235:U:H2'	15:D:1236:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:P:57:VAL:O	27:P:58:ASN:ND2	2.53	0.42
32:U:6:LEU:HG	32:U:17:TYR:HB3	2.00	0.42
38:a:1082:U:N3	38:a:1086:A:C6	2.87	0.42
38:a:1250:G:OP2	58:u:21:ARG:NH2	2.53	0.42
38:a:1394:U:C4	38:a:1395:A:C6	3.07	0.42
38:a:2273:A:H2'	38:a:2274:A:C8	2.55	0.42
11:AA:400:VAL:HG21	11:AA:452:ARG:HE	1.84	0.41
11:AA:587:LEU:HD23	11:AA:587:LEU:HA	1.89	0.41
11:AA:1029:LEU:HD21	11:AA:1033:ARG:CZ	2.51	0.41
11:AA:1046:VAL:HG22	11:AA:1049:ILE:CG1	2.50	0.41
13:AE:385:LEU:CD2	13:AE:390:LEU:HB2	2.50	0.41
13:AE:515:ARG:HG2	13:AE:516:ASP:H	1.85	0.41
13:AE:1106:ILE:O	13:AE:1123:ARG:N	2.45	0.41
13:AE:1350:ASN:HA	13:AE:1353:VAL:HG12	2.02	0.41
10:B:26:G:C2	10:B:45:G:N2	2.88	0.41
15:D:537:G:OP1	29:R:110:ARG:NH2	2.48	0.41
15:D:563:A:C2	15:D:884:U:O4	2.62	0.41
18:G:208:ARG:NH1	19:H:29:VAL:HG11	2.34	0.41
19:H:152:LEU:CB	19:H:171:ARG:H	2.32	0.41
19:H:342:ILE:HG22	19:H:344:LEU:HD12	2.01	0.41
21:J:61:VAL:CG2	21:J:200:ILE:HD11	2.39	0.41
22:K:133:PRO:HA	22:K:136:VAL:HG12	2.02	0.41
38:a:2189:U:O2'	38:a:2190:G:O4'	2.36	0.41
38:a:2788:C:H2'	38:a:2789:C:C6	2.55	0.41
2:1:92:ARG:NE	2:1:94:ASP:OD1	2.53	0.41
8:7:8:A:O5'	8:7:8:A:C8	2.70	0.41
9:9:8:LYS:HZ1	38:a:1046:A:H61	1.68	0.41
9:9:25:ALA:HA	9:9:96:PHE:HE1	1.85	0.41
9:9:61:ARG:C	9:9:65:GLU:HB2	2.45	0.41
9:9:71:CYS:SG	9:9:117:LEU:HB2	2.60	0.41
11:AA:976:ARG:HA	11:AA:979:LEU:HB2	2.02	0.41
11:AA:1009:ASN:ND2	11:AA:1012:GLU:HB3	2.35	0.41
13:AE:26:SER:CB	13:AE:236:TRP:CZ2	2.95	0.41
13:AE:144:TYR:N	13:AE:144:TYR:CD1	2.88	0.41
13:AE:950:ILE:HB	13:AE:1018:ALA:HB3	2.01	0.41
15:D:1227:A:C5'	35:X:110:LYS:HZ1	2.24	0.41
17:F:67:ARG:HD3	17:F:67:ARG:H	1.85	0.41
37:Z:23:ILE:HD12	37:Z:23:ILE:HA	1.77	0.41
37:Z:30:PHE:HD1	37:Z:30:PHE:HA	1.75	0.41
38:a:476:G:H4'	38:a:502:A:N1	2.35	0.41
38:a:984:A:N3	38:a:984:A:H2'	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:l:149:ILE:HD11	49:l:188:MET:HE3	2.02	0.41
51:n:171:ALA:O	51:n:174:ASP:N	2.53	0.41
8:7:13:G:H8	8:7:13:G:C5'	2.33	0.41
9:9:80:THR:O	38:a:1108:U:OP1	2.38	0.41
10:A:26:G:H1	10:A:44:A:N6	2.18	0.41
10:A:58:A:OP2	10:A:58:A:H8	2.02	0.41
11:AA:69:GLN:HE21	11:AA:101:ARG:HD2	1.85	0.41
11:AA:302:ILE:O	11:AA:330:HIS:NE2	2.34	0.41
13:AE:616:PRO:HA	13:AE:619:ILE:HG22	2.02	0.41
13:AE:797:THR:HG22	13:AE:924:GLY:HA3	2.01	0.41
13:AE:930:LEU:HA	13:AE:1244:GLN:HG3	2.02	0.41
15:D:543:U:OP1	21:J:14:ARG:NE	2.47	0.41
38:a:214:G:N2	38:a:216:A:N3	2.66	0.41
46:i:43:ILE:HG22	46:i:49:TYR:HB2	2.01	0.41
53:p:52:PHE:CZ	53:p:72:LEU:HD22	2.56	0.41
6:5:98:DA:H2'	6:5:99:DT:H72	2.02	0.41
9:9:9:GLN:CD	9:9:9:GLN:C	2.85	0.41
9:9:18:VAL:HA	9:9:86:MET:CE	2.44	0.41
9:9:48:ALA:HB3	9:9:51:TYR:HD2	1.86	0.41
11:AA:26:TYR:HE2	11:AA:32:LEU:HD12	1.86	0.41
11:AA:318:SER:OG	11:AA:320:ASP:OD1	2.31	0.41
11:AA:1253:LEU:HD23	11:AA:1253:LEU:HA	1.90	0.41
13:AE:47:ARG:NE	13:AE:47:ARG:CA	2.83	0.41
13:AE:68:TYR:O	13:AE:75:TYR:CD2	2.70	0.41
13:AE:279:LEU:HD13	13:AE:299:LEU:HD13	2.02	0.41
13:AE:820:ILE:HG12	13:AE:884:SER:HB2	2.02	0.41
13:AE:1050:THR:HG23	13:AE:1057:SER:HB3	2.03	0.41
15:D:860:A:H2'	15:D:861:G:O4'	2.21	0.41
15:D:1061:G:H5'	27:P:61:ALA:HB2	2.02	0.41
38:a:36:G:N3	38:a:450:G:O2'	2.53	0.41
38:a:244:A:OP2	52:o:8:ARG:NH2	2.50	0.41
38:a:2683:C:O2	57:t:70:ARG:NH2	2.52	0.41
49:l:134:LEU:HB2	49:l:160:ALA:HB1	2.02	0.41
50:m:12:ARG:CG	50:m:44:VAL:HG11	2.50	0.41
8:7:13:G:H8	8:7:13:G:H5''	1.85	0.41
8:7:20:G:H21	13:AE:427:PRO:HD3	1.86	0.41
9:9:23:LEU:HA	9:9:118:ILE:CG1	2.51	0.41
11:AA:867:GLU:HB3	20:I:75:ILE:CG1	2.49	0.41
11:AA:1102:GLY:HA2	11:AA:1106:ARG:HH11	1.85	0.41
13:AE:576:ARG:HD3	13:AE:593:ASN:HA	2.03	0.41
13:AE:647:PRO:HG3	13:AE:697:MET:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:G:187:VAL:HG21	18:G:199:VAL:HG23	2.02	0.41
35:X:4:ILE:CG1	35:X:9:ILE:HD12	2.50	0.41
36:Y:78:LEU:CD1	36:Y:108:ILE:HG22	2.50	0.41
36:Y:102:ARG:HD2	36:Y:103:ALA:N	2.35	0.41
38:a:17:G:H2'	38:a:18:U:C6	2.56	0.41
38:a:207:A:H2'	38:a:208:C:O4'	2.21	0.41
38:a:1169:A:H5''	38:a:1169:A:N3	2.36	0.41
38:a:2311:A:C2	51:n:85:ILE:HD11	2.55	0.41
2:1:75:PHE:CZ	2:1:104:THR:HG21	2.56	0.41
3:2:46:ALA:O	3:2:50:LEU:HB2	2.21	0.41
7:6:27:DG:H1'	7:6:28:DA:C5	2.55	0.41
11:AA:867:GLU:CB	20:I:75:ILE:HG13	2.49	0.41
11:AA:914:LYS:C	11:AA:914:LYS:HE3	2.45	0.41
11:AA:960:LEU:HD21	11:AA:1028:LYS:HB3	2.02	0.41
12:AC:116:THR:O	12:AC:116:THR:OG1	2.35	0.41
13:AE:68:TYR:HB3	13:AE:75:TYR:HE2	1.81	0.41
15:D:1225:A:H2'	15:D:1226:C:C5	2.56	0.41
18:G:19:GLN:HG2	19:H:75:VAL:HG22	1.91	0.41
24:M:22:LEU:HD13	24:M:97:ASN:ND2	2.35	0.41
31:T:43:PHE:CE2	31:T:56:LEU:HD22	2.56	0.41
36:Y:20:SER:CB	36:Y:21:PRO:HD3	2.39	0.41
38:a:126:A:OP1	50:m:45:SER:OG	2.38	0.41
38:a:320:A:H2'	49:l:131:THR:HG21	2.01	0.41
38:a:910:A:N3	38:a:2264:C:O2'	2.49	0.41
38:a:1406:U:O2'	38:a:1407:G:OP2	2.39	0.41
45:h:76:ALA:HB2	45:h:96:TYR:CE1	2.55	0.41
58:u:109:LYS:HG2	58:u:126:ARG:HB2	2.02	0.41
8:7:0:U:O2	8:7:0:U:H3'	2.21	0.41
10:A:22:G:HO2'	10:A:23:C:P	2.44	0.41
11:AA:888:THR:HG22	11:AA:914:LYS:HD2	2.02	0.41
11:AA:933:VAL:O	11:AA:933:VAL:CG1	2.68	0.41
11:AA:963:GLU:CA	11:AA:966:ILE:HD12	2.49	0.41
11:AA:1251:TYR:CE2	11:AA:1301:ARG:NH1	2.88	0.41
19:H:155:LYS:O	19:H:169:SER:CB	2.69	0.41
22:K:136:VAL:O	22:K:140:THR:HG23	2.20	0.41
29:R:110:ARG:NH1	29:R:112:GLN:O	2.53	0.41
38:a:1047:G:N2	38:a:1110:G:O2'	2.50	0.41
38:a:1421:G:C2	38:a:1422:G:C8	3.09	0.41
38:a:1548:A:H2'	38:a:1549:A:C8	2.55	0.41
38:a:2298:A:C5	38:a:2321:U:C4	3.09	0.41
55:r:9:VAL:HG11	55:r:12:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:w:67:PHE:O	60:w:71:ARG:HG2	2.21	0.41
7:6:21:DA:H5''	11:AA:141:THR:HG21	2.03	0.41
8:7:-2:U:O2	8:7:-2:U:H3'	2.20	0.41
9:9:8:LYS:NZ	38:a:1046:A:N6	2.69	0.41
11:AA:56:VAL:HG11	11:AA:468:LEU:HD13	2.02	0.41
13:AE:390:LEU:N	13:AE:390:LEU:HD13	2.35	0.41
10:B:15:G:H1	10:B:20:U:H3	1.68	0.41
15:D:218:U:H2'	15:D:219:U:O4'	2.21	0.41
15:D:429:U:O2	15:D:430:A:N7	2.53	0.41
15:D:548:G:C6	15:D:549:C:C4	3.08	0.41
15:D:791:G:N2	15:D:1497:G:O3'	2.53	0.41
38:a:197:A:N6	38:a:2430:A:H2'	2.36	0.41
9:9:7:ASP:OD1	9:9:7:ASP:N	2.36	0.41
9:9:73:LYS:CB	9:9:117:LEU:HD11	2.51	0.41
10:A:8:U:H6	10:A:8:U:OP2	2.04	0.41
10:A:56:C:OP1	38:a:2168:G:N3	2.53	0.41
11:AA:218:GLU:HG2	11:AA:299:LYS:HA	2.02	0.41
11:AA:593:LYS:HB3	11:AA:602:GLU:HG3	2.02	0.41
11:AA:731:ARG:HG3	11:AA:731:ARG:HH11	1.86	0.41
11:AA:936:ARG:HG3	11:AA:936:ARG:HH21	1.86	0.41
11:AA:1072:ASN:OD1	11:AA:1072:ASN:N	2.47	0.41
11:AA:1286:THR:O	11:AA:1290:MET:HB2	2.21	0.41
12:AC:120:ASP:OD1	27:P:90:LEU:HD21	2.20	0.41
12:AD:111:THR:OG1	12:AD:112:ALA:N	2.54	0.41
13:AE:68:TYR:CB	13:AE:75:TYR:HE2	2.34	0.41
13:AE:605:LEU:HD23	13:AE:605:LEU:HA	1.93	0.41
10:B:7:G:O6	10:B:49:G:O6	2.39	0.41
10:B:8:U:H6	10:B:8:U:OP2	2.04	0.41
10:B:26:G:H1	10:B:44:A:N6	2.18	0.41
15:D:579:A:O2'	31:T:54:ARG:NH1	2.54	0.41
15:D:915:A:C6	15:D:916:U:C4	3.08	0.41
15:D:1330:U:OP2	35:X:26:GLY:HA3	2.21	0.41
18:G:35:ARG:CG	19:H:10:GLU:OE2	2.63	0.41
19:H:332:VAL:HG12	19:H:334:ASP:N	2.33	0.41
21:J:100:ASN:OD1	21:J:111:ARG:NH1	2.54	0.41
22:K:150:PRO:HA	22:K:153:VAL:HG22	2.03	0.41
35:X:16:VAL:HG13	35:X:34:LEU:CD1	2.51	0.41
36:Y:124:MET:HE2	36:Y:124:MET:HB2	1.77	0.41
38:a:851:C:H2'	38:a:852:U:C6	2.55	0.41
38:a:1082:U:C4	38:a:1086:A:N6	2.88	0.41
38:a:1182:G:H2'	38:a:1183:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1570:A:H2'	38:a:1571:A:C8	2.55	0.41
38:a:2627:G:O2'	38:a:2781:A:N1	2.37	0.41
45:h:29:PRO:HG2	45:h:34:LEU:HD11	2.03	0.41
45:h:119:GLY:O	45:h:130:LEU:HB3	2.20	0.41
45:h:232:HIS:HA	45:h:242:LYS:HE3	2.03	0.41
51:n:122:PHE:CZ	51:n:167:ARG:HA	2.56	0.41
55:r:57:LYS:O	55:r:61:VAL:HG13	2.21	0.41
60:w:29:VAL:HG11	60:w:75:ILE:HG23	2.03	0.41
63:z:18:LEU:HD13	63:z:18:LEU:HA	1.95	0.41
8:7:-9:G:C5'	15:D:1501:C:N4	2.83	0.41
10:A:46:G:H2'	10:A:47:U:OP2	2.21	0.41
11:AA:1105:SER:OG	13:AE:731:ARG:NH2	2.54	0.41
12:AD:97:GLU:HG3	12:AD:147:GLN:HG2	2.03	0.41
13:AE:109:SER:CB	13:AE:296:LYS:HG2	2.51	0.41
10:B:65:C:C2'	10:B:66:C:H5'	2.49	0.41
15:D:1526:G:P	17:F:42:THR:HG23	2.61	0.41
22:K:154:ALA:HA	22:K:164:ILE:HD11	2.03	0.41
36:Y:52:LEU:HD21	36:Y:81:LYS:HD3	2.03	0.41
38:a:67:U:C4	38:a:74:A:C6	3.04	0.41
38:a:1839:G:C4	38:a:1927:A:C5	3.08	0.41
38:a:2006:C:O2'	38:a:2823:A:N3	2.47	0.41
38:a:2294:G:OP1	61:x:10:ARG:HD3	2.21	0.41
38:a:2641:G:OP1	56:s:78:THR:HG22	2.21	0.41
61:x:53:THR:HG23	61:x:74:VAL:HG21	2.03	0.41
63:z:66:ASN:OD1	63:z:70:ARG:NE	2.54	0.41
10:A:26:G:C2	10:A:45:G:N2	2.89	0.40
10:A:34:C:H41	24:M:83:SER:HA	1.86	0.40
11:AA:801:ARG:HH12	11:AA:1119:MET:HE1	1.86	0.40
11:AA:867:GLU:N	20:I:75:ILE:HG13	2.36	0.40
11:AA:884:VAL:CG1	11:AA:1050:VAL:HG11	2.51	0.40
11:AA:1020:GLU:HA	11:AA:1023:HIS:CD2	2.56	0.40
36:Y:35:MET:O	36:Y:35:MET:SD	2.79	0.40
38:a:5:A:H2'	38:a:6:A:C8	2.56	0.40
38:a:753:A:C5	38:a:754:U:C5	3.09	0.40
38:a:1406:U:C2'	38:a:1407:G:OP2	2.69	0.40
38:a:2572:A:N7	47:j:150:GLN:NE2	2.69	0.40
40:c:33:LEU:O	40:c:34:HIS:CG	2.74	0.40
49:l:188:MET:HE2	49:l:193:VAL:HA	2.03	0.40
59:v:73:ILE:HG21	59:v:91:TYR:CZ	2.55	0.40
9:9:42:ARG:H	9:9:42:ARG:HG3	1.62	0.40
11:AA:6:THR:HA	11:AA:9:LYS:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:590:PRO:HB2	11:AA:655:VAL:HG21	2.04	0.40
12:AC:46:ILE:HD11	12:AC:224:LEU:HD13	2.03	0.40
12:AC:158:ARG:HH12	12:AC:172:LEU:HD23	1.86	0.40
12:AD:152:TYR:HE2	13:AE:535:ARG:HH21	1.68	0.40
14:C:12:ARG:NH2	19:H:268:VAL:CG2	2.71	0.40
15:D:197:A:C5	15:D:221:C:H4'	2.53	0.40
15:D:1370:G:C2	15:D:1371:G:C8	3.09	0.40
26:O:10:GLY:HA3	26:O:78:ALA:O	2.21	0.40
35:X:16:VAL:O	35:X:20:THR:HG23	2.21	0.40
36:Y:116:MET:HA	36:Y:116:MET:CE	2.50	0.40
38:a:2315:G:C5'	51:n:157:THR:HG23	2.52	0.40
56:s:104:ALA:O	56:s:108:MET:HG3	2.21	0.40
10:A:15:G:N2	10:A:20:U:H3	2.20	0.40
11:AA:732:ILE:HD12	11:AA:783:LEU:HB3	2.03	0.40
11:AA:859:GLU:CG	20:I:109:PRO:HG2	2.52	0.40
11:AA:867:GLU:N	20:I:75:ILE:CG1	2.85	0.40
12:AD:81:ILE:O	12:AD:85:LEU:HB2	2.22	0.40
12:AD:154:PRO:HG2	12:AD:157:THR:HG22	2.04	0.40
13:AE:111:THR:HG23	13:AE:300:GLN:HA	2.03	0.40
13:AE:113:HIS:ND1	13:AE:115:TRP:HB2	2.37	0.40
15:D:977:A:H1'	15:D:982:U:O4	2.20	0.40
15:D:1368:A:OP1	26:O:113:ARG:NH2	2.54	0.40
18:G:28:LYS:N	18:G:29:PRO:CD	2.85	0.40
19:H:110:GLY:N	19:H:153:GLU:HA	2.37	0.40
20:I:112:ASP:HB3	20:I:115:LEU:HD12	2.03	0.40
24:M:27:VAL:HG12	24:M:43:VAL:HG21	2.04	0.40
30:S:16:LEU:HD13	30:S:54:ASP:HB2	2.03	0.40
36:Y:71:LYS:HB3	36:Y:72:THR:H	1.58	0.40
36:Y:122:GLU:O	36:Y:122:GLU:HG2	2.21	0.40
38:a:493:G:H2'	38:a:494:G:O4'	2.20	0.40
39:b:59:LEU:HD12	39:b:80:ILE:HD12	2.03	0.40
58:u:74:THR:HG22	58:u:107:PHE:HB2	2.04	0.40
9:9:118:ILE:H	9:9:119:PRO:HD2	1.85	0.40
10:A:71:C:H2'	10:A:72:A:C1'	2.52	0.40
13:AE:50:LYS:HD3	13:AE:50:LYS:HA	1.72	0.40
15:D:798:U:H2'	15:D:799:G:O4'	2.22	0.40
36:Y:21:PRO:HD2	36:Y:22:PRO:HD2	2.03	0.40
38:a:548:G:H3'	38:a:549:G:O4'	2.20	0.40
38:a:1736:U:H2'	38:a:1737:G:O4'	2.21	0.40
38:a:2602:A:H5''	38:a:2603:G:H5''	2.03	0.40
47:j:175:LEU:CD1	47:j:193:VAL:HG12	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:p:25:THR:HG22	53:p:34:THR:HG23	2.02	0.40
63:z:83:LEU:HD23	63:z:83:LEU:HA	1.93	0.40
9:9:72:LEU:C	9:9:72:LEU:CD2	2.94	0.40
10:A:15:G:N2	10:A:20:U:C2	2.89	0.40
11:AA:868:SER:OG	11:AA:941:LYS:HB2	2.21	0.40
13:AE:244:VAL:HA	13:AE:269:TYR:CZ	2.57	0.40
13:AE:1350:ASN:ND2	13:AE:1355:ARG:HD2	2.37	0.40
15:D:152:A:N6	15:D:170:U:C2	2.89	0.40
26:O:21:ILE:HD13	26:O:63:LEU:HB3	2.04	0.40
38:a:2225:A:H4'	38:a:2226:C:O5'	2.22	0.40
38:a:2756:U:OP2	54:q:19:ARG:NE	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	46
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	46
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	8
11	AA	1318/1342 (98%)	1150 (87%)	136 (10%)	32 (2%)	4	30
12	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	49
12	AD	226/329 (69%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1407 (94%)	1200 (90%)	120 (9%)	9 (1%)	18	55
14	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
17	F	68/71 (96%)	68 (100%)	0	0	100	100
18	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
19	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	19
20	I	206/233 (88%)	197 (96%)	8 (4%)	1 (0%)	24	61
21	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
22	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	58
23	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	46
24	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	18	55
25	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	52
26	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	52
27	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	12	46
28	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	36
29	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100
30	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
31	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
32	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	41
33	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
34	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
35	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	6	35
36	Y	139/141 (99%)	102 (73%)	25 (18%)	12 (9%)	0	10
37	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	13
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
43	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
45	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	30	65
46	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
47	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
48	k	50/55 (91%)	50 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	61
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	11	44
52	o	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
53	p	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
54	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
55	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
56	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
57	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
58	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
59	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
60	w	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
61	x	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
62	y	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	49
All	All	9274/10209 (91%)	8519 (92%)	653 (7%)	102 (1%)	14	44

All (102) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU
11	AA	873	ILE
11	AA	937	ASP
11	AA	993	PRO
19	H	139	ARG
19	H	153	GLU
19	H	169	SER
19	H	306	VAL
19	H	340	ARG
26	O	56	ASP
35	X	103	LYS
36	Y	48	ILE
9	9	33	VAL

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Mol	Chain	Res	Type
9	9	119	PRO
11	AA	375	PRO
11	AA	856	ASN
11	AA	870	ILE
11	AA	940	GLU
11	AA	985	GLU
11	AA	1003	THR
11	AA	1158	LYS
13	AE	175	GLU
19	H	108	VAL
19	H	309	MET
19	H	333	LEU
36	Y	93	ASN
45	h	158	ALA
49	l	142	ALA
63	z	3	ARG
9	9	48	ALA
9	9	91	ALA
9	9	118	ILE
9	9	130	PRO
11	AA	376	PRO
11	AA	723	VAL
11	AA	728	ASP
11	AA	935	THR
11	AA	980	VAL
11	AA	1005	GLU
11	AA	1045	GLY
12	AC	164	ASP
12	AC	165	GLU
13	AE	51	PRO
13	AE	805	GLN
19	H	76	GLU
19	H	142	ARG
24	M	130	ASN
27	P	58	ASN
28	Q	119	ASN
36	Y	20	SER
36	Y	64	ARG
36	Y	106	GLN
9	9	69	PHE
9	9	73	LYS
9	9	108	VAL

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Mol	Chain	Res	Type
9	9	129	LEU
9	9	133	GLU
11	AA	850	ILE
11	AA	943	LYS
11	AA	995	ASP
13	AE	174	ASP
13	AE	193	ASP
19	H	82	THR
20	I	80	LYS
35	X	105	ASN
36	Y	83	ALA
37	Z	21	GLU
51	n	40	VAL
9	9	28	ALA
11	AA	917	SER
11	AA	991	LYS
11	AA	997	TRP
11	AA	1044	PRO
13	AE	91	GLU
19	H	70	VAL
36	Y	22	PRO
36	Y	71	LYS
36	Y	89	SER
37	Z	7	ILE
4	3	39	ILE
13	AE	49	PHE
13	AE	73	GLY
13	AE	904	ALA
36	Y	62	ALA
23	L	96	VAL
36	Y	23	VAL
36	Y	100	ILE
1	0	44	GLY
11	AA	697	LYS
11	AA	1159	VAL
11	AA	1317	PRO
22	K	44	GLY
28	Q	74	VAL
32	U	64	GLY
9	9	54	VAL
51	n	62	GLY
11	AA	933	VAL

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Mol	Chain	Res	Type
25	N	75	ILE

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	0	84/84 (100%)	76 (90%)	8 (10%)	8	27
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	35
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	46
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	42
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	51
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1140/1157 (98%)	1027 (90%)	113 (10%)	7	26
12	AC	198/286 (69%)	183 (92%)	15 (8%)	12	35
12	AD	196/286 (68%)	193 (98%)	3 (2%)	57	70
13	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15	39
14	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
16	E	65/66 (98%)	61 (94%)	4 (6%)	16	41
17	F	60/61 (98%)	57 (95%)	3 (5%)	22	45
18	G	187/199 (94%)	174 (93%)	13 (7%)	14	38
19	H	137/461 (30%)	124 (90%)	13 (10%)	8	27
20	I	171/190 (90%)	163 (95%)	8 (5%)	23	47
21	J	172/172 (100%)	164 (95%)	8 (5%)	23	47
22	K	119/126 (94%)	111 (93%)	8 (7%)	15	39
23	L	91/116 (78%)	84 (92%)	7 (8%)	12	34
24	M	124/124 (100%)	113 (91%)	11 (9%)	9	30
25	N	104/104 (100%)	101 (97%)	3 (3%)	37	58
26	O	105/105 (100%)	99 (94%)	6 (6%)	18	43
27	P	86/86 (100%)	76 (88%)	10 (12%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Q	90/90 (100%)	88 (98%)	2 (2%)	45	64
29	R	101/103 (98%)	95 (94%)	6 (6%)	18	42
30	S	83/84 (99%)	79 (95%)	4 (5%)	23	46
31	T	76/77 (99%)	65 (86%)	11 (14%)	3	16
32	U	65/65 (100%)	60 (92%)	5 (8%)	12	34
33	V	74/78 (95%)	71 (96%)	3 (4%)	27	50
34	W	72/72 (100%)	66 (92%)	6 (8%)	10	32
35	X	94/94 (100%)	87 (93%)	7 (7%)	13	35
36	Y	109/109 (100%)	69 (63%)	40 (37%)	0	1
37	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
39	b	58/58 (100%)	57 (98%)	1 (2%)	53	68
40	c	67/68 (98%)	64 (96%)	3 (4%)	24	48
42	e	54/54 (100%)	51 (94%)	3 (6%)	19	43
43	f	48/48 (100%)	43 (90%)	5 (10%)	7	24
44	g	59/59 (100%)	54 (92%)	5 (8%)	10	32
45	h	216/216 (100%)	199 (92%)	17 (8%)	11	34
46	i	47/47 (100%)	41 (87%)	6 (13%)	4	19
47	j	164/164 (100%)	156 (95%)	8 (5%)	22	46
48	k	47/49 (96%)	44 (94%)	3 (6%)	16	40
49	l	165/165 (100%)	151 (92%)	14 (8%)	10	32
50	m	38/38 (100%)	36 (95%)	2 (5%)	20	44
51	n	148/148 (100%)	130 (88%)	18 (12%)	5	20
52	o	51/51 (100%)	47 (92%)	4 (8%)	11	34
53	p	136/136 (100%)	130 (96%)	6 (4%)	25	48
54	q	34/34 (100%)	31 (91%)	3 (9%)	9	31
55	r	114/114 (100%)	102 (90%)	12 (10%)	6	24
56	s	116/116 (100%)	106 (91%)	10 (9%)	10	32
57	t	104/104 (100%)	97 (93%)	7 (7%)	15	39
58	u	103/103 (100%)	96 (93%)	7 (7%)	14	38
59	v	109/109 (100%)	105 (96%)	4 (4%)	30	52
60	w	99/99 (100%)	91 (92%)	8 (8%)	11	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	x	86/86 (100%)	80 (93%)	6 (7%)	14	38
62	y	99/99 (100%)	91 (92%)	8 (8%)	11	33
63	z	89/89 (100%)	85 (96%)	4 (4%)	24	48
All	All	7705/8430 (91%)	7064 (92%)	641 (8%)	12	32

All (641) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	10	LYS
1	0	38	VAL
1	0	47	VAL
1	0	48	LYS
1	0	51	VAL
1	0	68	ARG
1	0	86	GLN
1	0	96	VAL
2	1	19	LEU
2	1	30	SER
2	1	41	LYS
2	1	69	LEU
2	1	97	LEU
2	1	107	VAL
2	1	110	ARG
3	2	1	MET
3	2	24	MET
3	2	37	ASP
3	2	93	LEU
4	3	52	LEU
4	3	70	VAL
4	3	72	ILE
4	3	99	ASN
4	3	101	GLU
5	4	40	ILE
5	4	69	GLU
5	4	71	LYS
9	9	1	MET
9	9	3	LEU
9	9	4	ASN
9	9	5	LEU
9	9	6	GLN
9	9	7	ASP

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Mol	Chain	Res	Type
9	9	11	ILE
9	9	14	GLU
9	9	23	LEU
9	9	24	SER
9	9	27	VAL
9	9	31	ARG
9	9	33	VAL
9	9	34	THR
9	9	35	VAL
9	9	36	ASP
9	9	37	LYS
9	9	39	THR
9	9	42	ARG
9	9	43	LYS
9	9	52	MET
9	9	54	VAL
9	9	55	VAL
9	9	56	ARG
9	9	57	ASN
9	9	61	ARG
9	9	69	PHE
9	9	70	GLU
9	9	71	CYS
9	9	72	LEU
9	9	73	LYS
9	9	81	LEU
9	9	86	MET
9	9	94	ARG
9	9	96	PHE
9	9	98	GLU
9	9	106	PHE
9	9	107	GLU
9	9	109	LYS
9	9	113	PHE
9	9	117	LEU
9	9	122	GLN
9	9	123	ILE
9	9	125	ARG
9	9	133	GLU
9	9	134	GLU
9	9	138	ARG
9	9	142	THR

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Mol	Chain	Res	Type
9	9	143	MET
11	AA	39	ILE
11	AA	145	ILE
11	AA	376	PRO
11	AA	615	VAL
11	AA	723	VAL
11	AA	727	VAL
11	AA	728	ASP
11	AA	731	ARG
11	AA	732	ILE
11	AA	752	ASN
11	AA	753	LEU
11	AA	802	VAL
11	AA	817	LEU
11	AA	840	SER
11	AA	844	LYS
11	AA	845	LEU
11	AA	851	THR
11	AA	854	ILE
11	AA	855	PRO
11	AA	857	VAL
11	AA	862	LEU
11	AA	864	LYS
11	AA	865	LEU
11	AA	866	ASP
11	AA	867	GLU
11	AA	868	SER
11	AA	871	VAL
11	AA	873	ILE
11	AA	876	GLU
11	AA	884	VAL
11	AA	886	LYS
11	AA	887	VAL
11	AA	890	LYS
11	AA	912	ASP
11	AA	913	VAL
11	AA	914	LYS
11	AA	918	LEU
11	AA	933	VAL
11	AA	936	ARG
11	AA	939	VAL
11	AA	941	LYS

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Mol	Chain	Res	Type
11	AA	943	LYS
11	AA	944	ARG
11	AA	946	LEU
11	AA	947	GLU
11	AA	949	GLU
11	AA	950	GLU
11	AA	951	MET
11	AA	952	GLN
11	AA	953	LEU
11	AA	954	LYS
11	AA	955	GLN
11	AA	957	LYS
11	AA	958	LYS
11	AA	959	ASP
11	AA	960	LEU
11	AA	962	GLU
11	AA	963	GLU
11	AA	964	LEU
11	AA	965	GLN
11	AA	967	LEU
11	AA	968	GLU
11	AA	971	LEU
11	AA	973	SER
11	AA	974	ARG
11	AA	979	LEU
11	AA	980	VAL
11	AA	985	GLU
11	AA	988	LYS
11	AA	989	LEU
11	AA	991	LYS
11	AA	992	LEU
11	AA	994	ARG
11	AA	995	ASP
11	AA	997	TRP
11	AA	998	LEU
11	AA	999	GLU
11	AA	1002	LEU
11	AA	1005	GLU
11	AA	1006	GLU
11	AA	1008	GLN
11	AA	1009	ASN
11	AA	1013	GLN

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Mol	Chain	Res	Type
11	AA	1014	LEU
11	AA	1019	ASP
11	AA	1020	GLU
11	AA	1023	HIS
11	AA	1024	GLU
11	AA	1025	PHE
11	AA	1026	GLU
11	AA	1027	LYS
11	AA	1029	LEU
11	AA	1032	LYS
11	AA	1034	ARG
11	AA	1035	LYS
11	AA	1037	THR
11	AA	1038	GLN
11	AA	1041	ASP
11	AA	1042	LEU
11	AA	1046	VAL
11	AA	1047	LEU
11	AA	1048	LYS
11	AA	1076	ILE
11	AA	1151	LEU
11	AA	1159	VAL
11	AA	1248	THR
11	AA	1250	SER
11	AA	1252	SER
11	AA	1253	LEU
11	AA	1254	VAL
11	AA	1256	GLN
11	AA	1259	LEU
11	AA	1298	VAL
12	AC	62	ASP
12	AC	65	LEU
12	AC	72	GLU
12	AC	91	ARG
12	AC	134	THR
12	AC	158	ARG
12	AC	159	ILE
12	AC	160	HIS
12	AC	162	GLU
12	AC	163	GLU
12	AC	165	GLU
12	AC	166	ARG

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Mol	Chain	Res	Type
12	AC	168	ILE
12	AC	170	ARG
12	AC	171	LEU
12	AD	110	VAL
12	AD	187	VAL
12	AD	208	ASN
13	AE	40	LYS
13	AE	42	GLU
13	AE	44	ILE
13	AE	46	TYR
13	AE	47	ARG
13	AE	49	PHE
13	AE	50	LYS
13	AE	52	GLU
13	AE	53	ARG
13	AE	54	ASP
13	AE	56	LEU
13	AE	60	ARG
13	AE	66	LYS
13	AE	67	ASP
13	AE	70	CYS
13	AE	74	LYS
13	AE	76	LYS
13	AE	78	LEU
13	AE	80	HIS
13	AE	81	ARG
13	AE	87	LYS
13	AE	88	CYS
13	AE	91	GLU
13	AE	94	GLN
13	AE	95	THR
13	AE	96	LYS
13	AE	99	ARG
13	AE	100	GLU
13	AE	114	ILE
13	AE	117	LEU
13	AE	119	SER
13	AE	123	ARG
13	AE	132	LEU
13	AE	135	ILE
13	AE	142	GLU
13	AE	144	TYR

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Mol	Chain	Res	Type
13	AE	145	VAL
13	AE	146	VAL
13	AE	147	ILE
13	AE	152	THR
13	AE	154	LEU
13	AE	157	GLN
13	AE	159	ILE
13	AE	175	GLU
13	AE	180	MET
13	AE	190	LYS
13	AE	193	ASP
13	AE	196	GLN
13	AE	210	SER
13	AE	212	THR
13	AE	216	LYS
13	AE	222	LYS
13	AE	223	LEU
13	AE	227	PHE
13	AE	233	LYS
13	AE	237	MET
13	AE	238	ILE
13	AE	239	LEU
13	AE	240	THR
13	AE	244	VAL
13	AE	271	ARG
13	AE	324	LEU
13	AE	385	LEU
13	AE	386	GLU
13	AE	387	LEU
13	AE	390	LEU
13	AE	393	THR
13	AE	394	ILE
13	AE	395	LYS
13	AE	506	VAL
13	AE	514	THR
13	AE	839	VAL
13	AE	1172	LYS
13	AE	1233	ILE
14	C	33	ILE
14	C	74	HIS
16	E	6	SER
16	E	10	ARG

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Mol	Chain	Res	Type
16	E	48	GLN
16	E	64	LYS
17	F	34	ARG
17	F	62	ARG
17	F	67	ARG
18	G	8	ASP
18	G	45	LYS
18	G	59	LYS
18	G	105	LYS
18	G	108	ARG
18	G	117	LEU
18	G	128	LYS
18	G	129	LEU
18	G	132	LYS
18	G	135	LEU
18	G	161	LEU
18	G	174	LYS
18	G	208	ARG
19	H	9	PHE
19	H	31	ILE
19	H	43	LYS
19	H	54	LYS
19	H	62	ILE
19	H	70	VAL
19	H	294	VAL
19	H	305	HIS
19	H	336	ASP
19	H	337	GLU
19	H	338	GLU
19	H	339	ARG
19	H	340	ARG
20	I	14	ILE
20	I	21	THR
20	I	33	LEU
20	I	75	ILE
20	I	89	LYS
20	I	175	LEU
20	I	178	LEU
20	I	200	VAL
21	J	47	ARG
21	J	48	LEU
21	J	95	GLU

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Mol	Chain	Res	Type
21	J	104	ARG
21	J	105	MET
21	J	116	GLN
21	J	138	SER
21	J	143	VAL
22	K	10	GLU
22	K	15	LEU
22	K	60	ILE
22	K	114	VAL
22	K	115	LEU
22	K	138	ARG
22	K	141	ILE
22	K	162	GLU
23	L	7	VAL
23	L	16	GLU
23	L	24	ARG
23	L	36	ILE
23	L	38	ARG
23	L	54	LEU
23	L	86	ARG
24	M	7	ILE
24	M	17	LYS
24	M	21	GLU
24	M	23	LEU
24	M	27	VAL
24	M	50	LEU
24	M	79	ARG
24	M	91	VAL
24	M	109	ARG
24	M	130	ASN
24	M	146	GLU
25	N	96	MET
25	N	104	VAL
25	N	117	ARG
26	O	27	LYS
26	O	60	LYS
26	O	61	LEU
26	O	63	LEU
26	O	116	VAL
26	O	118	LEU
27	P	17	LEU
27	P	18	ILE

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Mol	Chain	Res	Type
27	P	24	GLU
27	P	25	ILE
27	P	27	GLU
27	P	37	ARG
27	P	87	LEU
27	P	89	ARG
27	P	90	LEU
27	P	102	LEU
28	Q	15	GLN
28	Q	107	ILE
29	R	5	ASN
29	R	12	ARG
29	R	24	LEU
29	R	62	GLU
29	R	74	LEU
29	R	102	LEU
30	S	45	VAL
30	S	46	LEU
30	S	89	MET
30	S	92	GLU
31	T	10	LYS
31	T	22	THR
31	T	39	LEU
31	T	40	GLN
31	T	64	ARG
31	T	66	LEU
31	T	67	LEU
31	T	70	LEU
31	T	73	LYS
31	T	84	ARG
31	T	85	LEU
32	U	1	MET
32	U	2	VAL
32	U	6	LEU
32	U	19	VAL
32	U	50	THR
33	V	46	VAL
33	V	75	LEU
33	V	81	LYS
34	W	21	LYS
34	W	33	THR
34	W	49	ILE

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Mol	Chain	Res	Type
34	W	58	VAL
34	W	79	THR
34	W	81	ARG
35	X	16	VAL
35	X	25	VAL
35	X	29	ARG
35	X	59	GLU
35	X	93	ARG
35	X	101	ARG
35	X	117	LYS
36	Y	4	VAL
36	Y	10	LEU
36	Y	16	MET
36	Y	23	VAL
36	Y	27	LEU
36	Y	30	GLN
36	Y	36	GLU
36	Y	44	LYS
36	Y	45	THR
36	Y	48	ILE
36	Y	50	LYS
36	Y	52	LEU
36	Y	57	VAL
36	Y	58	ILE
36	Y	60	VAL
36	Y	61	TYR
36	Y	64	ARG
36	Y	65	SER
36	Y	67	THR
36	Y	71	LYS
36	Y	78	LEU
36	Y	80	LYS
36	Y	81	LYS
36	Y	91	LYS
36	Y	94	LYS
36	Y	95	ASP
36	Y	99	LYS
36	Y	100	ILE
36	Y	102	ARG
36	Y	104	GLN
36	Y	108	ILE
36	Y	112	LYS

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Mol	Chain	Res	Type
36	Y	116	MET
36	Y	124	MET
36	Y	125	THR
36	Y	126	ARG
36	Y	133	ARG
36	Y	135	MET
36	Y	137	LEU
36	Y	138	VAL
37	Z	1	SER
37	Z	2	ILE
37	Z	3	THR
37	Z	4	LYS
37	Z	6	GLN
37	Z	7	ILE
37	Z	8	ILE
37	Z	14	MET
37	Z	16	VAL
37	Z	17	MET
37	Z	19	VAL
37	Z	23	ILE
37	Z	26	MET
37	Z	28	GLU
37	Z	29	LYS
37	Z	30	PHE
39	b	70	GLU
40	c	33	LEU
40	c	48	THR
40	c	71	LEU
42	e	18	LEU
42	e	58	ASN
42	e	60	LYS
43	f	3	LYS
43	f	11	ARG
43	f	25	LEU
43	f	45	ARG
43	f	55	VAL
44	g	3	LYS
44	g	16	CYS
44	g	24	ILE
44	g	36	VAL
44	g	47	LYS
45	h	51	THR

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Mol	Chain	Res	Type
45	h	94	VAL
45	h	105	LEU
45	h	118	SER
45	h	125	LYS
45	h	130	LEU
45	h	141	VAL
45	h	156	ARG
45	h	183	LYS
45	h	187	ASP
45	h	195	VAL
45	h	202	LEU
45	h	203	ARG
45	h	204	VAL
45	h	205	LEU
45	h	242	LYS
45	h	271	ARG
46	i	9	THR
46	i	12	LYS
46	i	26	THR
46	i	27	SER
46	i	29	SER
46	i	40	ARG
47	j	13	ARG
47	j	18	ASP
47	j	91	THR
47	j	99	GLU
47	j	104	VAL
47	j	177	VAL
47	j	189	VAL
47	j	193	VAL
48	k	5	ILE
48	k	17	THR
48	k	24	THR
49	l	17	THR
49	l	22	ASP
49	l	40	ARG
49	l	48	THR
49	l	57	LYS
49	l	69	ARG
49	l	77	ILE
49	l	80	SER
49	l	108	ILE

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Mol	Chain	Res	Type
49	l	109	LEU
49	l	111	GLU
49	l	122	GLU
49	l	149	ILE
49	l	179	SER
50	m	22	MET
50	m	42	LEU
51	n	6	ASP
51	n	10	ASP
51	n	26	MET
51	n	40	VAL
51	n	47	LYS
51	n	49	LEU
51	n	57	LEU
51	n	79	ILE
51	n	80	ARG
51	n	95	ARG
51	n	105	THR
51	n	117	LEU
51	n	122	PHE
51	n	123	ASP
51	n	132	VAL
51	n	140	GLU
51	n	141	ILE
51	n	163	ASP
52	o	8	ARG
52	o	30	ARG
52	o	31	HIS
52	o	55	LEU
53	p	11	VAL
53	p	85	LYS
53	p	95	ARG
53	p	125	CYS
53	p	168	VAL
53	p	171	THR
54	q	3	VAL
54	q	26	ILE
54	q	34	LYS
55	r	1	MET
55	r	9	VAL
55	r	11	ASN
55	r	12	LEU

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Mol	Chain	Res	Type
55	r	15	LEU
55	r	41	LYS
55	r	66	ASN
55	r	72	ILE
55	r	76	GLU
55	r	94	ILE
55	r	101	ASP
55	r	127	GLU
56	s	1	MET
56	s	30	THR
56	s	31	GLU
56	s	43	GLU
56	s	57	LEU
56	s	123	LYS
56	s	124	VAL
56	s	139	VAL
56	s	140	LEU
56	s	142	ILE
57	t	7	MET
57	t	35	VAL
57	t	49	ARG
57	t	67	LYS
57	t	70	ARG
57	t	80	ASP
57	t	104	THR
58	u	5	THR
58	u	27	LEU
58	u	59	ARG
58	u	73	ILE
58	u	76	GLU
58	u	78	ARG
58	u	84	LYS
59	v	110	GLU
59	v	126	ILE
59	v	127	LYS
59	v	128	THR
60	w	2	ARG
60	w	20	MET
60	w	24	MET
60	w	51	LEU
60	w	65	LEU
60	w	69	ARG

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Mol	Chain	Res	Type
60	w	95	THR
60	w	116	VAL
61	x	13	ARG
61	x	31	THR
61	x	47	VAL
61	x	48	LEU
61	x	91	SER
61	x	116	GLN
62	y	8	LEU
62	y	10	GLN
62	y	27	GLU
62	y	40	LEU
62	y	81	VAL
62	y	85	SER
62	y	102	GLU
62	y	114	LEU
63	z	18	LEU
63	z	51	ARG
63	z	109	LEU
63	z	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	86	GLN
2	1	61	ASN
3	2	28	ASN
3	2	59	ASN
4	3	54	GLN
5	4	12	GLN
9	9	103	ASN
9	9	122	GLN
11	AA	69	GLN
11	AA	273	HIS
11	AA	761	GLN
11	AA	808	ASN
11	AA	965	GLN
11	AA	1157	GLN
11	AA	1236	ASN
12	AC	41	ASN
12	AC	132	HIS
12	AD	41	ASN

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Mol	Chain	Res	Type
12	AD	93	GLN
12	AD	103	ASN
13	AE	94	GLN
13	AE	196	GLN
13	AE	469	HIS
13	AE	817	HIS
13	AE	865	HIS
13	AE	1238	GLN
13	AE	1249	ASN
16	E	3	ASN
16	E	55	GLN
16	E	61	GLN
18	G	18	HIS
18	G	58	ASN
18	G	94	HIS
20	I	6	HIS
20	I	123	GLN
21	J	36	GLN
21	J	40	GLN
21	J	41	HIS
22	K	97	GLN
23	L	11	HIS
23	L	63	ASN
23	L	94	HIS
24	M	148	ASN
26	O	81	HIS
27	P	58	ASN
29	R	72	HIS
31	T	40	GLN
32	U	59	HIS
35	X	12	HIS
35	X	105	ASN
45	h	70	ASN
46	i	5	GLN
48	k	26	ASN
51	n	63	GLN
52	o	28	ASN
53	p	88	GLN
55	r	18	GLN
55	r	20	ASN
55	r	133	GLN
57	t	88	ASN

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Mol	Chain	Res	Type
62	y	15	GLN
62	y	66	ASN
63	z	44	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
15	D	1515/1542 (98%)	289 (19%)	35 (2%)
38	a	2859/2904 (98%)	541 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	31/32 (96%)	21 (67%)	3 (9%)
All	All	4674/4750 (98%)	932 (19%)	50 (1%)

All (932) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-9	G
8	7	-8	U
8	7	-7	U
8	7	-5	U
8	7	-4	U
8	7	-3	U
8	7	-2	U
8	7	-1	U
8	7	0	U
8	7	1	U
8	7	2	U
8	7	3	U
8	7	4	U
8	7	5	U
8	7	6	U
8	7	7	G
8	7	8	A
8	7	9	U
8	7	10	U
8	7	12	G
8	7	13	G
10	A	2	G
10	A	6	G

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Mol	Chain	Res	Type
10	A	7	G
10	A	8	U
10	A	10	G
10	A	13	C
10	A	14	A
10	A	15	G
10	A	16	C
10	A	17	C
10	A	18	G
10	A	19	G
10	A	20	U
10	A	21	A
10	A	22	G
10	A	23	C
10	A	46	G
10	A	47	U
10	A	48	C
10	A	49	G
10	A	52	G
10	A	57	A
10	A	58	A
10	A	59	A
10	A	61	C
10	A	66	C
10	A	69	C
10	A	71	C
10	A	73	A
10	B	2	G
10	B	6	G
10	B	7	G
10	B	8	U
10	B	10	G
10	B	13	C
10	B	14	A
10	B	15	G
10	B	16	C
10	B	17	C
10	B	18	G
10	B	19	G
10	B	20	U
10	B	21	A
10	B	22	G

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Mol	Chain	Res	Type
10	B	23	C
10	B	30	G
10	B	31	G
10	B	32	C
10	B	36	U
10	B	37	A
10	B	38	A
10	B	46	G
10	B	47	U
10	B	48	C
10	B	49	G
10	B	52	G
10	B	57	A
10	B	58	A
10	B	59	A
10	B	61	C
10	B	66	C
10	B	69	C
10	B	71	C
10	B	73	A
15	D	4	U
15	D	5	U
15	D	9	G
15	D	22	G
15	D	29	U
15	D	32	A
15	D	39	G
15	D	41	G
15	D	47	C
15	D	48	C
15	D	50	A
15	D	51	A
15	D	52	C
15	D	54	C
15	D	69	G
15	D	70	U
15	D	71	A
15	D	72	A
15	D	74	A
15	D	76	G
15	D	82	G
15	D	83	C

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Mol	Chain	Res	Type
15	D	84	U
15	D	87	C
15	D	90	C
15	D	94	G
15	D	95	C
15	D	96	U
15	D	108	G
15	D	120	A
15	D	122	G
15	D	128	G
15	D	131	A
15	D	141	G
15	D	144	G
15	D	148	G
15	D	149	A
15	D	160	A
15	D	164	G
15	D	173	U
15	D	181	A
15	D	182	A
15	D	197	A
15	D	198	G
15	D	204	G
15	D	208	U
15	D	209	U
15	D	210	C
15	D	211	G
15	D	212	G
15	D	216	U
15	D	226	G
15	D	245	U
15	D	247	G
15	D	251	G
15	D	258	G
15	D	262	A
15	D	266	G
15	D	267	C
15	D	271	C
15	D	279	A
15	D	289	G
15	D	299	G
15	D	306	A

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Mol	Chain	Res	Type
15	D	321	A
15	D	328	C
15	D	329	A
15	D	332	G
15	D	347	G
15	D	352	C
15	D	353	A
15	D	354	G
15	D	355	C
15	D	367	U
15	D	372	C
15	D	373	A
15	D	376	G
15	D	382	A
15	D	384	G
15	D	392	C
15	D	393	A
15	D	397	A
15	D	406	G
15	D	412	A
15	D	413	G
15	D	414	A
15	D	421	U
15	D	422	C
15	D	424	G
15	D	429	U
15	D	446	G
15	D	451	A
15	D	457	G
15	D	458	U
15	D	460	A
15	D	463	U
15	D	464	U
15	D	467	U
15	D	468	A
15	D	469	C
15	D	478	A
15	D	479	U
15	D	481	G
15	D	484	G
15	D	485	U
15	D	486	U

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Mol	Chain	Res	Type
15	D	505	G
15	D	509	A
15	D	511	C
15	D	518	C
15	D	519	C
15	D	526	C
15	D	531	U
15	D	532	A
15	D	533	A
15	D	542	G
15	D	547	A
15	D	559	A
15	D	562	U
15	D	568	G
15	D	572	A
15	D	573	A
15	D	576	C
15	D	577	G
15	D	579	A
15	D	596	A
15	D	628	G
15	D	633	G
15	D	641	U
15	D	642	A
15	D	649	A
15	D	650	G
15	D	653	U
15	D	665	A
15	D	666	G
15	D	687	A
15	D	700	G
15	D	723	U
15	D	724	G
15	D	731	G
15	D	734	G
15	D	747	A
15	D	748	G
15	D	755	G
15	D	760	G
15	D	777	A
15	D	793	U
15	D	794	A

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Mol	Chain	Res	Type
15	D	815	A
15	D	817	C
15	D	828	U
15	D	829	G
15	D	832	G
15	D	841	C
15	D	844	G
15	D	845	A
15	D	849	G
15	D	874	G
15	D	887	G
15	D	902	G
15	D	914	A
15	D	916	U
15	D	926	G
15	D	934	C
15	D	935	A
15	D	954	G
15	D	960	U
15	D	963	G
15	D	969	A
15	D	972	C
15	D	975	A
15	D	976	G
15	D	991	U
15	D	992	U
15	D	993	G
15	D	996	A
15	D	999	C
15	D	1004	A
15	D	1008	U
15	D	1009	U
15	D	1017	U
15	D	1018	G
15	D	1021	A
15	D	1024	G
15	D	1026	G
15	D	1028	C
15	D	1030	U
15	D	1031	C
15	D	1037	C
15	D	1043	G

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Mol	Chain	Res	Type
15	D	1044	A
15	D	1046	A
15	D	1065	U
15	D	1085	U
15	D	1086	U
15	D	1094	G
15	D	1095	U
15	D	1099	G
15	D	1101	A
15	D	1124	G
15	D	1133	G
15	D	1135	U
15	D	1136	C
15	D	1137	C
15	D	1139	G
15	D	1140	C
15	D	1141	C
15	D	1142	G
15	D	1143	G
15	D	1145	A
15	D	1146	A
15	D	1151	A
15	D	1152	A
15	D	1158	C
15	D	1159	U
15	D	1167	A
15	D	1171	A
15	D	1174	G
15	D	1175	G
15	D	1176	A
15	D	1184	G
15	D	1196	A
15	D	1197	A
15	D	1206	G
15	D	1211	U
15	D	1212	U
15	D	1213	A
15	D	1214	C
15	D	1215	G
15	D	1226	C
15	D	1227	A
15	D	1228	C

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Mol	Chain	Res	Type
15	D	1238	A
15	D	1256	A
15	D	1257	A
15	D	1260	G
15	D	1275	A
15	D	1276	G
15	D	1278	G
15	D	1279	G
15	D	1280	A
15	D	1285	A
15	D	1286	U
15	D	1287	A
15	D	1299	A
15	D	1300	G
15	D	1302	C
15	D	1305	G
15	D	1312	G
15	D	1317	C
15	D	1320	C
15	D	1323	G
15	D	1329	A
15	D	1338	G
15	D	1340	A
15	D	1346	A
15	D	1347	G
15	D	1353	G
15	D	1363	A
15	D	1370	G
15	D	1378	C
15	D	1379	G
15	D	1381	U
15	D	1391	U
15	D	1396	A
15	D	1397	C
15	D	1398	A
15	D	1404	C
15	D	1419	G
15	D	1429	A
15	D	1441	A
15	D	1446	A
15	D	1447	A
15	D	1448	C

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Mol	Chain	Res	Type
15	D	1452	C
15	D	1453	G
15	D	1475	G
15	D	1487	G
15	D	1492	A
15	D	1493	A
15	D	1494	G
15	D	1495	U
15	D	1497	G
15	D	1503	A
15	D	1506	U
15	D	1517	G
15	D	1529	G
15	D	1530	G
15	D	1534	A
38	a	10	A
38	a	15	G
38	a	34	U
38	a	35	G
38	a	46	G
38	a	58	G
38	a	60	G
38	a	63	A
38	a	71	A
38	a	74	A
38	a	75	G
38	a	83	A
38	a	84	A
38	a	85	G
38	a	93	G
38	a	96	C
38	a	102	U
38	a	103	A
38	a	110	G
38	a	114	U
38	a	118	A
38	a	119	A
38	a	120	U
38	a	122	G
38	a	131	A
38	a	136	G
38	a	139	U

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Mol	Chain	Res	Type
38	a	140	C
38	a	141	G
38	a	145	C
38	a	163	C
38	a	165	A
38	a	181	A
38	a	196	A
38	a	199	A
38	a	200	U
38	a	215	G
38	a	216	A
38	a	222	A
38	a	225	C
38	a	248	G
38	a	249	C
38	a	261	G
38	a	264	C
38	a	265	A
38	a	266	G
38	a	267	C
38	a	271	G
38	a	272	A
38	a	275	C
38	a	276	U
38	a	278	A
38	a	285	G
38	a	311	A
38	a	324	A
38	a	329	G
38	a	330	A
38	a	353	C
38	a	359	G
38	a	361	G
38	a	362	A
38	a	371	A
38	a	372	G
38	a	373	U
38	a	375	G
38	a	383	C
38	a	386	G
38	a	396	G
38	a	405	U

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Mol	Chain	Res	Type
38	a	411	G
38	a	412	A
38	a	420	C
38	a	424	G
38	a	435	C
38	a	451	U
38	a	456	C
38	a	457	A
38	a	477	A
38	a	481	G
38	a	491	G
38	a	501	A
38	a	503	A
38	a	504	A
38	a	505	A
38	a	509	C
38	a	522	A
38	a	529	A
38	a	532	A
38	a	543	G
38	a	546	U
38	a	547	A
38	a	548	G
38	a	549	G
38	a	551	G
38	a	563	A
38	a	569	U
38	a	573	U
38	a	575	A
38	a	588	U
38	a	603	A
38	a	609	A
38	a	613	A
38	a	614	A
38	a	615	U
38	a	616	A
38	a	618	G
38	a	620	G
38	a	621	A
38	a	627	A
38	a	637	A
38	a	645	C

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Mol	Chain	Res	Type
38	a	647	G
38	a	654	A
38	a	664	G
38	a	668	A
38	a	685	A
38	a	686	U
38	a	710	U
38	a	717	C
38	a	730	A
38	a	738	G
38	a	757	G
38	a	764	A
38	a	765	C
38	a	775	G
38	a	776	G
38	a	782	A
38	a	784	G
38	a	785	G
38	a	800	A
38	a	802	A
38	a	805	G
38	a	812	C
38	a	819	A
38	a	827	U
38	a	828	U
38	a	845	A
38	a	846	U
38	a	858	G
38	a	859	G
38	a	869	G
38	a	878	A
38	a	881	G
38	a	883	G
38	a	884	U
38	a	885	C
38	a	888	C
38	a	891	G
38	a	892	A
38	a	893	C
38	a	895	U
38	a	896	A
38	a	897	C

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Mol	Chain	Res	Type
38	a	899	A
38	a	907	G
38	a	910	A
38	a	914	G
38	a	915	C
38	a	931	U
38	a	941	A
38	a	945	A
38	a	946	C
38	a	953	G
38	a	961	C
38	a	974	G
38	a	983	A
38	a	984	A
38	a	985	C
38	a	995	C
38	a	996	A
38	a	999	U
38	a	1005	C
38	a	1012	U
38	a	1013	C
38	a	1022	G
38	a	1023	U
38	a	1026	G
38	a	1033	U
38	a	1041	G
38	a	1042	G
38	a	1045	C
38	a	1046	A
38	a	1047	G
38	a	1060	U
38	a	1061	U
38	a	1062	G
38	a	1063	G
38	a	1064	C
38	a	1065	U
38	a	1066	U
38	a	1067	A
38	a	1068	G
38	a	1069	A
38	a	1070	A
38	a	1071	G

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Mol	Chain	Res	Type
38	a	1073	A
38	a	1074	G
38	a	1076	C
38	a	1079	C
38	a	1080	A
38	a	1081	U
38	a	1082	U
38	a	1083	U
38	a	1084	A
38	a	1087	G
38	a	1088	A
38	a	1090	A
38	a	1095	A
38	a	1096	A
38	a	1107	G
38	a	1110	G
38	a	1111	A
38	a	1112	G
38	a	1119	U
38	a	1122	G
38	a	1132	U
38	a	1134	A
38	a	1135	C
38	a	1142	A
38	a	1143	A
38	a	1169	A
38	a	1170	C
38	a	1173	U
38	a	1174	U
38	a	1175	A
38	a	1176	U
38	a	1177	G
38	a	1178	C
38	a	1179	G
38	a	1180	U
38	a	1186	G
38	a	1238	G
38	a	1248	G
38	a	1253	A
38	a	1256	G
38	a	1266	G
38	a	1271	G

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Mol	Chain	Res	Type
38	a	1272	A
38	a	1273	U
38	a	1301	A
38	a	1321	A
38	a	1345	C
38	a	1352	U
38	a	1365	A
38	a	1368	G
38	a	1378	A
38	a	1379	U
38	a	1380	G
38	a	1383	A
38	a	1387	A
38	a	1392	A
38	a	1395	A
38	a	1406	U
38	a	1407	G
38	a	1408	G
38	a	1411	U
38	a	1414	C
38	a	1415	U
38	a	1416	G
38	a	1417	C
38	a	1419	A
38	a	1420	A
38	a	1428	C
38	a	1452	G
38	a	1453	A
38	a	1460	U
38	a	1478	G
38	a	1482	G
38	a	1490	A
38	a	1491	G
38	a	1497	U
38	a	1503	A
38	a	1508	A
38	a	1509	A
38	a	1510	G
38	a	1515	A
38	a	1529	G
38	a	1534	U
38	a	1535	A

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Mol	Chain	Res	Type
38	a	1536	C
38	a	1537	G
38	a	1554	U
38	a	1559	U
38	a	1566	A
38	a	1569	A
38	a	1578	U
38	a	1580	A
38	a	1581	G
38	a	1582	C
38	a	1583	A
38	a	1584	U
38	a	1589	U
38	a	1590	A
38	a	1608	A
38	a	1609	A
38	a	1610	A
38	a	1647	U
38	a	1648	U
38	a	1649	G
38	a	1651	G
38	a	1674	G
38	a	1677	A
38	a	1703	G
38	a	1714	U
38	a	1715	G
38	a	1718	G
38	a	1729	U
38	a	1730	C
38	a	1732	C
38	a	1738	G
38	a	1750	G
38	a	1755	A
38	a	1758	U
38	a	1764	C
38	a	1773	A
38	a	1791	A
38	a	1800	C
38	a	1801	A
38	a	1808	A
38	a	1811	G
38	a	1816	C

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Mol	Chain	Res	Type
38	a	1829	A
38	a	1833	C
38	a	1847	A
38	a	1848	A
38	a	1858	A
38	a	1859	U
38	a	1862	G
38	a	1864	U
38	a	1869	G
38	a	1870	C
38	a	1872	A
38	a	1873	G
38	a	1905	C
38	a	1906	G
38	a	1907	G
38	a	1913	A
38	a	1914	C
38	a	1919	A
38	a	1920	C
38	a	1922	G
38	a	1923	U
38	a	1924	C
38	a	1925	C
38	a	1926	U
38	a	1928	A
38	a	1929	G
38	a	1930	G
38	a	1936	A
38	a	1938	A
38	a	1955	U
38	a	1965	C
38	a	1967	C
38	a	1970	A
38	a	1971	U
38	a	1972	G
38	a	1987	A
38	a	1991	U
38	a	1992	G
38	a	1993	U
38	a	1997	C
38	a	2002	G
38	a	2022	U

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Mol	Chain	Res	Type
38	a	2023	C
38	a	2027	G
38	a	2033	A
38	a	2043	C
38	a	2051	A
38	a	2052	A
38	a	2055	C
38	a	2056	G
38	a	2060	A
38	a	2061	G
38	a	2062	A
38	a	2063	C
38	a	2077	A
38	a	2097	A
38	a	2099	U
38	a	2100	G
38	a	2108	A
38	a	2110	G
38	a	2111	U
38	a	2113	U
38	a	2115	G
38	a	2116	G
38	a	2117	A
38	a	2118	U
38	a	2121	G
38	a	2122	U
38	a	2124	G
38	a	2125	G
38	a	2126	A
38	a	2127	G
38	a	2128	G
38	a	2131	U
38	a	2132	U
38	a	2133	G
38	a	2134	A
38	a	2139	U
38	a	2141	G
38	a	2146	C
38	a	2147	A
38	a	2154	A
38	a	2157	G
38	a	2158	A

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Mol	Chain	Res	Type
38	a	2159	G
38	a	2162	G
38	a	2163	A
38	a	2164	C
38	a	2165	C
38	a	2169	A
38	a	2171	A
38	a	2172	U
38	a	2178	C
38	a	2182	U
38	a	2183	A
38	a	2185	U
38	a	2188	U
38	a	2189	U
38	a	2190	G
38	a	2191	A
38	a	2193	G
38	a	2194	U
38	a	2198	A
38	a	2204	G
38	a	2210	U
38	a	2211	A
38	a	2212	A
38	a	2213	U
38	a	2225	A
38	a	2226	C
38	a	2229	U
38	a	2238	G
38	a	2239	G
38	a	2244	U
38	a	2250	G
38	a	2268	A
38	a	2278	A
38	a	2283	C
38	a	2287	A
38	a	2297	A
38	a	2305	U
38	a	2308	G
38	a	2309	A
38	a	2315	G
38	a	2322	A
38	a	2325	G

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Mol	Chain	Res	Type
38	a	2327	A
38	a	2333	A
38	a	2339	C
38	a	2345	G
38	a	2347	C
38	a	2350	C
38	a	2361	G
38	a	2372	U
38	a	2376	A
38	a	2383	G
38	a	2385	C
38	a	2402	U
38	a	2403	C
38	a	2406	A
38	a	2423	U
38	a	2424	C
38	a	2425	A
38	a	2426	A
38	a	2429	G
38	a	2430	A
38	a	2431	U
38	a	2434	A
38	a	2435	A
38	a	2441	U
38	a	2447	G
38	a	2448	A
38	a	2470	G
38	a	2474	U
38	a	2476	A
38	a	2478	A
38	a	2484	G
38	a	2491	U
38	a	2502	G
38	a	2506	U
38	a	2507	C
38	a	2512	C
38	a	2513	A
38	a	2518	A
38	a	2520	C
38	a	2525	G
38	a	2529	G
38	a	2535	G

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Mol	Chain	Res	Type
38	a	2547	A
38	a	2554	U
38	a	2566	A
38	a	2567	G
38	a	2572	A
38	a	2573	C
38	a	2574	G
38	a	2585	U
38	a	2586	U
38	a	2602	A
38	a	2603	G
38	a	2609	U
38	a	2610	C
38	a	2611	C
38	a	2613	U
38	a	2629	U
38	a	2663	G
38	a	2669	G
38	a	2671	G
38	a	2689	U
38	a	2690	U
38	a	2714	G
38	a	2722	G
38	a	2726	A
38	a	2744	G
38	a	2748	A
38	a	2757	A
38	a	2758	A
38	a	2765	A
38	a	2777	G
38	a	2778	A
38	a	2791	G
38	a	2793	C
38	a	2796	U
38	a	2797	U
38	a	2798	U
38	a	2799	A
38	a	2801	G
38	a	2818	U
38	a	2820	A
38	a	2823	A
38	a	2825	G

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Mol	Chain	Res	Type
38	a	2849	U
38	a	2850	A
38	a	2859	G
38	a	2861	U
38	a	2867	G
38	a	2880	C
38	a	2884	U
38	a	2885	G
38	a	2891	U
38	a	2902	C
41	d	2	G
41	d	9	G
41	d	13	G
41	d	16	G
41	d	17	C
41	d	35	C
41	d	36	C
41	d	45	A
41	d	51	G
41	d	56	G
41	d	64	G
41	d	66	A
41	d	88	C
41	d	89	U
41	d	90	C
41	d	99	A
41	d	109	A

All (50) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	7	-8	U
8	7	-5	U
8	7	-3	U
10	A	6	G
10	A	7	G
10	A	9	G
10	A	22	G
10	A	60	U
10	A	70	G
10	B	6	G
10	B	7	G

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Mol	Chain	Res	Type
10	B	9	G
10	B	22	G
10	B	37	A
10	B	60	U
15	D	7	A
15	D	70	U
15	D	121	U
15	D	181	A
15	D	183	C
15	D	197	A
15	D	209	U
15	D	305	G
15	D	328	C
15	D	428	G
15	D	496	A
15	D	517	G
15	D	531	U
15	D	532	A
15	D	562	U
15	D	641	U
15	D	722	G
15	D	793	U
15	D	991	U
15	D	992	U
15	D	1109	C
15	D	1145	A
15	D	1196	A
15	D	1211	U
15	D	1212	U
15	D	1213	A
15	D	1214	C
15	D	1225	A
15	D	1299	A
15	D	1396	A
15	D	1432	G
15	D	1447	A
15	D	1491	G
15	D	1492	A
15	D	1493	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

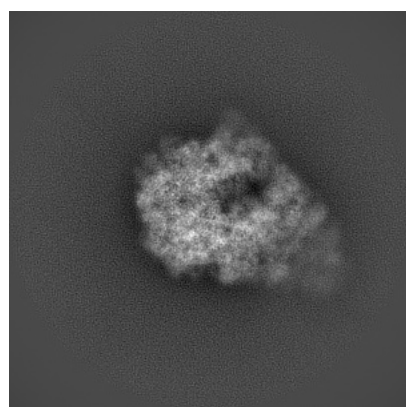
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21494. These allow visual inspection of the internal detail of the map and identification of artifacts.

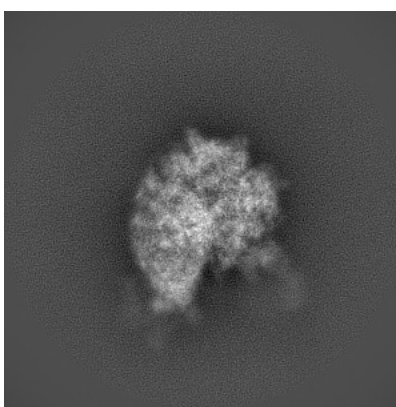
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

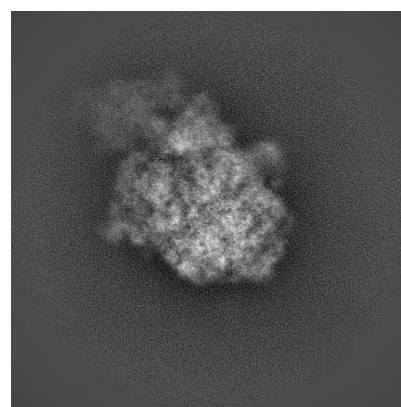
6.1.1 Primary map



X



Y

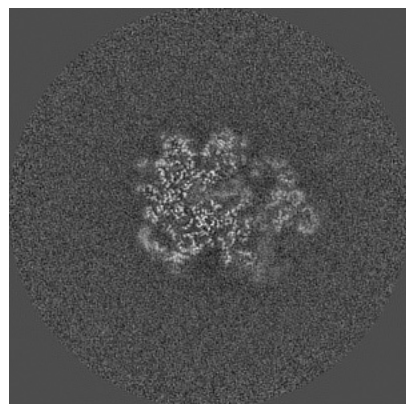


Z

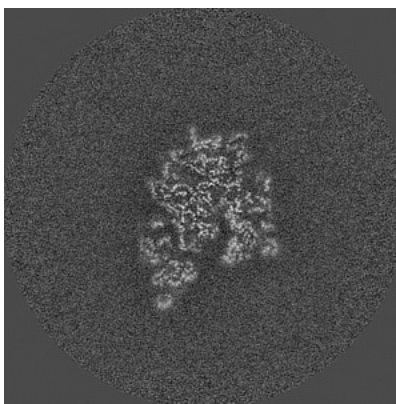
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

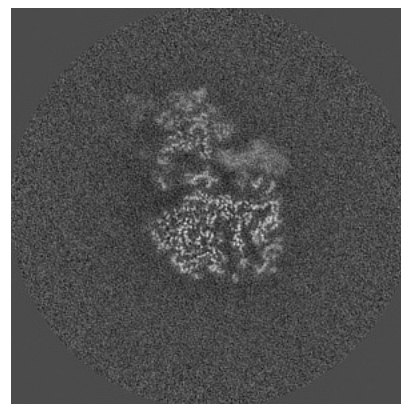
6.2.1 Primary map



X Index: 256



Y Index: 256

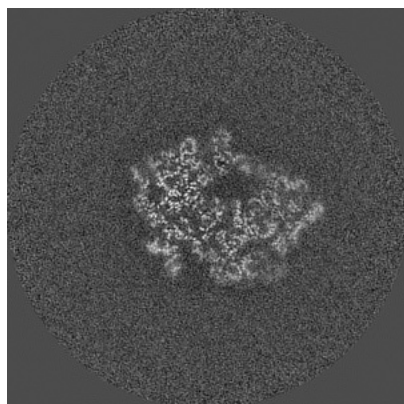


Z Index: 256

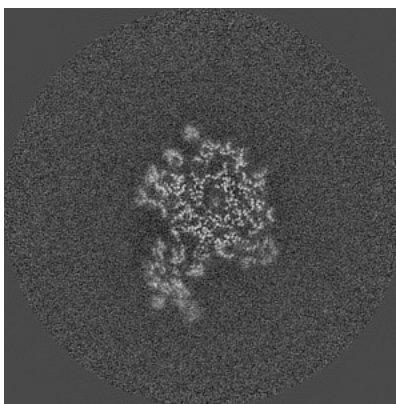
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

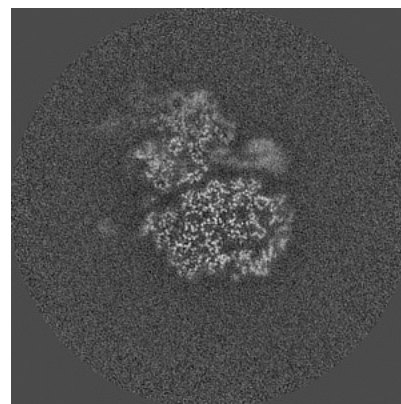
6.3.1 Primary map



X Index: 240



Y Index: 231

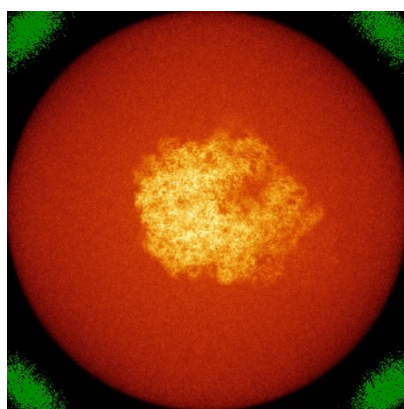


Z Index: 248

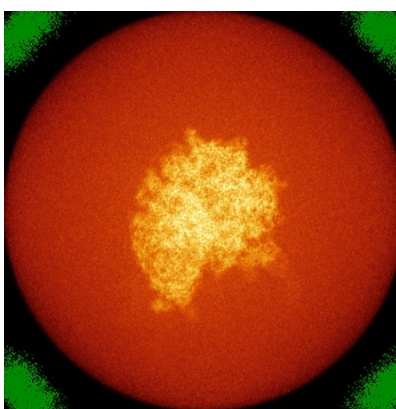
The images above show the largest variance slices of the map in three orthogonal directions.

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

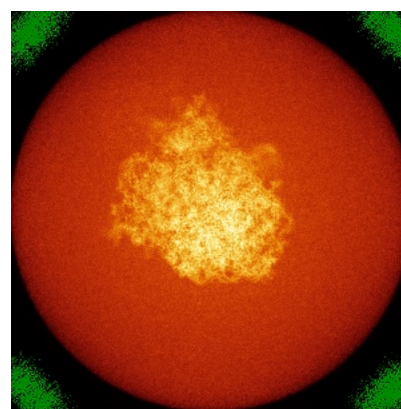
6.4.1 Primary map



X



Y

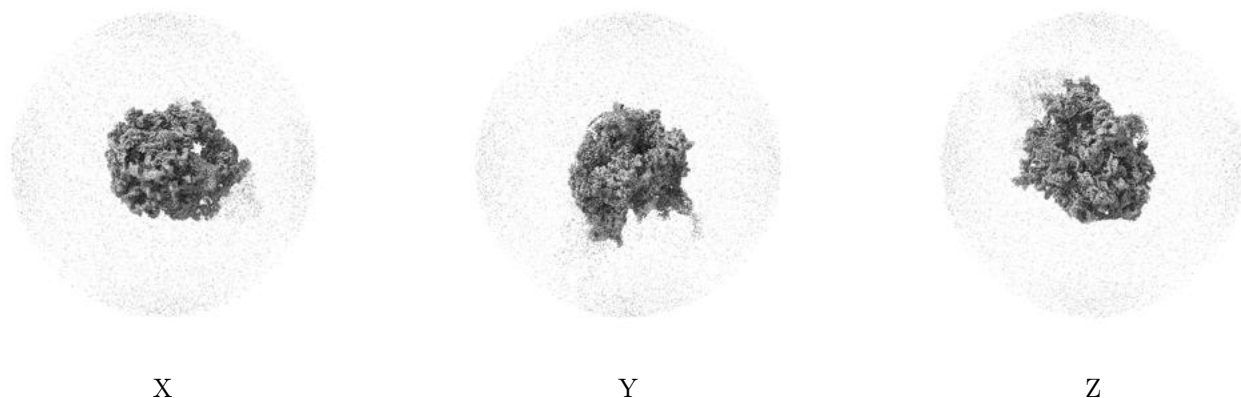


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

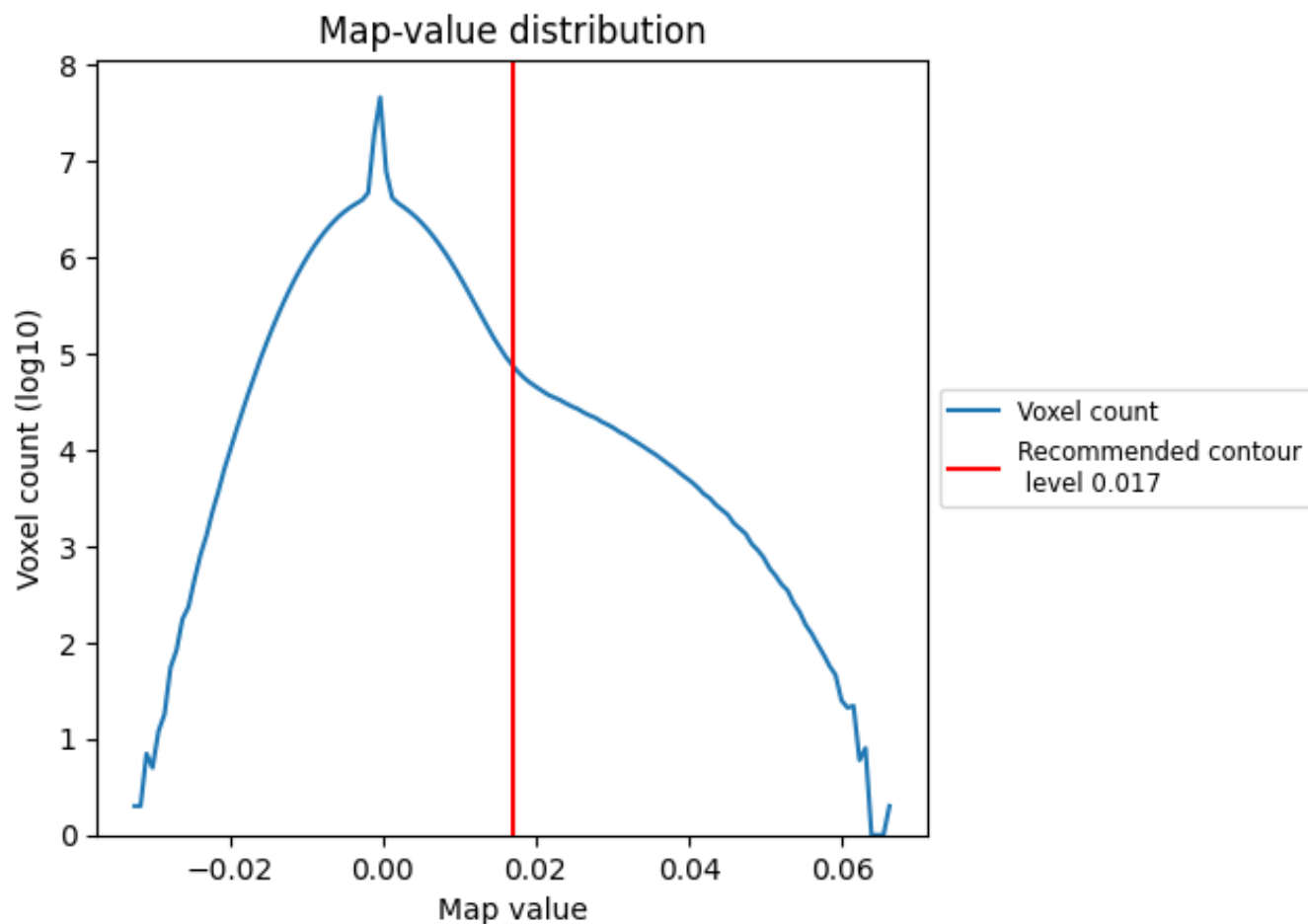
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

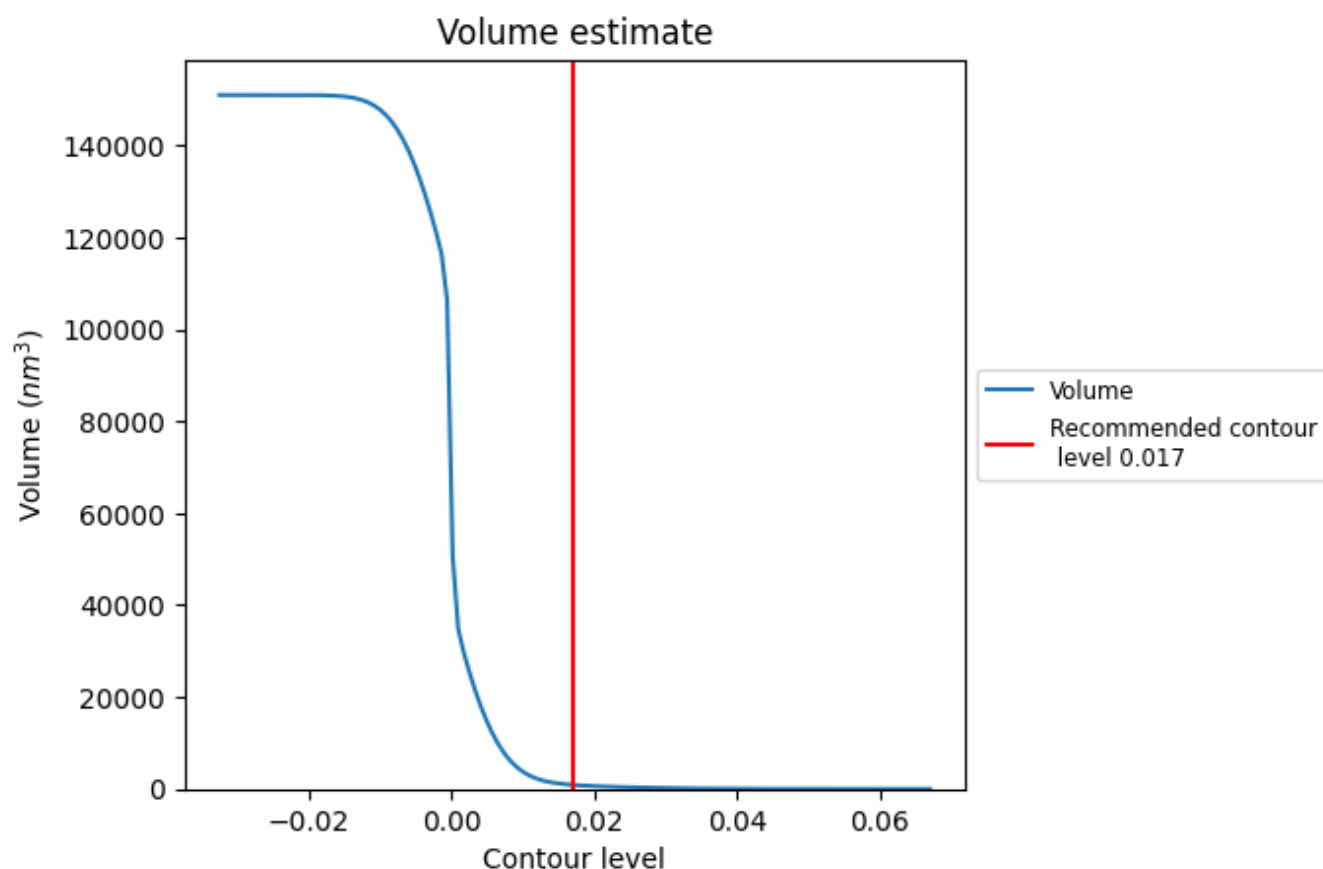
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

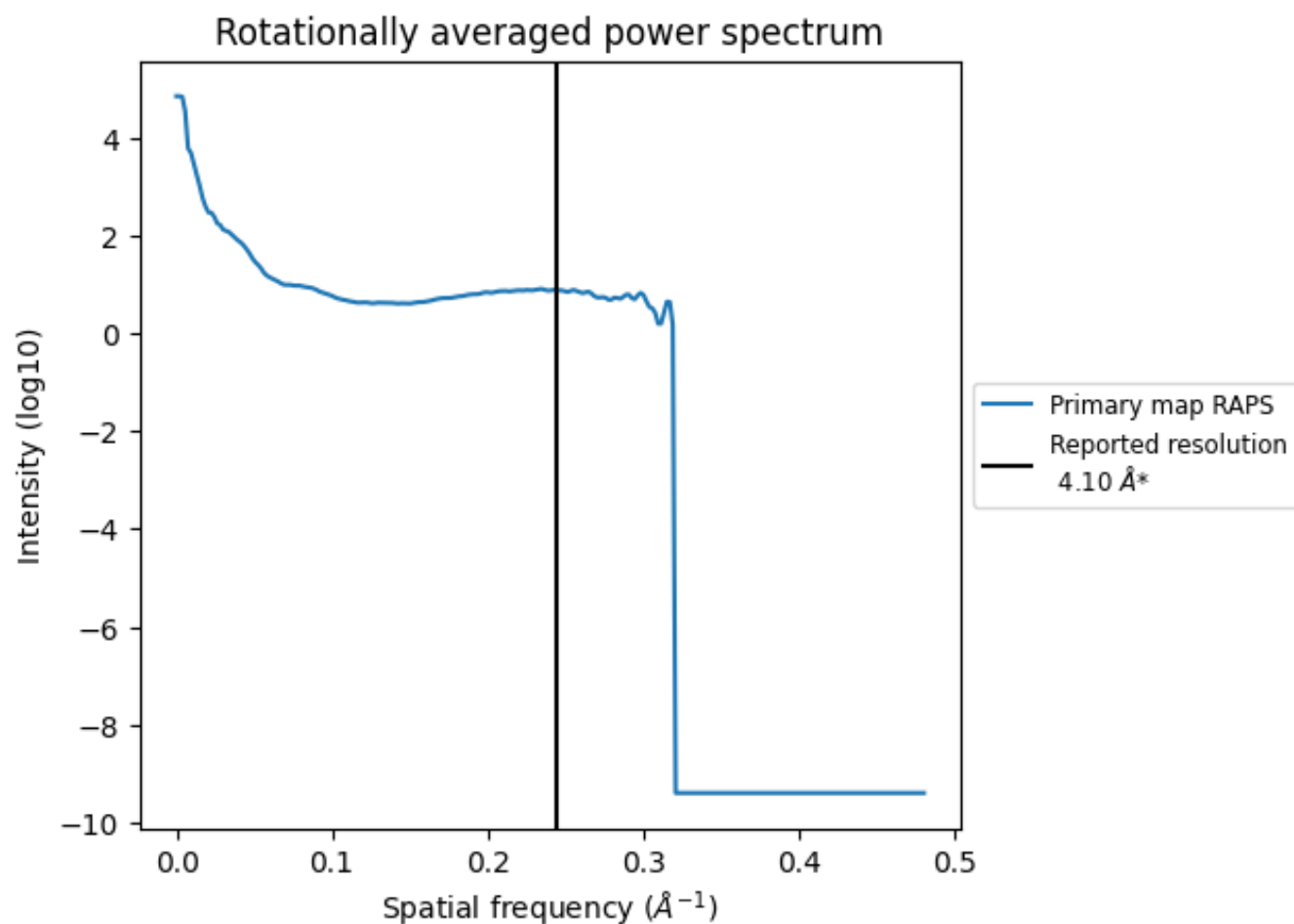
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 887 nm^3 ; this corresponds to an approximate mass of 801 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8 Fourier-Shell correlation

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

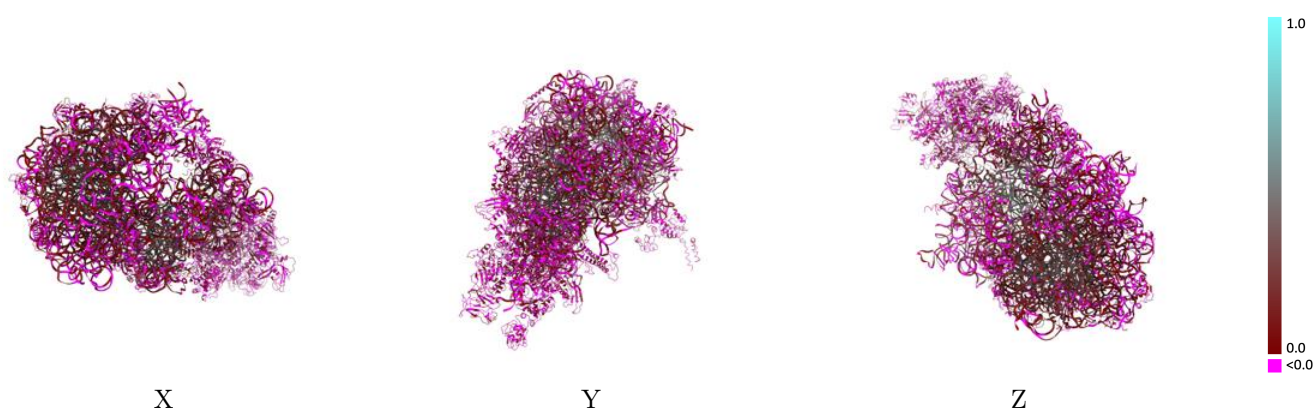
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21494 and PDB model 6VZJ. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

This section was not generated.

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

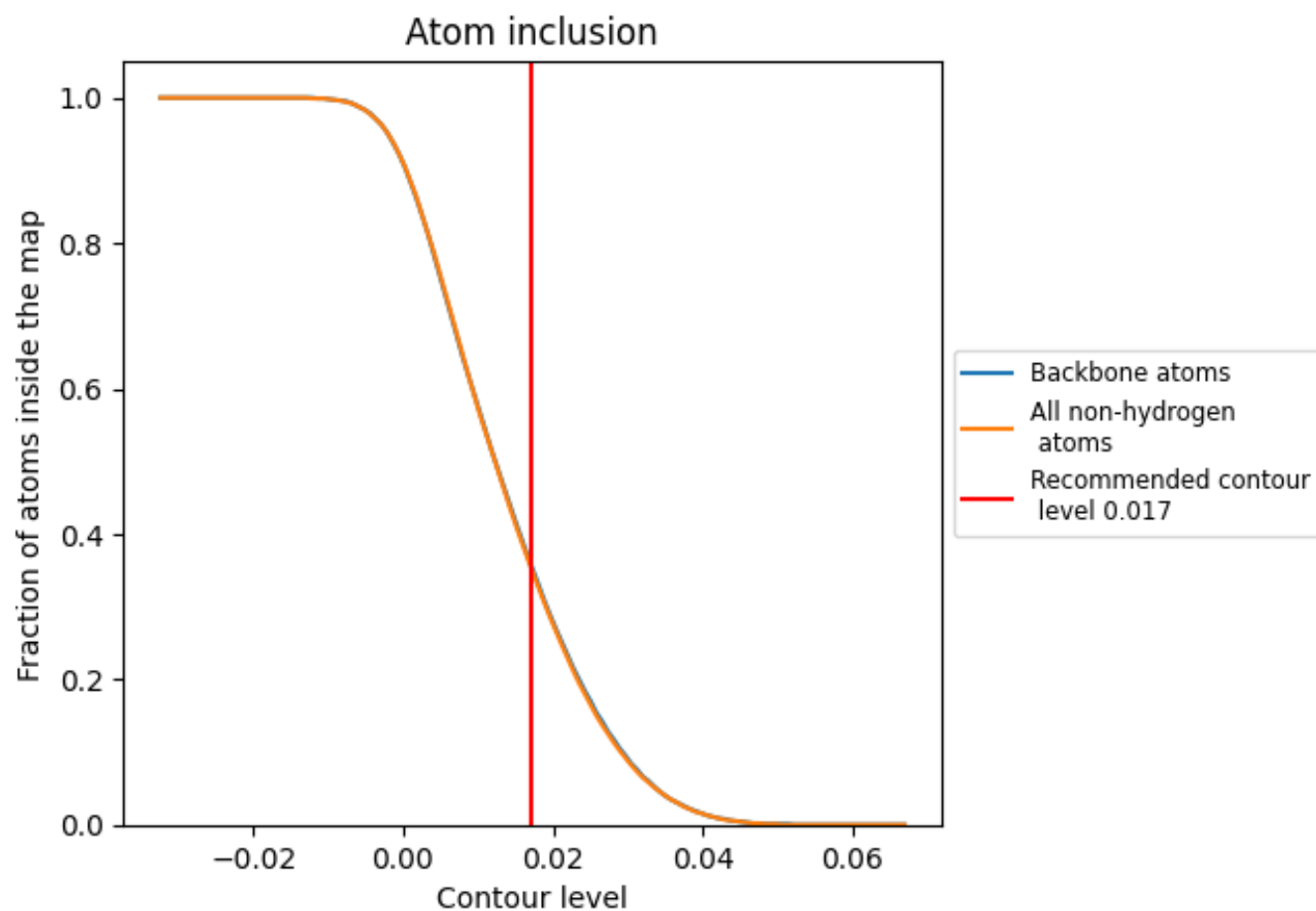


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 36% of all backbone atoms, 36% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3560	 0.1230
0	 0.3230	 0.1140
1	 0.4280	 0.2450
2	 0.2510	 0.0600
3	 0.2310	 0.0170
4	 0.2580	 0.0510
5	 0.0020	 -0.0050
6	 0.0050	 0.0520
7	 0.0130	 0.0190
9	 0.0700	 0.0020
A	 0.1760	 0.0960
AA	 0.0020	 0.0230
AC	 0.0020	 0.0180
AD	 0.0010	 0.0130
AE	 0.0020	 0.0180
B	 0.1270	 0.0350
C	 0.2410	 0.0790
D	 0.5260	 0.1880
E	 0.2120	 0.0040
F	 0.2200	 0.1780
G	 0.2310	 0.1020
H	 0.0080	 0.0140
I	 0.2080	 0.1290
J	 0.2270	 0.1030
K	 0.4110	 0.2670
L	 0.1620	 0.0260
M	 0.1900	 0.1040
N	 0.3250	 0.1810
O	 0.2000	 0.0480
P	 0.2030	 0.0890
Q	 0.2470	 0.1310
R	 0.4360	 0.3000
S	 0.2180	 0.0610
T	 0.3150	 0.1390
U	 0.1470	 -0.0110



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Chain	Atom inclusion	Q-score
V	 0.2770	 0.1500
W	 0.0910	 0.0010
X	 0.1420	 -0.0100
Y	 0.0440	 -0.0160
Z	 0.0130	 -0.0140
a	 0.5300	 0.1630
b	 0.2330	 0.0450
c	 0.2750	 0.0890
d	 0.4500	 0.0400
e	 0.2490	 0.0100
f	 0.3330	 0.1300
g	 0.0960	 -0.0160
h	 0.3070	 0.1140
i	 0.4580	 0.2290
j	 0.3760	 0.1720
k	 0.1790	 -0.0210
l	 0.2700	 0.0700
m	 0.4840	 0.2710
n	 0.1680	 0.0010
o	 0.2440	 0.0650
p	 0.1910	 0.0070
q	 0.3190	 0.1040
r	 0.0770	 -0.0010
s	 0.3690	 0.1680
t	 0.3700	 0.2120
u	 0.2880	 0.0750
v	 0.3430	 0.1570
w	 0.3980	 0.1670
x	 0.1890	 -0.0690
y	 0.2610	 0.1010
z	 0.4500	 0.2090