



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 06:27 AM UTC

PDB ID : 6X9Q / pdb_00006x9q
EMDB ID : EMD-22107
Title : Cryo-EM structure of an Escherichia coli coupled transcription-translational complex B3 (TTC-B3) containing an mRNA with a 27 nt long spacer, transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.
Deposited on : 2020-06-03
Resolution : 4.80 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:

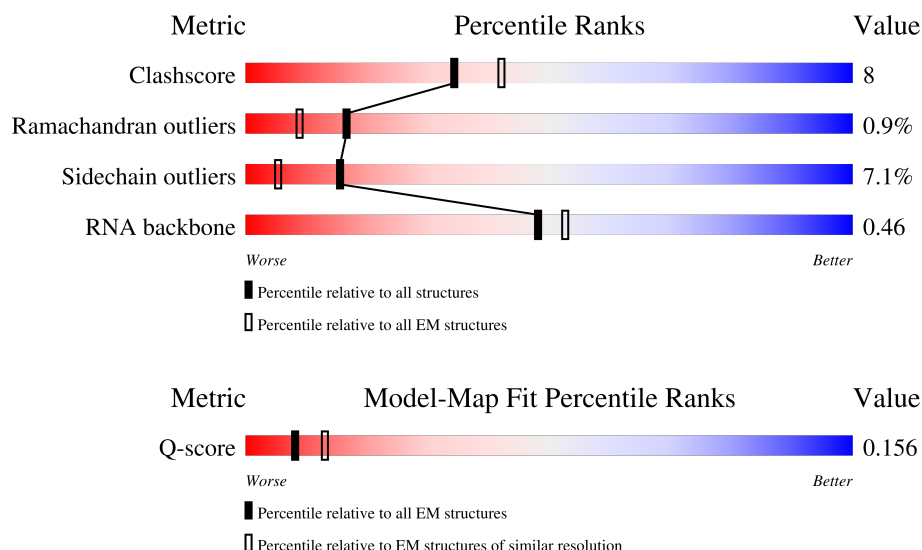
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.80 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	1575 (4.30 - 5.30)

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	
5	4	94	
6	5	36	
7	6	36	
8	7	44	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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Mol	Chain	Length	Quality of chain
52	l	201	
53	m	46	
54	n	179	
55	o	65	
56	p	177	
57	q	38	
58	r	149	
59	s	142	
60	t	123	
61	u	144	
62	v	136	
63	w	127	
64	x	117	
65	y	115	
66	z	118	

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 290203 atoms, of which 109912 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	33	Total	C	H	N	O	P	0	0
			784	307	97	96	251	33		

- 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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1276	813	221	235	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	301	Total	C	N	O	S	0	0
			2091	1295	379	411	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	298	Total	C	N	O	S	0	0
			2073	1284	377	406	6		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	variant	UNP A0A4S1NBU2

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 16 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AG	494	Total	C	N	O	0	0
			2442	1454	494	494		

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

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

- Molecule 18 is a RNA chain called 16S rRNA.

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

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

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

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

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

- Molecule 21 is a protein called 30S ribosomal protein S2.

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

- Molecule 22 is a protein called 30S ribosomal protein S1.

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

- Molecule 23 is a protein called 30S ribosomal protein S3.

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

- Molecule 24 is a protein called 30S ribosomal protein S4.

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

- Molecule 25 is a protein called 30S ribosomal protein S5.

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

- Molecule 26 is a protein called 30S ribosomal protein S6.

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

- Molecule 27 is a protein called 30S ribosomal protein S7.

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

- Molecule 28 is a protein called 30S ribosomal protein S8.

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

- Molecule 29 is a protein called 30S ribosomal protein S9.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S11.

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

- Molecule 32 is a protein called 30S ribosomal protein S12.

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

- Molecule 33 is a protein called 30S ribosomal protein S14.

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

- Molecule 34 is a protein called 30S ribosomal protein S15.

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

- Molecule 35 is a protein called 30S ribosomal protein S16.

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

- Molecule 36 is a protein called 30S ribosomal protein S17.

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

- Molecule 37 is a protein called 30S ribosomal protein S19.

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

- Molecule 38 is a protein called 30S ribosomal protein S13.

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

- Molecule 39 is a protein called 50S ribosomal protein L11.

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

- Molecule 40 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	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	variant	GB 937521852

- Molecule 42 is a protein called 50S ribosomal protein L27.

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

- Molecule 43 is a protein called 50S ribosomal protein L28.

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

- Molecule 44 is a RNA chain called 5S rRNA.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L2.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33.

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

- Molecule 52 is a protein called 50S ribosomal protein L4.

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

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L5.

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

- Molecule 55 is a protein called 50S ribosomal protein L35.

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

- Molecule 56 is a protein called 50S ribosomal protein L6.

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

- Molecule 57 is a protein called 50S ribosomal protein L36.

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

- Molecule 58 is a protein called 50S ribosomal protein L9.

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

- Molecule 59 is a protein called 50S ribosomal protein L13.

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

- Molecule 60 is a protein called 50S ribosomal protein L14.

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

- Molecule 61 is a protein called 50S ribosomal protein L15.

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

- Molecule 62 is a protein called 50S ribosomal protein L16.

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

- Molecule 63 is a protein called 50S ribosomal protein L17.

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

- Molecule 64 is a protein called 50S ribosomal protein L18.

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

- Molecule 65 is a protein called 50S ribosomal protein L19.

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

- Molecule 66 is a protein called 50S ribosomal protein L20.

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

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

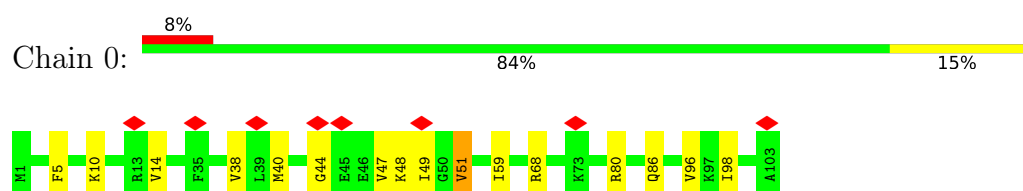
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

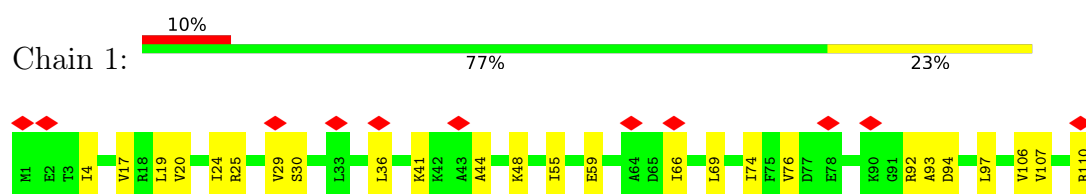
3 Residue-property plots [i](#)

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.

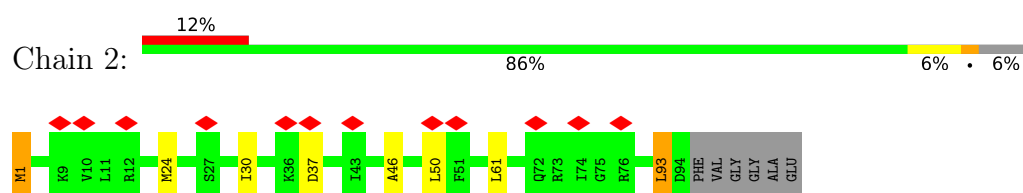
- Molecule 1: 50S ribosomal protein L21



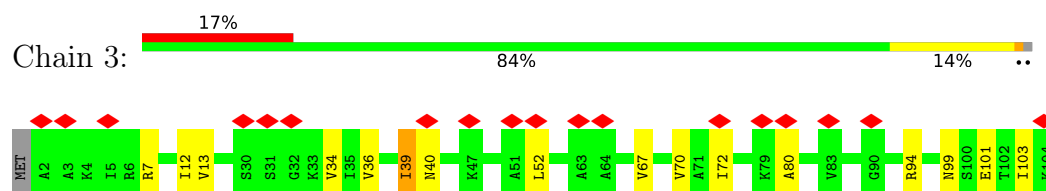
- Molecule 2: 50S ribosomal protein L22



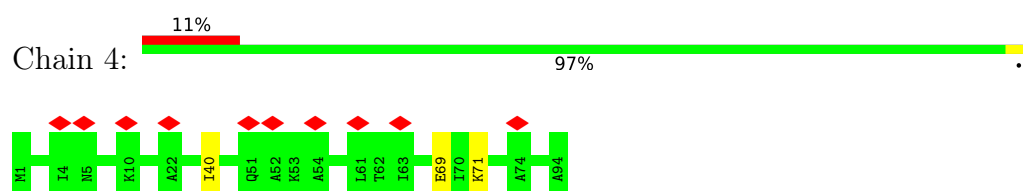
- Molecule 3: 50S ribosomal protein L23



- Molecule 4: 50S ribosomal protein L24



- Molecule 5: 50S ribosomal protein L25



Chain 5:

Node Type	Count
DC	2
DG	1
DT	2
DA	2
T96	1
C97	1
A98	1
T99	1
A100	1
T101	1
T102	1
A103	1
T108	1
T109	1
A110	1
C111	1
C114	1
A115	1
G116	1
A117	1
G122	1

Chain 6:

Category	Percentage
Red	44%
Green	36%
Yellow	39%
Grey	25%

Sequence of 32 items (diamonds): C2, C3, C4, C5, T5, G6, G7, T8, T9, G10, G11, C12, G13, T14, C15, C16, T17, C18, T19, C20, A21, C22, C23, T24, T25, A26, T26, G27, A28, DT, DC, DA, DT, DT, DG, DA, DG, DC, DG, DG.

Chain 7:

Chain 9:

47%

27%

36%

24%

10%

M1 A2 L3 N4 L5 Q6 D7 K8 Q9 A10 I11 V12 E14 S16 E17 V18 A19 K20 L23 S24 A25 V26 V27 A28 D29 S30 R31 G32 V33 T34 V35 D36 K37 M38 T39 E40 L41 R42 K43 A44 G45 R46 E47 G48 V50 Y51 M52 R53 V54 V55 R56 M57 T58 L59 L60 R61 R62 A63 E64 E65 G66 T67 P68 F69 E70 C71 L72 K73 D74 A75 F76 V77 G78 P79 L81 I82 A83 Y84 S85 M86 E87 H88 P89 G90 A91 A92 A93 R94 L95 F96 K97 E98 F99 K101 A102 N103 A104 K105 F106 E107 V108 K109 A110 A111 A112 F113 E114 G115 E116 L117 I118 P119 A120 S121 Q122 I123 D124 A125 L126 A127 T128 L129 P130 Y131 Y132 E133 E134 A135 L136 A137 R138 L139 M140 A141 T142 M143 K144 E145 A146 S147 A148 GLY LYS LEU VAL ARG THR LEU ALA VAL ARG ASP ALA LYS GLU ALA

Chain A:

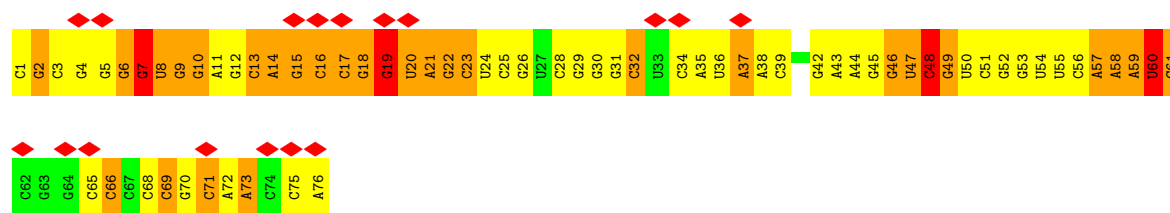
7% 12% 47% 36% 5%

C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 C13 C14 C15 C16 C17 C18 C19 C20 C21 C22 C23 C24 C25 C26 C27 C28 C29 C30 C31 C32 C33 C34 C35 C36 C37 C38 C39 C40 C41 C42 C43 C44 C45 C46 C47 C48 C49 C50 C51 C52 C53

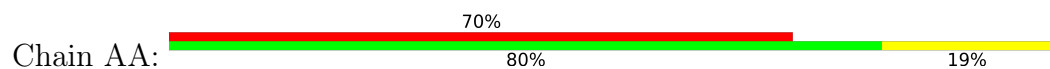
C61 C62 C63 C64 C65 C66 C67 C68 C69 C70 C71 C72 C73 C74 C75 C76 C77 C78 C79 C80 C81 C82 C83 C84 C85 C86 C87 C88 C89 C90 C91 C92 C93 C94 C95 C96 C97 C98 C99 C100

A76

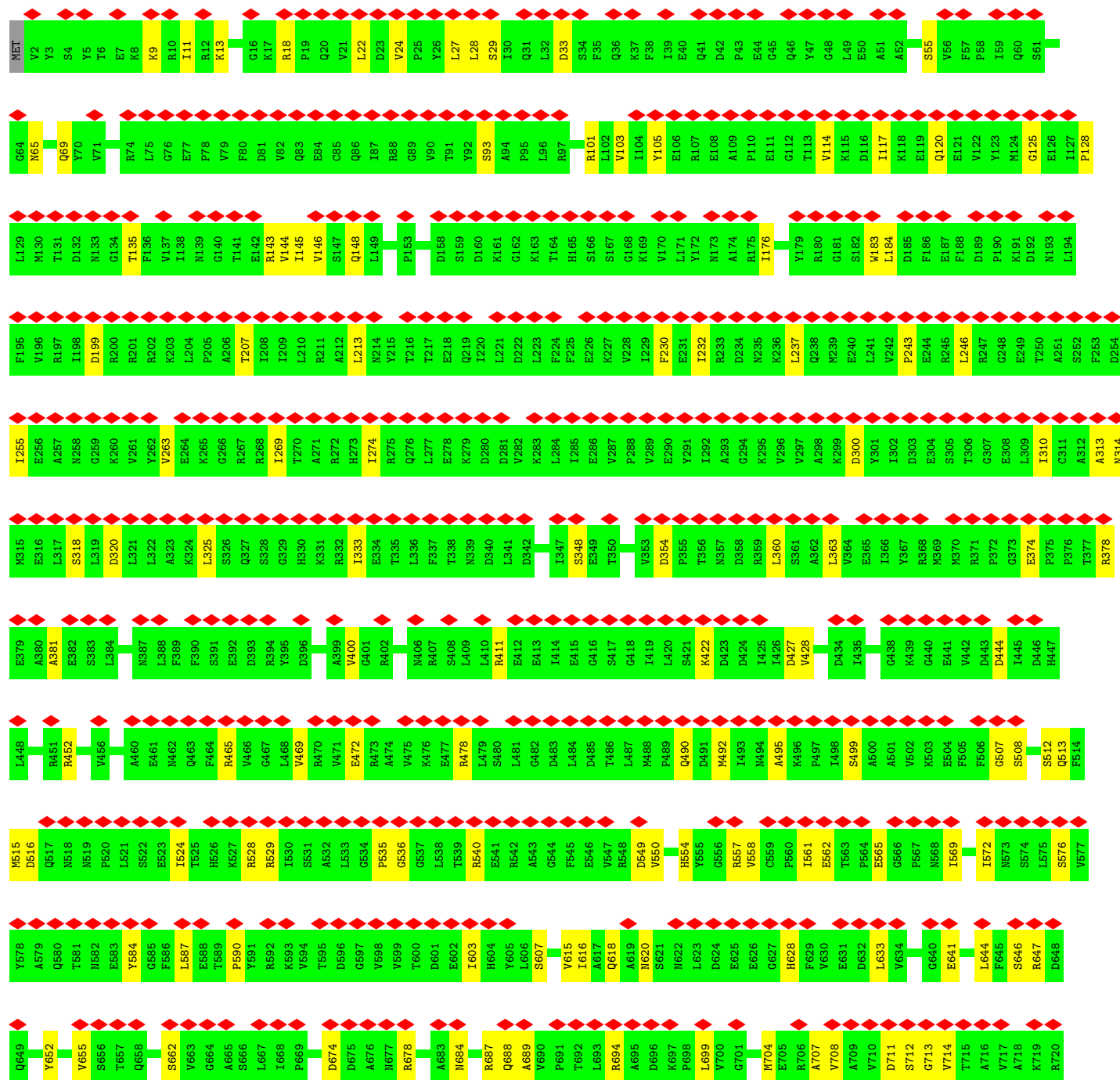
Chain B: 12% 46% 37% 5%

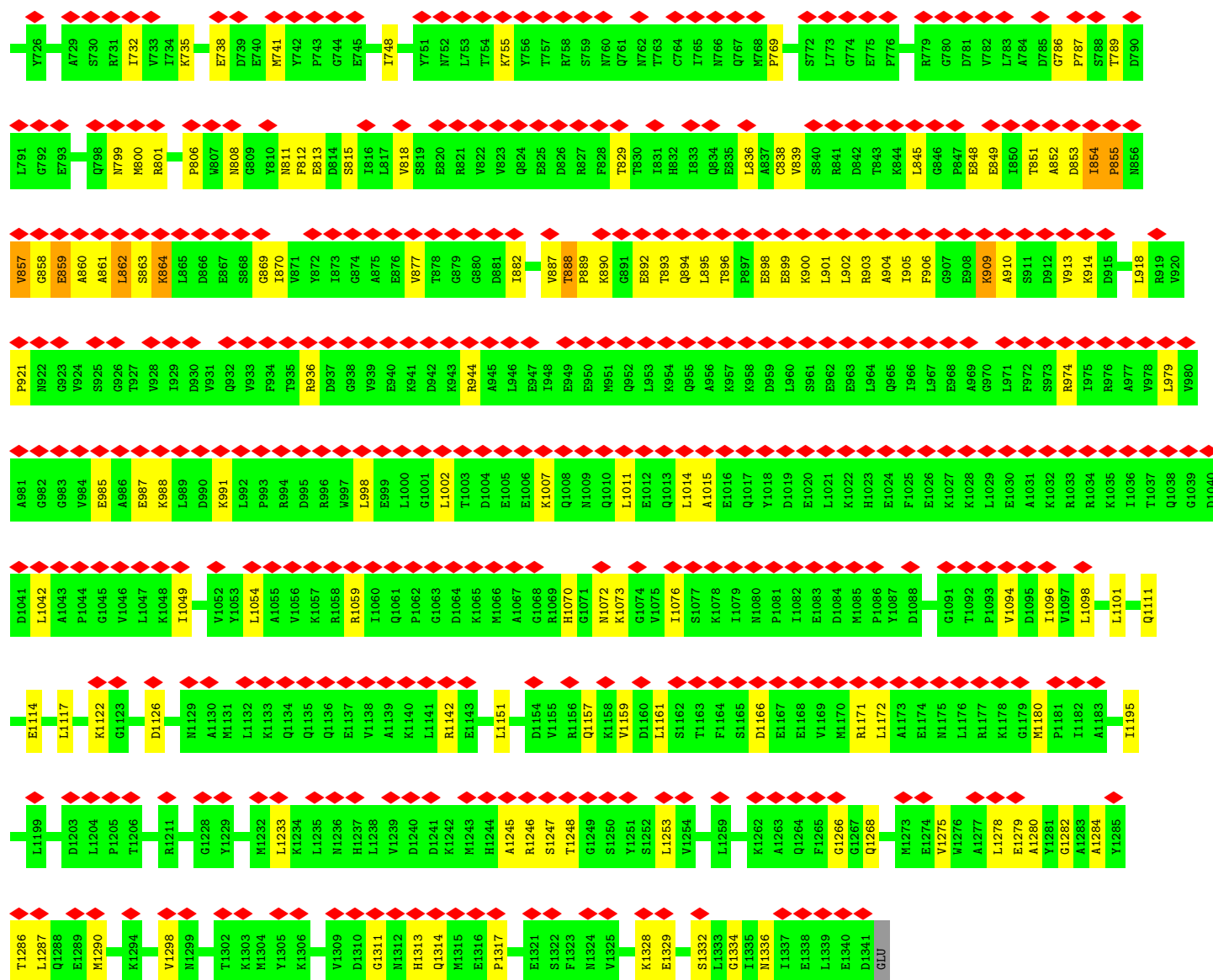


• Molecule 11: DNA-directed RNA polymerase subunit beta

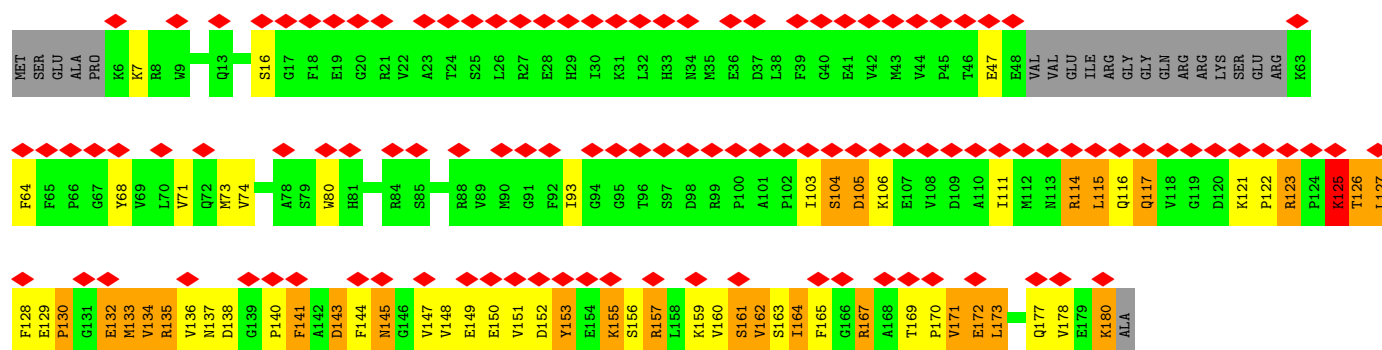


Chain AA:

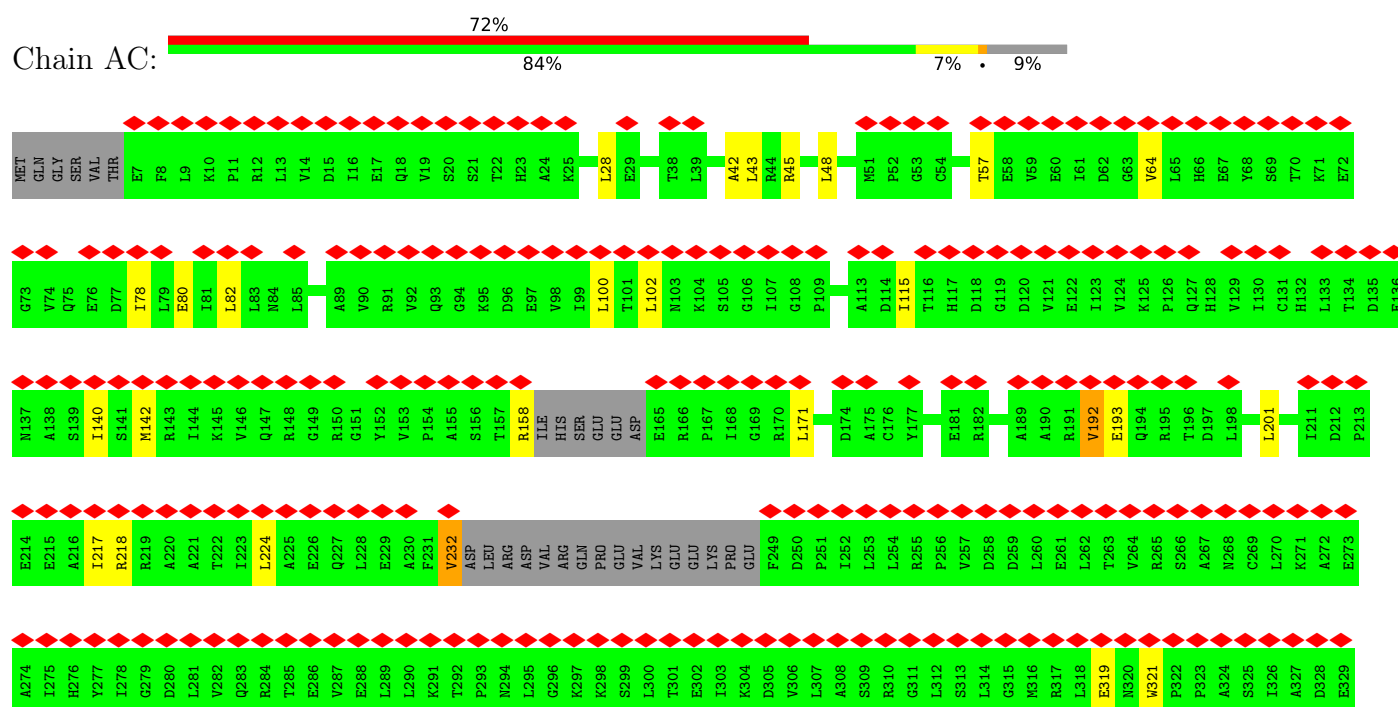




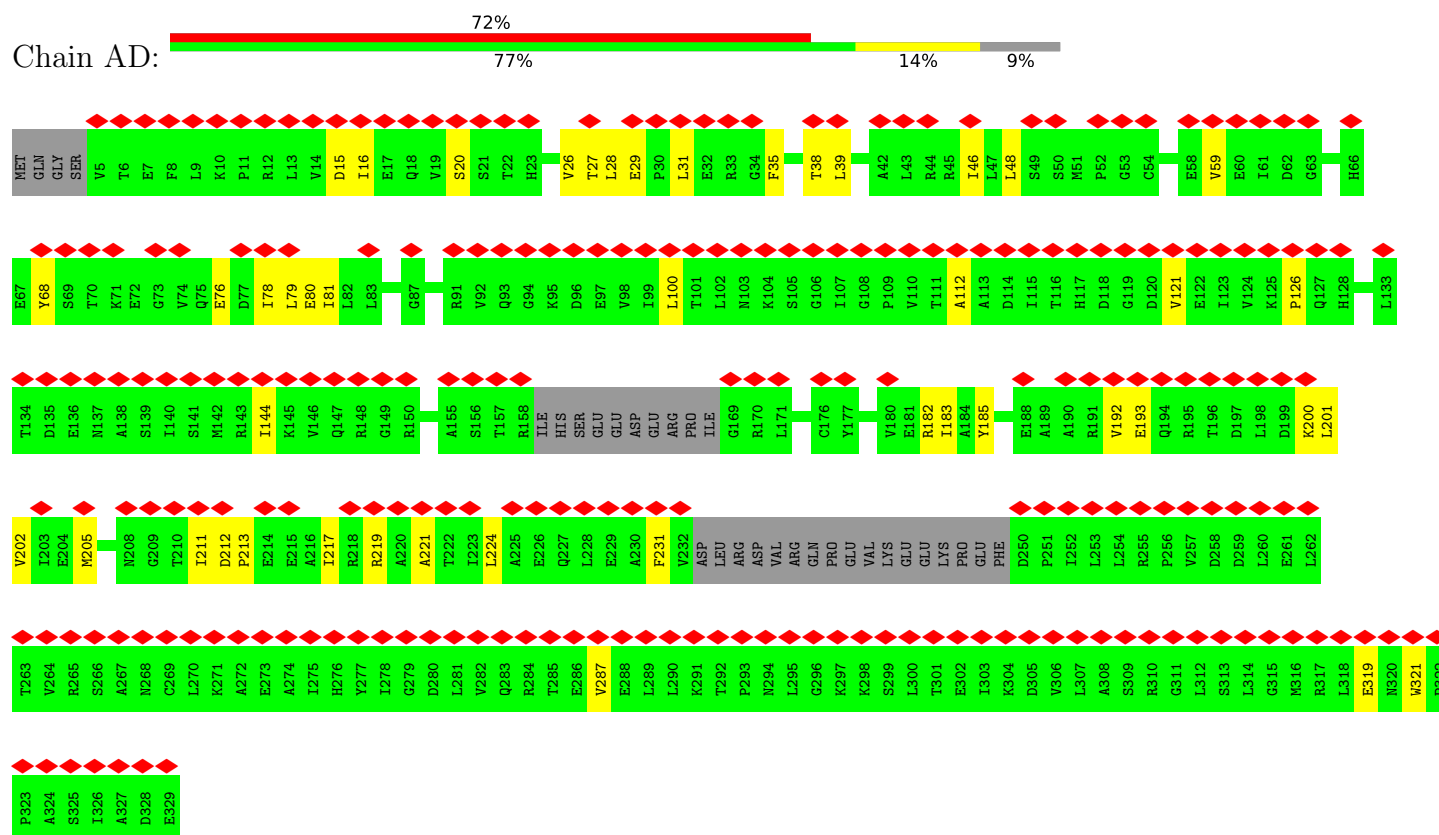
• Molecule 12: Transcription termination/antitermination protein NusG



• Molecule 13: DNA-directed RNA polymerase subunit alpha

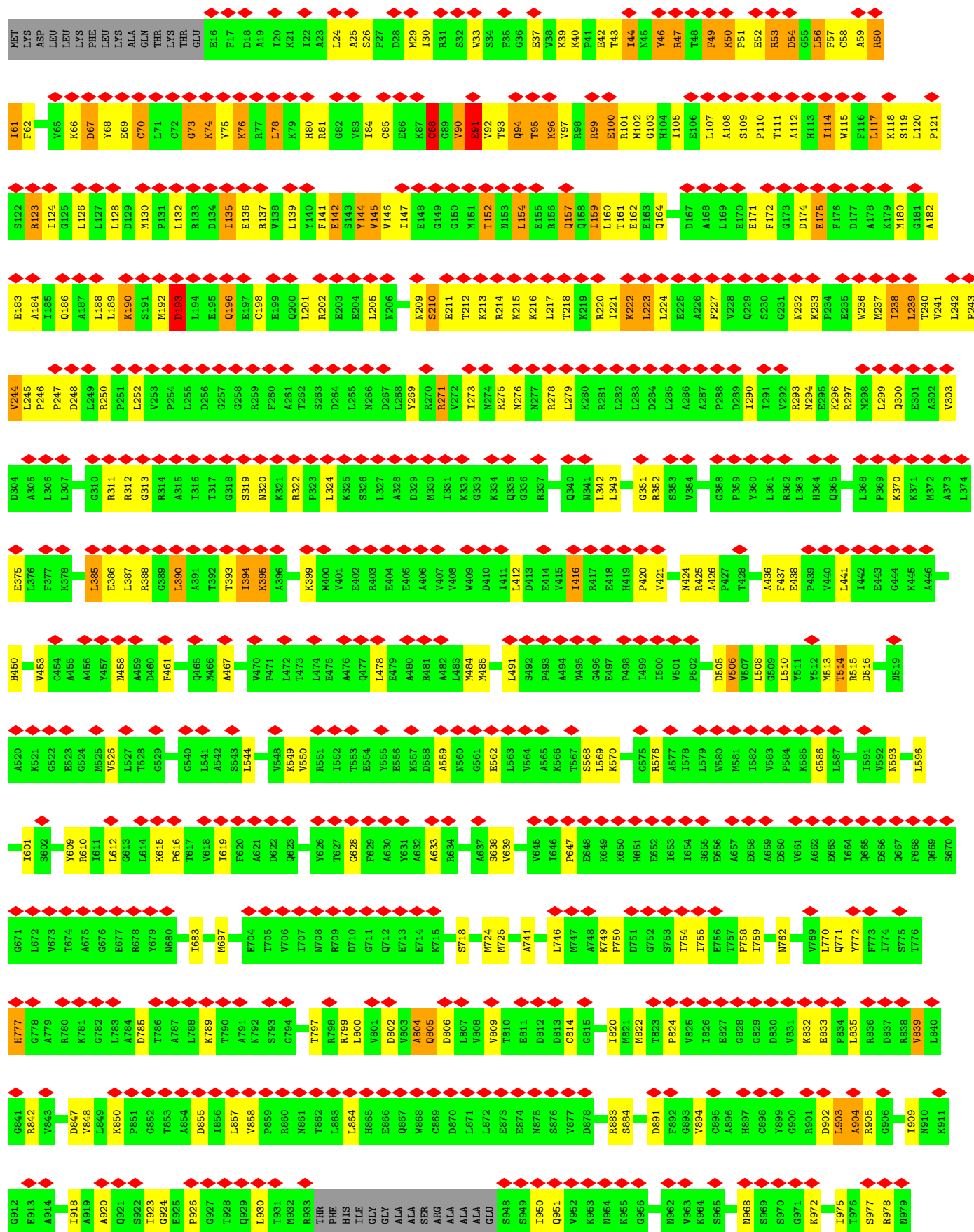


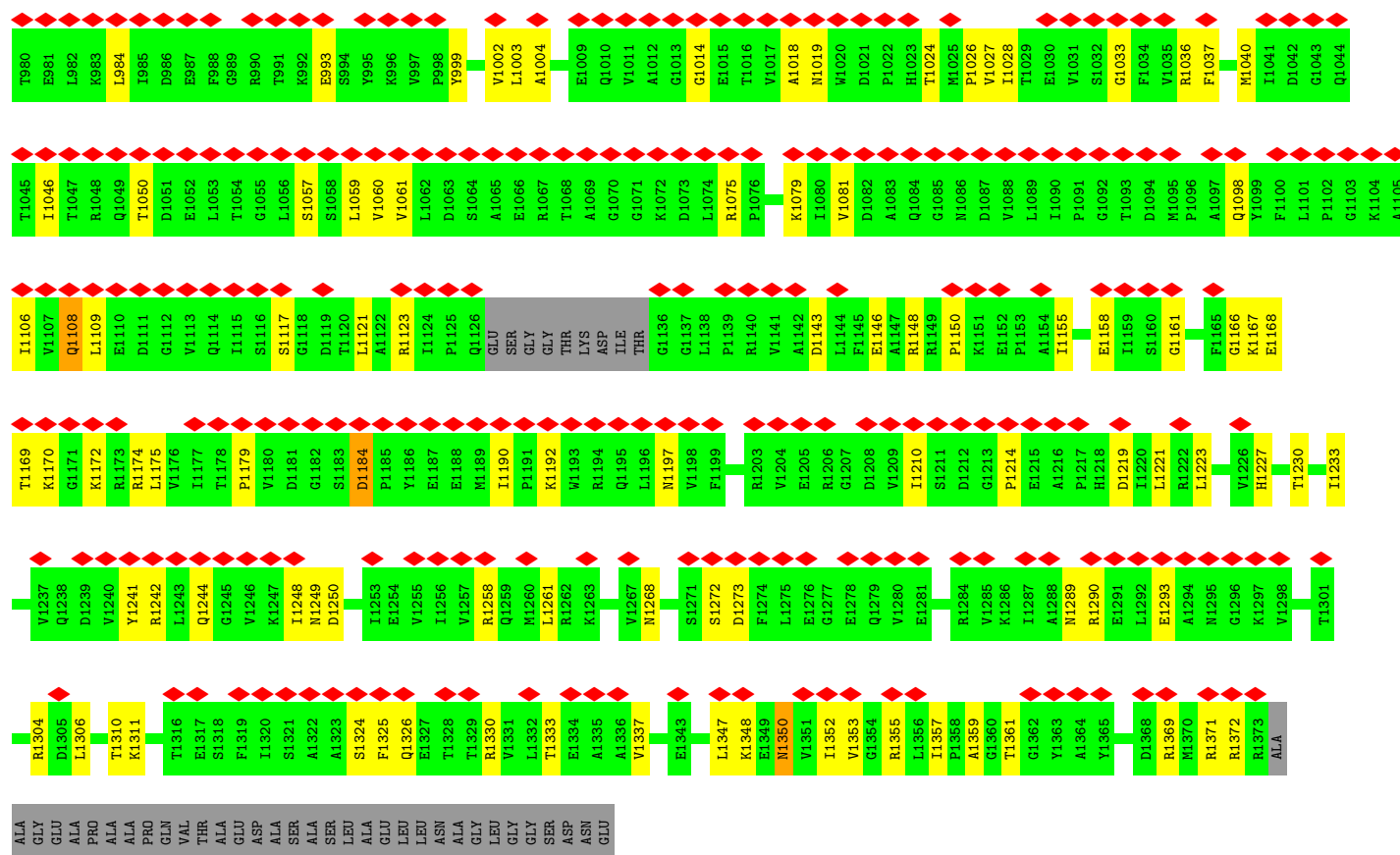
• Molecule 13: DNA-directed RNA polymerase subunit alpha



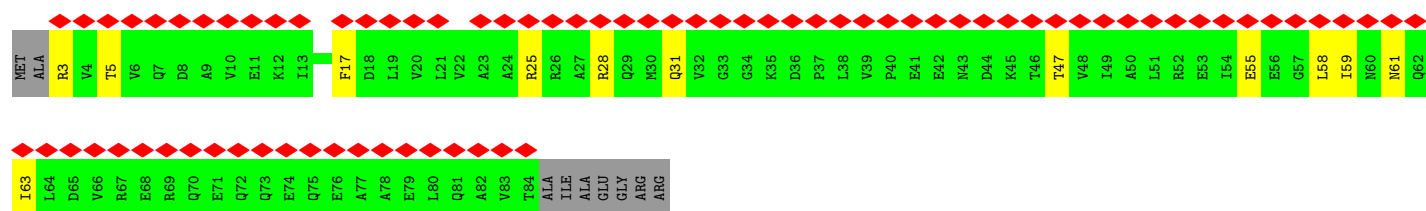
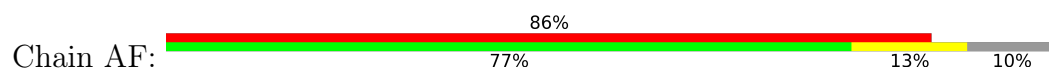
• Molecule 14: DNA-directed RNA polymerase subunit beta'



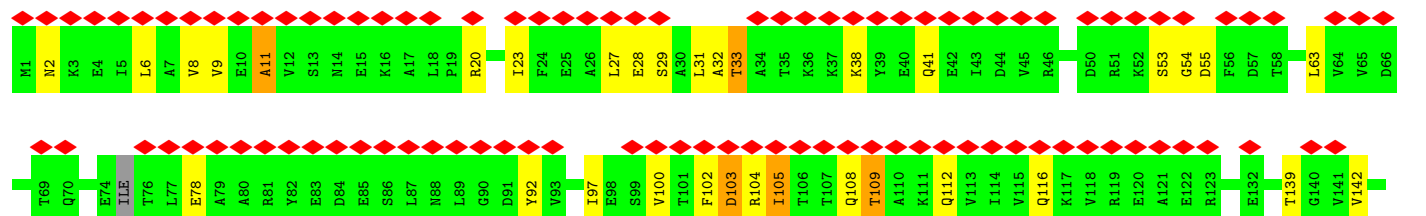


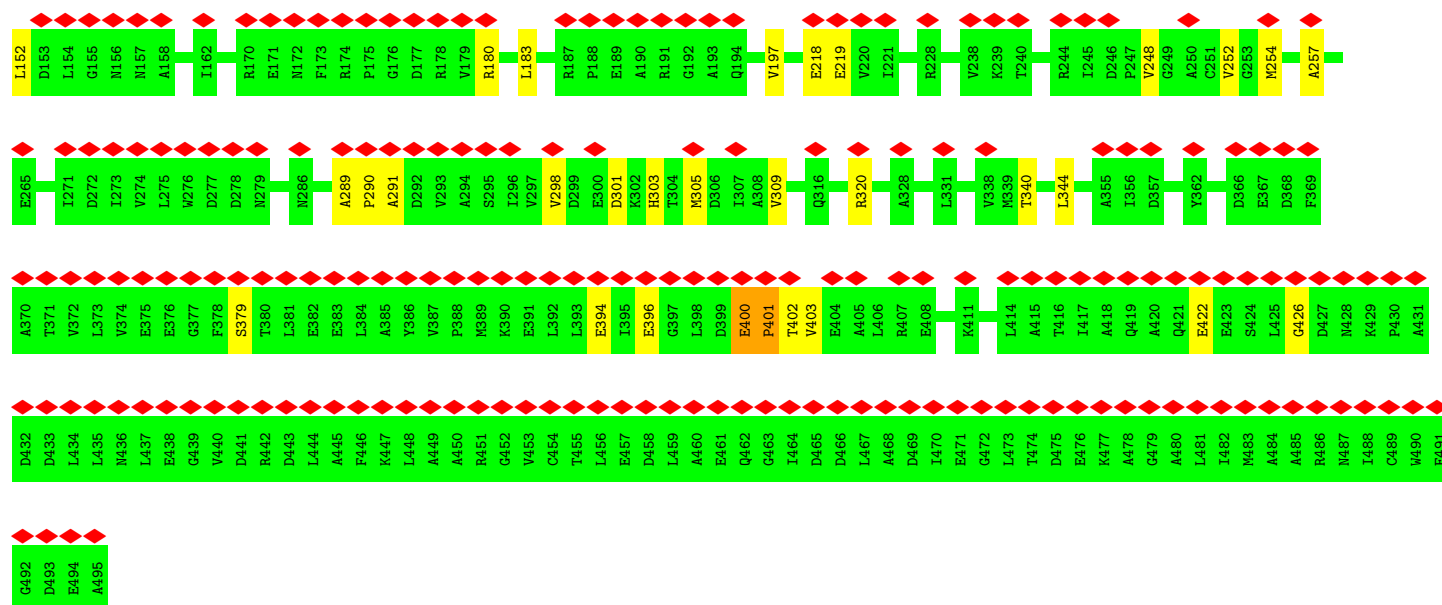


• Molecule 15: DNA-directed RNA polymerase subunit omega

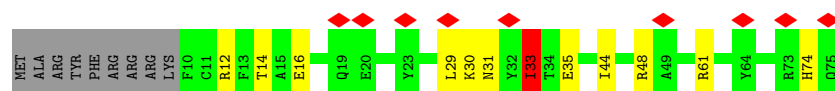
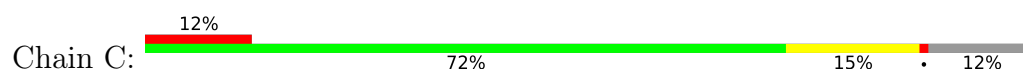


• Molecule 16: Transcription termination/antitermination protein NusA

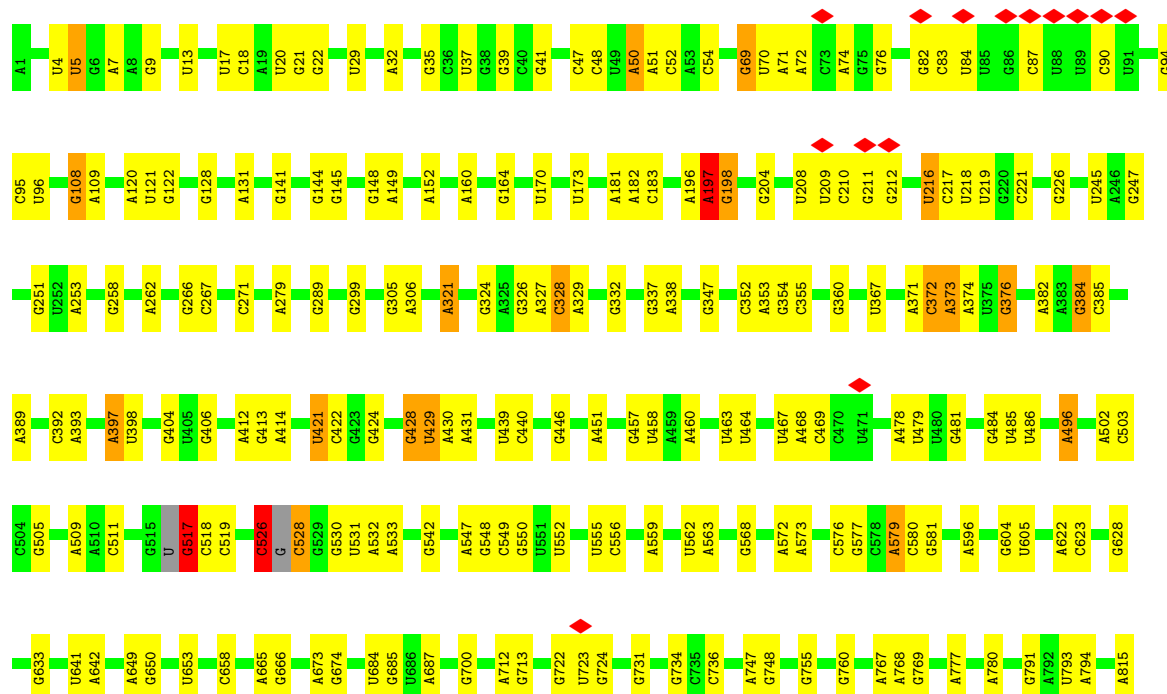


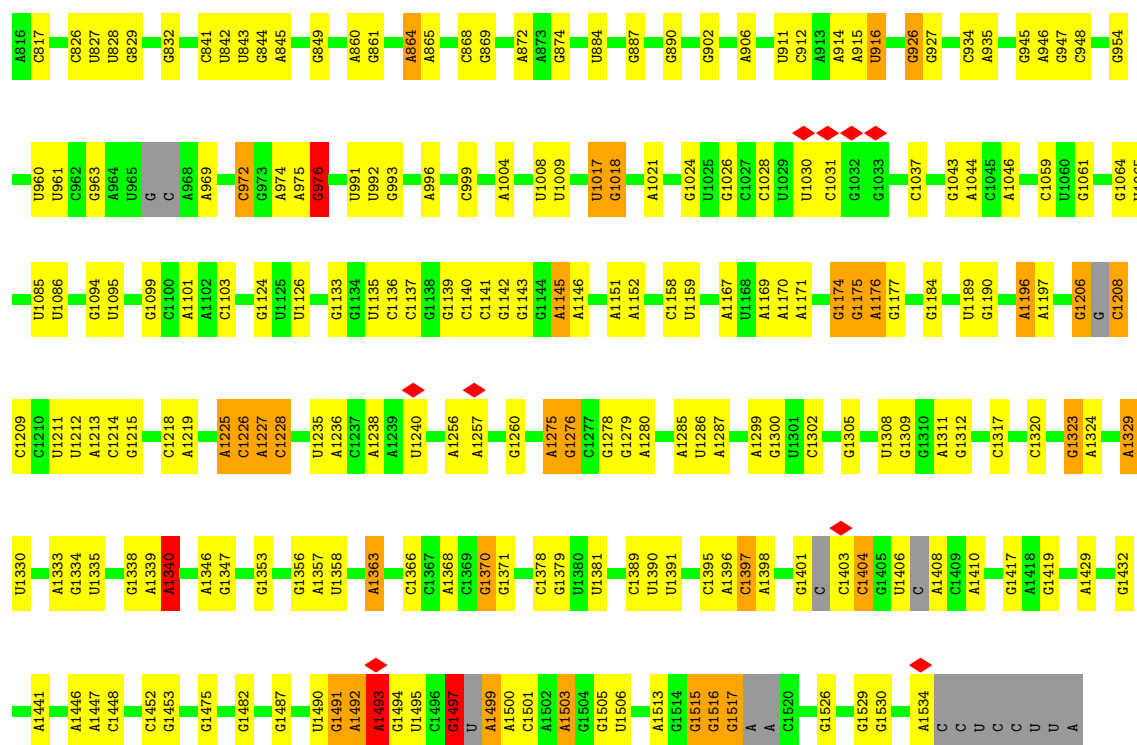


- Molecule 17: 30S ribosomal protein S18

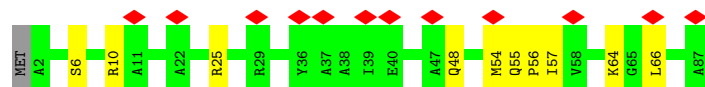
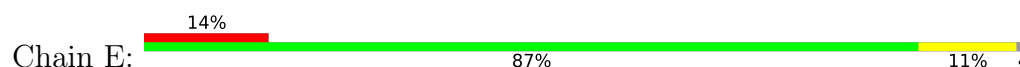


- Molecule 18: 16S rRNA

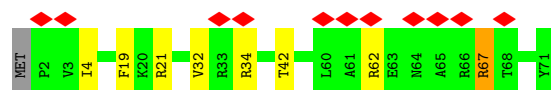
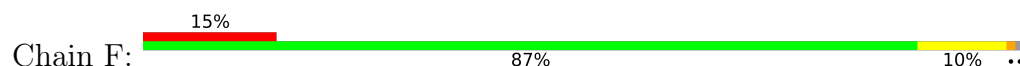




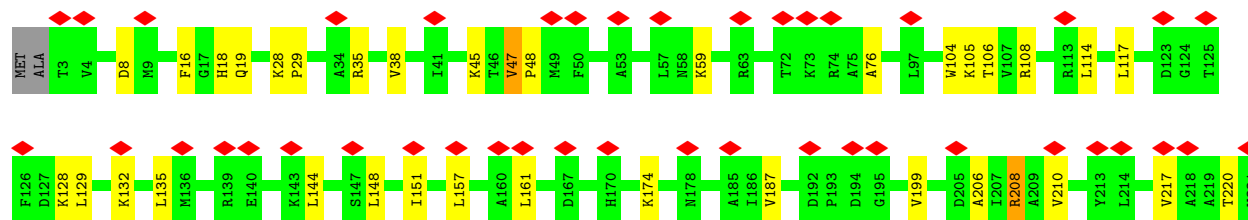
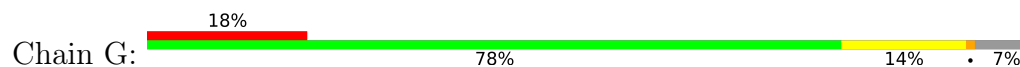
• Molecule 19: 30S ribosomal protein S20

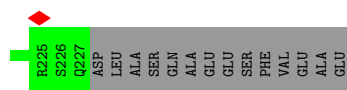


• Molecule 20: 30S ribosomal protein S21

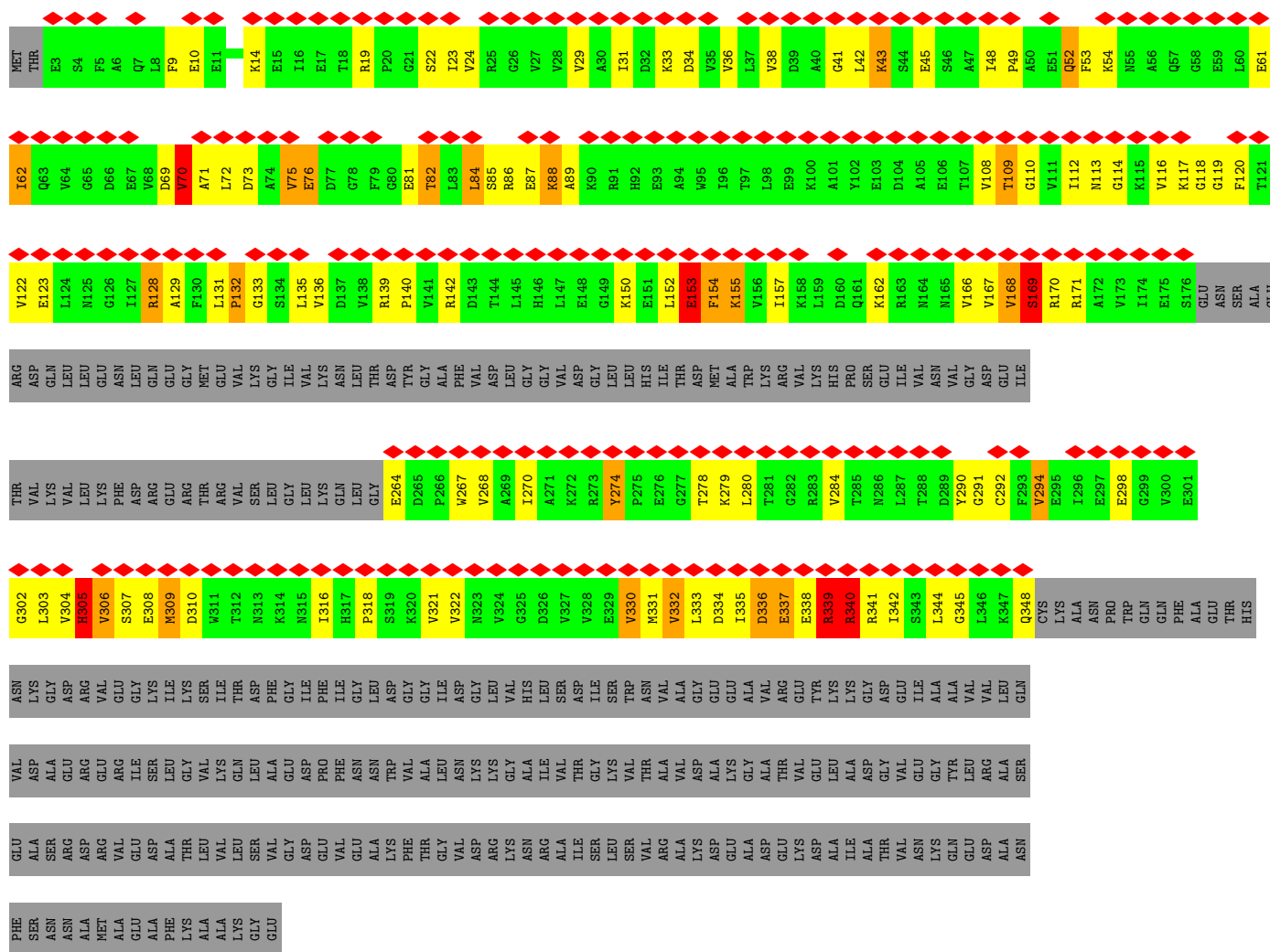
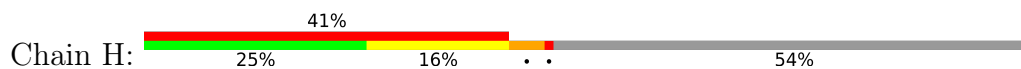


• Molecule 21: 30S ribosomal protein S2

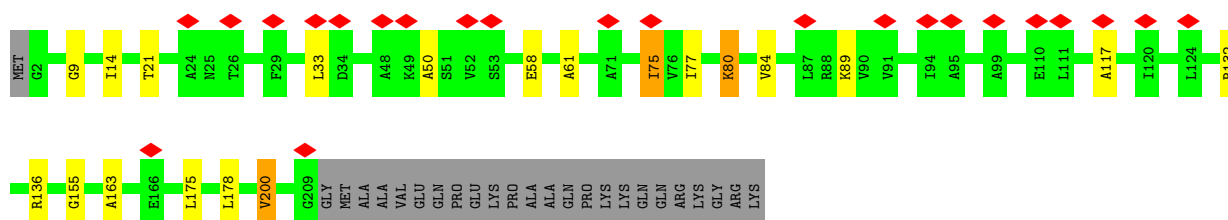
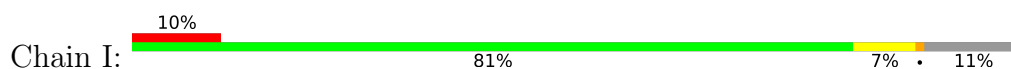




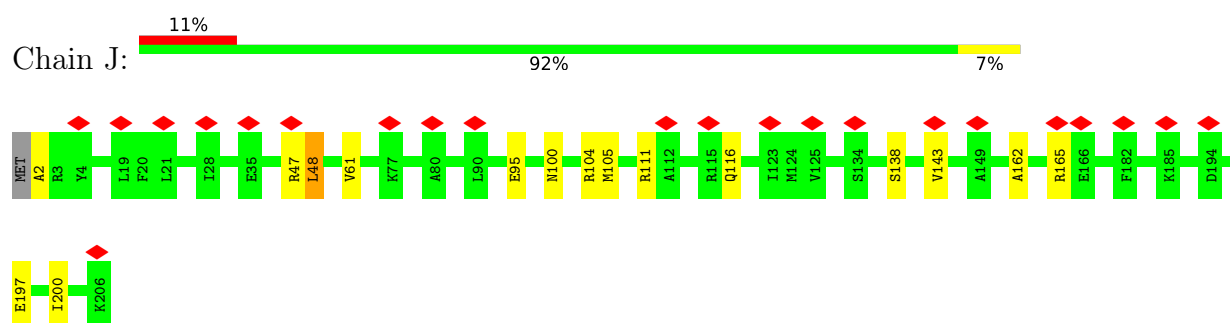
• Molecule 22: 30S ribosomal protein S1



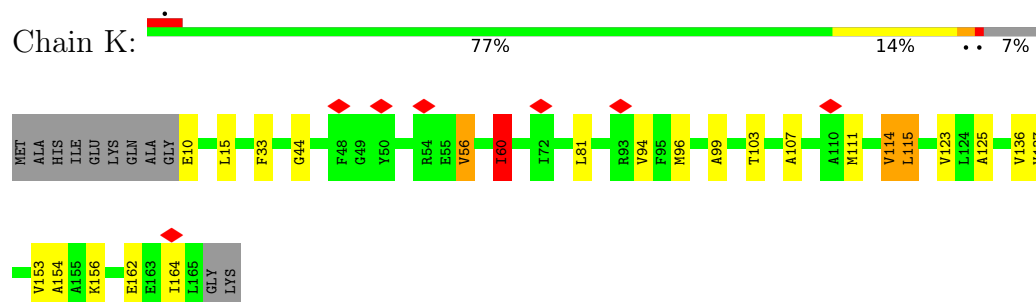
• Molecule 23: 30S ribosomal protein S3



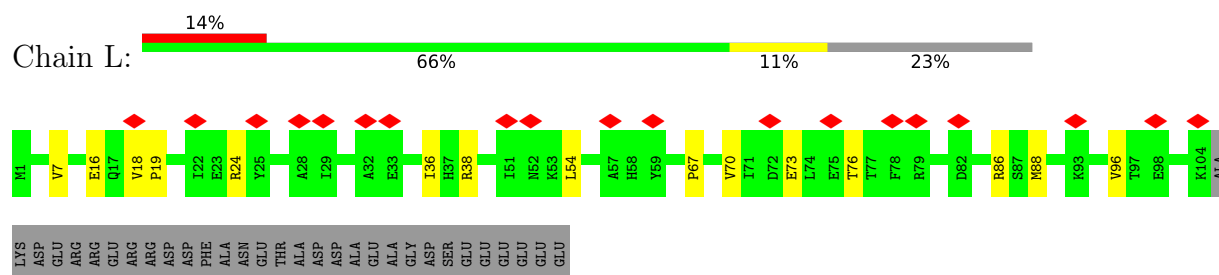
• Molecule 24: 30S ribosomal protein S4



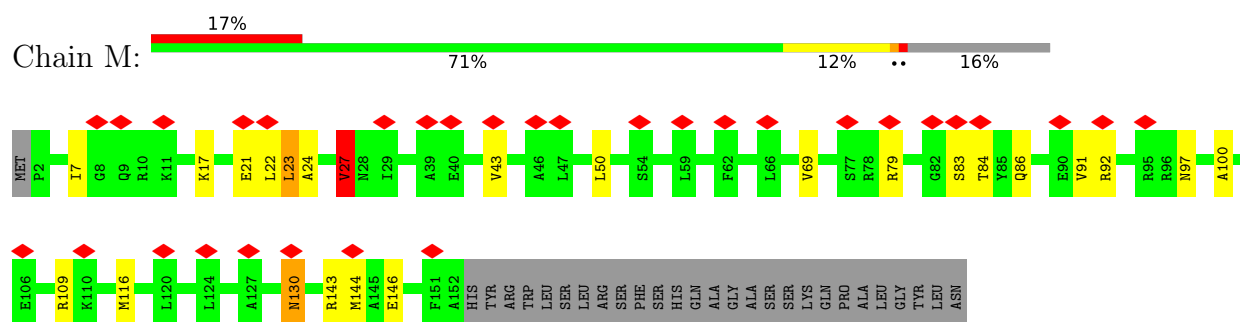
- Molecule 25: 30S ribosomal protein S5



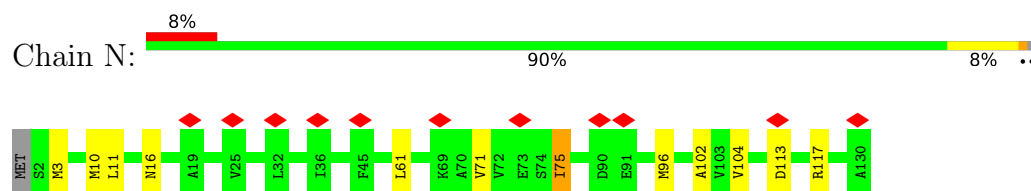
- Molecule 26: 30S ribosomal protein S6



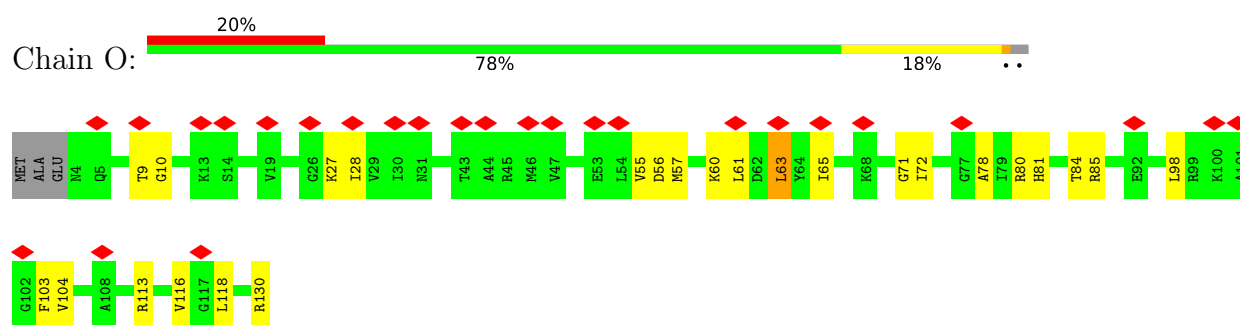
- Molecule 27: 30S ribosomal protein S7



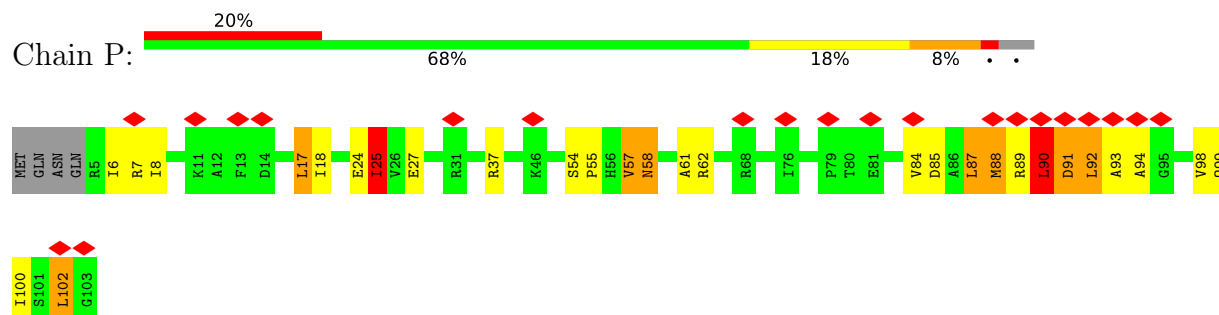
- Molecule 28: 30S ribosomal protein S8



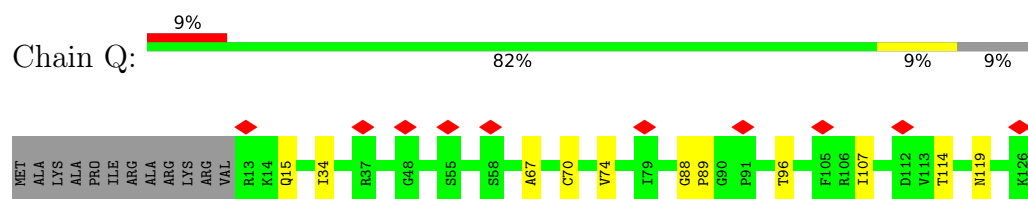
- Molecule 29: 30S ribosomal protein S9



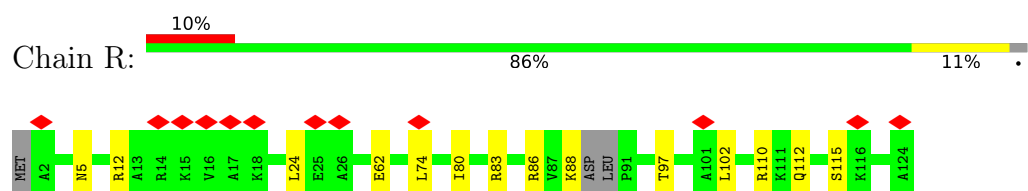
- Molecule 30: 30S ribosomal protein S10



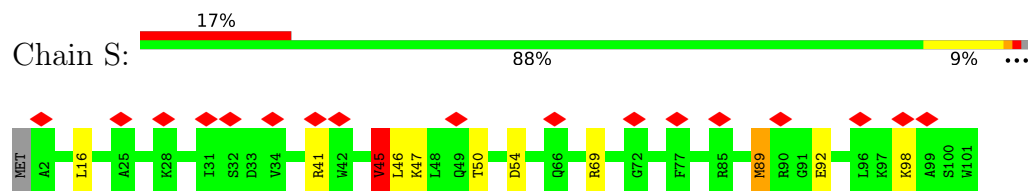
- Molecule 31: 30S ribosomal protein S11



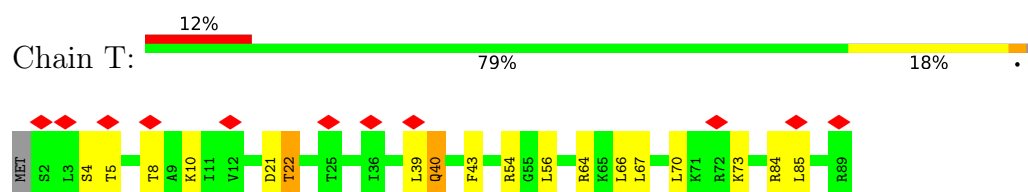
- Molecule 32: 30S ribosomal protein S12



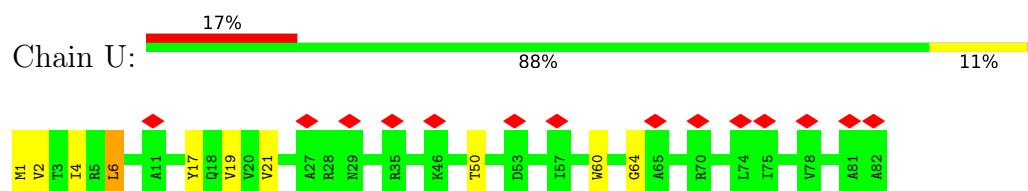
- Molecule 33: 30S ribosomal protein S14



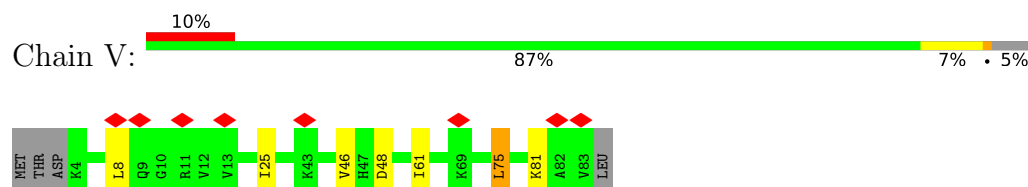
- Molecule 34: 30S ribosomal protein S15



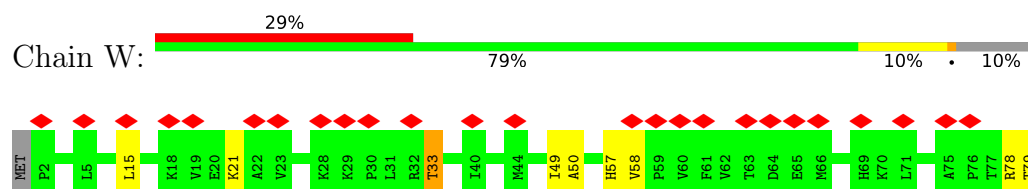
- Molecule 35: 30S ribosomal protein S16



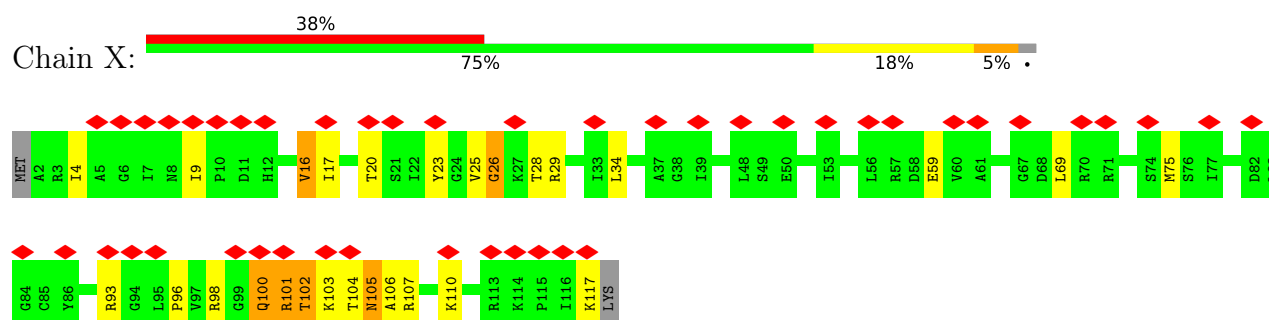
- Molecule 36: 30S ribosomal protein S17



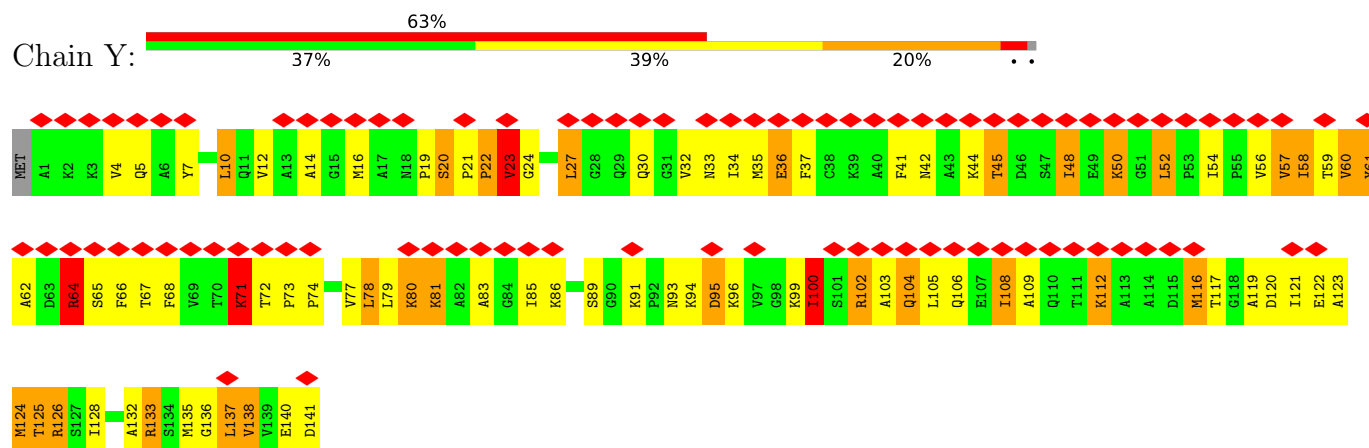
- Molecule 37: 30S ribosomal protein S19



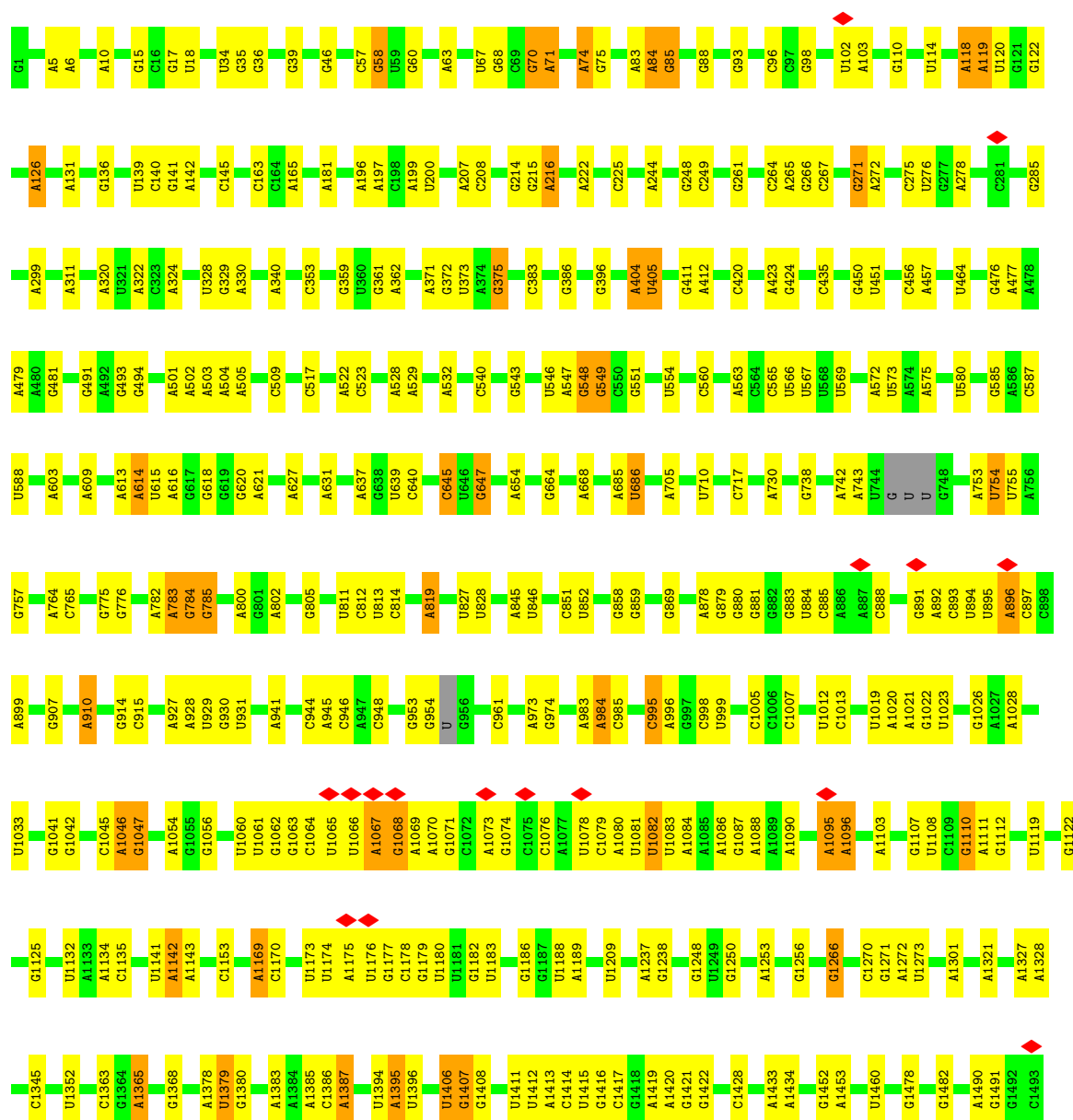
- Molecule 38: 30S ribosomal protein S13

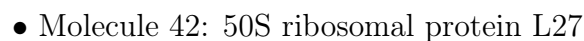


- Molecule 39: 50S ribosomal protein L11

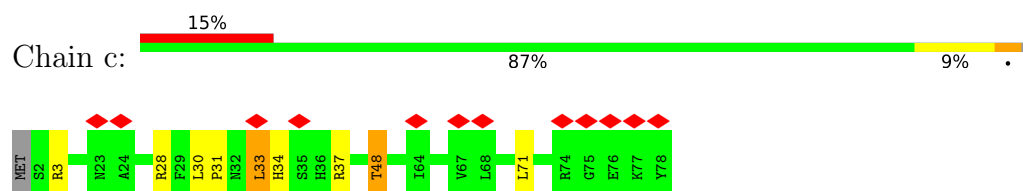


- Molecule 40: 50S ribosomal protein L7/L12

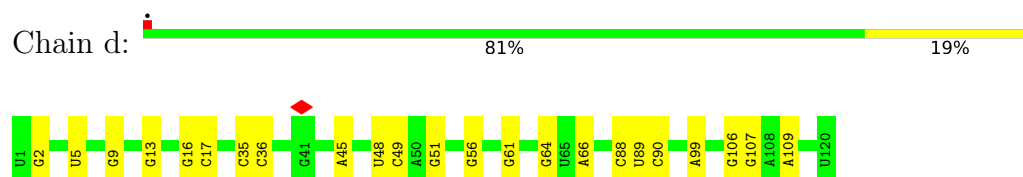




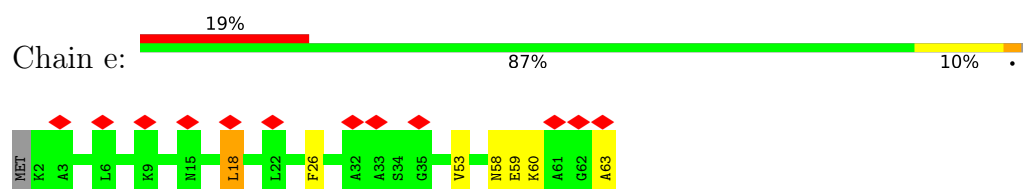
- Molecule 43: 50S ribosomal protein L28



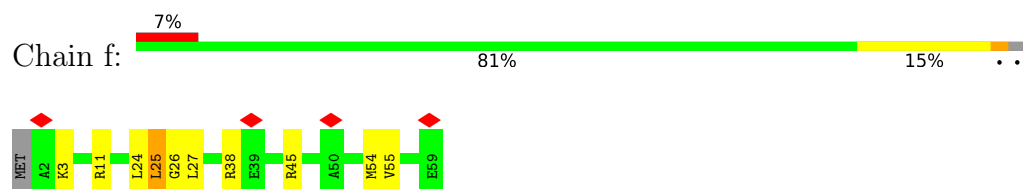
- Molecule 44: 5S rRNA



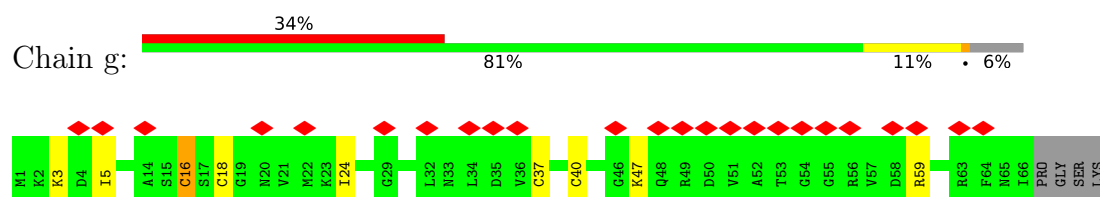
- Molecule 45: 50S ribosomal protein L29



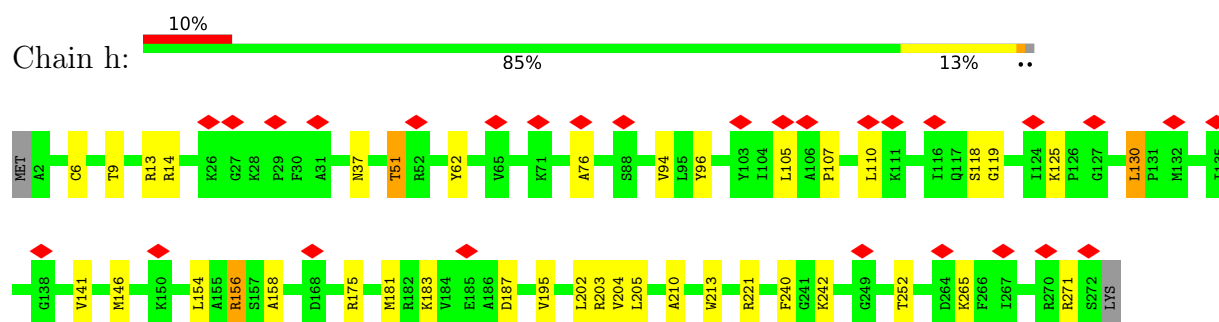
- Molecule 46: 50S ribosomal protein L30



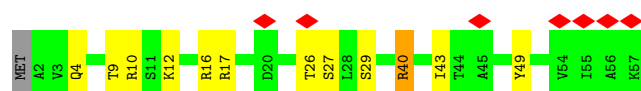
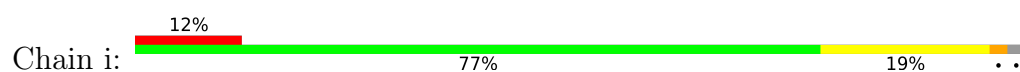
- Molecule 47: 50S ribosomal protein L31



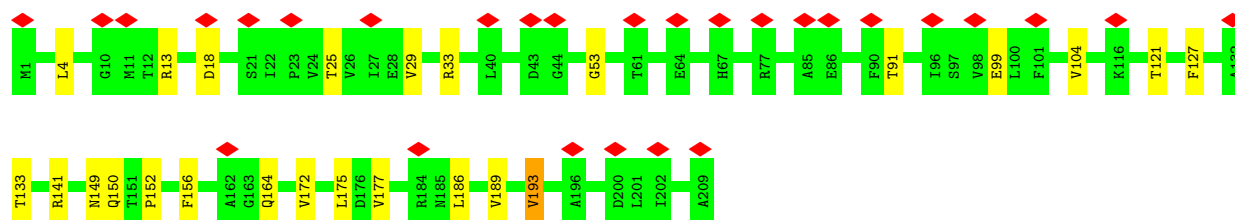
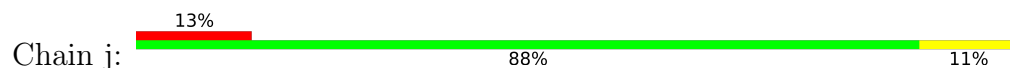
- Molecule 48: 50S ribosomal protein L2



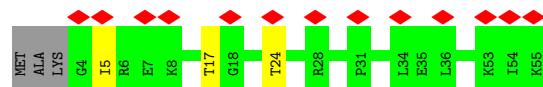
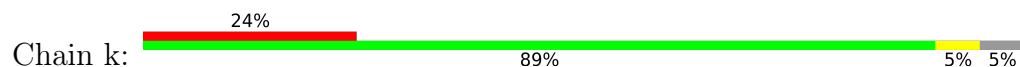
- Molecule 49: 50S ribosomal protein L32



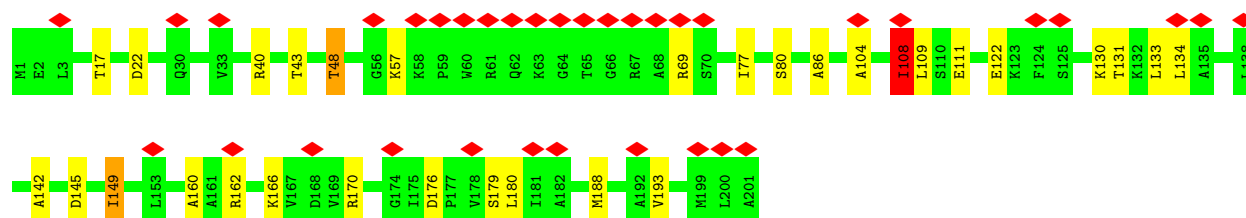
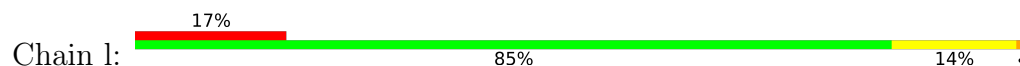
- Molecule 50: 50S ribosomal protein L3



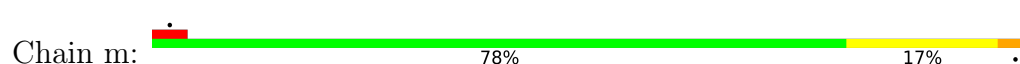
- Molecule 51: 50S ribosomal protein L33



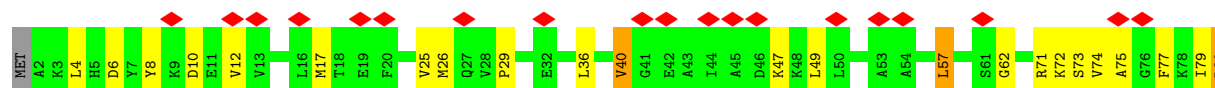
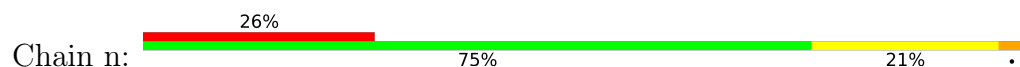
- Molecule 52: 50S ribosomal protein L4

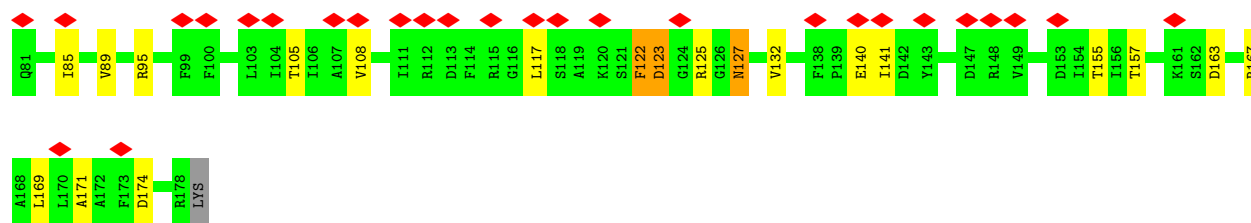


- Molecule 53: 50S ribosomal protein L34

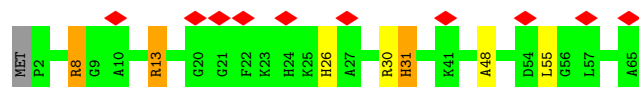
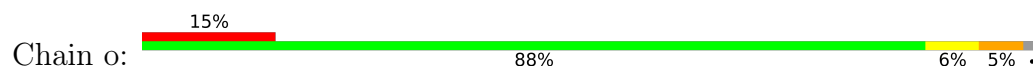


- Molecule 54: 50S ribosomal protein L5

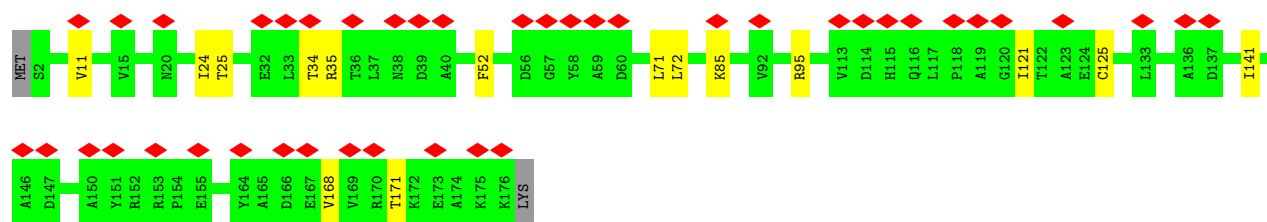
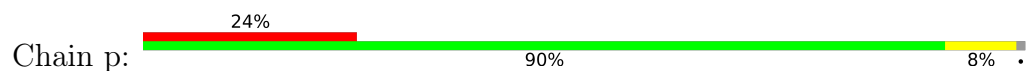




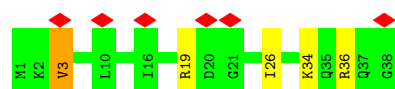
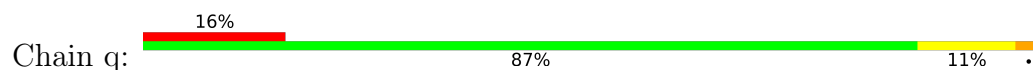
• Molecule 55: 50S ribosomal protein L35



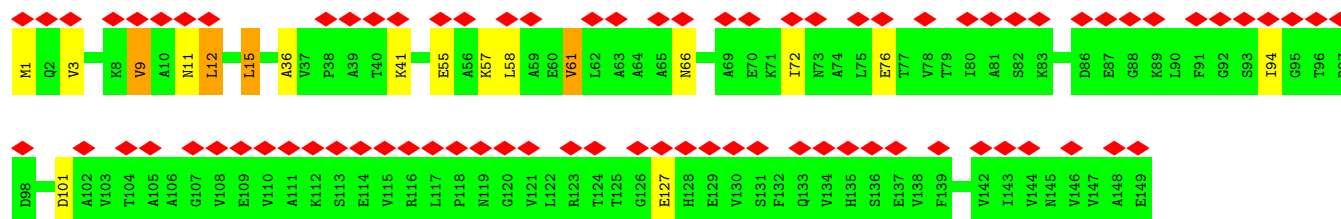
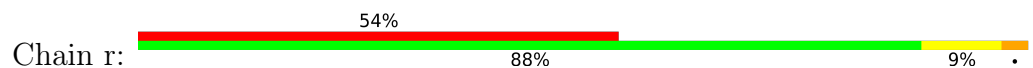
• Molecule 56: 50S ribosomal protein L6



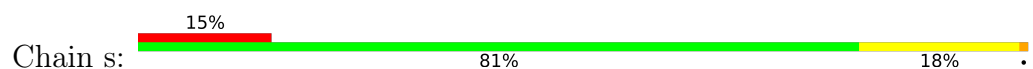
• Molecule 57: 50S ribosomal protein L36

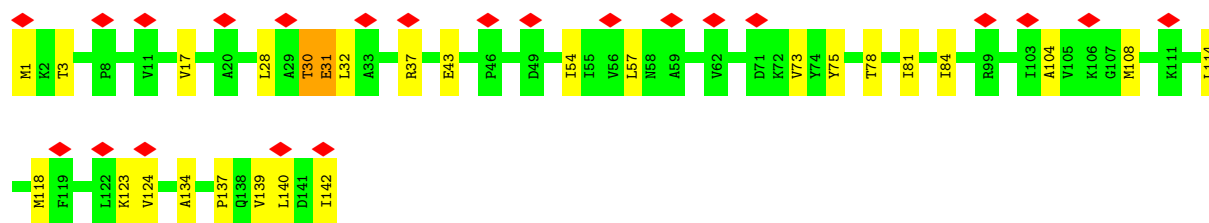


• Molecule 58: 50S ribosomal protein L9

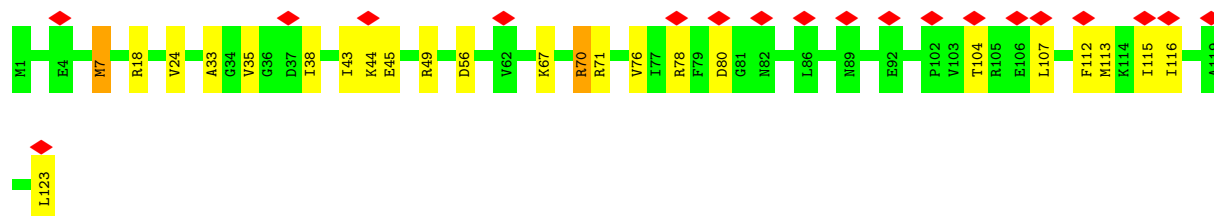
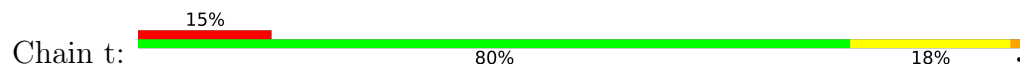


• Molecule 59: 50S ribosomal protein L13

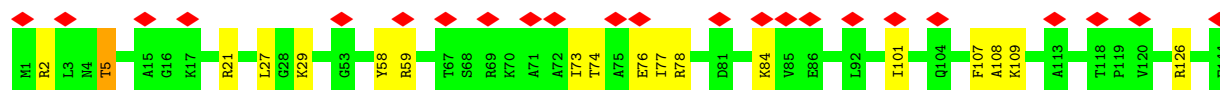
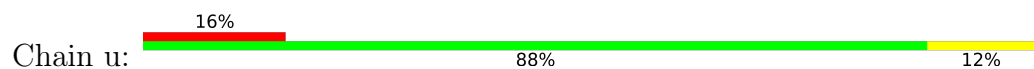




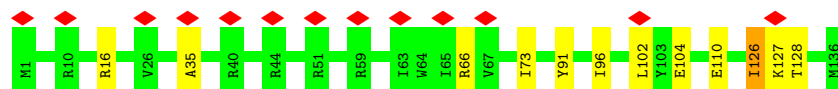
- Molecule 60: 50S ribosomal protein L14



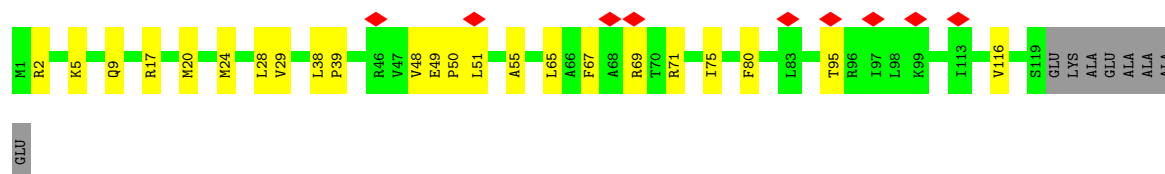
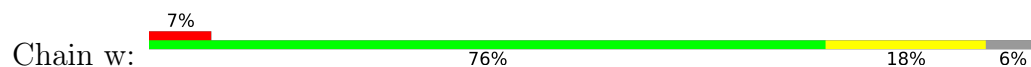
- Molecule 61: 50S ribosomal protein L15



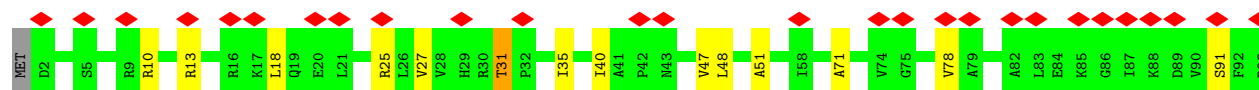
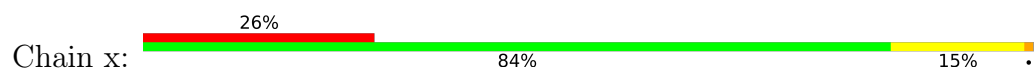
- Molecule 62: 50S ribosomal protein L16

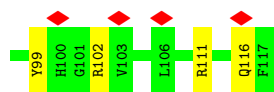


- Molecule 63: 50S ribosomal protein L17

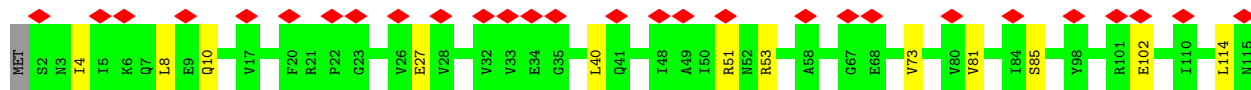
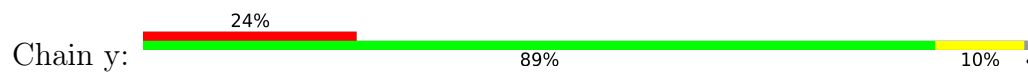


- Molecule 64: 50S ribosomal protein L18

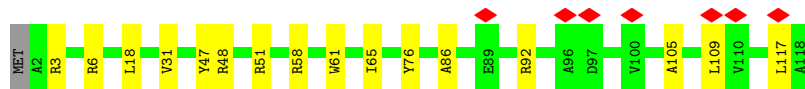
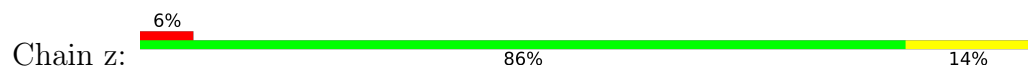




- Molecule 65: 50S ribosomal protein L19



- Molecule 66: 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	11509	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	0.031	Depositor
Minimum map value	-0.009	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00868	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	0.78	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	0.56	1/603 (0.2%)	0.56	0/926
8	7	0.61	3/761 (0.4%)	0.89	4/1178 (0.3%)
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	0.40	0/10736	0.64	0/14487
12	AB	0.71	0/1304	0.90	1/1759 (0.1%)
13	AC	0.35	0/2110	0.61	0/2873
13	AD	0.29	0/2091	0.59	0/2847
14	AE	0.54	10/10545 (0.1%)	0.74	23/14236 (0.2%)
15	AF	0.29	0/652	0.61	0/879
16	AG	0.64	0/2440	0.90	6/3396 (0.2%)
17	C	0.66	0/553	1.14	2/743 (0.3%)
18	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
19	E	0.76	0/675	1.32	0/895
20	F	0.71	0/597	1.20	0/792
21	G	0.65	0/1791	1.08	1/2413 (0.0%)
22	H	0.76	4/1746 (0.2%)	1.58	33/2382 (1.4%)
23	I	0.59	0/1663	0.98	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.64	1/1165 (0.1%)	1.06	2/1568 (0.1%)
26	L	0.58	0/867	0.94	0/1171
27	M	0.68	0/1195	1.19	3/1602 (0.2%)
28	N	0.55	0/989	0.91	0/1326
29	O	0.59	0/1034	1.02	1/1375 (0.1%)
30	P	0.64	0/800	1.13	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.55	0/893	0.91	0/1205
32	R	0.49	0/952	0.81	0/1274
33	S	0.64	0/817	1.11	1/1088 (0.1%)
34	T	0.69	0/722	1.21	0/964
35	U	0.58	0/659	0.99	0/884
36	V	0.46	0/657	0.72	0/881
37	W	0.51	0/680	0.83	0/915
38	X	0.67	0/909	1.21	3/1215 (0.2%)
39	Y	1.04	0/1046	1.09	1/1410 (0.1%)
40	Z	1.02	0/227	1.12	0/304
41	a	0.40	3/69247 (0.0%)	0.75	57/107985 (0.1%)
42	b	0.51	0/589	0.76	0/779
43	c	0.63	0/635	0.97	0/848
44	d	0.37	0/2872	0.69	0/4478
45	e	0.69	0/502	1.19	0/667
46	f	0.62	0/452	1.02	0/605
47	g	0.56	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.52	0/450	0.94	0/599
50	j	0.60	0/1586	0.87	0/2134
51	k	0.47	0/433	0.80	0/576
52	l	0.61	0/1571	1.03	1/2113 (0.0%)
53	m	0.68	0/380	1.22	0/498
54	n	0.63	0/1434	1.18	10/1926 (0.5%)
55	o	0.64	0/513	1.11	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.51	0/303	0.88	0/397
58	r	0.63	0/1122	0.97	1/1515 (0.1%)
59	s	0.68	0/1152	1.02	2/1551 (0.1%)
60	t	0.57	0/955	0.88	0/1279
61	u	0.55	0/1062	0.95	1/1413 (0.1%)
62	v	0.60	0/1093	0.97	0/1460
63	w	0.68	0/964	1.13	0/1289
64	x	0.61	0/902	1.09	0/1209
65	y	0.53	0/929	0.79	0/1242
66	z	0.80	0/960	1.25	0/1278
All	All	0.49	35/193531 (0.0%)	0.82	212/284843 (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
10	B	0	2
11	AA	0	1
13	AC	0	3
13	AD	0	3
14	AE	0	5
16	AG	0	1
22	H	0	3
38	X	0	1
All	All	0	21

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.30	1.70	1.47
14	AE	93	THR	CA-C	12.25	1.69	1.52
22	H	169	SER	N-CA	11.74	1.61	1.46
18	D	1516	G	O3'-P	-10.75	1.45	1.61
14	AE	70	CYS	CA-CB	-8.77	1.41	1.53
18	D	1339	A	O3'-P	8.47	1.73	1.61
8	7	19	G	C1'-N9	-7.43	1.36	1.48
22	H	88	LYS	N-CA	7.05	1.55	1.46
8	7	-19	U	C1'-N1	7.05	1.59	1.48
6	5	109	DT	O3'-P	6.97	1.71	1.61
18	D	145	G	O3'-P	6.77	1.71	1.61
18	D	196	A	O3'-P	6.62	1.71	1.61
22	H	168	VAL	C-N	6.37	1.42	1.33
18	D	1275	A	O3'-P	6.21	1.70	1.61
41	a	2434	A	O3'-P	6.08	1.70	1.61
18	D	1395	C	O3'-P	5.85	1.70	1.61
18	D	1515	G	O3'-P	-5.85	1.52	1.61
14	AE	90	VAL	CA-C	5.70	1.60	1.52
22	H	88	LYS	CA-C	5.68	1.60	1.52
25	K	56	VAL	CA-CB	5.53	1.57	1.54
18	D	1490	U	O3'-P	5.47	1.69	1.61
7	6	10	DG	C1'-N9	-5.40	1.35	1.46
8	7	-3	U	C1'-N1	5.37	1.56	1.48
18	D	1492	A	O3'-P	5.35	1.69	1.61
41	a	1905	C	O3'-P	5.28	1.69	1.61
41	a	2167	U	O3'-P	5.25	1.69	1.61
14	AE	1350	ASN	CG-ND2	-5.21	1.22	1.33
14	AE	424	ASN	CG-ND2	-5.21	1.22	1.33
9	9	116	GLU	N-CA	5.16	1.49	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	AE	777	HIS	ND1-CE1	5.16	1.37	1.32
14	AE	777	HIS	CD2-NE2	-5.14	1.32	1.37
9	9	129	LEU	C-N	5.13	1.45	1.33
14	AE	1268	ASN	CG-OD1	5.04	1.33	1.23
14	AE	1108	GLN	CD-OE1	5.03	1.33	1.23
14	AE	450	HIS	CD2-NE2	-5.01	1.32	1.37

All (212) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1516	G	O3'-P-O5'	17.43	130.15	104.00
22	H	88	LYS	CA-C-N	16.96	143.62	120.38
22	H	88	LYS	C-N-CA	16.96	143.62	120.38
10	B	29	G	C3'-C2'-O2'	15.95	134.62	110.70
9	9	129	LEU	CA-C-N	15.79	139.58	119.84
9	9	129	LEU	C-N-CA	15.79	139.58	119.84
18	D	1516	G	P-O3'-C3'	-15.55	96.87	120.20
22	H	332	VAL	N-CA-C	13.70	124.59	110.62
22	H	169	SER	N-CA-C	12.80	138.07	110.80
22	H	330	VAL	N-CA-C	12.19	126.94	109.51
22	H	305	HIS	N-CA-C	11.95	131.09	111.37
14	AE	90	VAL	N-CA-C	9.88	122.18	107.75
41	a	2244	U	C1'-C2'-O2'	-9.80	93.70	108.40
54	n	73	SER	N-CA-CB	-9.58	94.56	110.47
18	D	1206	G	C4'-C3'-O3'	9.51	127.27	113.00
30	P	54	SER	CA-C-N	9.34	129.03	118.85
30	P	54	SER	C-N-CA	9.34	129.03	118.85
41	a	2250	G	C4'-C3'-O3'	-9.25	95.52	109.40
16	AG	104	ARG	N-CA-C	-9.10	96.59	110.70
18	D	1401	G	C4'-C3'-O3'	8.81	126.22	113.00
18	D	428	G	C4'-C3'-O3'	8.71	122.47	109.40
8	7	-20	A	O3'-P-O5'	-8.61	91.08	104.00
9	9	130	PRO	CA-N-CD	-8.59	99.98	112.00
22	H	339	ARG	CA-C-N	8.51	137.80	121.54
22	H	339	ARG	C-N-CA	8.51	137.80	121.54
18	D	1515	G	O3'-P-O5'	-8.48	91.28	104.00
33	S	45	VAL	N-CA-CB	8.44	120.43	110.55
41	a	2296	U	C4'-C3'-O3'	8.42	122.03	109.40
8	7	-17	U	C2'-C3'-O3'	8.37	122.05	109.50
41	a	404	A	C2'-C3'-O3'	8.33	122.00	109.50
30	P	57	VAL	N-CA-C	8.28	120.02	107.77
41	a	2252	G	N9-C1'-C2'	-8.17	99.75	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	197	A	C2'-C3'-O3'	8.17	121.75	109.50
18	D	1401	G	N9-C1'-C2'	-7.92	100.11	112.00
22	H	155	LYS	CA-C-N	-7.87	110.79	121.66
22	H	155	LYS	C-N-CA	-7.87	110.79	121.66
41	a	2425	A	C2'-C3'-O3'	7.84	121.25	109.50
41	a	2071	A	C4'-C3'-O3'	-7.74	101.39	113.00
22	H	168	VAL	CA-C-N	7.68	136.22	121.54
22	H	168	VAL	C-N-CA	7.68	136.22	121.54
18	D	1493	A	C2'-C3'-O3'	7.68	125.22	113.70
14	AE	903	LEU	CA-C-N	7.67	136.18	121.54
14	AE	903	LEU	C-N-CA	7.67	136.18	121.54
22	H	84	LEU	N-CA-C	7.63	121.00	110.24
22	H	52	GLN	N-CA-C	-7.61	104.14	113.50
18	D	1339	A	P-O3'-C3'	7.60	131.60	120.20
25	K	60	ILE	N-CA-CB	7.57	119.41	110.55
38	X	102	THR	CB-CA-C	7.56	123.38	110.84
54	n	75	ALA	CA-C-N	7.52	129.54	120.14
54	n	75	ALA	C-N-CA	7.52	129.54	120.14
18	D	1499	A	N9-C1'-C2'	-7.52	100.72	112.00
18	D	528	C	N1-C1'-C2'	-7.47	100.80	112.00
54	n	73	SER	CB-CA-C	7.43	122.90	110.79
22	H	336	ASP	CB-CA-C	-7.42	98.70	110.79
10	B	28	C	P-O3'-C3'	7.39	131.28	120.20
21	G	47	VAL	O-C-N	7.36	125.13	120.42
25	K	56	VAL	O-C-N	7.35	125.12	120.42
41	a	783	A	C4'-C3'-O3'	7.34	124.01	113.00
41	a	2602	A	C4'-C3'-O3'	7.26	120.28	109.40
54	n	108	VAL	O-C-N	7.26	125.22	120.07
18	D	1497	G	C1'-C2'-O2'	-7.22	97.57	108.40
10	B	29	G	N9-C1'-C2'	-7.20	101.20	112.00
18	D	196	A	P-O3'-C3'	7.15	130.92	120.20
41	a	2162	G	C4'-C3'-O3'	7.13	120.09	109.40
41	a	896	A	C4'-C3'-O3'	7.08	120.03	109.40
41	a	1379	U	C2'-C3'-O3'	7.03	124.25	113.70
41	a	2225	A	C4'-C3'-O3'	7.00	119.90	109.40
41	a	2244	U	C4'-C3'-O3'	6.97	123.46	113.00
27	M	27	VAL	N-CA-CB	6.95	118.68	110.55
22	H	340	ARG	CA-C-N	-6.87	112.44	123.23
22	H	340	ARG	C-N-CA	-6.87	112.44	123.23
22	H	140	PRO	N-CA-CB	6.86	110.45	103.25
41	a	2252	G	C4'-C3'-O3'	6.83	123.25	113.00
54	n	71	ARG	CA-C-N	6.78	134.02	122.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	n	71	ARG	C-N-CA	6.78	134.02	122.37
16	AG	103	ASP	O-C-N	6.70	131.51	123.33
18	D	526	C	C4'-C3'-O3'	6.68	123.02	113.00
22	H	170	ARG	N-CA-C	6.68	119.66	110.24
41	a	2243	U	C4'-C3'-O3'	6.67	123.00	113.00
18	D	517	G	C5'-C4'-C3'	6.65	125.17	115.20
22	H	87	GLU	N-CA-C	-6.62	104.07	111.28
22	H	132	PRO	N-CA-CB	6.59	110.30	103.38
41	a	894	U	C2'-C3'-O3'	6.56	119.34	109.50
22	H	303	LEU	N-CA-C	6.56	121.12	112.13
22	H	112	ILE	N-CA-C	6.56	117.14	106.72
29	O	72	ILE	N-CA-C	-6.54	105.33	111.48
22	H	155	LYS	N-CA-C	-6.54	98.24	108.90
58	r	61	VAL	N-CA-CB	6.53	118.19	110.55
41	a	2167	U	P-O3'-C3'	6.53	129.99	120.20
41	a	2189	U	C1'-C2'-O2'	-6.51	102.03	111.80
54	n	127	ASN	CB-CA-C	6.49	121.61	110.77
14	AE	450	HIS	CB-CG-CD2	-6.46	122.80	131.20
18	D	526	C	N1-C1'-C2'	-6.46	102.30	112.00
55	o	13	ARG	N-CA-C	6.44	120.98	113.18
54	n	127	ASN	CA-CB-CG	-6.43	106.17	112.60
18	D	1340	A	C1'-C2'-O2'	6.42	118.03	108.40
14	AE	93	THR	CA-C-N	6.39	133.07	121.06
14	AE	93	THR	C-N-CA	6.39	133.07	121.06
18	D	69	G	C4'-C3'-O3'	-6.37	103.44	113.00
41	a	754	U	N1-C1'-C2'	6.37	121.56	112.00
14	AE	61	ILE	CA-C-N	-6.34	114.03	121.64
14	AE	61	ILE	C-N-CA	-6.34	114.03	121.64
41	a	2434	A	P-O3'-C3'	6.34	129.71	120.20
18	D	1208	C	N1-C1'-C2'	-6.29	102.56	112.00
14	AE	777	HIS	CB-CG-CD2	-6.27	123.04	131.20
22	H	153	GLU	N-CA-C	-6.27	97.45	110.80
8	7	11	U	C4'-C3'-O3'	6.25	118.77	109.40
22	H	113	ASN	N-CA-C	6.25	118.17	111.36
41	a	2425	A	C4'-C3'-O3'	6.24	118.75	109.40
10	B	28	C	O3'-P-O5'	-6.22	94.67	104.00
17	C	33	ILE	CA-C-O	-6.15	115.04	121.93
18	D	1206	G	N9-C1'-C2'	-6.14	102.79	112.00
14	AE	70	CYS	CB-CA-C	6.12	120.32	110.29
18	D	1516	G	OP1-P-O3'	-6.06	89.83	108.00
27	M	92	ARG	CA-C-N	6.06	125.54	119.24
27	M	92	ARG	C-N-CA	6.06	125.54	119.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	2210	U	C4'-C3'-O3'	6.02	118.43	109.40
14	AE	90	VAL	CA-C-O	-6.01	114.14	120.39
41	a	271	G	C4'-C3'-O3'	6.00	118.40	109.40
18	D	1408	A	C4'-C3'-O3'	5.98	121.97	113.00
18	D	550	G	C3'-C2'-O2'	5.98	119.67	110.70
41	a	1913	A	C2'-C3'-O3'	5.97	118.46	109.50
12	AB	122	PRO	N-CA-CB	5.95	109.87	103.33
41	a	2308	G	C2'-C3'-O3'	-5.92	104.83	113.70
41	a	2820	A	C4'-C3'-O3'	-5.91	104.13	113.00
22	H	150	LYS	N-CA-C	5.88	118.30	110.53
52	l	108	ILE	N-CA-CB	5.87	118.52	110.54
22	H	109	THR	N-CA-C	-5.86	99.10	109.06
22	H	75	VAL	N-CA-C	5.83	116.52	108.12
41	a	2756	U	C4'-C3'-O3'	5.82	118.14	109.40
38	X	26	GLY	N-CA-C	-5.82	104.33	112.13
54	n	72	LYS	N-CA-C	-5.81	99.19	109.06
18	D	1275	A	P-O3'-C3'	5.79	128.89	120.20
10	B	29	G	O5'-C5'-C4'	-5.77	102.84	111.50
18	D	1406	U	N1-C1'-C2'	-5.76	103.37	112.00
14	AE	91	GLU	N-CA-C	5.75	123.05	110.80
41	a	70	G	C4'-C3'-O3'	5.75	118.03	109.40
16	AG	11	ALA	CA-C-N	5.75	132.05	121.70
16	AG	11	ALA	C-N-CA	5.75	132.05	121.70
41	a	1905	C	P-O3'-C3'	5.75	128.82	120.20
18	D	976	G	C4'-C3'-O3'	-5.74	104.39	113.00
10	A	48	C	N1-C1'-C2'	5.73	120.59	112.00
41	a	2168	G	C4'-C3'-O3'	-5.70	104.46	113.00
18	D	1490	U	P-O3'-C3'	5.69	128.74	120.20
18	D	1340	A	C5'-C4'-C3'	5.67	124.50	116.00
18	D	1492	A	P-O3'-C3'	5.67	128.70	120.20
10	B	48	C	N1-C1'-C2'	5.66	120.48	112.00
41	a	2017	U	C2'-C3'-O3'	-5.63	105.25	113.70
22	H	114	GLY	N-CA-C	5.62	121.25	111.14
14	AE	450	HIS	CB-CG-ND1	5.61	131.11	122.70
41	a	2731	G	C4'-C3'-O3'	-5.59	104.62	113.00
41	a	1757	A	C4'-C3'-O3'	-5.58	104.63	113.00
18	D	780	A	C4'-C3'-O3'	-5.57	104.65	113.00
41	a	1568	G	C4'-C3'-O3'	-5.53	104.70	113.00
41	a	2447	G	C2'-C3'-O3'	-5.52	101.22	109.50
14	AE	93	THR	CB-CA-C	5.43	121.22	110.42
14	AE	69	GLU	CA-C-N	-5.40	113.89	121.72
14	AE	69	GLU	C-N-CA	-5.40	113.89	121.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1499	A	C4'-C3'-O3'	5.38	121.08	113.00
10	B	35	A	P-O3'-C3'	5.38	128.27	120.20
41	a	2572	A	C4'-C3'-O3'	-5.38	101.33	109.40
41	a	944	C	C4'-C3'-O3'	-5.38	104.93	113.00
18	D	864	A	N9-C1'-C2'	5.37	120.06	112.00
41	a	2481	G	C4'-C3'-O3'	-5.37	104.94	113.00
14	AE	70	CYS	N-CA-C	-5.37	101.04	109.25
14	AE	777	HIS	CB-CG-ND1	5.36	130.73	122.70
41	a	1270	C	C2'-C3'-O3'	-5.35	105.67	113.70
18	D	517	G	C4'-C3'-O3'	-5.33	101.40	109.40
47	g	5	ILE	N-CA-C	5.33	117.71	111.05
41	a	2529	G	C4'-C3'-O3'	-5.33	105.01	113.00
18	D	145	G	P-O3'-C3'	5.32	128.18	120.20
41	a	375	G	C2'-C3'-O3'	5.32	121.68	113.70
41	a	2068	U	C4'-C3'-O3'	-5.31	105.03	113.00
14	AE	90	VAL	O-C-N	-5.30	117.58	123.20
18	D	1145	A	C4'-C3'-O3'	-5.30	105.06	113.00
14	AE	73	GLY	N-CA-C	5.29	125.72	113.18
8	7	-11	U	C2'-C3'-O3'	5.29	117.43	109.50
41	a	2020	A	C4'-C3'-O3'	-5.28	105.08	113.00
18	D	1395	C	P-O3'-C3'	5.26	128.09	120.20
41	a	2231	U	C1'-C2'-O2'	5.26	116.29	108.40
38	X	102	THR	CA-C-O	-5.25	114.88	121.02
14	AE	88	CYS	N-CA-C	5.23	120.31	113.88
10	B	60	U	C2'-C3'-O3'	5.22	117.32	109.50
22	H	128	ARG	CA-C-N	-5.20	114.07	122.81
22	H	128	ARG	C-N-CA	-5.20	114.07	122.81
41	a	423	A	C2'-C3'-O3'	-5.19	105.92	113.70
14	AE	61	ILE	CA-C-O	-5.18	115.57	120.95
41	a	1834	U	C4'-C3'-O3'	-5.17	105.24	113.00
41	a	2245	U	N1-C1'-C2'	-5.17	104.24	112.00
10	A	60	U	C2'-C3'-O3'	5.17	117.25	109.50
39	Y	5	GLN	O-C-N	5.16	124.65	120.83
41	a	126	A	C4'-C3'-O3'	-5.16	105.26	113.00
61	u	101	ILE	N-CA-C	5.13	116.43	112.12
18	D	1335	U	C4'-C3'-O3'	-5.12	105.33	113.00
22	H	154	PHE	N-CA-C	-5.11	100.38	109.06
30	P	25	ILE	N-CA-CB	5.08	117.45	110.54
41	a	528	A	C4'-C3'-O3'	-5.08	105.38	113.00
17	C	35	GLU	N-CA-C	-5.08	105.93	111.82
59	s	28	LEU	CA-C-N	5.08	127.04	120.44
59	s	28	LEU	C-N-CA	5.08	127.04	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	328	U	C4'-C3'-O3'	-5.07	105.40	113.00
41	a	1864	U	C4'-C3'-O3'	-5.04	105.44	113.00
16	AG	104	ARG	CA-C-N	5.04	131.04	121.97
16	AG	104	ARG	C-N-CA	5.04	131.04	121.97
41	a	479	A	C4'-C3'-O3'	5.03	116.95	109.40
41	a	614	A	C2'-C3'-O3'	5.03	117.05	109.50
14	AE	1184	ASP	N-CA-C	5.02	120.91	109.81
41	a	2335	A	C4'-C3'-O3'	-5.01	105.49	113.00
9	9	115	GLY	CA-C-O	-5.00	118.24	122.29
10	B	19	G	N9-C1'-C2'	5.00	119.50	112.00
41	a	1078	U	C2'-C3'-O3'	-5.00	106.19	113.70
41	a	1991	U	C3'-C2'-O2'	5.00	118.20	110.70

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	910	ALA	Peptide
13	AC	192	VAL	Peptide
13	AC	319	GLU	Peptide
13	AC	321	TRP	Peptide
13	AD	20	SER	Peptide
13	AD	319	GLU	Peptide
13	AD	321	TRP	Peptide
14	AE	1184	ASP	Peptide
14	AE	1326	GLN	Peptide
14	AE	313	GLY	Peptide
14	AE	416	ILE	Peptide
14	AE	804	ALA	Peptide
16	AG	379	SER	Peptide
10	B	19	G	Sidechain
10	B	7	G	Sidechain
22	H	274	TYR	Peptide
22	H	81	GLU	Peptide
22	H	82	THR	Peptide
38	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	13	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	260	21	0
7	6	542	305	306	24	0
8	7	687	97	341	102	0
9	9	1117	0	1153	165	0
10	A	1620	826	826	170	0
10	B	1620	813	827	140	0
11	AA	10567	0	10582	276	0
12	AB	1276	0	1244	209	0
13	AC	2091	0	1892	16	0
13	AD	2073	0	1889	30	0
14	AE	10388	10612	10611	366	0
15	AF	650	0	658	12	0
16	AG	2442	0	1177	81	0
17	C	544	559	560	23	0
18	D	32703	16423	16459	219	0
19	E	669	719	719	3	0
20	F	589	629	629	8	0
21	G	1760	1785	1785	53	0
22	H	1730	1454	1454	212	0
23	I	1636	1710	1710	23	0
24	J	1643	1707	1707	16	0
25	K	1152	1196	1196	21	0
26	L	848	846	846	4	0
27	M	1181	1235	1235	33	0
28	N	979	1031	1031	6	0
29	O	1022	1070	1070	13	0
30	P	790	831	831	120	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	7	0
33	S	805	844	844	6	0
34	T	714	734	734	8	0
35	U	649	666	666	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	4	0
37	W	663	688	688	3	0
38	X	900	964	964	57	0
39	Y	1032	0	1088	85	0
40	Z	227	0	237	17	0
41	a	61841	31077	31123	303	0
42	b	582	599	599	3	0
43	c	625	652	652	5	0
44	d	2569	1301	1301	3	0
45	e	501	531	531	4	0
46	f	448	488	488	6	0
47	g	522	520	520	11	0
48	h	2082	2154	2154	19	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	15	0
51	k	426	464	464	0	0
52	l	1552	1619	1619	14	0
53	m	377	418	418	10	0
54	n	1410	1443	1444	29	0
55	o	504	572	572	4	0
56	p	1313	1358	1358	7	0
57	q	302	343	343	2	0
58	r	1111	1148	1148	6	0
59	s	1129	1162	1162	15	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	9	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	9	0
64	x	892	923	923	8	0
65	y	917	962	962	4	0
66	z	947	1020	1019	11	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	180291	109912	130171	2511	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 (2511) 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)
11:AA:902:LEU:HD13	16:AG:27:LEU:CB	1.23	1.58
17:C:12:ARG:HG3	22:H:264:GLU:CB	1.30	1.58
11:AA:902:LEU:CD1	16:AG:27:LEU:CB	1.78	1.57
22:H:131:LEU:CB	22:H:167:VAL:CA	1.78	1.55
22:H:131:LEU:CB	22:H:167:VAL:HA	1.03	1.47
9:9:130:PRO:N	9:9:130:PRO:CA	1.70	1.43
9:9:31:ARG:NE	41:a:1054:A:H5'	1.31	1.41
12:AB:140:PRO:CD	30:P:102:LEU:HD22	1.51	1.41
12:AB:140:PRO:HG2	30:P:102:LEU:CB	1.52	1.38
22:H:71:ALA:C	22:H:72:LEU:HD12	1.49	1.38
18:D:1358:U:O4	18:D:1363:A:N1	1.60	1.35
9:9:57:ASN:OD1	9:9:62:ARG:CG	1.75	1.34
22:H:118:GLY:O	22:H:133:GLY:CA	1.74	1.34
41:a:1839:G:H1'	41:a:1927:A:C8	1.62	1.33
8:7:-7:U:H5'	23:I:132:ARG:NH1	1.40	1.32
22:H:118:GLY:O	22:H:133:GLY:HA3	1.27	1.30
41:a:1021:A:N1	41:a:1141:U:O4	1.63	1.29
9:9:31:ARG:CZ	41:a:1054:A:H5'	1.63	1.28
11:AA:905:ILE:HG12	16:AG:54:GLY:O	1.30	1.27
18:D:1227:A:OP2	38:X:110:LYS:HE3	1.34	1.27
12:AB:145:ASN:HD22	14:AE:53:ARG:NH2	1.35	1.25
18:D:1308:U:H2'	38:X:98:ARG:NH2	1.48	1.25
10:A:32:C:O4'	27:M:144:MET:HE1	1.09	1.25
17:C:12:ARG:CG	22:H:264:GLU:CB	2.15	1.25
12:AB:165:PHE:CD2	30:P:92:LEU:HD11	1.73	1.24
18:D:948:C:OP2	38:X:105:ASN:OD1	1.53	1.23
10:A:18:G:N7	10:A:57:A:N6	1.87	1.23
12:AB:140:PRO:HD2	30:P:102:LEU:CD2	1.68	1.22
11:AA:858:GLY:H	11:AA:861:ALA:CB	1.49	1.22
12:AB:141:PHE:N	30:P:84:VAL:HG11	1.54	1.22
10:B:18:G:N7	10:B:57:A:N6	1.87	1.22
22:H:267:TRP:CZ2	22:H:340:ARG:HG2	1.75	1.21
16:AG:32:ALA:HB1	16:AG:102:PHE:O	1.36	1.20
18:D:563:A:N1	18:D:884:U:O4	1.73	1.20
18:D:1308:U:C2'	38:X:98:ARG:NH2	2.03	1.20
12:AB:140:PRO:HD3	30:P:102:LEU:CD1	1.72	1.20
9:9:88:HIS:HB3	9:9:89:PRO:CD	1.70	1.20
18:D:1308:U:H3'	38:X:98:ARG:CZ	1.44	1.20
9:9:142:THR:HG21	40:Z:7:ILE:HG12	1.21	1.19
12:AB:140:PRO:CG	30:P:102:LEU:HB2	1.74	1.17
9:9:31:ARG:NE	41:a:1054:A:C5'	2.07	1.17
12:AB:47:GLU:HG3	12:AB:64:PHE:HE1	1.01	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:47:GLU:HG3	12:AB:64:PHE:CE1	1.80	1.16
12:AB:164:ILE:HD11	12:AB:169:THR:OG1	1.01	1.15
12:AB:140:PRO:HG2	30:P:102:LEU:HB3	1.22	1.15
11:AA:854:ILE:HG12	11:AA:855:PRO:HD2	1.17	1.15
18:D:1329:A:OP1	38:X:28:THR:HB	1.47	1.15
11:AA:859:GLU:O	11:AA:863:SER:HB3	1.46	1.14
12:AB:140:PRO:CG	30:P:102:LEU:CB	2.25	1.14
11:AA:848:GLU:HG2	11:AA:888:THR:HG22	1.15	1.14
10:B:70:G:H2'	10:B:71:C:H5''	1.23	1.14
11:AA:855:PRO:CB	16:AG:109:THR:H	1.59	1.14
21:G:19:GLN:CD	22:H:76:GLU:CB	2.19	1.14
21:G:19:GLN:CD	22:H:76:GLU:HB3	1.67	1.14
9:9:57:ASN:OD1	9:9:62:ARG:HG3	1.44	1.14
17:C:44:ILE:HD13	22:H:339:ARG:CG	1.78	1.14
11:AA:906:PHE:CE2	16:AG:31:LEU:CB	2.32	1.13
22:H:119:GLY:HA2	22:H:133:GLY:HA2	1.14	1.13
8:7:11:U:O2	11:AA:1253:LEU:HD12	1.48	1.13
11:AA:854:ILE:HG12	11:AA:855:PRO:CD	1.77	1.13
22:H:135:LEU:CB	22:H:167:VAL:CB	2.27	1.13
17:C:44:ILE:HD13	22:H:339:ARG:HG2	1.18	1.12
10:A:32:C:O4'	27:M:144:MET:CE	1.97	1.12
11:AA:855:PRO:HG3	16:AG:108:GLN:CB	1.79	1.12
11:AA:904:ALA:N	16:AG:8:VAL:CB	2.12	1.12
12:AB:164:ILE:CD1	12:AB:169:THR:OG1	1.97	1.12
22:H:267:TRP:CE2	22:H:340:ARG:HG2	1.84	1.12
12:AB:169:THR:HG21	30:P:98:VAL:HG23	1.26	1.11
10:A:70:G:H2'	10:A:71:C:H5''	1.23	1.11
12:AB:141:PHE:CE2	12:AB:171:VAL:HG21	1.84	1.11
12:AB:141:PHE:CZ	12:AB:171:VAL:HG21	1.86	1.10
9:9:129:LEU:N	9:9:130:PRO:HD3	1.66	1.10
12:AB:144:PHE:HE2	30:P:85:ASP:HA	1.09	1.10
12:AB:167:ARG:HA	23:I:61:ALA:HB2	1.22	1.10
18:D:1308:U:C2'	38:X:98:ARG:HH21	1.63	1.10
14:AE:24:LEU:HG	14:AE:232:ASN:HD21	1.17	1.10
41:a:1839:G:C8	41:a:1927:A:H1'	1.87	1.09
18:D:1308:U:C3'	38:X:98:ARG:CZ	2.31	1.09
9:9:50:VAL:HG22	39:Y:119:ALA:CB	1.82	1.09
22:H:267:TRP:CH2	22:H:340:ARG:HG2	1.87	1.09
30:P:87:LEU:HD23	30:P:100:ILE:HD13	1.32	1.09
12:AB:140:PRO:CD	30:P:102:LEU:CD2	2.28	1.09
18:D:1308:U:C3'	38:X:98:ARG:NH2	2.16	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:140:PRO:CD	30:P:102:LEU:HD13	1.82	1.08
11:AA:858:GLY:H	11:AA:861:ALA:HB3	1.12	1.08
22:H:71:ALA:O	22:H:72:LEU:HD12	1.53	1.08
24:J:162:ALA:HA	24:J:165:ARG:CZ	1.83	1.08
9:9:88:HIS:CB	9:9:89:PRO:HD3	1.82	1.07
12:AB:144:PHE:CE2	30:P:85:ASP:HA	1.89	1.07
11:AA:857:VAL:HG12	11:AA:861:ALA:CB	1.84	1.07
12:AB:140:PRO:HD3	30:P:102:LEU:HD13	1.09	1.07
12:AB:144:PHE:HE2	30:P:85:ASP:CA	1.66	1.07
21:G:19:GLN:CG	22:H:75:VAL:HG22	1.84	1.07
8:7:-7:U:C5'	23:I:132:ARG:HH12	1.68	1.06
12:AB:165:PHE:CD1	30:P:90:LEU:O	2.08	1.06
12:AB:169:THR:CG2	30:P:98:VAL:HG23	1.86	1.06
8:7:-18:G:H5''	18:D:1500:A:N6	1.70	1.05
11:AA:902:LEU:HD12	16:AG:27:LEU:CB	1.85	1.05
13:AC:232:VAL:C	13:AD:221:ALA:HB3	1.80	1.05
10:A:18:G:N2	10:A:55:U:O2	1.90	1.05
12:AB:128:PHE:HB2	12:AB:180:LYS:HB2	1.36	1.05
21:G:19:GLN:HG3	22:H:75:VAL:HG22	1.38	1.05
10:B:56:C:H2'	10:B:57:A:H5''	1.39	1.04
16:AG:32:ALA:CB	16:AG:102:PHE:O	2.05	1.04
22:H:162:LYS:CB	22:H:298:GLU:CD	2.30	1.04
8:7:-10:U:O2'	25:K:33:PHE:CE1	2.11	1.04
11:AA:1313:HIS:CD2	15:AF:31:GLN:HE22	1.75	1.04
12:AB:165:PHE:HD1	30:P:90:LEU:O	1.40	1.04
10:B:56:C:O4'	54:n:80:ARG:NH2	1.91	1.04
18:D:1227:A:OP2	38:X:110:LYS:CE	2.06	1.04
10:A:56:C:H2'	10:A:57:A:H5''	1.39	1.04
10:A:70:G:C2'	10:A:71:C:H5''	1.89	1.03
22:H:19:ARG:O	22:H:72:LEU:HB2	1.58	1.03
10:B:18:G:N2	10:B:55:U:O2	1.90	1.03
12:AB:144:PHE:CE2	30:P:85:ASP:HB2	1.94	1.03
11:AA:857:VAL:HG12	11:AA:861:ALA:HB1	1.03	1.02
9:9:129:LEU:H	9:9:130:PRO:HD3	0.90	1.02
12:AB:145:ASN:ND2	14:AE:53:ARG:NH2	2.05	1.02
10:B:70:G:C2'	10:B:71:C:H5''	1.89	1.02
11:AA:549:ASP:OD2	14:AE:750:PRO:HB3	1.60	1.02
30:P:17:LEU:HD21	30:P:93:ALA:CB	1.90	1.02
11:AA:855:PRO:HB3	16:AG:109:THR:H	1.22	1.02
12:AB:140:PRO:C	30:P:84:VAL:HG11	1.85	1.02
10:B:56:C:H5'	54:n:80:ARG:CZ	1.90	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:1329:A:OP1	38:X:28:THR:CB	2.07	1.01
9:9:93:ALA:O	9:9:129:LEU:HD12	1.60	1.01
22:H:290:TYR:O	22:H:305:HIS:O	1.77	1.01
14:AE:111:THR:HG23	14:AE:300:GLN:CD	1.86	1.00
21:G:38:VAL:CG2	22:H:75:VAL:HG21	1.90	1.00
18:D:13:U:N3	18:D:915:A:C6	2.29	1.00
41:a:2297:A:N1	41:a:2321:U:C4	2.29	1.00
10:A:32:C:C4'	27:M:144:MET:HE1	1.93	0.99
18:D:13:U:O4	18:D:20:U:O4	1.79	0.98
18:D:1308:U:H3'	38:X:98:ARG:NH2	1.76	0.98
22:H:131:LEU:CB	22:H:167:VAL:CB	2.40	0.98
12:AB:140:PRO:HG2	30:P:102:LEU:HB2	1.32	0.98
12:AB:165:PHE:HZ	30:P:87:LEU:CD1	1.77	0.98
13:AC:232:VAL:C	13:AD:221:ALA:CB	2.37	0.98
11:AA:887:VAL:HG22	11:AA:913:VAL:HG22	1.45	0.98
9:9:129:LEU:H	9:9:130:PRO:CD	1.77	0.98
22:H:118:GLY:O	22:H:133:GLY:HA2	1.63	0.97
11:AA:1268:GLN:NE2	14:AE:352:ARG:HD2	1.78	0.97
12:AB:47:GLU:CG	12:AB:64:PHE:HE1	1.76	0.97
41:a:1839:G:O4'	41:a:1927:A:O4'	1.82	0.97
9:9:31:ARG:CD	41:a:1054:A:H5'	1.94	0.97
10:A:32:C:O2'	27:M:86:GLN:CG	2.12	0.97
11:AA:904:ALA:H	16:AG:8:VAL:CB	1.76	0.97
11:AA:901:LEU:HA	16:AG:9:VAL:HA	1.43	0.97
41:a:1839:G:C1'	41:a:1927:A:C8	2.46	0.97
9:9:142:THR:HG21	40:Z:7:ILE:CG1	1.95	0.97
22:H:119:GLY:CA	22:H:133:GLY:HA2	1.95	0.97
9:9:57:ASN:OD1	9:9:62:ARG:HG2	1.64	0.96
8:7:-19:U:P	18:D:1505:G:H8	1.87	0.96
21:G:38:VAL:HG22	22:H:75:VAL:HG21	1.44	0.96
12:AB:141:PHE:CA	30:P:84:VAL:HG11	1.95	0.96
11:AA:849:GLU:HB2	11:AA:887:VAL:CG1	1.96	0.96
11:AA:906:PHE:CZ	16:AG:31:LEU:CB	2.48	0.96
11:AA:903:ARG:HB3	16:AG:8:VAL:CB	1.94	0.95
12:AB:144:PHE:HE2	30:P:85:ASP:CB	1.79	0.95
12:AB:141:PHE:CA	30:P:84:VAL:CG1	2.45	0.95
7:6:15:DC:N4	7:6:16:DC:N4	2.15	0.95
8:7:-7:U:C5'	23:I:132:ARG:NH1	2.26	0.95
12:AB:128:PHE:CZ	12:AB:178:VAL:HG21	2.01	0.95
14:AE:68:TYR:O	14:AE:75:TYR:CE2	2.20	0.94
41:a:1839:G:O4'	41:a:1927:A:C1'	2.15	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:72:A:H2'	10:A:73:A:H5''	1.49	0.94
16:AG:400:GLU:O	16:AG:401:PRO:O	1.85	0.94
11:AA:1313:HIS:HD2	15:AF:31:GLN:HE22	0.99	0.94
10:B:72:A:H2'	10:B:73:A:H5''	1.49	0.94
22:H:135:LEU:HA	22:H:157:ILE:CB	1.98	0.94
11:AA:887:VAL:CG2	11:AA:913:VAL:CG2	2.46	0.94
18:D:13:U:C4	18:D:915:A:N6	2.36	0.94
10:B:68:C:H2'	10:B:69:C:H5''	1.51	0.93
22:H:71:ALA:C	22:H:72:LEU:CD1	2.42	0.93
41:a:67:U:N3	41:a:74:A:C6	2.35	0.93
30:P:87:LEU:CD2	30:P:100:ILE:HD13	1.99	0.93
22:H:119:GLY:HA3	22:H:131:LEU:O	1.68	0.93
18:D:13:U:N3	18:D:915:A:N6	2.16	0.92
10:A:68:C:H2'	10:A:69:C:H5''	1.51	0.92
10:B:75:C:OP1	41:a:2602:A:C8	2.22	0.92
11:AA:857:VAL:CG1	11:AA:861:ALA:HB1	1.97	0.92
12:AB:138:ASP:HB3	12:AB:177:GLN:HA	1.51	0.92
8:7:-17:U:O2'	18:D:1403:C:O2	1.87	0.92
11:AA:858:GLY:H	11:AA:861:ALA:HB2	1.34	0.92
30:P:17:LEU:HD21	30:P:93:ALA:HB1	1.49	0.92
10:A:32:C:O2'	27:M:86:GLN:HG3	1.68	0.92
11:AA:858:GLY:N	11:AA:861:ALA:CB	2.33	0.91
11:AA:855:PRO:HB2	16:AG:109:THR:H	1.34	0.91
11:AA:887:VAL:HG22	11:AA:913:VAL:CG2	2.00	0.91
12:AB:125:LYS:HG2	12:AB:153:TYR:HB2	1.52	0.91
12:AB:140:PRO:HG3	30:P:102:LEU:HB2	1.50	0.91
10:A:56:C:H1'	41:a:2112:G:C6	2.06	0.91
9:9:88:HIS:HB3	9:9:89:PRO:HD3	0.93	0.91
8:7:-19:U:P	18:D:1505:G:C8	2.64	0.91
12:AB:128:PHE:CE1	12:AB:178:VAL:CG2	2.55	0.90
41:a:2013:A:N6	41:a:2613:U:H3	1.68	0.90
12:AB:165:PHE:CZ	30:P:87:LEU:HG	2.06	0.90
41:a:1406:U:O2'	41:a:1407:G:C5'	2.19	0.90
18:D:13:U:C4	18:D:20:U:O4	2.24	0.90
12:AB:164:ILE:HD11	12:AB:169:THR:CB	2.02	0.90
14:AE:24:LEU:HB2	14:AE:232:ASN:OD1	1.72	0.90
9:9:93:ALA:O	9:9:129:LEU:CD1	2.19	0.90
11:AA:641:GLU:OE2	14:AE:749:LYS:NZ	2.03	0.90
12:AB:93:ILE:HG22	14:AE:290:ILE:CG2	2.02	0.90
12:AB:165:PHE:CZ	30:P:87:LEU:CD1	2.54	0.90
10:A:18:G:N2	10:A:58:A:N7	2.19	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:144:PHE:CE2	30:P:85:ASP:CB	2.53	0.89
14:AE:136:GLU:OE1	14:AE:312:ARG:NH1	2.04	0.89
6:5:114:DC:H5'	14:AE:1148:ARG:NH2	1.87	0.89
9:9:50:VAL:HG22	39:Y:119:ALA:HB1	1.50	0.89
22:H:279:LYS:HA	22:H:331:MET:HB3	1.54	0.89
12:AB:141:PHE:HA	30:P:84:VAL:CG1	2.02	0.89
11:AA:906:PHE:HE2	16:AG:31:LEU:CB	1.79	0.89
12:AB:128:PHE:HB2	12:AB:180:LYS:CB	2.02	0.89
8:7:-18:G:C5'	18:D:1500:A:H62	1.85	0.89
12:AB:117:GLN:HE21	12:AB:117:GLN:HA	1.36	0.89
14:AE:68:TYR:C	14:AE:75:TYR:HE2	1.80	0.89
9:9:142:THR:CG2	40:Z:7:ILE:HG12	2.02	0.89
18:D:1308:U:H2'	38:X:98:ARG:HH21	1.06	0.89
11:AA:857:VAL:HG11	11:AA:862:LEU:HD12	1.53	0.89
12:AB:163:SER:O	30:P:88:MET:HG3	1.71	0.89
39:Y:104:GLN:HG2	39:Y:108:ILE:HD11	1.53	0.89
9:9:88:HIS:CB	9:9:89:PRO:CD	2.41	0.89
10:B:18:G:N2	10:B:58:A:N7	2.19	0.89
30:P:17:LEU:CD2	30:P:93:ALA:HB3	2.03	0.89
22:H:162:LYS:N	22:H:298:GLU:OE2	2.06	0.88
11:AA:1313:HIS:HD2	15:AF:31:GLN:NE2	1.71	0.88
11:AA:888:THR:HB	11:AA:889:PRO:HD2	1.55	0.88
14:AE:202:ARG:HG2	14:AE:202:ARG:HH11	1.35	0.88
30:P:87:LEU:HD23	30:P:100:ILE:CD1	2.02	0.88
21:G:18:HIS:HA	22:H:43:LYS:HD2	1.55	0.88
22:H:119:GLY:HA2	22:H:133:GLY:CA	2.01	0.88
11:AA:857:VAL:HG11	11:AA:862:LEU:CD1	2.04	0.87
12:AB:167:ARG:HA	23:I:61:ALA:CB	2.01	0.87
39:Y:21:PRO:HB2	39:Y:22:PRO:HD3	1.54	0.87
12:AB:128:PHE:CZ	12:AB:178:VAL:CG2	2.58	0.87
9:9:50:VAL:CG2	39:Y:119:ALA:HB3	2.04	0.87
16:AG:219:GLU:O	21:G:157:LEU:HD12	1.74	0.87
11:AA:848:GLU:HG2	11:AA:888:THR:CG2	2.02	0.87
9:9:129:LEU:N	9:9:130:PRO:CD	2.34	0.87
17:C:31:ASN:OD1	22:H:268:VAL:HG22	1.74	0.87
41:a:2314:A:H1'	54:n:155:THR:HG21	1.54	0.87
24:J:162:ALA:HB2	24:J:165:ARG:NH2	1.90	0.87
12:AB:136:VAL:HG22	12:AB:178:VAL:HG12	1.57	0.87
47:g:16:CYS:CB	47:g:37:CYS:HB3	2.05	0.87
22:H:162:LYS:CA	22:H:298:GLU:OE2	2.17	0.86
9:9:31:ARG:CZ	41:a:1054:A:C5'	2.49	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:173:LEU:CD1	30:P:102:LEU:CD2	2.53	0.86
14:AE:24:LEU:HG	14:AE:232:ASN:ND2	1.90	0.86
22:H:131:LEU:CB	22:H:167:VAL:N	2.37	0.86
22:H:332:VAL:HG11	22:H:335:ILE:HG13	1.58	0.86
11:AA:901:LEU:CD2	16:AG:23:ILE:CB	2.53	0.86
22:H:348:GLN:N	22:H:348:GLN:OE1	2.08	0.86
14:AE:425:ARG:NH1	14:AE:458:ASN:O	2.08	0.86
9:9:31:ARG:HH11	9:9:31:ARG:HG3	1.41	0.86
39:Y:81:LYS:O	39:Y:81:LYS:HE3	1.75	0.86
9:9:52:MET:C	9:9:52:MET:HE3	2.00	0.85
41:a:783:A:N3	41:a:783:A:H2'	1.89	0.85
11:AA:855:PRO:HB3	16:AG:108:GLN:N	1.90	0.85
11:AA:858:GLY:O	11:AA:861:ALA:N	2.07	0.85
8:7:-18:G:H5''	18:D:1500:A:H62	1.40	0.85
11:AA:887:VAL:CG2	11:AA:913:VAL:HG22	2.05	0.85
12:AB:128:PHE:CE2	12:AB:134:VAL:HG11	2.11	0.85
41:a:67:U:N3	41:a:74:A:N6	2.25	0.85
9:9:31:ARG:CD	41:a:1054:A:H4'	2.06	0.85
10:A:33:U:H5''	27:M:84:THR:HG21	1.55	0.85
12:AB:111:ILE:O	12:AB:115:LEU:HD22	1.77	0.85
12:AB:165:PHE:CZ	30:P:87:LEU:HD12	2.12	0.85
22:H:267:TRP:CD2	22:H:340:ARG:HG2	2.11	0.85
18:D:197:A:C6	18:D:221:C:H4'	2.11	0.85
22:H:267:TRP:CZ3	22:H:340:ARG:HG2	2.11	0.85
10:A:18:G:N7	10:A:57:A:C6	2.44	0.85
24:J:61:VAL:HG21	24:J:200:ILE:HD11	1.57	0.84
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.58	0.84
12:AB:140:PRO:CD	30:P:102:LEU:CD1	2.49	0.84
14:AE:68:TYR:HB3	14:AE:75:TYR:OH	1.77	0.84
9:9:125:ARG:NH1	9:9:125:ARG:HA	1.92	0.84
10:A:16:C:O2	41:a:2181:U:H5'	1.76	0.84
10:B:18:G:N7	10:B:57:A:C6	2.44	0.84
22:H:131:LEU:CB	22:H:166:VAL:O	2.26	0.84
17:C:12:ARG:HH22	22:H:268:VAL:CG2	1.91	0.84
22:H:135:LEU:CB	22:H:167:VAL:C	2.50	0.84
39:Y:20:SER:HB3	39:Y:21:PRO:HD3	1.59	0.84
41:a:2303:G:C2	41:a:2314:A:C2	2.66	0.84
10:A:68:C:C2'	10:A:69:C:H5''	2.08	0.84
14:AE:26:SER:HB2	14:AE:236:TRP:CZ2	2.12	0.84
22:H:267:TRP:CH2	22:H:340:ARG:CG	2.61	0.83
9:9:50:VAL:HG22	39:Y:119:ALA:HB3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:60:VAL:HG13	39:Y:66:PHE:HB3	1.58	0.83
25:K:111:MET:HE2	25:K:125:ALA:HB1	1.59	0.83
12:AB:133:MET:H	12:AB:133:MET:HE2	1.42	0.83
10:B:56:C:H5'	54:n:80:ARG:NE	1.93	0.83
10:A:72:A:C2'	10:A:73:A:H5''	2.08	0.83
18:D:1227:A:H5'	38:X:110:LYS:NZ	1.93	0.83
7:6:21:DA:N1	8:7:15:G:N2	2.26	0.83
8:7:-19:U:OP2	18:D:1505:G:C8	2.32	0.83
39:Y:102:ARG:HB3	39:Y:141:ASP:HA	1.61	0.83
41:a:1406:U:O2'	41:a:1407:G:H5''	1.79	0.83
41:a:1021:A:N6	41:a:1141:U:H3	1.77	0.83
9:9:62:ARG:HG2	9:9:62:ARG:HH21	1.44	0.83
10:B:68:C:C2'	10:B:69:C:H5''	2.08	0.83
10:B:72:A:C2'	10:B:73:A:H5''	2.09	0.83
7:6:18:DC:H42	8:7:17:G:H1	1.27	0.82
10:A:54:U:H3	10:A:58:A:N6	1.78	0.82
9:9:31:ARG:CD	41:a:1054:A:C4'	2.56	0.82
14:AE:68:TYR:O	14:AE:75:TYR:HE2	1.58	0.82
8:7:-7:U:H5'	23:I:132:ARG:HH12	1.01	0.82
11:AA:913:VAL:HG12	16:AG:108:GLN:CB	2.09	0.82
14:AE:141:PHE:HE2	14:AE:296:LYS:HB2	1.44	0.82
10:B:54:U:H3	10:B:58:A:N6	1.77	0.82
8:7:-19:U:OP1	18:D:1505:G:C8	2.32	0.82
9:9:3:LEU:HD13	9:9:5:LEU:HG	1.62	0.82
9:9:43:LYS:HD2	9:9:43:LYS:C	2.05	0.82
41:a:1839:G:C1'	41:a:1927:A:N9	2.43	0.82
8:7:-19:U:OP1	18:D:1505:G:H8	1.63	0.82
22:H:122:VAL:O	22:H:129:ALA:N	2.13	0.82
22:H:305:HIS:CD2	22:H:306:VAL:H	1.98	0.82
41:a:1019:U:H3	41:a:1142:A:N6	1.77	0.82
18:D:37:U:N3	18:D:397:A:N6	2.28	0.82
21:G:16:PHE:HB3	22:H:43:LYS:HA	1.60	0.82
12:AB:117:GLN:HA	12:AB:117:GLN:NE2	1.94	0.81
14:AE:1169:THR:OG1	14:AE:1192:LYS:NZ	2.13	0.81
10:B:76:A:H1'	41:a:2494:G:P	2.20	0.81
22:H:155:LYS:CB	22:H:169:SER:CB	2.58	0.81
9:9:57:ASN:OD1	9:9:62:ARG:CD	2.27	0.81
10:A:56:C:C2'	10:A:57:A:H5''	2.11	0.81
11:AA:808:ASN:H	14:AE:633:ALA:HB2	1.44	0.81
9:9:28:ALA:H	9:9:110:ALA:HA	1.44	0.81
11:AA:905:ILE:CG1	16:AG:54:GLY:O	2.24	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:972:C:O2'	30:P:57:VAL:CG2	2.29	0.81
18:D:1397:C:OP1	18:D:1397:C:H2'	1.80	0.81
22:H:267:TRP:CZ3	22:H:340:ARG:CG	2.63	0.81
12:AB:173:LEU:HD12	30:P:102:LEU:HD21	1.62	0.81
10:B:56:C:C2'	10:B:57:A:H5''	2.11	0.81
41:a:585:G:N7	66:z:6:ARG:NH1	2.29	0.81
10:A:22:G:H2'	10:A:23:C:C6	2.16	0.81
39:Y:27:LEU:HD12	39:Y:27:LEU:O	1.81	0.81
7:6:21:DA:N1	8:7:15:G:C2	2.49	0.81
10:A:7:G:H4'	10:A:8:U:OP1	1.81	0.81
12:AB:148:VAL:HB	12:AB:160:VAL:HG22	1.63	0.81
9:9:50:VAL:CG2	39:Y:119:ALA:CB	2.59	0.81
11:AA:854:ILE:HG13	11:AA:887:VAL:HB	1.62	0.81
11:AA:901:LEU:HD23	16:AG:23:ILE:CB	2.11	0.81
11:AA:887:VAL:HG21	11:AA:913:VAL:HG21	1.63	0.80
14:AE:141:PHE:CE2	14:AE:296:LYS:HB2	2.15	0.80
14:AE:144:TYR:HE1	14:AE:162:GLU:OE2	1.64	0.80
24:J:162:ALA:HA	24:J:165:ARG:NH2	1.95	0.80
24:J:162:ALA:CB	24:J:165:ARG:NH2	2.44	0.80
30:P:17:LEU:CD2	30:P:93:ALA:CB	2.57	0.80
14:AE:37:GLU:O	14:AE:61:ILE:HD11	1.81	0.80
9:9:31:ARG:HD2	41:a:1054:A:H4'	1.62	0.80
41:a:2297:A:N1	41:a:2321:U:O4	2.14	0.80
10:B:7:G:H4'	10:B:8:U:OP1	1.81	0.80
17:C:12:ARG:CB	22:H:264:GLU:CB	2.59	0.80
41:a:1021:A:H61	41:a:1141:U:H3	1.28	0.80
47:g:18:CYS:HB3	47:g:40:CYS:CB	2.12	0.80
54:n:125:ARG:O	54:n:127:ASN:ND2	2.14	0.80
11:AA:858:GLY:N	11:AA:861:ALA:HB3	1.94	0.80
12:AB:141:PHE:HA	30:P:84:VAL:HG12	1.63	0.80
11:AA:848:GLU:CG	11:AA:888:THR:HG22	2.06	0.80
10:B:22:G:H2'	10:B:23:C:C6	2.16	0.80
41:a:2298:A:C4	41:a:2321:U:C5	2.70	0.80
8:7:-18:G:C5'	18:D:1500:A:N6	2.42	0.80
9:9:78:GLY:N	9:9:79:PRO:HD2	1.97	0.80
11:AA:855:PRO:CB	16:AG:109:THR:N	2.42	0.80
39:Y:72:THR:OG1	39:Y:73:PRO:HD2	1.81	0.80
14:AE:111:THR:HG23	14:AE:300:GLN:OE1	1.81	0.80
10:B:58:A:O2'	10:B:59:A:H3'	1.81	0.80
8:7:0:U:OP1	23:I:80:LYS:HA	1.81	0.79
16:AG:401:PRO:O	16:AG:403:VAL:N	2.11	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:g:16:CYS:HB2	47:g:37:CYS:HB3	1.63	0.79
22:H:123:GLU:HA	22:H:128:ARG:HA	1.63	0.79
41:a:2189:U:OP1	41:a:2189:U:O4'	2.00	0.79
24:J:162:ALA:CA	24:J:165:ARG:NH2	2.44	0.79
10:B:18:G:N2	10:B:58:A:C5	2.50	0.79
11:AA:618:GLN:HG3	14:AE:770:LEU:HD13	1.64	0.79
12:AB:164:ILE:HA	30:P:88:MET:HA	1.63	0.79
12:AB:165:PHE:HD2	30:P:92:LEU:HD11	1.41	0.79
14:AE:90:VAL:HG13	14:AE:90:VAL:O	1.82	0.79
12:AB:165:PHE:CE1	30:P:87:LEU:HA	2.18	0.79
30:P:17:LEU:HD21	30:P:93:ALA:HB3	1.62	0.79
41:a:1406:U:O2'	41:a:1407:G:O5'	2.01	0.79
9:9:11:ILE:HD11	9:9:62:ARG:HA	1.65	0.79
10:A:58:A:O2'	10:A:59:A:H3'	1.82	0.79
12:AB:140:PRO:CD	30:P:102:LEU:CG	2.61	0.79
41:a:1019:U:H3	41:a:1142:A:H61	1.28	0.79
11:AA:855:PRO:HB3	16:AG:109:THR:N	1.96	0.78
24:J:162:ALA:HB2	24:J:165:ARG:HH22	1.47	0.78
41:a:1406:U:O2'	41:a:1407:G:P	2.41	0.78
9:9:39:THR:HA	9:9:42:ARG:HD2	1.64	0.78
22:H:19:ARG:HD3	22:H:73:ASP:CG	2.09	0.78
22:H:270:ILE:CG2	22:H:337:GLU:HB3	2.12	0.78
12:AB:145:ASN:HD22	14:AE:53:ARG:HH22	1.28	0.78
18:D:1329:A:P	38:X:28:THR:HB	2.22	0.78
12:AB:173:LEU:CD1	30:P:102:LEU:HD21	2.14	0.78
14:AE:1075:ARG:NH2	14:AE:1168:GLU:OE2	2.17	0.78
21:G:16:PHE:CZ	22:H:41:GLY:O	2.36	0.78
39:Y:32:VAL:HG13	39:Y:60:VAL:HG21	1.66	0.78
16:AG:32:ALA:CA	16:AG:102:PHE:O	2.32	0.78
9:9:3:LEU:H	9:9:3:LEU:HD12	1.47	0.78
10:A:18:G:N2	10:A:58:A:C5	2.50	0.78
12:AB:165:PHE:CZ	30:P:87:LEU:CG	2.67	0.78
10:A:70:G:H2'	10:A:71:C:C5'	2.11	0.78
10:A:18:G:C5	10:A:57:A:C6	2.72	0.77
12:AB:141:PHE:HZ	12:AB:171:VAL:HG21	1.49	0.77
14:AE:186:GLN:HG3	14:AE:238:ILE:HG13	1.65	0.77
10:B:15:G:N1	10:B:20:U:O2	2.17	0.77
10:B:70:G:H2'	10:B:71:C:C5'	2.11	0.77
41:a:2756:U:N3	41:a:2758:A:C6	2.53	0.77
10:A:15:G:N1	10:A:20:U:O2	2.17	0.77
10:A:33:U:O3'	27:M:84:THR:OG1	2.02	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:135:ARG:HG2	12:AB:135:ARG:HH11	1.50	0.77
10:B:5:G:H2'	10:B:6:G:H5'	1.66	0.77
12:AB:141:PHE:CA	30:P:84:VAL:HG12	2.15	0.77
10:B:18:G:C5	10:B:57:A:C6	2.72	0.77
10:A:5:G:H2'	10:A:6:G:H5'	1.66	0.77
10:A:68:C:C3'	10:A:69:C:H5''	2.15	0.77
7:6:18:DC:N3	8:7:17:G:N2	2.31	0.77
11:AA:887:VAL:CG2	11:AA:913:VAL:HG21	2.11	0.77
41:a:2756:U:N3	41:a:2758:A:N6	2.32	0.77
10:B:68:C:C3'	10:B:69:C:H5''	2.15	0.76
10:A:76:A:H2'	41:a:2394:C:H42	1.48	0.76
16:AG:298:VAL:HA	16:AG:305:MET:HA	1.65	0.76
7:6:15:DC:C4	7:6:16:DC:N4	2.53	0.76
9:9:31:ARG:NE	41:a:1054:A:C4'	2.48	0.76
21:G:35:ARG:HD2	22:H:14:LYS:HD3	1.66	0.76
22:H:305:HIS:CD2	22:H:306:VAL:N	2.53	0.76
11:AA:902:LEU:HD11	16:AG:27:LEU:CB	2.11	0.76
12:AB:141:PHE:HE2	12:AB:171:VAL:HG21	1.45	0.76
50:j:4:LEU:HD23	50:j:29:VAL:HG11	1.65	0.76
11:AA:906:PHE:CZ	16:AG:28:GLU:HA	2.20	0.76
18:D:1358:U:C4	18:D:1363:A:N1	2.52	0.76
64:x:31:THR:O	64:x:102:ARG:NH1	2.19	0.76
9:9:97:LYS:HD3	9:9:127:ALA:HA	1.68	0.76
11:AA:854:ILE:CG1	11:AA:855:PRO:HD2	2.08	0.76
18:D:1227:A:H5'	38:X:110:LYS:HZ3	1.50	0.76
39:Y:74:PRO:HG2	39:Y:77:VAL:HB	1.67	0.76
17:C:44:ILE:CD1	22:H:339:ARG:CG	2.62	0.75
47:g:18:CYS:CB	47:g:40:CYS:HB3	2.16	0.75
10:A:32:C:C1'	27:M:144:MET:HE1	2.17	0.75
22:H:109:THR:HA	22:H:153:GLU:HA	1.69	0.75
18:D:197:A:N6	18:D:221:C:H4'	2.01	0.75
10:A:41:C:O4'	27:M:143:ARG:NH1	2.20	0.75
11:AA:858:GLY:N	11:AA:861:ALA:HB2	1.96	0.75
41:a:2013:A:N6	41:a:2613:U:N3	2.33	0.75
9:9:27:VAL:HG23	9:9:83:ALA:HB3	1.67	0.75
22:H:131:LEU:CB	22:H:166:VAL:C	2.60	0.75
25:K:137:VAL:O	25:K:140:THR:OG1	2.04	0.75
21:G:35:ARG:HG3	22:H:10:GLU:OE2	1.86	0.75
9:9:60:LEU:HD23	9:9:64:VAL:HG21	1.67	0.74
41:a:2298:A:C4	41:a:2321:U:H5	2.04	0.74
10:B:6:G:O2'	10:B:7:G:O5'	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:19:GLN:CD	22:H:76:GLU:HB2	2.08	0.74
9:9:52:MET:HG3	9:9:95:LEU:HD11	1.68	0.74
9:9:78:GLY:N	9:9:79:PRO:CD	2.50	0.74
18:D:1228:C:OP1	38:X:107:ARG:NH1	2.20	0.74
21:G:19:GLN:OE1	22:H:75:VAL:O	1.85	0.74
14:AE:110:PRO:HG2	14:AE:183:GLU:HG3	1.68	0.74
10:B:18:G:H1'	10:B:58:A:C2	2.23	0.74
8:7:14:U:H4'	14:AE:322:ARG:CD	2.18	0.74
14:AE:202:ARG:HG2	14:AE:202:ARG:NH1	1.99	0.74
4:3:36:VAL:HG11	4:3:39:ILE:HD12	1.68	0.74
22:H:109:THR:CA	22:H:153:GLU:HA	2.18	0.74
6:5:115:DA:OP1	14:AE:1148:ARG:NE	2.21	0.74
10:A:6:G:O2'	10:A:7:G:O5'	2.06	0.74
21:G:19:GLN:CG	22:H:76:GLU:HB2	2.18	0.74
10:B:70:G:C3'	10:B:71:C:H5''	2.17	0.74
11:AA:857:VAL:CG1	11:AA:862:LEU:CD1	2.65	0.74
14:AE:123:ARG:HG3	14:AE:1337:VAL:HG11	1.67	0.74
10:B:18:G:O2'	10:B:60:U:C2	2.41	0.74
10:A:41:C:H1'	27:M:143:ARG:HH12	1.52	0.73
14:AE:44:ILE:HD12	14:AE:252:LEU:CD2	2.18	0.73
14:AE:211:GLU:HG2	14:AE:215:LYS:HE3	1.70	0.73
22:H:110:GLY:CA	22:H:153:GLU:O	2.36	0.73
12:AB:169:THR:HG23	30:P:98:VAL:O	1.88	0.73
14:AE:120:LEU:O	14:AE:1330:ARG:NH1	2.21	0.73
17:C:44:ILE:HD13	22:H:339:ARG:HG3	1.69	0.73
11:AA:864:LYS:HE3	11:AA:877:VAL:HG12	1.70	0.73
10:A:18:G:H1'	10:A:58:A:C2	2.23	0.73
12:AB:165:PHE:CD1	30:P:87:LEU:O	2.41	0.73
14:AE:157:GLN:OE1	14:AE:157:GLN:HA	1.89	0.73
14:AE:210:SER:HB3	14:AE:213:LYS:HB2	1.71	0.73
10:B:76:A:H1'	41:a:2494:G:OP1	1.88	0.73
18:D:517:G:O2'	18:D:530:G:H4'	1.88	0.73
10:A:70:G:C3'	10:A:71:C:H5''	2.18	0.73
14:AE:105:ILE:HD12	14:AE:242:LEU:HD22	1.71	0.73
16:AG:219:GLU:CB	21:G:157:LEU:HG	2.19	0.73
22:H:19:ARG:HB2	22:H:73:ASP:OD2	1.88	0.73
39:Y:36:GLU:OE1	39:Y:36:GLU:HA	1.88	0.73
9:9:31:ARG:CD	41:a:1054:A:C5'	2.58	0.73
32:R:86:ARG:HG3	32:R:86:ARG:O	1.89	0.73
22:H:267:TRP:CE3	22:H:340:ARG:CG	2.72	0.73
39:Y:85:ILE:H	39:Y:85:ILE:HD12	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:84:THR:HG21	29:O:103:PHE:HB3	1.71	0.73
41:a:67:U:C4	41:a:74:A:N6	2.57	0.73
12:AB:165:PHE:CG	30:P:92:LEU:HD11	2.24	0.73
22:H:304:VAL:HG12	22:H:309:MET:SD	2.28	0.73
10:A:18:G:O2'	10:A:60:U:C2	2.41	0.72
14:AE:44:ILE:HD12	14:AE:252:LEU:HD21	1.71	0.72
41:a:1021:A:N1	41:a:1141:U:C4	2.55	0.72
41:a:1839:G:H1'	41:a:1927:A:N9	2.03	0.72
14:AE:1143:ASP:OD1	14:AE:1148:ARG:NH1	2.21	0.72
10:B:76:A:H2'	10:B:76:A:N3	2.03	0.72
14:AE:68:TYR:C	14:AE:75:TYR:CE2	2.65	0.72
14:AE:142:GLU:HG3	14:AE:142:GLU:O	1.89	0.72
7:6:21:DA:C6	8:7:15:G:N2	2.57	0.72
11:AA:845:LEU:HD23	11:AA:889:PRO:HB2	1.70	0.72
12:AB:155:LYS:HE3	18:D:1276:G:OP2	1.90	0.72
41:a:1913:A:OP2	41:a:1913:A:H3'	1.89	0.72
12:AB:164:ILE:HD13	12:AB:167:ARG:O	1.89	0.72
41:a:1839:G:C1'	41:a:1927:A:C1'	2.67	0.72
10:A:33:U:H5''	27:M:84:THR:CG2	2.18	0.72
10:A:46:G:H1'	10:A:47:U:C5	2.25	0.72
16:AG:401:PRO:C	16:AG:403:VAL:H	1.97	0.72
11:AA:901:LEU:HA	16:AG:9:VAL:CA	2.17	0.72
12:AB:133:MET:HE2	12:AB:133:MET:N	2.05	0.72
18:D:1308:U:C3'	38:X:98:ARG:HH21	1.92	0.72
22:H:267:TRP:CE3	22:H:340:ARG:HG2	2.24	0.72
10:B:46:G:H1'	10:B:47:U:C5	2.25	0.71
10:B:76:A:H2'	41:a:2493:U:H5''	1.72	0.71
18:D:1308:U:O5'	38:X:98:ARG:HG3	1.90	0.71
22:H:70:VAL:HA	22:H:85:SER:CB	2.20	0.71
8:7:0:U:P	23:I:80:LYS:HG3	2.30	0.71
10:A:72:A:C3'	10:A:73:A:H5''	2.20	0.71
14:AE:220:ARG:HG2	14:AE:220:ARG:HH11	1.55	0.71
10:B:72:A:C3'	10:B:73:A:H5''	2.20	0.71
14:AE:107:LEU:HD11	14:AE:242:LEU:HB2	1.70	0.71
17:C:12:ARG:HB2	22:H:264:GLU:CB	2.19	0.71
8:7:-12:U:N3	18:D:1196:A:C8	2.57	0.71
9:9:77:VAL:HG12	9:9:82:ILE:HG21	1.71	0.71
22:H:86:ARG:O	22:H:89:ALA:HB3	1.91	0.71
9:9:3:LEU:HD12	9:9:3:LEU:N	2.05	0.71
10:A:18:G:C5	10:A:57:A:N6	2.59	0.71
12:AB:145:ASN:ND2	14:AE:53:ARG:CZ	2.52	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:16:PHE:CB	22:H:43:LYS:HA	2.20	0.71
38:X:96:PRO:HG2	38:X:102:THR:CG2	2.21	0.71
9:9:18:VAL:HA	9:9:86:MET:HE2	1.71	0.71
10:A:15:G:H2'	10:A:15:G:N3	2.06	0.70
11:AA:855:PRO:HB2	16:AG:109:THR:N	2.05	0.70
18:D:827:U:H3	18:D:872:A:N6	1.87	0.70
16:AG:32:ALA:HA	16:AG:103:ASP:O	1.91	0.70
10:B:18:G:C5	10:B:57:A:N6	2.59	0.70
41:a:2314:A:C1'	54:n:155:THR:HG21	2.21	0.70
11:AA:903:ARG:C	16:AG:8:VAL:CB	2.63	0.70
8:7:-12:U:O4	18:D:1196:A:N9	2.24	0.70
13:AC:232:VAL:C	13:AD:221:ALA:HB1	2.16	0.70
10:A:41:C:C1'	27:M:143:ARG:NH1	2.55	0.70
30:P:102:LEU:HG	30:P:102:LEU:O	1.89	0.70
12:AB:141:PHE:CD1	30:P:84:VAL:HG13	2.27	0.70
18:D:915:A:N6	18:D:916:U:C4	2.60	0.70
22:H:19:ARG:HD3	22:H:73:ASP:OD1	1.92	0.70
39:Y:21:PRO:CB	39:Y:22:PRO:HD3	2.22	0.70
12:AB:144:PHE:CE2	30:P:85:ASP:CA	2.56	0.70
41:a:742:A:H2'	41:a:743:A:C8	2.26	0.70
8:7:0:U:H5''	23:I:80:LYS:HE2	1.74	0.69
10:A:11:A:H2'	10:A:12:G:O4'	1.92	0.69
11:AA:905:ILE:HA	16:AG:54:GLY:C	2.17	0.69
18:D:972:C:O2'	30:P:57:VAL:HG23	1.92	0.69
11:AA:905:ILE:HG12	16:AG:54:GLY:C	2.14	0.69
12:AB:140:PRO:CG	30:P:102:LEU:HD13	2.21	0.69
10:B:15:G:H2'	10:B:15:G:N3	2.06	0.69
9:9:31:ARG:HD2	41:a:1054:A:C5'	2.22	0.69
11:AA:849:GLU:HB2	11:AA:887:VAL:HG12	1.72	0.69
11:AA:888:THR:HB	11:AA:889:PRO:CD	2.22	0.69
18:D:1309:G:H8	38:X:98:ARG:NH2	1.89	0.69
10:A:32:C:C4'	27:M:144:MET:CE	2.66	0.69
12:AB:161:SER:HA	12:AB:170:PRO:HA	1.75	0.69
22:H:19:ARG:HD3	22:H:73:ASP:OD2	1.92	0.69
48:h:146:MET:HE3	48:h:154:LEU:HD21	1.74	0.69
22:H:70:VAL:HA	22:H:85:SER:CA	2.22	0.69
41:a:1839:G:C4	41:a:1927:A:C4	2.81	0.69
47:g:18:CYS:CB	47:g:40:CYS:CB	2.68	0.69
10:A:32:C:C1'	27:M:144:MET:CE	2.69	0.69
11:AA:905:ILE:HG23	16:AG:55:ASP:HA	1.75	0.69
10:A:16:C:O2	41:a:2181:U:C5'	2.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:140:PRO:HD2	30:P:102:LEU:HD22	0.74	0.69
14:AE:128:LEU:HD11	14:AE:189:LEU:HG	1.73	0.69
10:B:11:A:H2'	10:B:12:G:O4'	1.92	0.69
12:AB:173:LEU:CD1	30:P:102:LEU:HD23	2.21	0.69
18:D:37:U:H3	18:D:397:A:N6	1.90	0.69
41:a:1021:A:H3'	41:a:1021:A:N3	2.07	0.69
7:6:21:DA:C2	8:7:15:G:N2	2.61	0.69
12:AB:128:PHE:HB2	12:AB:180:LYS:CG	2.23	0.69
41:a:1596:A:H2'	41:a:1597:A:C8	2.28	0.69
1:0:80:ARG:NH2	41:a:572:A:OP2	2.25	0.68
18:D:13:U:O4	18:D:21:G:C2	2.46	0.68
38:X:96:PRO:CG	38:X:102:THR:CG2	2.71	0.68
14:AE:39:LYS:O	14:AE:273:ILE:CG2	2.41	0.68
41:a:2756:U:C4	41:a:2758:A:N6	2.61	0.68
9:9:50:VAL:HG13	39:Y:119:ALA:CB	2.22	0.68
10:A:5:G:H2'	10:A:6:G:C5'	2.24	0.68
14:AE:54:ASP:OD1	14:AE:54:ASP:N	2.24	0.68
14:AE:94:GLN:HB2	14:AE:97:VAL:HG23	1.75	0.68
11:AA:1332:SER:O	14:AE:243:PRO:HG2	1.93	0.68
14:AE:117:LEU:HD12	14:AE:117:LEU:O	1.94	0.68
41:a:1839:G:H8	41:a:1927:A:H1'	1.55	0.68
7:6:8:DC:C6	7:6:9:DT:H72	2.29	0.68
8:7:14:U:H4'	14:AE:322:ARG:HD2	1.74	0.68
11:AA:65:ASN:HB3	11:AA:105:TYR:HB2	1.73	0.68
22:H:19:ARG:O	22:H:72:LEU:CB	2.41	0.68
9:9:58:THR:HG21	9:9:81:LEU:HG	1.74	0.68
14:AE:111:THR:CG2	14:AE:300:GLN:CD	2.66	0.68
22:H:110:GLY:HA3	22:H:153:GLU:O	1.93	0.68
39:Y:14:ALA:HB2	39:Y:54:ILE:HD12	1.76	0.68
41:a:1839:G:C8	41:a:1927:A:C1'	2.74	0.68
41:a:2310:C:O2'	54:n:74:VAL:CG1	2.40	0.68
9:9:118:ILE:HB	9:9:119:PRO:HD3	1.76	0.68
41:a:927:A:H2'	41:a:928:A:C8	2.28	0.68
41:a:2310:C:O2'	54:n:74:VAL:HG12	1.94	0.68
12:AB:128:PHE:HB2	12:AB:180:LYS:HG3	1.74	0.68
22:H:117:LYS:CB	22:H:279:LYS:O	2.41	0.68
9:9:67:THR:N	9:9:68:PRO:CD	2.58	0.67
14:AE:161:THR:HG22	14:AE:164:GLN:HB2	1.75	0.67
41:a:1779:U:H5	41:a:1784:A:N7	1.93	0.67
22:H:267:TRP:CD2	22:H:340:ARG:CG	2.76	0.67
9:9:73:LYS:HB2	9:9:117:LEU:HD21	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:141:PHE:CD2	14:AE:293:ARG:O	2.47	0.67
22:H:70:VAL:HA	22:H:85:SER:HA	1.77	0.67
12:AB:149:GLU:N	12:AB:149:GLU:OE1	2.27	0.67
7:6:16:DC:H1'	14:AE:426:ALA:HB1	1.77	0.67
14:AE:832:LYS:C	14:AE:1242:ARG:HH12	2.01	0.67
18:D:563:A:N1	18:D:884:U:C4	2.61	0.67
41:a:1153:C:OP1	66:z:92:ARG:NH1	2.27	0.67
8:7:-12:U:O4	18:D:1196:A:O4'	2.13	0.67
12:AB:140:PRO:CG	30:P:102:LEU:CG	2.72	0.67
16:AG:219:GLU:CB	21:G:157:LEU:H	2.08	0.67
10:B:5:G:H2'	10:B:6:G:C5'	2.24	0.67
41:a:1920:C:O5'	41:a:1920:C:H6	1.77	0.67
9:9:60:LEU:HA	9:9:64:VAL:HB	1.77	0.67
23:I:75:ILE:O	23:I:75:ILE:HD13	1.95	0.67
9:9:11:ILE:CD1	9:9:62:ARG:HD3	2.24	0.67
12:AB:141:PHE:CB	30:P:84:VAL:HG12	2.24	0.67
22:H:110:GLY:N	22:H:153:GLU:C	2.53	0.67
9:9:43:LYS:HD2	9:9:43:LYS:O	1.94	0.66
14:AE:1037:PHE:HB3	14:AE:1040:MET:HB2	1.78	0.66
12:AB:164:ILE:HD13	12:AB:164:ILE:H	1.60	0.66
39:Y:58:ILE:HD13	39:Y:58:ILE:N	2.09	0.66
10:A:56:C:C5	41:a:2168:G:C6	2.84	0.66
22:H:162:LYS:CB	22:H:298:GLU:OE1	2.44	0.66
11:AA:858:GLY:C	11:AA:861:ALA:H	2.03	0.66
9:9:50:VAL:CG1	39:Y:119:ALA:HB3	2.26	0.66
14:AE:108:ALA:CB	14:AE:279:LEU:HD22	2.25	0.66
22:H:110:GLY:H	22:H:153:GLU:CA	2.08	0.66
11:AA:904:ALA:HB2	16:AG:9:VAL:H	1.61	0.66
38:X:96:PRO:CG	38:X:102:THR:HG22	2.25	0.66
8:7:-6:U:OP1	23:I:136:ARG:NH2	2.28	0.66
14:AE:108:ALA:HB3	14:AE:279:LEU:HD22	1.77	0.66
22:H:270:ILE:HG23	22:H:337:GLU:HB3	1.77	0.66
14:AE:1355:ARG:NH1	14:AE:1369:ARG:HH12	1.93	0.66
21:G:16:PHE:HZ	22:H:41:GLY:O	1.77	0.66
12:AB:125:LYS:CG	12:AB:153:TYR:HB2	2.24	0.66
13:AD:48:LEU:HB2	13:AD:183:ILE:HD11	1.76	0.66
10:B:66:C:H5'	10:B:66:C:H6	1.60	0.66
10:B:21:A:H4'	10:B:21:A:OP1	1.95	0.66
10:B:37:A:H3'	10:B:37:A:OP2	1.96	0.66
22:H:135:LEU:CA	22:H:157:ILE:CB	2.74	0.66
39:Y:116:MET:HB3	39:Y:124:MET:HG2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:165:PHE:HB2	30:P:92:LEU:HD12	1.78	0.65
14:AE:141:PHE:HD2	14:AE:293:ARG:O	1.80	0.65
8:7:-12:U:N3	18:D:1196:A:N7	2.44	0.65
9:9:142:THR:HG21	40:Z:7:ILE:CD1	2.26	0.65
10:A:18:G:C8	10:A:57:A:C6	2.85	0.65
18:D:197:A:C6	18:D:221:C:C4'	2.80	0.65
10:A:21:A:H4'	10:A:21:A:OP1	1.95	0.65
18:D:1227:A:OP2	38:X:110:LYS:NZ	2.29	0.65
9:9:78:GLY:H	9:9:79:PRO:CD	2.10	0.65
18:D:1308:U:O5'	38:X:98:ARG:CG	2.45	0.65
9:9:61:ARG:NH1	41:a:1047:G:N7	2.44	0.65
10:B:56:C:H5'	54:n:80:ARG:NH2	2.10	0.65
56:p:24:ILE:HD13	56:p:72:LEU:HD21	1.77	0.65
14:AE:984:LEU:HB3	14:AE:993:GLU:HB2	1.77	0.65
10:A:3:C:H2'	10:A:4:G:H8	1.62	0.65
22:H:267:TRP:CE2	22:H:340:ARG:CG	2.73	0.65
22:H:267:TRP:CE3	22:H:340:ARG:HG3	2.32	0.65
8:7:-13:U:OP2	18:D:1397:C:N3	2.30	0.65
10:A:66:C:H6	10:A:66:C:H5'	1.60	0.65
18:D:827:U:N3	18:D:872:A:N6	2.45	0.65
21:G:19:GLN:CG	22:H:75:VAL:CG2	2.70	0.65
33:S:47:LYS:O	33:S:50:THR:OG1	2.12	0.65
36:V:25:ILE:HD11	36:V:61:ILE:HD11	1.77	0.65
18:D:1358:U:O4	18:D:1363:A:C2	2.47	0.65
21:G:35:ARG:HH21	22:H:10:GLU:HG2	1.62	0.65
22:H:52:GLN:O	22:H:53:PHE:CD1	2.50	0.65
22:H:85:SER:O	22:H:88:LYS:CB	2.45	0.65
14:AE:67:ASP:OD1	14:AE:95:THR:OG1	2.15	0.65
14:AE:975:ILE:HG22	14:AE:977:SER:H	1.62	0.65
10:B:3:C:H2'	10:B:4:G:H8	1.62	0.65
9:9:57:ASN:CG	9:9:62:ARG:CG	2.68	0.64
11:AA:887:VAL:HG21	11:AA:913:VAL:CG2	2.20	0.64
12:AB:173:LEU:HD11	30:P:102:LEU:CD2	2.27	0.64
10:B:18:G:C8	10:B:57:A:C6	2.85	0.64
39:Y:116:MET:HE2	39:Y:116:MET:HA	1.79	0.64
41:a:1082:U:N3	41:a:1086:A:N6	2.45	0.64
55:o:26:HIS:CE1	55:o:48:ALA:HB2	2.32	0.64
24:J:162:ALA:CB	24:J:165:ARG:HH22	2.08	0.64
11:AA:1280:ALA:HB1	14:AE:918:ILE:HG22	1.79	0.64
21:G:18:HIS:HA	22:H:43:LYS:CD	2.27	0.64
22:H:72:LEU:HD12	22:H:72:LEU:N	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:p:121:ILE:HD12	56:p:141:ILE:HG22	1.79	0.64
7:6:15:DC:N4	7:6:16:DC:H41	1.96	0.64
14:AE:68:TYR:HB3	14:AE:75:TYR:CE2	2.32	0.64
10:B:76:A:H1'	41:a:2493:U:O3'	1.96	0.64
22:H:267:TRP:CZ2	22:H:340:ARG:CG	2.68	0.64
41:a:1923:U:H2'	41:a:1923:U:OP2	1.96	0.64
11:AA:901:LEU:HD21	16:AG:23:ILE:CB	2.27	0.64
14:AE:978:ARG:HG2	14:AE:1197:ASN:HD21	1.60	0.64
10:B:50:U:H2'	10:B:51:C:C6	2.33	0.64
10:B:75:C:OP1	41:a:2602:A:N9	2.30	0.64
18:D:1308:U:H5''	38:X:98:ARG:HG2	1.78	0.64
18:D:1358:U:H3	18:D:1363:A:N6	1.96	0.64
11:AA:1268:GLN:HE22	14:AE:352:ARG:HD2	1.57	0.64
12:AB:152:ASP:HB2	12:AB:157:ARG:HB3	1.78	0.64
41:a:1909:C:O5'	41:a:1909:C:H6	1.80	0.64
12:AB:133:MET:H	12:AB:133:MET:CE	2.08	0.64
14:AE:84:ILE:O	14:AE:84:ILE:HG13	1.96	0.64
22:H:332:VAL:HG12	22:H:334:ASP:H	1.62	0.64
11:AA:901:LEU:HD21	16:AG:20:ARG:O	1.97	0.64
12:AB:93:ILE:HG22	14:AE:290:ILE:HG22	1.78	0.64
14:AE:193:ASP:HB3	14:AE:196:GLN:HB2	1.78	0.64
6:5:98:DA:C2'	6:5:99:DT:H72	2.28	0.64
9:9:11:ILE:HG13	9:9:65:GLU:HB3	1.79	0.64
11:AA:849:GLU:HB2	11:AA:887:VAL:HG13	1.76	0.64
14:AE:136:GLU:CD	14:AE:312:ARG:HH22	2.06	0.64
18:D:1358:U:N3	18:D:1363:A:N6	2.46	0.64
41:a:2303:G:N3	41:a:2314:A:C2	2.66	0.64
59:s:114:LEU:HG	59:s:118:MET:HE3	1.78	0.64
11:AA:855:PRO:CG	16:AG:108:GLN:CB	2.69	0.63
21:G:19:GLN:CG	22:H:76:GLU:CB	2.76	0.63
30:P:17:LEU:HD11	30:P:94:ALA:O	1.98	0.63
10:A:41:C:C4'	27:M:143:ARG:NH1	2.60	0.63
12:AB:164:ILE:HD13	12:AB:164:ILE:O	1.98	0.63
18:D:13:U:O4	18:D:20:U:C4	2.52	0.63
38:X:96:PRO:HG3	38:X:102:THR:HG22	1.78	0.63
6:5:101:DT:OP2	14:AE:275:ARG:NH2	2.31	0.63
9:9:11:ILE:HD12	9:9:62:ARG:HD3	1.80	0.63
9:9:57:ASN:OD1	9:9:62:ARG:HD2	1.98	0.63
18:D:1309:G:C8	38:X:98:ARG:NH2	2.66	0.63
12:AB:47:GLU:CG	12:AB:64:PHE:CE1	2.64	0.63
10:B:69:C:H2'	10:B:70:G:O4'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2885:G:N7	49:i:40:ARG:NH2	2.46	0.63
10:A:19:G:N2	41:a:2112:G:C8	2.62	0.63
10:A:31:G:O2'	27:M:144:MET:SD	2.56	0.63
10:A:37:A:O2'	10:A:38:A:H5'	1.99	0.63
14:AE:44:ILE:CD1	14:AE:252:LEU:HD21	2.29	0.63
14:AE:92:VAL:O	14:AE:92:VAL:HG12	1.99	0.63
18:D:1059:C:O2	30:P:55:PRO:HG3	1.99	0.63
30:P:87:LEU:CD2	30:P:100:ILE:CD1	2.71	0.63
41:a:1789:A:OP2	48:h:221:ARG:NH1	2.32	0.63
10:A:56:C:O2	41:a:2112:G:C4	2.52	0.63
11:AA:314:ASN:HD21	11:AA:348:SER:HA	1.62	0.63
14:AE:128:LEU:HA	14:AE:192:MET:HE1	1.81	0.63
14:AE:1355:ARG:NH1	14:AE:1369:ARG:NH1	2.47	0.63
10:B:6:G:HO2'	10:B:7:G:H8	1.44	0.63
22:H:270:ILE:HG21	22:H:337:GLU:HB3	1.80	0.63
39:Y:32:VAL:HA	39:Y:60:VAL:HG11	1.81	0.63
9:9:29:ASP:HB2	9:9:56:ARG:HD3	1.79	0.63
14:AE:245:LEU:HG	14:AE:246:PRO:HD2	1.79	0.63
10:A:50:U:H2'	10:A:51:C:C6	2.33	0.63
11:AA:549:ASP:OD2	14:AE:750:PRO:CB	2.44	0.63
12:AB:128:PHE:CE1	12:AB:178:VAL:HG23	2.34	0.63
12:AB:141:PHE:N	30:P:84:VAL:CG1	2.45	0.63
21:G:38:VAL:HG22	22:H:75:VAL:CG2	2.25	0.63
22:H:304:VAL:HG12	22:H:304:VAL:O	1.99	0.63
8:7:20:G:OP1	11:AA:1073:LYS:NZ	2.26	0.62
9:9:23:LEU:HB3	9:9:92:ALA:HA	1.81	0.62
14:AE:162:GLU:OE1	14:AE:162:GLU:HA	1.97	0.62
14:AE:201:LEU:HB2	14:AE:221:ILE:HD13	1.80	0.62
18:D:37:U:O2	18:D:548:G:C2	2.52	0.62
2:1:36:LEU:HD13	2:1:48:LYS:HA	1.80	0.62
11:AA:813:GLU:HB2	14:AE:461:PHE:HD2	1.63	0.62
22:H:49:PRO:CD	22:H:84:LEU:HD11	2.29	0.62
41:a:1021:A:C2	41:a:1141:U:O4	2.50	0.62
1:0:40:MET:HE1	66:z:105:ALA:HB1	1.80	0.62
12:AB:162:VAL:CG1	12:AB:164:ILE:HG23	2.29	0.62
12:AB:165:PHE:CB	30:P:90:LEU:O	2.48	0.62
14:AE:395:LYS:HZ2	14:AE:399:LYS:CD	2.12	0.62
9:9:92:ALA:HB3	9:9:129:LEU:HB2	1.82	0.62
10:A:69:C:H2'	10:A:70:G:O4'	1.99	0.62
11:AA:120:GLN:NE2	11:AA:490:GLN:OE1	2.32	0.62
11:AA:1101:LEU:HD23	14:AE:725:MET:SD	2.40	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:141:PHE:CD1	30:P:84:VAL:CG1	2.82	0.62
14:AE:111:THR:CG2	14:AE:300:GLN:NE2	2.63	0.62
22:H:110:GLY:N	22:H:153:GLU:O	2.32	0.62
22:H:270:ILE:CG2	22:H:337:GLU:CB	2.77	0.62
41:a:2297:A:C2	41:a:2321:U:C4	2.86	0.62
3:2:50:LEU:HD23	45:e:26:PHE:CE1	2.35	0.62
16:AG:142:VAL:HA	16:AG:152:LEU:HA	1.81	0.62
21:G:19:GLN:CD	22:H:75:VAL:HG22	2.25	0.62
22:H:119:GLY:CA	22:H:131:LEU:O	2.46	0.62
41:a:1839:G:O4'	41:a:1927:A:H1'	1.97	0.62
41:a:1839:G:N9	41:a:1927:A:N9	2.48	0.62
41:a:2189:U:O4'	41:a:2189:U:P	2.57	0.62
9:9:18:VAL:HG13	9:9:71:CYS:HB2	1.81	0.62
12:AB:144:PHE:CZ	30:P:85:ASP:HB2	2.33	0.62
14:AE:395:LYS:NZ	14:AE:399:LYS:HD3	2.15	0.62
41:a:1998:A:OP2	50:j:141:ARG:NH2	2.32	0.62
41:a:2683:C:OP1	65:y:51:ARG:NH2	2.32	0.62
13:AD:211:ILE:HG12	13:AD:219:ARG:HH12	1.65	0.62
10:A:3:C:H2'	10:A:4:G:C8	2.35	0.61
11:AA:55:SER:OG	11:AA:465:ARG:NH1	2.33	0.61
16:AG:219:GLU:CB	21:G:157:LEU:N	2.63	0.61
17:C:29:LEU:O	17:C:33:ILE:HG23	2.00	0.61
27:M:23:LEU:O	27:M:27:VAL:HG13	1.99	0.61
14:AE:24:LEU:CG	14:AE:232:ASN:ND2	2.63	0.61
22:H:84:LEU:HD22	22:H:84:LEU:N	2.16	0.61
22:H:305:HIS:O	22:H:306:VAL:HB	2.00	0.61
41:a:754:U:H2'	41:a:755:U:C6	2.35	0.61
10:B:42:G:H2'	10:B:43:A:H8	1.65	0.61
38:X:101:ARG:O	38:X:101:ARG:HD3	2.00	0.61
10:A:33:U:H4'	27:M:84:THR:HB	1.82	0.61
10:B:56:C:C4'	54:n:80:ARG:NH2	2.63	0.61
8:7:-7:U:OP1	23:l:132:ARG:NH1	2.33	0.61
11:AA:862:LEU:HD22	11:AA:862:LEU:N	2.14	0.61
22:H:280:LEU:N	22:H:330:VAL:O	2.32	0.61
30:P:57:VAL:O	30:P:58:ASN:CG	2.43	0.61
8:7:17:G:OP2	11:AA:540:ARG:NH1	2.33	0.61
9:9:62:ARG:CG	9:9:62:ARG:HH21	2.14	0.61
14:AE:342:LEU:HD23	14:AE:1352:ILE:HG23	1.83	0.61
7:6:15:DC:C4	7:6:16:DC:C4	2.89	0.61
9:9:136:ILE:HD12	9:9:139:LEU:HD12	1.83	0.61
18:D:13:U:C5	18:D:20:U:O4	2.53	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-7:U:H5'	23:I:132:ARG:CZ	2.26	0.61
10:A:41:C:C1'	27:M:143:ARG:HH12	2.12	0.61
12:AB:141:PHE:CZ	12:AB:171:VAL:CG2	2.74	0.61
12:AB:159:LYS:O	12:AB:159:LYS:HG2	2.00	0.61
14:AE:68:TYR:HB3	14:AE:75:TYR:CZ	2.35	0.61
18:D:1329:A:P	38:X:28:THR:CB	2.83	0.61
9:9:47:GLU:HG3	9:9:95:LEU:HD21	1.83	0.61
9:9:57:ASN:CG	9:9:62:ARG:HG2	2.24	0.61
12:AB:135:ARG:HH11	12:AB:135:ARG:CG	2.14	0.61
9:9:6:GLN:OE1	9:9:6:GLN:HA	2.00	0.61
11:AA:1072:ASN:ND2	11:AA:1111:GLN:OE1	2.34	0.61
11:AA:1287:LEU:HD13	14:AE:1357:ILE:HD11	1.81	0.61
14:AE:90:VAL:O	14:AE:90:VAL:CG1	2.48	0.61
21:G:19:GLN:HG3	22:H:76:GLU:HB2	1.82	0.61
11:AA:862:LEU:HD22	11:AA:862:LEU:H	1.66	0.60
41:a:2297:A:C2	41:a:2321:U:C5	2.89	0.60
13:AC:45:ARG:HD3	13:AD:38:THR:HB	1.82	0.60
8:7:-14:U:H5''	8:7:-14:U:H6	1.64	0.60
10:A:34:C:P	27:M:84:THR:OG1	2.60	0.60
11:AA:857:VAL:CG1	11:AA:862:LEU:HD13	2.31	0.60
10:A:42:G:H2'	10:A:43:A:H8	1.65	0.60
12:AB:128:PHE:CB	12:AB:180:LYS:HB2	2.23	0.60
17:C:44:ILE:CD1	22:H:339:ARG:HG2	2.12	0.60
18:D:1218:C:H2'	18:D:1219:A:C8	2.36	0.60
22:H:117:LYS:CB	22:H:278:THR:HG23	2.32	0.60
22:H:162:LYS:CB	22:H:298:GLU:OE2	2.45	0.60
10:A:41:C:H4'	27:M:143:ARG:CZ	2.31	0.60
10:A:22:G:H2'	10:A:23:C:H6	1.62	0.60
11:AA:528:ARG:NH2	11:AA:576:SER:O	2.30	0.60
12:AB:128:PHE:HZ	12:AB:178:VAL:HG21	1.61	0.60
12:AB:133:MET:HE2	12:AB:133:MET:CA	2.32	0.60
13:AD:112:ALA:HB3	13:AD:126:PRO:HA	1.83	0.60
14:AE:144:TYR:CE1	14:AE:162:GLU:OE2	2.51	0.60
10:B:3:C:H2'	10:B:4:G:C8	2.35	0.60
10:B:65:C:H2'	10:B:66:C:H5'	1.82	0.60
22:H:305:HIS:HD2	22:H:306:VAL:H	1.49	0.60
12:AB:125:LYS:HG2	12:AB:153:TYR:CB	2.30	0.60
22:H:118:GLY:C	22:H:133:GLY:CA	2.67	0.60
35:U:21:VAL:HG21	35:U:60:TRP:CD1	2.36	0.60
39:Y:54:ILE:O	39:Y:54:ILE:HG22	2.00	0.60
41:a:2720:U:OP1	65:y:53:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:65:C:H2'	10:A:66:C:H5'	1.82	0.60
14:AE:201:LEU:HD11	14:AE:220:ARG:HH11	1.67	0.60
11:AA:903:ARG:CB	16:AG:8:VAL:CB	2.76	0.60
11:AA:906:PHE:HZ	16:AG:31:LEU:CB	2.12	0.60
10:B:54:U:N3	10:B:58:A:N6	2.47	0.60
22:H:305:HIS:CD2	22:H:307:SER:H	2.20	0.60
22:H:331:MET:N	22:H:331:MET:SD	2.75	0.60
12:AB:133:MET:HE2	12:AB:133:MET:O	2.01	0.60
14:AE:118:LYS:HD2	14:AE:312:ARG:NH2	2.17	0.60
14:AE:926:PRO:HG2	14:AE:1248:ILE:HD11	1.84	0.60
41:a:1406:U:HO2'	41:a:1407:G:C5'	2.06	0.60
41:a:1921:G:O5'	41:a:1921:G:H8	1.84	0.59
53:m:31:LEU:HD22	53:m:42:LEU:HD13	1.84	0.59
14:AE:99:ARG:HG3	14:AE:99:ARG:NH1	2.17	0.59
14:AE:154:LEU:HD21	14:AE:160:LEU:HD21	1.83	0.59
14:AE:416:ILE:HG13	14:AE:441:LEU:HD11	1.83	0.59
22:H:284:VAL:HG12	22:H:294:VAL:HB	1.84	0.59
25:K:107:ALA:HB2	25:K:125:ALA:HB3	1.83	0.59
27:M:69:VAL:HG23	27:M:100:ALA:HB1	1.83	0.59
10:A:54:U:N3	10:A:58:A:N6	2.47	0.59
12:AB:165:PHE:CE1	30:P:87:LEU:HD12	2.38	0.59
18:D:658:C:H1'	34:T:22:THR:HG21	1.83	0.59
35:U:4:ILE:HG12	35:U:21:VAL:HG22	1.84	0.59
12:AB:145:ASN:N	12:AB:145:ASN:OD1	2.34	0.59
12:AB:165:PHE:CG	30:P:90:LEU:O	2.56	0.59
14:AE:370:LYS:HG2	14:AE:441:LEU:HD23	1.84	0.59
17:C:44:ILE:CD1	22:H:339:ARG:HG3	2.29	0.59
18:D:321:A:N7	18:D:328:C:O2'	2.35	0.59
18:D:1225:A:H4'	37:W:78:ARG:NH1	2.18	0.59
8:7:-10:U:O2'	25:K:33:PHE:HE1	1.76	0.59
10:A:6:G:HO2'	10:A:7:G:H8	1.51	0.59
12:AB:164:ILE:CD1	12:AB:169:THR:CB	2.74	0.59
12:AB:165:PHE:CD2	30:P:92:LEU:CD1	2.67	0.59
14:AE:223:LEU:HG	14:AE:223:LEU:O	2.00	0.59
18:D:13:U:C2	18:D:915:A:N6	2.70	0.59
18:D:563:A:N6	18:D:884:U:N3	2.51	0.59
20:F:4:ILE:CD1	20:F:19:PHE:HA	2.33	0.59
21:G:217:VAL:O	21:G:220:THR:HG22	2.02	0.59
9:9:52:MET:HE3	9:9:52:MET:O	2.03	0.59
11:AA:1142:ARG:NH1	11:AA:1161:LEU:O	2.36	0.59
14:AE:951:GLN:NE2	14:AE:1014:GLY:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:270:ILE:HG21	22:H:337:GLU:CB	2.32	0.59
41:a:1406:U:HO2'	41:a:1407:G:P	2.25	0.59
21:G:35:ARG:HD2	22:H:14:LYS:CD	2.32	0.59
11:AA:901:LEU:CA	16:AG:9:VAL:HA	2.25	0.59
10:B:22:G:H2'	10:B:23:C:H6	1.62	0.59
22:H:36:VAL:HB	22:H:48:ILE:HB	1.84	0.59
40:Z:7:ILE:HG23	40:Z:7:ILE:O	2.01	0.59
10:A:47:U:O2'	10:A:50:U:P	2.61	0.59
11:AA:69:GLN:HE21	11:AA:101:ARG:HD2	1.67	0.59
11:AA:1328:LYS:HE2	14:AE:100:GLU:HA	1.85	0.59
14:AE:275:ARG:NH1	14:AE:278:ARG:NH1	2.51	0.59
14:AE:412:LEU:HD22	14:AE:441:LEU:HD21	1.84	0.59
18:D:404:G:N7	24:J:2:ALA:HB3	2.17	0.59
40:Z:20:VAL:O	40:Z:20:VAL:HG12	2.02	0.59
46:f:24:LEU:HD11	46:f:54:MET:HE2	1.84	0.59
14:AE:395:LYS:HZ2	14:AE:399:LYS:HD3	1.67	0.59
14:AE:1161:GLY:HA3	14:AE:1179:PRO:HA	1.83	0.59
10:B:47:U:O2'	10:B:50:U:P	2.61	0.59
10:B:58:A:H1'	10:B:60:U:C5	2.38	0.59
39:Y:78:LEU:HD13	39:Y:108:ILE:HG22	1.85	0.59
9:9:77:VAL:HG12	9:9:77:VAL:O	2.01	0.58
10:A:58:A:H1'	10:A:60:U:C5	2.38	0.58
18:D:1308:U:C5'	38:X:98:ARG:HG2	2.32	0.58
41:a:70:G:H4'	41:a:71:A:OP1	2.02	0.58
50:j:33:ARG:NH1	50:j:53:GLY:O	2.36	0.58
11:AA:1282:GLY:HA3	15:AF:17:PHE:HE1	1.67	0.58
14:AE:67:ASP:OD1	14:AE:67:ASP:N	2.34	0.58
14:AE:161:THR:HG23	14:AE:164:GLN:H	1.68	0.58
19:E:25:ARG:HA	19:E:66:LEU:HD21	1.85	0.58
8:7:-11:U:H5''	8:7:-11:U:O2	2.03	0.58
11:AA:707:ALA:O	11:AA:711:ASP:HB2	2.03	0.58
14:AE:438:GLU:HG3	14:AE:485:MET:HE1	1.84	0.58
41:a:2572:A:C8	50:j:149:ASN:OD1	2.56	0.58
22:H:119:GLY:HA3	22:H:132:PRO:C	2.28	0.58
9:9:31:ARG:HG3	9:9:31:ARG:NH1	2.17	0.58
11:AA:618:GLN:CG	14:AE:770:LEU:HD13	2.32	0.58
11:AA:838:CYS:HB2	11:AA:918:LEU:HD22	1.85	0.58
12:AB:164:ILE:CD1	12:AB:164:ILE:H	2.17	0.58
12:AB:165:PHE:CB	30:P:92:LEU:CD1	2.82	0.58
14:AE:491:LEU:HB2	14:AE:904:ALA:HA	1.86	0.58
22:H:291:GLY:HA2	22:H:305:HIS:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1590:A:H2'	41:a:1591:A:C8	2.38	0.58
13:AD:287:VAL:CB	16:AG:78:GLU:CB	2.82	0.58
9:9:19:ALA:HA	9:9:70:GLU:HG2	1.84	0.58
9:9:61:ARG:CZ	41:a:1047:G:N7	2.66	0.58
14:AE:124:ILE:HG22	14:AE:124:ILE:O	2.04	0.58
14:AE:514:THR:HG21	14:AE:596:LEU:HD12	1.84	0.58
14:AE:615:LYS:HG2	15:AF:5:THR:HG21	1.85	0.58
14:AE:802:ASP:OD1	14:AE:1348:LYS:NZ	2.31	0.58
18:D:1329:A:P	38:X:28:THR:OG1	2.62	0.58
22:H:330:VAL:HB	22:H:344:LEU:HD23	1.86	0.58
18:D:496:A:N3	18:D:496:A:H2'	2.19	0.58
9:9:78:GLY:H	9:9:79:PRO:HD2	1.68	0.58
10:A:35:A:H2'	10:A:36:U:C6	2.37	0.58
10:A:76:A:H2'	41:a:2394:C:N4	2.11	0.58
13:AC:82:LEU:HD11	13:AC:171:LEU:HD23	1.86	0.58
14:AE:97:VAL:HG11	14:AE:101:ARG:NH2	2.18	0.58
10:B:18:G:C8	10:B:57:A:N6	2.69	0.58
41:a:404:A:O2'	41:a:405:U:OP2	2.22	0.58
6:5:100:DA:H4'	12:AB:16:SER:OG	2.03	0.58
9:9:34:THR:HG22	9:9:38:MET:HE3	1.85	0.58
14:AE:1046:ILE:HD12	14:AE:1059:LEU:HB3	1.86	0.58
22:H:110:GLY:N	22:H:153:GLU:CA	2.67	0.58
14:AE:37:GLU:O	14:AE:61:ILE:CD1	2.52	0.57
10:B:56:C:C5'	54:n:80:ARG:NH2	2.67	0.57
41:a:1839:G:N9	41:a:1927:A:C4	2.72	0.57
41:a:2314:A:O2'	54:n:155:THR:CG2	2.52	0.57
4:3:36:VAL:CG1	4:3:39:ILE:HD12	2.32	0.57
12:AB:156:SER:O	12:AB:156:SER:OG	2.16	0.57
12:AB:165:PHE:HA	30:P:90:LEU:O	2.04	0.57
10:B:60:U:P	10:B:61:C:H41	2.27	0.57
22:H:267:TRP:CH2	22:H:340:ARG:CB	2.87	0.57
47:g:16:CYS:HB3	47:g:37:CYS:HB3	1.87	0.57
6:5:99:DT:H2''	6:5:100:DA:H5''	1.85	0.57
11:AA:1122:LYS:NZ	11:AA:1126:ASP:OD1	2.38	0.57
14:AE:241:VAL:HG12	14:AE:241:VAL:O	2.04	0.57
8:7:-12:U:O4	18:D:1196:A:C8	2.57	0.57
12:AB:141:PHE:CB	30:P:84:VAL:CG1	2.82	0.57
14:AE:638:SER:OG	14:AE:639:VAL:N	2.36	0.57
18:D:439:U:O2	18:D:440:C:C6	2.56	0.57
2:1:20:VAL:HG11	2:1:44:ALA:HA	1.86	0.57
8:7:-14:U:H5''	8:7:-14:U:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:858:GLY:O	11:AA:861:ALA:HB3	2.04	0.57
61:u:77:ILE:HD11	61:u:108:ALA:HB1	1.87	0.57
10:A:11:A:H2'	10:A:12:G:C8	2.40	0.57
10:A:60:U:P	10:A:61:C:H41	2.27	0.57
11:AA:818:VAL:HG22	11:AA:1096:ILE:HG12	1.87	0.57
10:B:60:U:O2'	10:B:61:C:OP1	2.23	0.57
18:D:1526:G:OP2	20:F:42:THR:HG23	2.04	0.57
25:K:56:VAL:O	25:K:60:ILE:HG23	2.04	0.57
39:Y:7:TYR:HB2	39:Y:57:VAL:HG22	1.86	0.57
8:7:-9:U:H3'	8:7:-9:U:H6	1.70	0.57
14:AE:160:LEU:HD22	14:AE:164:GLN:HB3	1.86	0.57
14:AE:247:PRO:HA	14:AE:250:ARG:HG3	1.87	0.57
14:AE:343:LEU:HD11	14:AE:1324:SER:HB3	1.87	0.57
21:G:19:GLN:NE2	22:H:75:VAL:HG22	2.19	0.57
31:Q:67:ALA:HB2	31:Q:96:THR:HG23	1.86	0.57
8:7:-12:U:O4	18:D:1196:A:C1'	2.52	0.57
12:AB:133:MET:N	12:AB:133:MET:SD	2.77	0.57
12:AB:157:ARG:HD2	12:AB:172:GLU:HB3	1.86	0.57
39:Y:59:THR:HG22	39:Y:61:TYR:HE1	1.70	0.57
14:AE:130:MET:HE2	14:AE:135:ILE:HG12	1.87	0.57
22:H:118:GLY:C	22:H:133:GLY:HA2	2.28	0.57
38:X:104:THR:O	38:X:104:THR:HG22	2.03	0.57
9:9:54:VAL:O	9:9:54:VAL:HG22	2.03	0.57
22:H:290:TYR:C	22:H:305:HIS:O	2.47	0.57
11:AA:516:ASP:OD1	11:AA:516:ASP:O	2.23	0.56
14:AE:102:MET:HG2	14:AE:246:PRO:HG3	1.87	0.56
22:H:49:PRO:HD3	22:H:84:LEU:HD11	1.86	0.56
39:Y:77:VAL:O	39:Y:77:VAL:HG12	2.05	0.56
39:Y:137:LEU:N	39:Y:137:LEU:HD23	2.19	0.56
8:7:-10:U:O2'	25:K:33:PHE:CZ	2.52	0.56
14:AE:510:LEU:HD22	14:AE:601:ILE:HD12	1.86	0.56
10:B:11:A:H2'	10:B:12:G:C8	2.39	0.56
39:Y:96:LYS:HE3	39:Y:136:GLY:HA3	1.87	0.56
1:0:51:VAL:HG23	66:z:86:ALA:O	2.05	0.56
6:5:115:DA:OP2	14:AE:1148:ARG:HG3	2.04	0.56
8:7:-12:U:C4	18:D:1196:A:C8	2.93	0.56
10:A:76:A:C2'	41:a:2394:C:H42	2.16	0.56
11:AA:854:ILE:HG12	11:AA:855:PRO:HD3	1.80	0.56
12:AB:93:ILE:HG22	14:AE:290:ILE:HG23	1.85	0.56
12:AB:141:PHE:HB3	30:P:84:VAL:HG12	1.88	0.56
28:N:10:MET:HE3	28:N:61:LEU:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:17:GLU:HB3	9:9:86:MET:HB2	1.87	0.56
14:AE:74:LYS:HD2	14:AE:85:CYS:SG	2.45	0.56
14:AE:741:ALA:O	14:AE:762:ASN:ND2	2.38	0.56
18:D:528:C:H6	18:D:528:C:H5''	1.71	0.56
22:H:110:GLY:H	22:H:153:GLU:C	2.12	0.56
22:H:332:VAL:CG1	22:H:335:ILE:HG13	2.33	0.56
41:a:580:U:O3'	66:z:31:VAL:HG13	2.05	0.56
9:9:31:ARG:HD2	41:a:1054:A:C4'	2.29	0.56
12:AB:129:GLU:H	12:AB:180:LYS:HD2	1.70	0.56
14:AE:99:ARG:HH11	14:AE:99:ARG:CG	2.18	0.56
16:AG:112:GLN:O	16:AG:116:GLN:CB	2.54	0.56
41:a:1818:U:OP2	48:h:156:ARG:NH1	2.38	0.56
10:A:56:C:C6	41:a:2168:G:C6	2.94	0.56
14:AE:171:GLU:HA	14:AE:171:GLU:OE1	2.05	0.56
14:AE:198:CYS:HA	14:AE:221:ILE:HD11	1.87	0.56
41:a:2245:U:O2'	41:a:2436:G:OP2	2.22	0.56
2:1:93:ALA:HB2	41:a:1614:A:C2	2.40	0.56
9:9:50:VAL:HG13	39:Y:119:ALA:HB3	1.88	0.56
12:AB:134:VAL:HG12	12:AB:180:LYS:HA	1.87	0.56
16:AG:218:GLU:HA	21:G:104:TRP:HD1	1.71	0.56
7:6:18:DC:N4	8:7:17:G:H1	1.99	0.56
9:9:35:VAL:HA	9:9:38:MET:HB2	1.88	0.56
11:AA:13:LYS:HB2	11:AA:1180:MET:HE2	1.86	0.56
11:AA:806:PRO:O	14:AE:633:ALA:HA	2.06	0.56
11:AA:839:VAL:HG12	11:AA:1049:ILE:HG12	1.87	0.56
12:AB:165:PHE:HZ	30:P:87:LEU:HD11	1.67	0.56
10:B:32:C:OP2	29:O:130:ARG:NH2	2.38	0.56
41:a:2000:C:OP1	63:w:5:LYS:NZ	2.36	0.56
47:g:18:CYS:HB3	47:g:40:CYS:HB2	1.88	0.56
8:7:-20:A:H2'	8:7:-19:U:H6	1.70	0.56
8:7:-10:U:O2	8:7:-10:U:H2'	2.06	0.56
9:9:7:ASP:OD1	9:9:7:ASP:N	2.36	0.56
12:AB:167:ARG:HB2	12:AB:167:ARG:HH11	1.70	0.56
14:AE:1175:LEU:HD22	14:AE:1190:ILE:HD11	1.88	0.56
21:G:19:GLN:HG3	22:H:75:VAL:CG2	2.23	0.56
22:H:267:TRP:CH2	22:H:340:ARG:HB3	2.41	0.56
52:l:104:ALA:O	52:l:108:ILE:HG23	2.05	0.56
62:v:66:ARG:NH1	62:v:104:GLU:OE1	2.39	0.56
7:6:26:DT:H2''	7:6:27:DG:H5'	1.89	0.56
12:AB:140:PRO:CG	30:P:102:LEU:CD1	2.84	0.56
7:6:21:DA:N6	8:7:15:G:H1	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:39:LYS:O	14:AE:273:ILE:HG21	2.06	0.55
30:P:6:ILE:HG23	30:P:100:ILE:HG23	1.87	0.55
41:a:2303:G:C4	41:a:2314:A:C2	2.94	0.55
8:7:-9:U:H5''	25:K:56:VAL:HG21	1.87	0.55
10:A:38:A:H2'	10:A:39:C:H5'	1.88	0.55
12:AB:140:PRO:CB	30:P:6:ILE:HD11	2.36	0.55
14:AE:144:TYR:HE1	14:AE:162:GLU:CD	2.14	0.55
10:A:50:U:H2'	10:A:51:C:H6	1.69	0.55
14:AE:1155:ILE:HG13	14:AE:1210:ILE:HB	1.89	0.55
21:G:148:LEU:HD22	21:G:151:ILE:HD11	1.86	0.55
8:7:-18:G:H5''	18:D:1501:C:N4	2.21	0.55
11:AA:985:GLU:HB3	11:AA:988:LYS:HB2	1.89	0.55
11:AA:1142:ARG:NH2	11:AA:1166:ASP:OD1	2.38	0.55
12:AB:148:VAL:HG13	12:AB:148:VAL:O	2.06	0.55
41:a:84:A:N1	41:a:98:G:O2'	2.33	0.55
43:c:31:PRO:HG2	43:c:33:LEU:HD13	1.87	0.55
16:AG:63:LEU:HA	16:AG:92:TYR:HA	1.87	0.55
10:B:11:A:H8	10:B:11:A:O5'	1.89	0.55
22:H:71:ALA:O	22:H:72:LEU:CD1	2.42	0.55
41:a:2249:U:H3'	41:a:2250:G:C5'	2.36	0.55
10:A:18:G:C8	10:A:57:A:N6	2.69	0.55
14:AE:903:LEU:HD21	14:AE:1249:ASN:HD22	1.70	0.55
10:B:50:U:H2'	10:B:51:C:H6	1.70	0.55
18:D:563:A:N6	18:D:884:U:H3	2.05	0.55
22:H:154:PHE:CB	22:H:168:VAL:CB	2.85	0.55
11:AA:143:ARG:NH2	11:AA:512:SER:O	2.40	0.55
12:AB:141:PHE:CE2	12:AB:171:VAL:CG2	2.75	0.55
18:D:769:G:H4'	18:D:1513:A:H4'	1.88	0.55
39:Y:57:VAL:O	39:Y:57:VAL:HG12	2.07	0.55
6:5:110:DA:N7	11:AA:183:TRP:CH2	2.75	0.55
8:7:-20:A:C4	8:7:-19:U:C5	2.95	0.55
9:9:43:LYS:HZ1	9:9:95:LEU:HD13	1.72	0.55
11:AA:905:ILE:HA	16:AG:55:ASP:N	2.22	0.55
14:AE:759:ILE:HG23	14:AE:771:GLN:HB3	1.89	0.55
41:a:523:C:O2	41:a:554:U:O2'	2.25	0.55
52:l:130:LYS:HB2	52:l:133:LEU:HD12	1.89	0.55
14:AE:58:CYS:SG	14:AE:59:ALA:N	2.80	0.55
14:AE:1166:GLY:HA3	14:AE:1174:ARG:HB2	1.88	0.55
22:H:332:VAL:O	22:H:334:ASP:N	2.40	0.55
24:J:61:VAL:HG21	24:J:200:ILE:CD1	2.35	0.55
37:W:15:LEU:HD13	37:W:33:THR:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:116:MET:HG3	39:Y:124:MET:HB3	1.89	0.55
40:Z:2:ILE:HB	40:Z:5:ASP:HB3	1.89	0.55
10:B:56:C:C5'	54:n:80:ARG:CZ	2.76	0.54
18:D:1515:G:H2'	18:D:1516:G:H8	1.72	0.54
22:H:84:LEU:HD22	22:H:84:LEU:H	1.72	0.54
7:6:2:DC:H2''	7:6:3:DC:C5	2.43	0.54
8:7:1:U:O2	8:7:1:U:H2'	2.06	0.54
10:A:11:A:O5'	10:A:11:A:H8	1.89	0.54
14:AE:124:ILE:HG23	14:AE:128:LEU:HD12	1.89	0.54
18:D:13:U:C2	18:D:915:A:C6	2.95	0.54
18:D:439:U:O2	18:D:440:C:C5	2.61	0.54
34:T:5:THR:O	34:T:8:THR:OG1	2.18	0.54
41:a:2314:A:O2'	54:n:155:THR:HG21	2.06	0.54
3:2:50:LEU:HD23	45:e:26:PHE:CZ	2.42	0.54
8:7:-13:U:H5'	18:D:1397:C:N3	2.22	0.54
14:AE:833:GLU:HB2	14:AE:1242:ARG:NH1	2.22	0.54
25:K:99:ALA:HB1	25:K:103:THR:HG21	1.89	0.54
41:a:1056:G:O2'	41:a:1103:A:N6	2.41	0.54
14:AE:46:TYR:CD1	14:AE:46:TYR:C	2.85	0.54
14:AE:1167:LYS:HZ2	14:AE:1170:LYS:HB2	1.72	0.54
18:D:961:U:O4	18:D:974:A:N1	2.40	0.54
42:b:37:ILE:HD11	42:b:82:ILE:HD11	1.90	0.54
7:6:22:DC:H4'	11:AA:508:SER:OG	2.07	0.54
10:A:60:U:O2'	10:A:61:C:OP1	2.23	0.54
11:AA:360:LEU:HD13	11:AA:378:ARG:HH11	1.72	0.54
13:AC:28:LEU:HD22	13:AC:201:LEU:HD23	1.88	0.54
14:AE:145:VAL:HG23	14:AE:159:ILE:HG22	1.89	0.54
10:B:12:G:H2'	10:B:13:C:OP1	2.08	0.54
18:D:1308:U:H2'	38:X:98:ARG:HH22	1.61	0.54
58:r:58:LEU:O	58:r:61:VAL:HG22	2.08	0.54
8:7:-18:G:C3'	18:D:1500:A:N6	2.71	0.54
9:9:93:ALA:O	9:9:129:LEU:HD13	2.06	0.54
11:AA:103:VAL:HB	11:AA:114:VAL:HG11	1.89	0.54
16:AG:289:ALA:HA	16:AG:291:ALA:H	1.72	0.54
9:9:139:LEU:HD11	40:Z:11:VAL:HG13	1.90	0.54
22:H:267:TRP:CZ3	22:H:340:ARG:HG3	2.43	0.54
22:H:321:VAL:HG13	22:H:322:VAL:HG23	1.90	0.54
11:AA:684:ASN:OD1	11:AA:687:ARG:NH2	2.41	0.54
14:AE:78:LEU:O	14:AE:78:LEU:HD13	2.08	0.54
14:AE:814:CYS:SG	14:AE:883:ARG:NH2	2.81	0.54
10:B:76:A:N3	41:a:2493:U:H4'	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:22:SER:N	22:H:69:ASP:OD2	2.40	0.54
22:H:116:VAL:C	22:H:279:LYS:HB2	2.33	0.54
39:Y:12:VAL:HG12	39:Y:23:VAL:HG21	1.90	0.54
10:A:17:C:O2	10:A:17:C:H2'	2.08	0.54
14:AE:205:LEU:HG	14:AE:217:LEU:HB3	1.90	0.54
15:AF:3:ARG:NH1	15:AF:55:GLU:OE2	2.40	0.54
18:D:1228:C:OP2	38:X:110:LYS:NZ	2.41	0.54
41:a:811:U:H2'	61:u:21:ARG:HA	1.89	0.54
64:x:27:VAL:HG21	64:x:40:ILE:HD12	1.89	0.54
9:9:51:TYR:CD1	9:9:51:TYR:C	2.85	0.54
11:AA:29:SER:O	11:AA:33:ASP:HB2	2.07	0.54
18:D:945:G:C2	18:D:946:A:C8	2.96	0.54
18:D:1227:A:H5'	38:X:110:LYS:HZ1	1.70	0.54
22:H:52:GLN:OE1	22:H:86:ARG:CB	2.56	0.54
22:H:84:LEU:H	22:H:84:LEU:CD2	2.21	0.54
12:AB:165:PHE:HE1	30:P:87:LEU:HA	1.68	0.53
39:Y:19:PRO:HG2	39:Y:24:GLY:H	1.73	0.53
64:x:35:ILE:HG21	64:x:71:ALA:HA	1.89	0.53
8:7:-4:U:H2'	8:7:-3:U:H5''	1.90	0.53
11:AA:628:HIS:HB3	11:AA:647:ARG:HH21	1.74	0.53
11:AA:811:ASN:HA	11:AA:815:SER:HB2	1.90	0.53
13:AD:100:LEU:HD21	13:AD:121:VAL:HG11	1.91	0.53
16:AG:32:ALA:HA	16:AG:102:PHE:O	2.06	0.53
39:Y:109:ALA:HB2	39:Y:128:ILE:HG13	1.89	0.53
52:l:108:ILE:HD11	52:l:180:LEU:HD13	1.89	0.53
8:7:20:G:O2'	14:AE:425:ARG:NH2	2.40	0.53
9:9:43:LYS:HG2	9:9:98:GLU:HG2	1.90	0.53
13:AC:100:LEU:HD23	13:AC:115:ILE:HG21	1.89	0.53
25:K:94:VAL:HG13	25:K:111:MET:HE1	1.91	0.53
8:7:-18:G:C4'	18:D:1500:A:H62	2.21	0.53
9:9:62:ARG:HG2	9:9:62:ARG:NH2	2.20	0.53
10:A:12:G:H2'	10:A:13:C:OP1	2.08	0.53
11:AA:633:LEU:HD13	11:AA:644:LEU:HD23	1.89	0.53
14:AE:975:ILE:HD11	14:AE:1003:LEU:HD11	1.91	0.53
18:D:1329:A:OP1	38:X:28:THR:N	2.41	0.53
22:H:135:LEU:CB	22:H:167:VAL:CA	2.86	0.53
32:R:80:ILE:HD12	32:R:97:THR:HG22	1.89	0.53
41:a:1209:U:O2'	41:a:1237:A:N1	2.40	0.53
52:l:131:THR:HG22	52:l:160:ALA:O	2.08	0.53
2:1:59:GLU:CG	2:1:66:ILE:HD11	2.38	0.53
8:7:0:U:OP2	23:I:80:LYS:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:18:G:C2	10:A:58:A:C5	2.96	0.53
11:AA:1284:ALA:HB3	14:AE:1361:THR:HB	1.90	0.53
14:AE:26:SER:HB2	14:AE:236:TRP:CE2	2.42	0.53
18:D:13:U:C4	18:D:21:G:C2	2.96	0.53
60:t:7:MET:HE1	60:t:44:LYS:HD2	1.91	0.53
8:7:15:G:H2'	8:7:16:A:C8	2.43	0.53
9:9:125:ARG:HA	9:9:125:ARG:CZ	2.38	0.53
11:AA:1117:LEU:HD12	11:AA:1195:ILE:HG12	1.90	0.53
12:AB:93:ILE:CG2	14:AE:290:ILE:HG22	2.39	0.53
13:AC:43:LEU:HD13	13:AC:217:ILE:HD11	1.90	0.53
13:AD:28:LEU:HD12	13:AD:201:LEU:HD23	1.91	0.53
14:AE:56:LEU:CD1	14:AE:273:ILE:HD12	2.39	0.53
14:AE:746:LEU:HG	14:AE:758:PRO:HG3	1.90	0.53
22:H:45:GLU:OE1	22:H:45:GLU:N	2.40	0.53
22:H:119:GLY:CA	22:H:133:GLY:CA	2.74	0.53
39:Y:138:VAL:HG12	39:Y:138:VAL:O	2.08	0.53
41:a:2192:U:H2'	41:a:2193:G:C8	2.43	0.53
41:a:2315:G:O2'	54:n:125:ARG:HD3	2.09	0.53
9:9:31:ARG:HD2	41:a:1054:A:H5'	1.80	0.53
10:A:56:C:C2	41:a:2112:G:C8	2.96	0.53
14:AE:39:LYS:O	14:AE:273:ILE:HG23	2.08	0.53
10:B:16:C:O2	10:B:16:C:H2'	2.08	0.53
22:H:135:LEU:CB	22:H:157:ILE:CB	2.87	0.53
14:AE:30:ILE:HG21	14:AE:241:VAL:O	2.08	0.53
10:B:18:G:C2	10:B:58:A:C5	2.97	0.53
18:D:767:A:H2'	18:D:768:A:O4'	2.09	0.53
41:a:2298:A:C5	41:a:2321:U:O4	2.62	0.53
8:7:-18:G:H3'	18:D:1500:A:N6	2.23	0.53
10:A:38:A:C2'	10:A:39:C:H5'	2.39	0.53
14:AE:111:THR:HG22	14:AE:300:GLN:NE2	2.23	0.53
14:AE:832:LYS:HB3	14:AE:1242:ARG:NH1	2.24	0.53
16:AG:139:THR:HA	16:AG:180:ARG:HA	1.91	0.53
22:H:19:ARG:O	22:H:72:LEU:HD22	2.09	0.53
9:9:58:THR:HG21	9:9:81:LEU:HA	1.90	0.53
13:AD:16:ILE:HG23	13:AD:26:VAL:HG22	1.91	0.53
14:AE:68:TYR:CA	14:AE:75:TYR:HE2	2.22	0.53
14:AE:99:ARG:HG3	14:AE:99:ARG:HH11	1.74	0.53
14:AE:850:LYS:HB2	14:AE:857:LEU:HB2	1.91	0.53
18:D:673:A:H2'	18:D:674:G:C8	2.44	0.53
30:P:8:ILE:HD12	30:P:25:ILE:HD11	1.89	0.53
39:Y:37:PHE:CZ	39:Y:56:VAL:HG11	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1906:G:H5''	41:a:1906:G:H8	1.73	0.53
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
12:AB:148:VAL:HA	12:AB:160:VAL:HA	1.90	0.52
14:AE:215:LYS:HA	14:AE:218:THR:HG22	1.91	0.52
29:O:98:LEU:HB3	29:O:104:VAL:HG13	1.91	0.52
11:AA:1070:HIS:NE2	11:AA:1114:GLU:OE1	2.36	0.52
14:AE:136:GLU:OE1	14:AE:312:ARG:CZ	2.55	0.52
22:H:49:PRO:HD2	22:H:84:LEU:CD1	2.39	0.52
60:t:71:ARG:NH2	60:t:123:LEU:O	2.42	0.52
8:7:15:G:H2'	8:7:16:A:H8	1.75	0.52
10:A:6:G:O2'	10:A:7:G:H8	1.92	0.52
10:A:22:G:O2'	10:A:23:C:P	2.67	0.52
14:AE:209:ASN:HA	14:AE:214:ARG:HH21	1.74	0.52
14:AE:785:ASP:O	14:AE:789:LYS:HB2	2.08	0.52
10:B:17:C:O2	10:B:17:C:H2'	2.08	0.52
63:w:38:LEU:N	63:w:39:PRO:CD	2.73	0.52
11:AA:246:LEU:HB3	11:AA:269:ILE:HD13	1.91	0.52
11:AA:786:GLY:N	11:AA:789:THR:OG1	2.41	0.52
9:9:71:CYS:HA	9:9:117:LEU:HD13	1.91	0.52
11:AA:125:GLY:HA2	11:AA:499:SER:HB2	1.92	0.52
14:AE:144:TYR:CE1	14:AE:162:GLU:CD	2.88	0.52
10:B:22:G:O2'	10:B:23:C:P	2.68	0.52
17:C:30:LYS:HA	17:C:33:ILE:HD13	1.91	0.52
18:D:864:A:C2	18:D:865:A:C2	2.98	0.52
39:Y:33:ASN:H	39:Y:66:PHE:HE1	1.56	0.52
41:a:1980:G:O2'	41:a:1982:U:OP2	2.28	0.52
8:7:11:U:C2	11:AA:1253:LEU:HD12	2.37	0.52
11:AA:374:GLU:HB2	12:AB:80:TRP:HH2	1.75	0.52
11:AA:524:ILE:HG21	11:AA:708:VAL:HG13	1.92	0.52
14:AE:804:ALA:O	14:AE:806:ASP:N	2.41	0.52
18:D:927:G:O2'	18:D:1503:A:N7	2.36	0.52
22:H:24:VAL:HG12	22:H:69:ASP:H	1.74	0.52
4:3:13:VAL:CG2	4:3:39:ILE:HD13	2.39	0.52
13:AD:205:MET:HE3	13:AD:213:PRO:HB3	1.91	0.52
14:AE:112:ALA:HA	14:AE:238:ILE:HA	1.91	0.52
10:B:6:G:O2'	10:B:7:G:H8	1.92	0.52
10:B:12:G:C2'	10:B:13:C:OP1	2.57	0.52
38:X:17:ILE:O	38:X:20:THR:OG1	2.22	0.52
39:Y:116:MET:HE2	39:Y:117:THR:H	1.74	0.52
41:a:587:C:OP2	61:u:21:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:243:PRO:HB2	11:AA:274:ILE:HG23	1.90	0.52
18:D:13:U:C4	18:D:915:A:C6	2.92	0.52
41:a:639:U:H2'	41:a:640:C:C6	2.45	0.52
41:a:929:U:H1'	46:f:26:GLY:O	2.10	0.52
9:9:11:ILE:CD1	9:9:11:ILE:N	2.73	0.52
10:A:12:G:C2'	10:A:13:C:OP1	2.58	0.52
12:AB:164:ILE:CD1	12:AB:164:ILE:N	2.73	0.52
39:Y:112:LYS:HZ2	39:Y:112:LYS:HB3	1.74	0.52
41:a:523:C:H4'	41:a:540:C:O2	2.10	0.52
44:d:106:G:H2'	44:d:107:G:O4'	2.10	0.52
10:B:56:C:C3'	10:B:57:A:H5''	2.40	0.52
8:7:16:A:H2'	8:7:17:G:C8	2.45	0.51
11:AA:143:ARG:NH1	11:AA:507:GLY:O	2.32	0.51
11:AA:714:VAL:HB	11:AA:787:PRO:HD2	1.92	0.51
10:B:56:C:H2'	10:B:57:A:C5'	2.27	0.51
18:D:1276:G:O5'	18:D:1276:G:H8	1.93	0.51
25:K:81:LEU:HD13	25:K:123:VAL:HG12	1.92	0.51
41:a:1266:G:OP2	49:i:17:ARG:NE	2.43	0.51
41:a:1693:U:O2'	48:h:14:ARG:NH2	2.43	0.51
41:a:2328:A:H2'	41:a:2329:U:C6	2.44	0.51
9:9:41:LEU:HD12	39:Y:117:THR:HG22	1.92	0.51
9:9:125:ARG:O	9:9:125:ARG:HG3	2.10	0.51
14:AE:683:ILE:HD12	14:AE:754:ILE:HG21	1.93	0.51
39:Y:27:LEU:HD12	39:Y:27:LEU:C	2.35	0.51
14:AE:88:CYS:HB3	14:AE:90:VAL:HG12	1.92	0.51
17:C:61:ARG:NH2	18:D:736:C:OP1	2.43	0.51
18:D:1404:C:H2'	18:D:1404:C:O2	2.10	0.51
22:H:49:PRO:HD2	22:H:84:LEU:HD11	1.92	0.51
41:a:1910:G:O5'	41:a:1910:G:H8	1.93	0.51
54:n:8:TYR:HA	54:n:12:VAL:HB	1.91	0.51
66:z:58:ARG:HA	66:z:61:TRP:CE3	2.45	0.51
10:A:15:G:N3	10:A:15:G:C2'	2.73	0.51
11:AA:1268:GLN:HE21	14:AE:352:ARG:HD2	1.66	0.51
18:D:5:U:O2	18:D:5:U:O4'	2.29	0.51
18:D:1308:U:P	38:X:98:ARG:HG3	2.50	0.51
23:I:77:ILE:HA	23:I:84:VAL:HG23	1.91	0.51
2:1:93:ALA:HB2	41:a:1614:A:N1	2.25	0.51
9:9:23:LEU:HA	9:9:118:ILE:HG13	1.93	0.51
10:A:16:C:O2	10:A:16:C:H2'	2.09	0.51
10:A:76:A:O2'	41:a:2395:C:C2	2.64	0.51
11:AA:1101:LEU:HD21	14:AE:508:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:165:PHE:CB	30:P:92:LEU:HD12	2.40	0.51
14:AE:201:LEU:HD12	14:AE:224:LEU:HD12	1.92	0.51
10:B:18:G:C2	10:B:58:A:C6	2.99	0.51
21:G:38:VAL:CG2	22:H:75:VAL:CG2	2.77	0.51
41:a:2093:G:O2'	41:a:2198:A:N1	2.41	0.51
56:p:121:ILE:HD12	56:p:141:ILE:CG2	2.41	0.51
11:AA:618:GLN:HG3	14:AE:770:LEU:CD1	2.38	0.51
11:AA:857:VAL:CG1	11:AA:861:ALA:CB	2.71	0.51
11:AA:974:ARG:HD2	11:AA:1014:LEU:HD21	1.92	0.51
53:m:31:LEU:HD22	53:m:42:LEU:CD1	2.40	0.51
4:3:12:ILE:HG21	4:3:80:ALA:HB2	1.93	0.51
11:AA:93:SER:HA	11:AA:128:PRO:HA	1.93	0.51
12:AB:164:ILE:CD1	12:AB:167:ARG:O	2.56	0.51
39:Y:100:ILE:HB	39:Y:105:LEU:HD11	1.92	0.51
44:d:5:U:OP1	44:d:61:G:O2'	2.26	0.51
59:s:17:VAL:HG23	59:s:137:PRO:HB2	1.93	0.51
10:A:41:C:H4'	27:M:143:ARG:NH1	2.25	0.51
10:A:56:C:C3'	10:A:57:A:H5''	2.40	0.51
11:AA:400:VAL:HG21	11:AA:452:ARG:HE	1.76	0.51
12:AB:123:ARG:H	12:AB:123:ARG:HD2	1.75	0.51
14:AE:275:ARG:HH12	14:AE:278:ARG:NH1	2.09	0.51
16:AG:29:SER:O	16:AG:33:THR:N	2.44	0.51
41:a:1964:G:H4'	41:a:1965:C:OP2	2.11	0.51
60:t:113:MET:O	60:t:116:ILE:HG13	2.11	0.51
8:7:-18:G:C4'	18:D:1500:A:N6	2.73	0.51
10:A:18:G:C2	10:A:58:A:C6	2.99	0.51
10:A:28:C:H2'	10:A:29:G:H8	1.76	0.51
10:A:56:C:H1'	41:a:2112:G:C5	2.46	0.51
12:AB:140:PRO:HB3	30:P:6:ILE:HD11	1.92	0.51
18:D:1499:A:O2'	18:D:1500:A:H5'	2.11	0.51
39:Y:59:THR:HG22	39:Y:61:TYR:CE1	2.45	0.51
41:a:1814:G:H4'	48:h:51:THR:HG21	1.93	0.51
60:t:43:ILE:HD12	60:t:56:ASP:HB2	1.93	0.51
2:1:59:GLU:HG3	2:1:66:ILE:HD11	1.92	0.51
8:7:-19:U:H2'	8:7:-18:G:C8	2.45	0.51
9:9:44:ALA:HB1	9:9:52:MET:HB3	1.93	0.51
12:AB:128:PHE:CE1	12:AB:178:VAL:HG22	2.41	0.51
10:B:34:C:O2	10:B:34:C:H2'	2.11	0.51
10:B:48:C:O2	10:B:48:C:H2'	2.11	0.51
30:P:57:VAL:O	30:P:57:VAL:HG13	2.10	0.51
39:Y:21:PRO:HB2	39:Y:22:PRO:CD	2.30	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:118:A:C8	41:a:119:A:C8	2.98	0.51
54:n:127:ASN:ND2	54:n:127:ASN:N	2.59	0.51
6:5:98:DA:N9	6:5:99:DT:H72	2.27	0.50
9:9:3:LEU:HD13	9:9:5:LEU:H	1.75	0.50
12:AB:172:GLU:N	12:AB:172:GLU:OE1	2.44	0.50
14:AE:99:ARG:HA	14:AE:248:ASP:HB2	1.92	0.50
41:a:1141:U:O2	41:a:1142:A:N6	2.44	0.50
4:3:94:ARG:HB3	4:3:103:ILE:HD12	1.92	0.50
8:7:-7:U:H6	8:7:-7:U:H3'	1.75	0.50
12:AB:117:GLN:HE21	12:AB:117:GLN:CA	2.16	0.50
14:AE:390:LEU:N	14:AE:390:LEU:CD1	2.73	0.50
14:AE:421:VAL:O	14:AE:436:ALA:HA	2.12	0.50
22:H:279:LYS:HA	22:H:331:MET:CB	2.34	0.50
39:Y:112:LYS:NZ	39:Y:112:LYS:CB	2.73	0.50
41:a:1824:G:O2'	48:h:252:THR:HG21	2.11	0.50
10:A:48:C:H2'	10:A:48:C:O2	2.11	0.50
11:AA:255:ILE:HB	11:AA:263:VAL:HB	1.93	0.50
11:AA:400:VAL:HG11	11:AA:452:ARG:HD2	1.94	0.50
18:D:1228:C:OP1	38:X:107:ARG:CZ	2.58	0.50
18:D:1366:C:O2'	30:P:62:ARG:NH2	2.44	0.50
21:G:18:HIS:CA	22:H:43:LYS:HD2	2.29	0.50
22:H:308:GLU:O	22:H:310:ASP:N	2.43	0.50
41:a:2557:G:H2'	41:a:2558:C:C6	2.47	0.50
10:A:56:C:C5	41:a:2168:G:O6	2.64	0.50
12:AB:135:ARG:CG	12:AB:135:ARG:NH1	2.73	0.50
14:AE:437:PHE:HZ	14:AE:453:VAL:HG11	1.76	0.50
21:G:35:ARG:NH2	22:H:10:GLU:HG2	2.25	0.50
22:H:332:VAL:C	22:H:334:ASP:H	2.18	0.50
6:5:96:DT:H2''	6:5:97:DC:C5	2.46	0.50
11:AA:18:ARG:HE	11:AA:620:ASN:HA	1.77	0.50
13:AC:140:ILE:HD12	13:AC:142:MET:HE3	1.92	0.50
14:AE:1371:ARG:HE	14:AE:1372:ARG:NH1	2.10	0.50
10:B:24:U:O2'	41:a:1922:G:O3'	2.29	0.50
18:D:1208:C:H2'	18:D:1209:C:C6	2.47	0.50
18:D:1410:A:C2	18:D:1491:G:C2	2.99	0.50
41:a:2243:U:H2'	41:a:2244:U:C6	2.46	0.50
47:g:16:CYS:CB	47:g:37:CYS:CB	2.82	0.50
11:AA:146:VAL:HG21	11:AA:513:GLN:HE21	1.77	0.50
14:AE:972:LYS:HD2	14:AE:1004:ALA:HA	1.93	0.50
10:B:15:G:N3	10:B:15:G:C2'	2.73	0.50
20:F:4:ILE:HD12	20:F:19:PHE:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:T:40:GLN:CA	34:T:40:GLN:HE21	2.23	0.50
56:p:35:ARG:HD3	56:p:71:LEU:HD13	1.93	0.50
2:1:24:ILE:HD13	2:1:36:LEU:HD11	1.93	0.50
2:1:55:ILE:HG23	2:1:66:ILE:HD12	1.93	0.50
8:7:-2:U:O2	8:7:-2:U:H2'	2.12	0.50
9:9:51:TYR:CG	9:9:89:PRO:HD2	2.47	0.50
10:A:11:A:H2'	10:A:12:G:C1'	2.42	0.50
10:A:19:G:C5	41:a:2112:G:H4'	2.44	0.50
11:AA:904:ALA:CB	16:AG:9:VAL:H	2.24	0.50
34:T:4:SER:O	34:T:8:THR:HG23	2.12	0.50
41:a:1869:G:N2	41:a:1871:A:O2'	2.44	0.50
41:a:2297:A:C6	41:a:2321:U:O4	2.65	0.50
9:9:62:ARG:CG	9:9:62:ARG:NH2	2.73	0.50
11:AA:529:ARG:HH11	11:AA:572:ILE:HG22	1.77	0.50
22:H:117:LYS:CB	22:H:278:THR:CG2	2.90	0.50
66:z:47:TYR:CD1	66:z:47:TYR:C	2.90	0.50
10:A:15:G:H22	10:A:20:U:H3	1.59	0.50
10:A:56:C:H2'	10:A:57:A:C5'	2.27	0.50
12:AB:71:VAL:HG12	12:AB:73:MET:HB2	1.93	0.50
34:T:21:ASP:O	34:T:22:THR:HG22	2.12	0.50
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.93	0.49
10:A:11:A:C2'	10:A:12:G:O4'	2.60	0.49
10:B:25:C:H2'	10:B:26:G:H5'	1.94	0.49
18:D:1311:A:OP1	47:g:59:ARG:NH1	2.45	0.49
22:H:132:PRO:N	22:H:167:VAL:CB	2.75	0.49
50:j:25:THR:HG21	50:j:193:VAL:HG22	1.94	0.49
59:s:32:LEU:CD2	59:s:54:ILE:HG21	2.42	0.49
11:AA:232:ILE:HG12	11:AA:237:LEU:HG	1.94	0.49
11:AA:845:LEU:HB3	11:AA:889:PRO:HB2	1.93	0.49
12:AB:141:PHE:HZ	12:AB:171:VAL:CG2	2.18	0.49
12:AB:165:PHE:CG	30:P:92:LEU:CD1	2.95	0.49
8:7:-15:U:C2	18:D:1493:A:C2	3.00	0.49
11:AA:411:ARG:NH2	11:AA:427:ASP:OD2	2.44	0.49
11:AA:862:LEU:O	11:AA:862:LEU:HD23	2.11	0.49
14:AE:145:VAL:HG12	14:AE:184:ALA:HB1	1.94	0.49
10:B:15:G:H22	10:B:20:U:H3	1.58	0.49
10:B:47:U:H2'	10:B:48:C:H4'	1.93	0.49
28:N:3:MET:HA	28:N:3:MET:HE3	1.94	0.49
41:a:742:A:C2	41:a:743:A:C6	3.00	0.49
59:s:30:THR:HG22	59:s:31:GLU:N	2.27	0.49
8:7:-13:U:OP2	18:D:1397:C:C2	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:39:C:O5'	10:B:39:C:H6	1.95	0.49
18:D:872:A:H2'	18:D:872:A:N3	2.27	0.49
18:D:1356:G:H2'	18:D:1357:A:C8	2.47	0.49
39:Y:80:LYS:HG3	39:Y:86:LYS:HA	1.94	0.49
41:a:2303:G:C6	41:a:2314:A:N1	2.81	0.49
6:5:101:DT:H72	14:AE:271:ARG:CZ	2.41	0.49
11:AA:904:ALA:HB2	16:AG:9:VAL:N	2.25	0.49
16:AG:103:ASP:C	16:AG:105:ILE:H	2.19	0.49
16:AG:103:ASP:C	16:AG:105:ILE:N	2.69	0.49
10:B:11:A:H2'	10:B:12:G:C1'	2.43	0.49
10:B:59:A:H2'	10:B:60:U:H5'	1.94	0.49
22:H:120:PHE:CB	22:H:136:VAL:CB	2.91	0.49
41:a:464:U:O3'	53:m:12:ARG:NH2	2.45	0.49
41:a:2038:G:H2'	41:a:2039:U:O4'	2.12	0.49
48:h:107:PRO:HD2	48:h:110:LEU:HD22	1.94	0.49
63:w:55:ALA:HA	63:w:80:PHE:CE1	2.47	0.49
9:9:52:MET:HE3	9:9:52:MET:CA	2.42	0.49
10:A:32:C:HO2'	27:M:86:GLN:HG3	1.73	0.49
10:A:47:U:H2'	10:A:48:C:H4'	1.94	0.49
10:A:76:A:C2'	41:a:2394:C:N4	2.75	0.49
11:AA:857:VAL:HB	11:AA:862:LEU:HD11	1.93	0.49
11:AA:1336:ASN:ND2	14:AE:29:MET:HG2	2.27	0.49
18:D:13:U:O4	18:D:21:G:N3	2.46	0.49
18:D:108:G:H5''	18:D:108:G:N3	2.27	0.49
42:b:37:ILE:HG21	42:b:80:ILE:HG21	1.95	0.49
64:x:51:ALA:HB3	64:x:78:VAL:HB	1.94	0.49
1:0:14:VAL:CG2	1:0:98:ILE:HG13	2.43	0.49
10:B:15:G:C2	10:B:20:U:O2	2.66	0.49
18:D:1499:A:H3'	18:D:1499:A:OP2	2.12	0.49
9:9:8:LYS:NZ	41:a:1046:A:H61	2.11	0.49
11:AA:732:ILE:HD11	11:AA:769:PRO:HB3	1.95	0.49
11:AA:857:VAL:HB	11:AA:862:LEU:CD1	2.43	0.49
12:AB:141:PHE:HE2	12:AB:171:VAL:CG2	2.20	0.49
13:AD:100:LEU:HB2	13:AD:144:ILE:HG23	1.94	0.49
14:AE:799:ARG:HG2	14:AE:1325:PHE:HZ	1.78	0.49
41:a:1412:U:C4	41:a:1413:A:N7	2.81	0.49
41:a:2646:C:O5'	41:a:2646:C:H6	1.95	0.49
58:r:3:VAL:HG22	58:r:36:ALA:HB1	1.95	0.49
63:w:67:PHE:O	63:w:71:ARG:N	2.45	0.49
8:7:-19:U:OP2	18:D:926:G:N2	2.45	0.49
9:9:31:ARG:HE	41:a:1054:A:C4'	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:554:HIS:HD2	11:AA:558:VAL:HB	1.77	0.49
25:K:114:VAL:HG21	25:K:141:ILE:HD12	1.94	0.49
41:a:1433:A:H2'	41:a:1434:A:O4'	2.13	0.49
41:a:2298:A:N3	41:a:2321:U:C5	2.80	0.49
48:h:210:ALA:HA	48:h:213:TRP:CE3	2.48	0.49
53:m:24:THR:HG23	53:m:27:GLY:H	1.78	0.49
10:A:59:A:H2'	10:A:60:U:H5'	1.94	0.49
14:AE:102:MET:HG2	14:AE:246:PRO:HD3	1.95	0.49
14:AE:114:ILE:HG12	14:AE:311:ARG:HD2	1.95	0.49
14:AE:800:LEU:HB3	14:AE:920:ALA:HB1	1.95	0.49
18:D:50:A:O2'	18:D:360:G:N2	2.45	0.49
18:D:1017:U:O2'	18:D:1018:G:O4'	2.31	0.49
18:D:1174:G:H2'	18:D:1175:G:H5'	1.95	0.49
22:H:52:GLN:O	22:H:53:PHE:HD1	1.95	0.49
29:O:81:HIS:O	29:O:84:THR:OG1	2.23	0.49
30:P:6:ILE:HG23	30:P:100:ILE:CG2	2.43	0.49
8:7:-15:U:C2	18:D:1493:A:H2	2.31	0.48
11:AA:9:LYS:HG2	11:AA:1171:ARG:HH12	1.77	0.48
11:AA:857:VAL:CB	11:AA:862:LEU:CD1	2.91	0.48
12:AB:93:ILE:O	14:AE:290:ILE:HG21	2.13	0.48
14:AE:201:LEU:HD11	14:AE:220:ARG:HG2	1.95	0.48
14:AE:550:VAL:O	14:AE:569:LEU:HA	2.13	0.48
14:AE:749:LYS:HB3	14:AE:755:ILE:HD11	1.93	0.48
10:B:11:A:C2'	10:B:12:G:O4'	2.60	0.48
18:D:1227:A:P	38:X:110:LYS:HZ1	2.36	0.48
25:K:99:ALA:CB	25:K:103:THR:HG21	2.43	0.48
36:V:48:ASP:HB3	36:V:75:LEU:HD23	1.94	0.48
45:e:18:LEU:HB2	45:e:53:VAL:HG11	1.95	0.48
46:f:24:LEU:HD11	46:f:54:MET:CE	2.42	0.48
11:AA:904:ALA:O	16:AG:53:SER:O	2.31	0.48
14:AE:115:TRP:O	14:AE:1333:THR:HG21	2.13	0.48
14:AE:395:LYS:NZ	14:AE:399:LYS:CD	2.74	0.48
18:D:1169:A:H2'	18:D:1170:A:C8	2.48	0.48
22:H:23:ILE:N	22:H:69:ASP:OD2	2.46	0.48
1:0:40:MET:HE3	1:0:49:ILE:CD1	2.44	0.48
11:AA:363:LEU:HB3	11:AA:381:ALA:HB1	1.96	0.48
12:AB:153:TYR:N	12:AB:153:TYR:CD2	2.81	0.48
14:AE:1027:VAL:HB	14:AE:1121:LEU:HB2	1.95	0.48
18:D:974:A:OP1	33:S:69:ARG:NH1	2.46	0.48
30:P:6:ILE:CG2	30:P:100:ILE:HG23	2.43	0.48
36:V:75:LEU:C	36:V:75:LEU:HD12	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1588:G:C6	41:a:1589:U:O4	2.67	0.48
50:j:156:PHE:CE1	59:s:81:ILE:HD13	2.48	0.48
6:5:110:DA:N7	11:AA:183:TRP:HH2	2.11	0.48
7:6:21:DA:N6	8:7:15:G:N1	2.61	0.48
10:A:37:A:H2'	10:A:38:A:C8	2.48	0.48
10:A:37:A:H2'	10:A:38:A:H8	1.77	0.48
11:AA:565:GLU:HA	11:AA:569:ILE:HG12	1.95	0.48
11:AA:862:LEU:C	11:AA:862:LEU:CD2	2.86	0.48
14:AE:809:VAL:HG21	14:AE:909:ILE:HG12	1.95	0.48
16:AG:183:LEU:HA	16:AG:197:VAL:HA	1.95	0.48
53:m:22:MET:O	53:m:28:ARG:NH1	2.45	0.48
9:9:51:TYR:CD1	9:9:88:HIS:HB2	2.49	0.48
10:A:18:G:C5	10:A:57:A:C5	3.01	0.48
10:A:76:A:N6	41:a:2422:C:O4'	2.46	0.48
12:AB:128:PHE:CB	12:AB:180:LYS:HG3	2.43	0.48
12:AB:129:GLU:N	12:AB:180:LYS:HG3	2.29	0.48
12:AB:141:PHE:CE2	12:AB:171:VAL:HG11	2.49	0.48
14:AE:103:GLY:H	14:AE:244:VAL:HG22	1.78	0.48
14:AE:190:LYS:HB2	14:AE:190:LYS:HE3	1.41	0.48
14:AE:833:GLU:N	14:AE:1242:ARG:HH12	2.12	0.48
28:N:102:ALA:HB3	28:N:113:ASP:HB3	1.96	0.48
43:c:3:ARG:HD2	43:c:30:LEU:HD22	1.94	0.48
2:1:25:ARG:NH1	2:1:74:ILE:O	2.46	0.48
4:3:7:ARG:HB2	41:a:85:G:OP2	2.13	0.48
10:A:15:G:C2	10:A:20:U:O2	2.66	0.48
14:AE:319:SER:HA	14:AE:320:ASN:HA	1.64	0.48
14:AE:1261:LEU:HD12	14:AE:1304:ARG:HH21	1.78	0.48
10:B:76:A:N3	10:B:76:A:C2'	2.74	0.48
18:D:911:U:H2'	18:D:912:C:C6	2.49	0.48
26:L:18:VAL:N	26:L:19:PRO:CD	2.76	0.48
41:a:565:C:H2'	41:a:566:U:O4'	2.13	0.48
6:5:108:DT:H73	11:AA:199:ASP:HB3	1.94	0.48
13:AD:182:ARG:O	13:AD:205:MET:HA	2.13	0.48
10:B:18:G:C5	10:B:57:A:C5	3.01	0.48
18:D:371:A:H2'	18:D:372:C:O4'	2.14	0.48
41:a:1839:G:N9	41:a:1927:A:C1'	2.77	0.48
41:a:2685:G:OP1	60:t:78:ARG:NH2	2.47	0.48
9:9:23:LEU:HD22	9:9:92:ALA:HB1	1.95	0.48
14:AE:891:ASP:OD2	14:AE:1290:ARG:NH2	2.47	0.48
14:AE:1347:LEU:HG	14:AE:1357:ILE:HG23	1.96	0.48
10:B:42:G:H2'	10:B:43:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:72:A:H2'	10:B:73:A:C5'	2.33	0.48
10:A:49:G:H8	10:A:49:G:O5'	1.96	0.48
12:AB:140:PRO:HD3	30:P:102:LEU:CD2	2.25	0.48
10:B:49:G:O5'	10:B:49:G:H8	1.96	0.48
55:o:13:ARG:HD3	61:u:58:TYR:O	2.14	0.48
8:7:-13:U:H5'	18:D:1397:C:C2	2.48	0.48
9:9:125:ARG:NH1	9:9:125:ARG:CA	2.73	0.48
10:A:25:C:H2'	10:A:26:G:H5'	1.95	0.48
10:A:41:C:H5'	27:M:143:ARG:HD2	1.96	0.48
11:AA:812:PHE:HA	14:AE:505:ASP:OD2	2.13	0.48
11:AA:836:LEU:HD13	11:AA:1054:LEU:HD13	1.95	0.48
11:AA:1286:THR:O	11:AA:1290:MET:HB2	2.14	0.48
14:AE:47:ARG:CZ	14:AE:47:ARG:HB2	2.44	0.48
14:AE:1060:VAL:HG13	14:AE:1106:ILE:HG12	1.96	0.48
18:D:13:U:O2	18:D:915:A:N7	2.47	0.48
18:D:1064:G:O2'	18:D:1190:G:N2	2.47	0.48
18:D:1329:A:OP1	38:X:28:THR:OG1	2.31	0.48
22:H:318:PRO:HA	22:H:321:VAL:HG12	1.95	0.48
39:Y:77:VAL:HG13	39:Y:80:LYS:HE3	1.95	0.48
41:a:686:U:O4	53:m:12:ARG:HB2	2.14	0.48
41:a:1067:A:O2'	41:a:1068:G:O4'	2.31	0.48
41:a:1839:G:N9	41:a:1927:A:H1'	2.23	0.48
41:a:2585:U:O2	41:a:2585:U:O4'	2.32	0.48
2:1:4:ILE:HG12	2:1:106:VAL:HG22	1.95	0.47
8:7:-14:U:C6	8:7:-14:U:C3'	2.97	0.47
10:A:58:A:OP2	10:A:58:A:C8	2.67	0.47
14:AE:395:LYS:NZ	14:AE:399:LYS:CE	2.77	0.47
10:B:58:A:C8	10:B:58:A:OP2	2.67	0.47
64:x:27:VAL:CG2	64:x:40:ILE:HD12	2.44	0.47
10:A:60:U:H4'	10:A:61:C:OP2	2.14	0.47
10:A:68:C:C4	10:A:69:C:C5	3.02	0.47
12:AB:145:ASN:HD21	14:AE:53:ARG:CZ	2.25	0.47
18:D:526:C:P	32:R:88:LYS:HE3	2.55	0.47
41:a:1993:U:H4'	50:j:133:THR:HG22	1.96	0.47
41:a:2303:G:C2	41:a:2314:A:N3	2.82	0.47
1:0:5:PHE:HB3	1:0:59:ILE:HD12	1.96	0.47
2:1:29:VAL:HB	2:1:55:ILE:HD11	1.96	0.47
10:A:5:G:C2'	10:A:6:G:H5'	2.39	0.47
10:A:33:U:H2'	10:A:35:A:OP2	2.14	0.47
10:A:42:G:H2'	10:A:43:A:C8	2.47	0.47
24:J:61:VAL:CG2	24:J:200:ILE:HD11	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:s:84:ILE:HG23	59:s:84:ILE:O	2.14	0.47
11:AA:1336:ASN:OD1	14:AE:33:TRP:HZ2	1.97	0.47
12:AB:165:PHE:CA	30:P:91:ASP:HA	2.45	0.47
14:AE:24:LEU:CB	14:AE:232:ASN:OD1	2.54	0.47
14:AE:1036:ARG:HE	14:AE:1081:VAL:HG11	1.79	0.47
14:AE:1150:PRO:HG3	14:AE:1214:PRO:HB2	1.97	0.47
18:D:604:G:H2'	18:D:605:U:O4'	2.14	0.47
18:D:1103:C:O2	21:G:106:THR:HG21	2.15	0.47
56:p:24:ILE:CD1	56:p:72:LEU:HD21	2.44	0.47
11:AA:400:VAL:HG22	11:AA:584:TYR:HB3	1.96	0.47
13:AC:102:LEU:HD12	13:AC:115:ILE:HG12	1.96	0.47
10:B:18:G:N3	10:B:58:A:C6	2.82	0.47
9:9:27:VAL:HG22	9:9:99:PHE:HE2	1.80	0.47
12:AB:165:PHE:HB2	30:P:92:LEU:CD1	2.41	0.47
14:AE:117:LEU:HG	14:AE:118:LYS:HG3	1.95	0.47
14:AE:202:ARG:HH11	14:AE:202:ARG:CG	2.14	0.47
14:AE:902:ASP:OD2	14:AE:905:ARG:HB2	2.15	0.47
10:B:14:A:N3	10:B:14:A:H2'	2.29	0.47
22:H:330:VAL:HG12	22:H:345:GLY:O	2.14	0.47
38:X:16:VAL:HG23	38:X:17:ILE:HD12	1.97	0.47
41:a:2627:G:O2'	41:a:2781:A:N1	2.37	0.47
50:j:121:THR:HB	50:j:127:PHE:CD2	2.49	0.47
9:9:17:GLU:HG2	9:9:88:HIS:NE2	2.29	0.47
9:9:139:LEU:HD21	40:Z:11:VAL:HG22	1.97	0.47
10:A:9:G:H5''	10:A:10:G:OP2	2.14	0.47
10:A:18:G:N3	10:A:58:A:C6	2.82	0.47
12:AB:126:THR:CG2	12:AB:130:PRO:HD3	2.44	0.47
12:AB:149:GLU:N	12:AB:149:GLU:CD	2.73	0.47
12:AB:173:LEU:HD13	30:P:102:LEU:HD23	1.97	0.47
14:AE:1167:LYS:NZ	14:AE:1170:LYS:HB2	2.30	0.47
16:AG:248:VAL:O	16:AG:252:VAL:CB	2.62	0.47
10:B:9:G:H5''	10:B:10:G:OP2	2.15	0.47
18:D:35:G:N3	32:R:115:SER:OG	2.47	0.47
18:D:373:A:C2	18:D:374:A:C8	3.03	0.47
18:D:1308:U:P	38:X:98:ARG:CG	3.03	0.47
19:E:54:MET:O	19:E:57:ILE:HG22	2.15	0.47
22:H:135:LEU:CB	22:H:167:VAL:O	2.63	0.47
23:I:75:ILE:HD13	23:I:75:ILE:C	2.40	0.47
26:L:67:PRO:O	26:L:70:VAL:HG22	2.15	0.47
39:Y:77:VAL:HG13	39:Y:80:LYS:CE	2.44	0.47
40:Z:18:ASP:HB3	40:Z:22:LEU:CD1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:299:A:N1	41:a:322:A:O2'	2.46	0.47
41:a:2168:G:H8	41:a:2168:G:OP1	1.97	0.47
41:a:2756:U:C4	41:a:2759:G:C6	3.03	0.47
50:j:152:PRO:HG3	50:j:156:PHE:CZ	2.50	0.47
9:9:31:ARG:NH1	9:9:31:ARG:CG	2.73	0.47
12:AB:162:VAL:HG13	12:AB:164:ILE:HG23	1.95	0.47
14:AE:108:ALA:HB1	14:AE:279:LEU:HD22	1.96	0.47
14:AE:128:LEU:HD21	14:AE:188:LEU:HB3	1.97	0.47
14:AE:1221:LEU:HD22	14:AE:1306:LEU:HB2	1.96	0.47
17:C:33:ILE:O	17:C:33:ILE:HG12	2.15	0.47
8:7:16:A:H2'	8:7:17:G:H8	1.80	0.47
14:AE:152:THR:HB	14:AE:172:PHE:CZ	2.48	0.47
17:C:12:ARG:NH2	22:H:268:VAL:CG2	2.71	0.47
22:H:69:ASP:O	22:H:85:SER:CB	2.63	0.47
22:H:309:MET:HE2	22:H:318:PRO:HB3	1.97	0.47
39:Y:79:LEU:HD13	39:Y:132:ALA:HA	1.97	0.47
41:a:1394:U:H4'	41:a:1603:A:H4'	1.97	0.47
54:n:36:LEU:HB3	54:n:57:LEU:HD21	1.97	0.47
10:A:14:A:H2'	10:A:14:A:N3	2.29	0.47
11:AA:887:VAL:HG21	11:AA:913:VAL:HG11	1.97	0.47
12:AB:165:PHE:CA	30:P:90:LEU:O	2.63	0.47
13:AD:35:PHE:HA	13:AD:38:THR:HG22	1.97	0.47
13:AD:59:VAL:HG22	13:AD:144:ILE:HA	1.96	0.47
14:AE:220:ARG:HG2	14:AE:220:ARG:NH1	2.26	0.47
14:AE:420:PRO:HA	14:AE:437:PHE:O	2.15	0.47
14:AE:1146:GLU:OE2	14:AE:1310:THR:HG22	2.14	0.47
10:B:18:G:C6	10:B:57:A:N7	2.83	0.47
10:B:68:C:C4	10:B:69:C:C5	3.02	0.47
39:Y:133:ARG:O	39:Y:133:ARG:HG2	2.14	0.47
41:a:784:G:H5'	41:a:785:G:OP1	2.15	0.47
41:a:995:C:O2	59:s:3:THR:OG1	2.24	0.47
41:a:1020:A:C6	41:a:1141:U:O2	2.68	0.47
9:9:48:ALA:HB3	9:9:51:TYR:CD2	2.50	0.46
9:9:132:TYR:CE1	40:Z:19:VAL:HG22	2.50	0.46
10:A:6:G:O2'	10:A:7:G:C5'	2.64	0.46
11:AA:852:ALA:HB2	11:AA:869:GLY:HA2	1.97	0.46
11:AA:858:GLY:C	11:AA:860:ALA:N	2.73	0.46
12:AB:141:PHE:HD1	30:P:84:VAL:HG13	1.79	0.46
14:AE:43:THR:HG22	14:AE:57:PHE:HE1	1.80	0.46
14:AE:50:LYS:HD3	14:AE:50:LYS:HA	1.71	0.46
10:B:68:C:H3'	10:B:69:C:H5''	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:1225:A:OP1	38:X:101:ARG:HB2	2.15	0.46
25:K:96:MET:CE	25:K:115:LEU:HD11	2.46	0.46
36:V:8:LEU:HD23	36:V:25:ILE:HG21	1.97	0.46
41:a:1814:G:C4'	48:h:51:THR:HG21	2.44	0.46
11:AA:689:ALA:HB2	11:AA:1233:LEU:HD23	1.97	0.46
11:AA:735:LYS:HA	11:AA:748:ILE:HG22	1.98	0.46
11:AA:858:GLY:O	11:AA:861:ALA:CB	2.62	0.46
12:AB:128:PHE:C	12:AB:180:LYS:HG3	2.40	0.46
14:AE:198:CYS:HA	14:AE:221:ILE:CD1	2.45	0.46
14:AE:1219:ASP:O	14:AE:1223:LEU:HB2	2.15	0.46
16:AG:401:PRO:C	16:AG:403:VAL:N	2.62	0.46
18:D:1308:U:O5'	38:X:98:ARG:HG2	2.16	0.46
18:D:1517:G:H1'	41:a:1919:A:O2'	2.16	0.46
22:H:291:GLY:HA2	22:H:305:HIS:O	2.15	0.46
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.46
10:A:18:G:C8	10:A:57:A:N1	2.83	0.46
10:A:18:G:C6	10:A:57:A:N7	2.83	0.46
13:AD:212:ASP:OD1	13:AD:212:ASP:N	2.48	0.46
10:B:5:G:C2'	10:B:6:G:H5'	2.40	0.46
18:D:1228:C:P	38:X:107:ARG:HH12	2.38	0.46
27:M:24:ALA:O	27:M:27:VAL:HG22	2.16	0.46
41:a:2298:A:C6	41:a:2299:U:C2	3.04	0.46
9:9:1:MET:SD	9:9:2:ALA:N	2.88	0.46
9:9:67:THR:H	9:9:68:PRO:HD3	1.80	0.46
9:9:118:ILE:HB	9:9:119:PRO:CD	2.45	0.46
14:AE:526:VAL:HG12	14:AE:549:LYS:HB2	1.96	0.46
14:AE:842:ARG:HH22	14:AE:1250:ASP:HB2	1.80	0.46
14:AE:968:ASN:HA	14:AE:1117:SER:HB2	1.96	0.46
18:D:868:C:H2'	18:D:869:G:O4'	2.16	0.46
18:D:915:A:C8	18:D:915:A:H3'	2.51	0.46
20:F:67:ARG:HD3	20:F:67:ARG:N	2.31	0.46
21:G:35:ARG:CD	22:H:14:LYS:HD3	2.40	0.46
22:H:332:VAL:HG13	22:H:342:ILE:HG23	1.98	0.46
40:Z:4:LYS:O	40:Z:4:LYS:HD2	2.15	0.46
41:a:1406:U:H3	41:a:1596:A:H2	1.59	0.46
41:a:1720:U:H2'	41:a:1721:G:O4'	2.16	0.46
47:g:18:CYS:HB2	47:g:40:CYS:HB3	1.96	0.46
1:0:51:VAL:HG22	1:0:51:VAL:O	2.15	0.46
9:9:39:THR:HA	9:9:42:ARG:HH11	1.81	0.46
12:AB:137:ASN:OD1	12:AB:143:ASP:N	2.45	0.46
10:B:18:G:C8	10:B:57:A:N1	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:429:U:N3	18:D:431:A:N6	2.64	0.46
31:Q:34:ILE:HG12	31:Q:70:CYS:SG	2.56	0.46
39:Y:21:PRO:CB	39:Y:22:PRO:CD	2.90	0.46
4:3:94:ARG:CB	4:3:103:ILE:HD12	2.45	0.46
9:9:58:THR:HB	9:9:82:ILE:H	1.80	0.46
10:A:14:A:H1'	10:A:22:G:N2	2.31	0.46
12:AB:155:LYS:HD3	12:AB:155:LYS:HA	1.53	0.46
14:AE:211:GLU:CG	14:AE:215:LYS:HE3	2.44	0.46
10:B:60:U:H4'	10:B:61:C:OP2	2.14	0.46
21:G:16:PHE:CD2	22:H:42:LEU:O	2.69	0.46
41:a:2168:G:OP1	41:a:2168:G:C8	2.68	0.46
9:9:127:ALA:O	9:9:130:PRO:HG2	2.16	0.46
10:A:72:A:H2'	10:A:73:A:C5'	2.32	0.46
11:AA:176:ILE:HD11	11:AA:428:VAL:HG21	1.98	0.46
11:AA:712:SER:OG	11:AA:713:GLY:N	2.49	0.46
11:AA:861:ALA:O	11:AA:882:ILE:HD13	2.15	0.46
12:AB:144:PHE:CE1	30:P:88:MET:SD	3.08	0.46
14:AE:385:LEU:HD23	14:AE:390:LEU:HB2	1.98	0.46
15:AF:25:ARG:NH1	15:AF:61:ASN:OD1	2.49	0.46
18:D:1176:A:H2'	18:D:1177:G:O4'	2.16	0.46
18:D:1308:U:OP1	38:X:100:GLN:OE1	2.23	0.46
30:P:99:GLN:O	30:P:99:GLN:HG2	2.16	0.46
41:a:517:C:OP2	49:i:10:ARG:NH2	2.48	0.46
6:5:110:DA:N1	11:AA:536:GLY:O	2.49	0.46
6:5:114:DC:H5''	14:AE:1148:ARG:CZ	2.46	0.46
11:AA:1002:LEU:HD21	11:AA:1007:LYS:HB2	1.98	0.46
12:AB:165:PHE:CE1	30:P:87:LEU:O	2.69	0.46
14:AE:123:ARG:HD3	14:AE:123:ARG:HA	1.48	0.46
16:AG:340:THR:O	16:AG:344:LEU:N	2.43	0.46
10:B:14:A:H1'	10:B:22:G:N2	2.31	0.46
10:B:58:A:C1'	10:B:60:U:C5	2.99	0.46
21:G:114:LEU:HD13	21:G:144:LEU:CB	2.46	0.46
22:H:84:LEU:N	22:H:84:LEU:CD2	2.78	0.46
9:9:50:VAL:CG2	39:Y:120:ASP:N	2.79	0.46
9:9:111:ALA:HB3	9:9:114:GLU:HG3	1.98	0.46
10:A:29:G:H2'	10:A:30:G:O4'	2.15	0.46
10:A:41:C:C5'	27:M:143:ARG:HD2	2.46	0.46
10:A:58:A:C1'	10:A:60:U:C5	2.99	0.46
11:AA:230:PHE:HB2	11:AA:333:ILE:HB	1.97	0.46
12:AB:123:ARG:H	12:AB:123:ARG:CD	2.27	0.46
12:AB:172:GLU:N	12:AB:172:GLU:CD	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:526:C:OP2	32:R:88:LYS:HE3	2.15	0.46
18:D:946:A:H2'	18:D:947:G:C8	2.50	0.46
41:a:2315:G:H5'	54:n:157:THR:HG23	1.97	0.46
9:9:24:SER:HB2	9:9:116:GLU:HG2	1.98	0.46
10:A:34:C:P	27:M:84:THR:HG1	2.31	0.46
10:A:68:C:H3'	10:A:69:C:H5''	1.96	0.46
11:AA:1268:GLN:NE2	14:AE:352:ARG:CD	2.66	0.46
11:AA:1311:GLY:O	15:AF:31:GLN:NE2	2.49	0.46
10:B:48:C:N4	10:B:59:A:C5	2.84	0.46
18:D:1175:G:N3	18:D:1176:A:C8	2.83	0.46
41:a:2291:U:H2'	41:a:2292:U:C6	2.51	0.46
7:6:15:DC:N3	7:6:16:DC:C4	2.84	0.45
8:7:17:G:H2'	8:7:18:A:H8	1.80	0.45
11:AA:28:LEU:HD21	11:AA:524:ILE:HG13	1.98	0.45
11:AA:557:ARG:NH2	11:AA:607:SER:O	2.50	0.45
11:AA:1245:ALA:O	14:AE:375:GLU:HG2	2.15	0.45
11:AA:1314:GLN:HB2	15:AF:28:ARG:HH12	1.81	0.45
22:H:19:ARG:O	22:H:72:LEU:HD13	2.16	0.45
22:H:72:LEU:CD1	22:H:72:LEU:N	2.73	0.45
22:H:316:ILE:HD11	22:H:321:VAL:HG11	1.97	0.45
24:J:162:ALA:O	24:J:165:ARG:O	2.33	0.45
50:j:4:LEU:HD23	50:j:29:VAL:CG1	2.39	0.45
8:7:-7:U:C3'	8:7:-7:U:C6	2.98	0.45
11:AA:207:THR:OG1	11:AA:354:ASP:OD2	2.32	0.45
11:AA:618:GLN:CD	14:AE:770:LEU:HD13	2.40	0.45
11:AA:862:LEU:HD11	16:AG:105:ILE:CB	2.46	0.45
11:AA:903:ARG:CA	16:AG:8:VAL:CB	2.94	0.45
17:C:61:ARG:HG2	26:L:88:MET:HE1	1.98	0.45
18:D:1240:U:OP1	27:M:116:MET:HB2	2.16	0.45
27:M:27:VAL:HG12	27:M:43:VAL:HG11	1.98	0.45
41:a:1906:G:H4'	41:a:1906:G:OP1	2.17	0.45
52:l:170:ARG:NH2	52:l:176:ASP:OD1	2.49	0.45
9:9:43:LYS:NZ	9:9:95:LEU:HD13	2.30	0.45
11:AA:103:VAL:HG12	11:AA:117:ILE:HG22	1.97	0.45
11:AA:318:SER:OG	11:AA:320:ASP:OD1	2.31	0.45
11:AA:845:LEU:HD13	11:AA:892:GLU:HB2	1.97	0.45
11:AA:906:PHE:CE1	16:AG:28:GLU:HA	2.52	0.45
11:AA:909:LYS:NZ	16:AG:2:ASN:O	2.48	0.45
12:AB:140:PRO:CG	30:P:102:LEU:CD2	2.94	0.45
12:AB:140:PRO:HG3	30:P:102:LEU:HD13	1.95	0.45
13:AC:64:VAL:HG11	13:AC:78:ILE:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:298:VAL:CA	16:AG:305:MET:HA	2.43	0.45
10:B:6:G:O2'	10:B:7:G:C5'	2.63	0.45
10:B:37:A:N3	10:B:37:A:H5''	2.32	0.45
17:C:12:ARG:CZ	22:H:264:GLU:HA	2.46	0.45
18:D:1340:A:H8	18:D:1340:A:O5'	2.00	0.45
22:H:290:TYR:O	22:H:305:HIS:C	2.56	0.45
34:T:21:ASP:OD1	34:T:22:THR:N	2.49	0.45
41:a:1327:A:H2'	41:a:1328:A:O4'	2.17	0.45
3:2:30:ILE:HD13	3:2:93:LEU:HD12	1.98	0.45
7:6:15:DC:C4	7:6:16:DC:C5	3.05	0.45
8:7:14:U:H2'	8:7:15:G:C8	2.52	0.45
11:AA:27:LEU:O	11:AA:528:ARG:NH1	2.43	0.45
12:AB:111:ILE:O	12:AB:114:ARG:O	2.33	0.45
12:AB:133:MET:HE2	12:AB:133:MET:C	2.40	0.45
14:AE:26:SER:HB2	14:AE:236:TRP:CH2	2.51	0.45
14:AE:75:TYR:CD2	14:AE:75:TYR:O	2.70	0.45
14:AE:209:ASN:HA	14:AE:214:ARG:NH2	2.31	0.45
14:AE:847:ASP:N	14:AE:847:ASP:OD1	2.49	0.45
14:AE:1158:GLU:HA	14:AE:1223:LEU:HD21	1.99	0.45
18:D:17:U:H2'	18:D:18:C:C6	2.52	0.45
18:D:552:U:O2'	32:R:83:ARG:O	2.27	0.45
39:Y:37:PHE:CE1	39:Y:56:VAL:HG11	2.51	0.45
41:a:930:G:H1'	46:f:25:LEU:HD11	1.98	0.45
54:n:77:PHE:N	54:n:77:PHE:CD1	2.82	0.45
60:t:18:ARG:HB2	60:t:45:GLU:HB3	1.97	0.45
62:v:96:ILE:HG21	62:v:126:ILE:HD12	1.98	0.45
9:9:60:LEU:HB2	9:9:61:ARG:NH2	2.31	0.45
10:A:48:C:N4	10:A:59:A:C5	2.84	0.45
11:AA:24:VAL:HG11	11:AA:704:MET:HE1	1.99	0.45
11:AA:1282:GLY:O	14:AE:1361:THR:OG1	2.33	0.45
12:AB:152:ASP:HB2	12:AB:157:ARG:CB	2.46	0.45
14:AE:115:TRP:HB3	14:AE:1333:THR:CG2	2.47	0.45
14:AE:213:LYS:HA	14:AE:213:LYS:HE3	1.99	0.45
14:AE:506:VAL:HG23	14:AE:628:GLY:HA3	1.99	0.45
14:AE:926:PRO:HB2	14:AE:1241:TYR:HE1	1.82	0.45
22:H:332:VAL:HG11	22:H:335:ILE:CG1	2.38	0.45
23:I:117:ALA:HB2	23:I:200:VAL:CG1	2.46	0.45
29:O:63:LEU:HD13	29:O:65:ILE:HD11	1.98	0.45
39:Y:71:LYS:HB3	39:Y:72:THR:H	1.58	0.45
39:Y:125:THR:HA	39:Y:128:ILE:HG12	1.98	0.45
41:a:39:G:H1'	52:l:43:THR:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-13:U:OP2	18:D:1397:C:O2	2.34	0.45
11:AA:694:ARG:HH22	13:AC:80:GLU:HG3	1.82	0.45
11:AA:887:VAL:HG21	11:AA:913:VAL:CG1	2.47	0.45
11:AA:1246:ARG:HH11	11:AA:1266:GLY:HA2	1.82	0.45
11:AA:1332:SER:C	14:AE:243:PRO:HG2	2.42	0.45
14:AE:395:LYS:NZ	14:AE:399:LYS:HE2	2.32	0.45
19:E:55:GLN:N	19:E:56:PRO:HD2	2.32	0.45
39:Y:95:ASP:OD2	39:Y:95:ASP:N	2.50	0.45
9:9:31:ARG:NE	41:a:1054:A:O4'	2.46	0.45
11:AA:1334:GLY:O	14:AE:25:ALA:HB3	2.17	0.45
12:AB:116:GLN:HG2	12:AB:116:GLN:O	2.17	0.45
12:AB:129:GLU:H	12:AB:180:LYS:CD	2.30	0.45
10:B:18:G:O2'	10:B:60:U:N3	2.48	0.45
10:B:48:C:C5	10:B:59:A:C8	3.05	0.45
48:h:76:ALA:HB2	48:h:96:TYR:CD1	2.51	0.45
52:l:149:ILE:CD1	52:l:188:MET:HE3	2.46	0.45
54:n:57:LEU:HD22	54:n:89:VAL:CG2	2.47	0.45
2:1:17:VAL:HG12	2:1:76:VAL:HG21	1.98	0.45
8:7:-8:U:H5''	8:7:-8:U:H6	1.82	0.45
9:9:106:PHE:C	9:9:106:PHE:CD2	2.95	0.45
10:A:48:C:C5	10:A:59:A:C8	3.05	0.45
11:AA:998:LEU:HG	11:AA:1011:LEU:HB3	1.99	0.45
13:AD:29:GLU:HB3	13:AD:200:LYS:HG3	1.99	0.45
13:AD:185:TYR:HA	13:AD:202:VAL:O	2.16	0.45
14:AE:395:LYS:HE3	14:AE:395:LYS:HB3	1.45	0.45
16:AG:254:MET:O	16:AG:257:ALA:HB2	2.17	0.45
18:D:1397:C:O5'	18:D:1397:C:C6	2.70	0.45
21:G:208:ARG:HH12	22:H:29:VAL:HG11	1.82	0.45
38:X:75:MET:HA	38:X:75:MET:HE3	1.99	0.45
41:a:645:C:H2'	41:a:647:G:C8	2.52	0.45
41:a:1668:A:O2'	41:a:1674:G:N7	2.44	0.45
46:f:25:LEU:C	46:f:25:LEU:HD13	2.41	0.45
54:n:29:PRO:HB2	54:n:169:LEU:HD22	1.99	0.45
7:6:21:DA:C6	8:7:15:G:C2	3.03	0.45
9:9:34:THR:HG22	9:9:38:MET:CE	2.46	0.45
9:9:106:PHE:CG	9:9:106:PHE:O	2.69	0.45
14:AE:201:LEU:CD1	14:AE:224:LEU:HD12	2.47	0.45
10:B:5:G:C2'	10:B:6:G:C5'	2.93	0.45
10:B:49:G:C2'	10:B:50:U:H5'	2.47	0.45
18:D:376:G:C2	18:D:389:A:C2	3.05	0.45
18:D:1493:A:C8	18:D:1493:A:OP1	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:84:THR:HG21	29:O:103:PHE:CB	2.45	0.45
30:P:8:ILE:HD12	30:P:25:ILE:CD1	2.46	0.45
38:X:106:ALA:HB3	38:X:110:LYS:CD	2.47	0.45
39:Y:42:ASN:HA	39:Y:45:THR:HB	1.98	0.45
39:Y:140:GLU:OE1	39:Y:140:GLU:N	2.50	0.45
41:a:1082:U:H3	41:a:1086:A:N6	2.15	0.45
41:a:2547:A:H2'	41:a:2548:U:C6	2.52	0.45
8:7:-12:U:C6	8:7:-12:U:OP2	2.70	0.45
9:9:50:VAL:HG22	39:Y:119:ALA:C	2.41	0.45
9:9:106:PHE:CD2	9:9:106:PHE:O	2.70	0.45
10:A:22:G:H2'	10:A:23:C:C5	2.52	0.45
11:AA:674:ASP:OD2	11:AA:1070:HIS:ND1	2.50	0.45
12:AB:165:PHE:HA	30:P:91:ASP:HA	1.99	0.45
14:AE:76:LYS:HB3	14:AE:76:LYS:NZ	2.32	0.45
14:AE:388:ARG:HG2	14:AE:388:ARG:NH1	2.32	0.45
14:AE:978:ARG:HD3	14:AE:999:TYR:H	1.82	0.45
10:B:58:A:HO2'	10:B:60:U:H5	1.62	0.45
18:D:337:G:H2'	18:D:338:A:C8	2.52	0.45
41:a:1385:A:O2'	41:a:1396:U:O2	2.35	0.45
50:j:186:LEU:HD21	65:y:4:ILE:HG21	1.98	0.45
54:n:17:MET:HE2	54:n:25:VAL:HA	1.98	0.45
64:x:18:LEU:HD23	64:x:25:ARG:HD2	1.99	0.45
10:A:76:A:C2	55:o:31:HIS:NE2	2.85	0.44
11:AA:800:MET:HE3	11:AA:800:MET:HB2	1.69	0.44
12:AB:126:THR:HG21	12:AB:130:PRO:HD3	1.98	0.44
13:AC:218:ARG:NH1	13:AD:231:PHE:O	2.50	0.44
10:B:34:C:O5'	10:B:34:C:C6	2.70	0.44
21:G:114:LEU:HA	21:G:144:LEU:HD13	1.98	0.44
22:H:38:VAL:HG22	22:H:48:ILE:HD11	1.99	0.44
22:H:294:VAL:HG21	22:H:330:VAL:HG21	1.99	0.44
39:Y:37:PHE:CD2	39:Y:37:PHE:O	2.71	0.44
41:a:1095:A:O2'	41:a:1096:A:O4'	2.33	0.44
41:a:1927:A:C8	41:a:1927:A:O5'	2.71	0.44
10:A:34:C:OP1	27:M:84:THR:OG1	2.35	0.44
10:A:49:G:C2'	10:A:50:U:H5'	2.47	0.44
11:AA:148:GLN:NE2	11:AA:535:PRO:O	2.40	0.44
11:AA:901:LEU:HA	16:AG:8:VAL:C	2.42	0.44
12:AB:115:LEU:HD13	12:AB:115:LEU:HA	1.72	0.44
14:AE:109:SER:HB2	14:AE:296:LYS:HG2	1.98	0.44
14:AE:128:LEU:CD2	14:AE:188:LEU:HB3	2.47	0.44
10:B:9:G:O2'	10:B:45:G:H2'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:7:TYR:CD2	39:Y:7:TYR:O	2.70	0.44
41:a:340:A:O2'	52:l:162:ARG:NH1	2.50	0.44
41:a:560:C:O2	66:z:48:ARG:NH1	2.41	0.44
41:a:1266:G:OP1	49:i:16:ARG:NE	2.45	0.44
41:a:2070:A:H2'	41:a:2071:A:O4'	2.17	0.44
41:a:2133:G:O2'	41:a:2157:G:N2	2.51	0.44
46:f:27:LEU:O	46:f:38:ARG:NE	2.46	0.44
9:9:57:ASN:CG	9:9:62:ARG:HG3	2.30	0.44
9:9:139:LEU:CD2	40:Z:11:VAL:HG22	2.47	0.44
12:AB:165:PHE:CE2	30:P:87:LEU:HG	2.48	0.44
14:AE:62:PHE:N	14:AE:62:PHE:CD1	2.86	0.44
14:AE:161:THR:H	14:AE:164:GLN:HB2	1.82	0.44
14:AE:1357:ILE:HG22	14:AE:1359:ALA:H	1.83	0.44
10:B:34:C:C5	10:B:34:C:OP1	2.70	0.44
38:X:106:ALA:HB3	38:X:110:LYS:HD2	1.98	0.44
40:Z:26:MET:HE2	40:Z:26:MET:HB2	1.71	0.44
41:a:1363:C:O2'	41:a:1809:A:N3	2.46	0.44
44:d:48:U:H2'	44:d:49:C:C6	2.52	0.44
6:5:108:DT:O4	11:AA:199:ASP:OD2	2.35	0.44
8:7:-20:A:H2'	8:7:-19:U:C6	2.50	0.44
8:7:-9:U:C3'	8:7:-9:U:C6	3.00	0.44
8:7:11:U:C5	8:7:11:U:OP2	2.71	0.44
11:AA:444:ASP:OD1	11:AA:444:ASP:N	2.51	0.44
11:AA:1298:VAL:HG11	14:AE:96:LYS:NZ	2.33	0.44
12:AB:133:MET:N	12:AB:133:MET:CE	2.73	0.44
14:AE:1026:PRO:HB2	14:AE:1028:ILE:HG23	2.00	0.44
14:AE:1227:HIS:HA	14:AE:1230:THR:HG22	1.99	0.44
18:D:109:A:C6	18:D:326:G:C6	3.05	0.44
25:K:111:MET:CE	25:K:125:ALA:HB1	2.39	0.44
26:L:73:GLU:O	26:L:76:THR:OG1	2.32	0.44
41:a:74:A:N7	41:a:88:G:C5	2.86	0.44
41:a:631:A:N3	41:a:2415:G:O2'	2.48	0.44
41:a:2252:G:O2'	41:a:2253:G:H5'	2.18	0.44
41:a:2898:U:O2'	59:s:134:ALA:O	2.29	0.44
6:5:115:DA:P	14:AE:1148:ARG:HG3	2.58	0.44
10:A:56:C:OP1	41:a:2168:G:C4	2.71	0.44
12:AB:157:ARG:HA	12:AB:157:ARG:HD3	1.33	0.44
14:AE:213:LYS:HE3	14:AE:213:LYS:CA	2.47	0.44
22:H:109:THR:C	22:H:153:GLU:HA	2.43	0.44
41:a:1007:C:OP1	59:s:37:ARG:NH2	2.50	0.44
41:a:1925:C:C5	41:a:1925:C:OP2	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2395:C:H2'	41:a:2396:G:O4'	2.18	0.44
48:h:6:CYS:SG	48:h:13:ARG:NH1	2.89	0.44
58:r:15:LEU:HD13	58:r:15:LEU:C	2.42	0.44
59:s:30:THR:CG2	59:s:31:GLU:N	2.79	0.44
6:5:98:DA:C2'	6:5:99:DT:C7	2.96	0.44
9:9:72:LEU:HD22	9:9:72:LEU:C	2.42	0.44
10:A:5:G:C2'	10:A:6:G:C5'	2.93	0.44
14:AE:478:LEU:HD21	15:AF:47:THR:HG23	1.99	0.44
14:AE:923:ILE:O	14:AE:1241:TYR:OH	2.31	0.44
10:B:22:G:H2'	10:B:23:C:C5	2.52	0.44
18:D:684:U:H2'	18:D:685:G:O4'	2.18	0.44
24:J:197:GLU:HA	24:J:200:ILE:HD12	1.99	0.44
58:r:55:GLU:HA	58:r:58:LEU:HD12	1.99	0.44
66:z:76:TYR:OH	66:z:92:ARG:NH1	2.51	0.44
9:9:9:GLN:CD	9:9:9:GLN:C	2.85	0.44
10:A:49:G:O5'	10:A:49:G:C8	2.71	0.44
11:AA:1247:SER:HB3	14:AE:375:GLU:O	2.17	0.44
13:AD:192:VAL:HG12	13:AD:193:GLU:H	1.83	0.44
14:AE:1046:ILE:HG22	14:AE:1061:VAL:HA	2.00	0.44
14:AE:1079:LYS:HD3	14:AE:1098:GLN:HB3	2.00	0.44
17:C:12:ARG:HD3	17:C:16:GLU:OE1	2.18	0.44
18:D:198:G:OP2	18:D:198:G:C8	2.70	0.44
18:D:397:A:H3'	18:D:397:A:N3	2.32	0.44
18:D:915:A:H8	18:D:915:A:O5'	2.00	0.44
21:G:16:PHE:CG	22:H:43:LYS:HA	2.53	0.44
59:s:73:VAL:HG11	59:s:75:TYR:CZ	2.53	0.44
63:w:28:LEU:HD23	63:w:48:VAL:HG21	1.98	0.44
10:A:22:G:O2'	10:A:23:C:O5'	2.36	0.44
11:AA:11:ILE:HG22	11:AA:1172:LEU:HD11	1.99	0.44
11:AA:855:PRO:HB3	16:AG:108:GLN:CA	2.48	0.44
14:AE:141:PHE:CE2	14:AE:296:LYS:CB	2.94	0.44
14:AE:222:LYS:HD2	14:AE:222:LYS:HA	1.32	0.44
14:AE:850:LYS:HB3	14:AE:855:ASP:HB2	2.00	0.44
10:B:25:C:C2'	10:B:26:G:H5'	2.47	0.44
18:D:13:U:C2	18:D:915:A:C5	3.05	0.44
20:F:21:ARG:HH22	22:H:341:ARG:HD2	1.82	0.44
21:G:76:ALA:CB	21:G:210:VAL:HG11	2.48	0.44
9:9:71:CYS:CA	9:9:117:LEU:HD13	2.48	0.44
10:A:9:G:O2'	10:A:45:G:H2'	2.18	0.44
11:AA:1157:GLN:HG3	11:AA:1159:VAL:HG13	2.00	0.44
18:D:324:G:N2	18:D:327:A:C8	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1695:G:N7	48:h:14:ARG:NH2	2.64	0.44
9:9:8:LYS:HZ2	41:a:1046:A:N6	2.16	0.43
11:AA:557:ARG:HB3	11:AA:587:LEU:HD13	2.00	0.43
11:AA:855:PRO:HG3	11:AA:913:VAL:HG12	1.99	0.43
12:AB:47:GLU:HG3	12:AB:64:PHE:CD1	2.44	0.43
12:AB:140:PRO:CG	30:P:102:LEU:HD22	2.34	0.43
13:AD:68:TYR:HE1	13:AD:79:LEU:HD13	1.82	0.43
14:AE:201:LEU:CB	14:AE:221:ILE:HD13	2.47	0.43
21:G:19:GLN:HG2	22:H:75:VAL:HG22	1.91	0.43
41:a:954:G:OP2	62:v:16:ARG:NH2	2.50	0.43
41:a:1021:A:N3	41:a:1021:A:C3'	2.78	0.43
41:a:1589:U:C2	41:a:1590:A:C8	3.06	0.43
60:t:24:VAL:HG13	60:t:33:ALA:HB2	2.00	0.43
10:A:26:G:N2	10:A:45:G:N2	2.66	0.43
11:AA:1314:GLN:HA	15:AF:28:ARG:HH22	1.82	0.43
12:AB:167:ARG:NH2	30:P:93:ALA:O	2.51	0.43
13:AD:78:ILE:HA	13:AD:81:ILE:HG22	2.00	0.43
14:AE:126:LEU:HD12	14:AE:223:LEU:HD22	1.99	0.43
14:AE:824:PRO:HD3	14:AE:835:LEU:HD12	2.00	0.43
14:AE:1108:GLN:HG3	14:AE:1109:LEU:HD12	1.99	0.43
18:D:421:U:O2	18:D:421:U:O4'	2.36	0.43
22:H:335:ILE:HG12	22:H:342:ILE:HG23	2.00	0.43
23:I:155:GLY:HA2	23:I:163:ALA:HB1	1.99	0.43
39:Y:124:MET:HE2	39:Y:124:MET:HB2	1.77	0.43
41:a:742:A:C2	41:a:755:U:N3	2.81	0.43
41:a:813:U:H2'	41:a:814:C:C6	2.53	0.43
62:v:35:ALA:HB2	62:v:102:LEU:HD11	2.00	0.43
8:7:-7:U:P	23:I:132:ARG:HH12	2.41	0.43
10:A:57:A:O5'	10:A:58:A:P	2.76	0.43
11:AA:811:ASN:ND2	11:AA:1098:LEU:O	2.51	0.43
13:AD:31:LEU:HD21	13:AD:39:LEU:HD12	2.00	0.43
14:AE:139:LEU:HD23	14:AE:139:LEU:HA	1.90	0.43
14:AE:568:SER:HB3	14:AE:570:LYS:NZ	2.34	0.43
14:AE:894:VAL:HG22	14:AE:1258:ARG:HH11	1.83	0.43
18:D:1126:U:OP1	30:P:7:ARG:NH2	2.51	0.43
21:G:114:LEU:HD13	21:G:144:LEU:HB3	1.99	0.43
21:G:206:ALA:O	21:G:210:VAL:HG23	2.18	0.43
22:H:280:LEU:HB2	22:H:330:VAL:O	2.18	0.43
24:J:165:ARG:NH1	24:J:165:ARG:HB2	2.32	0.43
38:X:23:TYR:CD2	38:X:69:LEU:HD23	2.53	0.43
41:a:57:C:H2'	41:a:58:G:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1095:A:H2'	41:a:1096:A:C8	2.53	0.43
8:7:-14:U:H6	8:7:-14:U:H3'	1.84	0.43
10:A:1:C:C5	10:A:2:G:N7	2.86	0.43
11:AA:900:LYS:HB2	16:AG:11:ALA:HB2	1.05	0.43
12:AB:68:TYR:OH	14:AE:294:ASN:ND2	2.51	0.43
14:AE:58:CYS:SG	14:AE:60:ARG:HG2	2.59	0.43
10:B:49:G:O5'	10:B:49:G:C8	2.71	0.43
10:B:57:A:O5'	10:B:58:A:P	2.76	0.43
29:O:80:ARG:O	29:O:84:THR:HG23	2.17	0.43
39:Y:34:ILE:HG22	39:Y:34:ILE:O	2.17	0.43
41:a:1921:G:C2'	41:a:1922:G:H5'	2.49	0.43
43:c:37:ARG:HG2	43:c:48:THR:HG23	2.00	0.43
9:9:16:SER:HB2	9:9:20:LYS:NZ	2.32	0.43
12:AB:163:SER:O	30:P:88:MET:CG	2.55	0.43
16:AG:422:GLU:O	16:AG:426:GLY:N	2.52	0.43
10:B:22:G:O2'	10:B:23:C:O5'	2.36	0.43
22:H:61:GLU:HG2	22:H:62:ILE:HG23	2.00	0.43
39:Y:123:ALA:HA	39:Y:126:ARG:HG3	2.00	0.43
41:a:68:G:N2	41:a:74:A:OP2	2.49	0.43
41:a:1386:C:H2'	41:a:1387:A:C8	2.53	0.43
45:e:59:GLU:O	45:e:63:ALA:HB3	2.18	0.43
47:g:37:CYS:N	47:g:40:CYS:SG	2.77	0.43
8:7:11:U:OP2	8:7:11:U:C4	2.70	0.43
10:A:18:G:N3	10:A:58:A:C5	2.87	0.43
12:AB:128:PHE:CD2	12:AB:128:PHE:O	2.72	0.43
14:AE:67:ASP:CG	14:AE:95:THR:HG1	2.23	0.43
14:AE:68:TYR:O	14:AE:75:TYR:CD2	2.70	0.43
14:AE:141:PHE:HE2	14:AE:296:LYS:CB	2.22	0.43
14:AE:201:LEU:HD11	14:AE:220:ARG:NH1	2.32	0.43
14:AE:586:GLY:HA3	14:AE:612:LEU:HD11	2.01	0.43
9:9:52:MET:HE1	9:9:85:SER:HB2	2.00	0.43
9:9:72:LEU:HD22	9:9:72:LEU:O	2.19	0.43
11:AA:561:ILE:HG21	14:AE:772:TYR:HE2	1.82	0.43
11:AA:590:PRO:HB2	11:AA:655:VAL:HG21	2.01	0.43
12:AB:7:LYS:HG2	12:AB:74:VAL:HG13	2.01	0.43
12:AB:132:GLU:CB	12:AB:147:VAL:HG13	2.49	0.43
14:AE:107:LEU:HA	14:AE:276:ASN:ND2	2.33	0.43
10:B:1:C:C5	10:B:2:G:N7	2.86	0.43
10:B:46:G:O2'	10:B:47:U:H5''	2.19	0.43
22:H:152:LEU:CB	22:H:171:ARG:H	2.32	0.43
23:I:58:GLU:OE1	30:P:94:ALA:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:121:ILE:HA	39:Y:124:MET:SD	2.58	0.43
41:a:126:A:O5'	53:m:19:ARG:HG3	2.19	0.43
41:a:1142:A:H2'	41:a:1142:A:N3	2.34	0.43
41:a:2469:A:N6	41:a:2481:G:O2'	2.52	0.43
60:t:76:VAL:HG12	65:y:73:VAL:HB	2.00	0.43
63:w:49:GLU:HB2	63:w:50:PRO:HD3	2.01	0.43
6:5:116:DG:C6	6:5:117:DA:C6	3.06	0.43
7:6:12:DC:O5'	7:6:12:DC:H6	2.01	0.43
7:6:18:DC:C2	8:7:17:G:N2	2.78	0.43
10:A:46:G:O2'	10:A:47:U:H5''	2.19	0.43
11:AA:300:ASP:OD1	11:AA:313:ALA:N	2.51	0.43
11:AA:829:THR:HG23	11:AA:1059:ARG:HG2	2.00	0.43
14:AE:111:THR:CG2	14:AE:300:GLN:HA	2.48	0.43
14:AE:126:LEU:CD1	14:AE:223:LEU:HD22	2.49	0.43
14:AE:950:ILE:HB	14:AE:1018:ALA:HB3	2.01	0.43
14:AE:1033:GLY:HA3	14:AE:1081:VAL:O	2.18	0.43
10:B:18:G:N3	10:B:58:A:C5	2.87	0.43
18:D:384:G:H2'	18:D:385:C:C6	2.54	0.43
25:K:156:LYS:HG2	28:N:71:VAL:HG13	2.00	0.43
39:Y:19:PRO:HG2	39:Y:24:GLY:N	2.32	0.43
11:AA:904:ALA:CB	16:AG:9:VAL:N	2.82	0.43
12:AB:127:LEU:HD12	12:AB:127:LEU:HA	1.87	0.43
14:AE:53:ARG:HA	14:AE:54:ASP:HA	1.56	0.43
14:AE:111:THR:HG21	14:AE:303:VAL:HB	2.00	0.43
14:AE:513:MET:HG3	14:AE:544:LEU:HD11	2.01	0.43
14:AE:515:ARG:NH2	14:AE:718:SER:O	2.48	0.43
14:AE:609:TYR:HD2	14:AE:610:ARG:NH1	2.17	0.43
14:AE:1024:THR:HG23	14:AE:1123:ARG:HA	2.00	0.43
10:B:58:A:OP2	10:B:58:A:H8	2.02	0.43
18:D:842:U:H3'	18:D:843:U:C5'	2.48	0.43
35:U:6:LEU:HG	35:U:17:TYR:HB3	2.00	0.43
39:Y:112:LYS:HB3	39:Y:112:LYS:NZ	2.34	0.43
41:a:2252:G:H2'	41:a:2253:G:H8	1.84	0.43
50:j:172:VAL:HG11	50:j:175:LEU:HD21	2.01	0.43
54:n:123:ASP:OD1	54:n:123:ASP:C	2.62	0.43
4:3:39:ILE:HG22	4:3:40:ASN:N	2.34	0.43
10:A:18:G:O2'	10:A:60:U:N3	2.48	0.43
10:A:58:A:OP2	10:A:58:A:H8	2.02	0.43
11:AA:22:LEU:HB3	11:AA:655:VAL:HG11	2.01	0.43
14:AE:68:TYR:HB3	14:AE:75:TYR:HE2	1.81	0.43
14:AE:224:LEU:HD23	14:AE:224:LEU:HA	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:244:VAL:HA	14:AE:269:TYR:OH	2.19	0.43
14:AE:388:ARG:HG2	14:AE:388:ARG:HH11	1.84	0.43
14:AE:515:ARG:HH12	14:AE:724:MET:HG2	1.83	0.43
10:B:26:G:N2	10:B:45:G:N2	2.66	0.43
18:D:1417:G:C6	18:D:1482:G:C6	3.06	0.43
25:K:150:PRO:O	25:K:153:VAL:HG22	2.18	0.43
41:a:705:A:O4'	48:h:9:THR:HG21	2.19	0.43
41:a:998:C:OP2	66:z:58:ARG:NH2	2.49	0.43
6:5:98:DA:H2'	6:5:99:DT:H72	2.01	0.42
10:A:36:U:H2'	10:A:37:A:O4'	2.19	0.42
11:AA:125:GLY:H	11:AA:495:ALA:HB1	1.84	0.42
12:AB:165:PHE:HZ	30:P:87:LEU:HD12	1.52	0.42
14:AE:144:TYR:OH	14:AE:162:GLU:OE1	2.34	0.42
10:B:53:G:C2	10:B:54:U:C5	3.07	0.42
18:D:622:A:C8	18:D:623:C:C6	3.08	0.42
18:D:826:C:O2	28:N:16:ASN:ND2	2.52	0.42
18:D:976:G:C8	18:D:1358:U:O2	2.71	0.42
22:H:76:GLU:HA	22:H:76:GLU:OE2	2.18	0.42
22:H:136:VAL:HA	22:H:168:VAL:O	2.18	0.42
25:K:153:VAL:HG23	25:K:164:ILE:HD13	2.00	0.42
41:a:879:G:H2'	41:a:880:G:O4'	2.19	0.42
53:m:12:ARG:HG3	53:m:44:VAL:HG11	2.00	0.42
60:t:38:ILE:HD11	60:t:112:PHE:CZ	2.54	0.42
10:A:56:C:C2	41:a:2112:G:C5	3.07	0.42
17:C:44:ILE:HG21	22:H:339:ARG:HA	2.01	0.42
18:D:37:U:O2	18:D:548:G:N2	2.53	0.42
18:D:1499:A:O2'	18:D:1500:A:C5'	2.67	0.42
22:H:119:GLY:O	22:H:120:PHE:C	2.62	0.42
31:Q:88:GLY:H	31:Q:114:THR:HG22	1.84	0.42
41:a:1028:A:N6	41:a:1125:G:H2'	2.34	0.42
49:i:43:ILE:HG22	49:i:49:TYR:HB2	2.01	0.42
9:9:18:VAL:HA	9:9:86:MET:CE	2.44	0.42
9:9:50:VAL:CG1	39:Y:119:ALA:CB	2.88	0.42
10:A:25:C:C2'	10:A:26:G:H5'	2.48	0.42
10:A:53:G:C2	10:A:54:U:C5	3.07	0.42
11:AA:901:LEU:HD11	16:AG:20:ARG:O	2.19	0.42
13:AD:211:ILE:HD12	13:AD:211:ILE:HA	1.92	0.42
14:AE:24:LEU:CD1	14:AE:232:ASN:ND2	2.82	0.42
14:AE:141:PHE:CD2	14:AE:297:ARG:HB2	2.54	0.42
14:AE:242:LEU:HA	14:AE:243:PRO:HD3	1.95	0.42
14:AE:839:VAL:HG12	14:AE:864:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AF:58:LEU:HD12	15:AF:59:ILE:HG12	2.00	0.42
18:D:791:G:N2	18:D:1497:G:O3'	2.53	0.42
18:D:1371:G:O3'	29:O:71:GLY:HA3	2.19	0.42
18:D:1515:G:H2'	18:D:1516:G:C8	2.52	0.42
22:H:302:GLY:HA3	22:H:344:LEU:HD13	2.00	0.42
23:I:50:ALA:HB2	23:I:75:ILE:HD12	2.01	0.42
29:O:28:ILE:HD12	29:O:28:ILE:N	2.35	0.42
41:a:214:G:N2	41:a:216:A:N3	2.66	0.42
41:a:1047:G:N2	41:a:1110:G:O2'	2.50	0.42
41:a:2511:U:O4	41:a:2575:C:N3	2.52	0.42
4:3:36:VAL:HG11	4:3:39:ILE:CD1	2.44	0.42
6:5:116:DG:OP1	14:AE:1311:LYS:NZ	2.46	0.42
10:A:26:G:H1	10:A:44:A:N6	2.17	0.42
14:AE:102:MET:HG2	14:AE:246:PRO:CG	2.49	0.42
18:D:197:A:C5	18:D:221:C:H4'	2.53	0.42
18:D:563:A:C2	18:D:884:U:O4	2.63	0.42
18:D:1323:G:H2'	18:D:1324:A:C8	2.54	0.42
18:D:1333:A:H2'	18:D:1334:G:O4'	2.19	0.42
21:G:208:ARG:NH1	22:H:29:VAL:HG11	2.34	0.42
41:a:320:A:H2'	52:l:131:THR:HG21	2.01	0.42
52:l:145:ASP:HA	52:l:166:LYS:HB3	2.01	0.42
59:s:32:LEU:HD23	59:s:54:ILE:HD13	2.01	0.42
4:3:12:ILE:CG2	4:3:80:ALA:HB2	2.49	0.42
8:7:-7:U:H3'	8:7:-7:U:C6	2.52	0.42
11:AA:562:GLU:OE1	11:AA:662:SER:OG	2.28	0.42
11:AA:808:ASN:N	14:AE:633:ALA:HB2	2.21	0.42
11:AA:1278:LEU:HD21	14:AE:484:MET:CE	2.50	0.42
11:AA:1279:GLU:HG2	14:AE:1357:ILE:HD13	2.02	0.42
13:AD:15:ASP:OD1	13:AD:27:THR:OG1	2.30	0.42
14:AE:47:ARG:HA	14:AE:47:ARG:NE	2.35	0.42
14:AE:105:ILE:HD12	14:AE:242:LEU:CD2	2.44	0.42
14:AE:1289:ASN:O	14:AE:1293:GLU:HB2	2.20	0.42
21:G:47:VAL:N	21:G:48:PRO:HD2	2.34	0.42
22:H:274:TYR:HD1	22:H:335:ILE:HD12	1.84	0.42
41:a:1925:C:OP2	41:a:1925:C:C6	2.73	0.42
52:l:134:LEU:HB2	52:l:160:ALA:HB1	2.02	0.42
14:AE:120:LEU:HA	14:AE:121:PRO:HA	1.84	0.42
14:AE:647:PRO:HG3	14:AE:697:MET:HB3	2.01	0.42
18:D:1208:C:H2'	18:D:1209:C:H6	1.85	0.42
41:a:1932:A:H2'	41:a:1933:G:O4'	2.19	0.42
60:t:113:MET:HE3	60:t:116:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1:MET:N	41:a:142:A:O2'	2.48	0.42
11:AA:478:ARG:HD2	11:AA:492:MET:HA	2.02	0.42
11:AA:524:ILE:HD12	11:AA:712:SER:HB2	2.02	0.42
11:AA:1268:GLN:NE2	14:AE:352:ARG:HB2	2.34	0.42
12:AB:136:VAL:HG21	12:AB:173:LEU:CD2	2.49	0.42
12:AB:162:VAL:HG12	12:AB:164:ILE:HG23	1.98	0.42
13:AD:46:ILE:HD11	13:AD:224:LEU:HD13	2.02	0.42
24:J:48:LEU:N	24:J:48:LEU:HD13	2.33	0.42
27:M:22:LEU:HD13	27:M:97:ASN:ND2	2.35	0.42
30:P:57:VAL:O	30:P:58:ASN:ND2	2.53	0.42
41:a:1020:A:C2	41:a:1141:U:C2	3.07	0.42
8:7:13:G:H5''	8:7:13:G:H8	1.85	0.42
9:9:47:GLU:HG3	9:9:95:LEU:CD2	2.49	0.42
14:AE:242:LEU:C	14:AE:242:LEU:HD23	2.44	0.42
14:AE:385:LEU:CD2	14:AE:390:LEU:HB2	2.50	0.42
22:H:119:GLY:CA	22:H:132:PRO:C	2.92	0.42
41:a:819:A:C4	41:a:1189:A:C2	3.07	0.42
41:a:910:A:N3	41:a:2264:C:O2'	2.49	0.42
41:a:1394:U:C4	41:a:1395:A:C6	3.07	0.42
41:a:2615:U:C2	49:i:4:GLN:HA	2.55	0.42
48:h:240:PHE:CD2	48:h:240:PHE:O	2.73	0.42
56:p:25:THR:HG22	56:p:34:THR:HG23	2.02	0.42
57:q:3:VAL:HA	57:q:36:ARG:O	2.19	0.42
60:t:107:LEU:HD21	60:t:115:ILE:HG21	2.01	0.42
8:7:2:U:H3'	8:7:2:U:H6	1.84	0.42
10:A:15:G:H1	10:A:20:U:H3	1.68	0.42
10:A:46:G:O2'	10:A:47:U:C6	2.73	0.42
11:AA:848:GLU:CG	11:AA:888:THR:CG2	2.83	0.42
12:AB:165:PHE:HB3	30:P:90:LEU:O	2.19	0.42
13:AD:79:LEU:HD11	14:AE:526:VAL:HG21	2.02	0.42
10:B:47:U:O2'	10:B:50:U:OP1	2.37	0.42
17:C:12:ARG:O	17:C:16:GLU:HG3	2.19	0.42
32:R:110:ARG:NH1	32:R:112:GLN:O	2.53	0.42
40:Z:18:ASP:HB3	40:Z:22:LEU:HD12	2.00	0.42
41:a:948:C:H1'	41:a:984:A:C8	2.55	0.42
41:a:984:A:N3	41:a:984:A:H2'	2.35	0.42
41:a:1082:U:C4	41:a:1086:A:N6	2.88	0.42
41:a:1250:G:OP2	61:u:21:ARG:NH2	2.52	0.42
41:a:2683:C:O2	60:t:70:ARG:NH2	2.52	0.42
41:a:2822:G:OP1	50:j:164:GLN:NE2	2.47	0.42
8:7:18:A:O3'	11:AA:688:GLN:NE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:71:CYS:SG	9:9:117:LEU:HB2	2.60	0.42
9:9:118:ILE:H	9:9:119:PRO:HD2	1.85	0.42
11:AA:469:VAL:HA	11:AA:472:GLU:HG2	2.01	0.42
11:AA:1245:ALA:HB3	14:AE:375:GLU:HB3	2.01	0.42
14:AE:848:VAL:HB	14:AE:858:VAL:HG22	2.02	0.42
14:AE:930:LEU:HA	14:AE:1244:GLN:HG3	2.02	0.42
18:D:429:U:O2	18:D:430:A:C8	2.72	0.42
41:a:36:G:N3	41:a:450:G:O2'	2.53	0.42
41:a:567:U:OP2	61:u:29:LYS:NZ	2.53	0.42
52:l:149:ILE:HD11	52:l:188:MET:HE3	2.02	0.42
54:n:171:ALA:O	54:n:174:ASP:N	2.53	0.42
59:s:114:LEU:HD12	59:s:114:LEU:HA	1.86	0.42
64:x:99:TYR:OH	64:x:111:ARG:NH1	2.53	0.42
11:AA:22:LEU:HD22	11:AA:603:ILE:HG21	2.02	0.41
13:AC:48:LEU:HA	13:AC:48:LEU:HD23	1.86	0.41
14:AE:390:LEU:HD13	14:AE:390:LEU:H	1.85	0.41
14:AE:616:PRO:HA	14:AE:619:ILE:HG22	2.02	0.41
10:B:26:G:H1	10:B:44:A:N6	2.18	0.41
18:D:1175:G:HO2'	18:D:1176:A:P	2.43	0.41
41:a:742:A:N1	41:a:755:U:O4	2.53	0.41
41:a:1570:A:H2'	41:a:1571:A:C8	2.55	0.41
41:a:2602:A:H5''	41:a:2603:G:C5'	2.50	0.41
41:a:2788:C:H2'	41:a:2789:C:C6	2.55	0.41
61:u:109:LYS:HG2	61:u:126:ARG:HB2	2.02	0.41
66:z:65:ILE:CD1	66:z:92:ARG:HB2	2.49	0.41
8:7:13:G:H8	8:7:13:G:C5'	2.33	0.41
10:B:26:G:C2	10:B:45:G:N2	2.88	0.41
17:C:14:THR:CG2	17:C:48:ARG:HE	2.33	0.41
18:D:1235:U:H2'	18:D:1236:A:O4'	2.20	0.41
22:H:19:ARG:CD	22:H:73:ASP:OD1	2.65	0.41
38:X:4:ILE:CG1	38:X:9:ILE:HD12	2.50	0.41
38:X:96:PRO:HG2	38:X:102:THR:HG23	1.97	0.41
39:Y:64:ARG:HE	39:Y:64:ARG:HB2	1.51	0.41
40:Z:28:GLU:H	40:Z:28:GLU:HG3	1.58	0.41
41:a:1565:C:O2'	41:a:1567:G:N7	2.48	0.41
41:a:2273:A:H2'	41:a:2274:A:C8	2.55	0.41
62:v:73:ILE:HG21	62:v:91:TYR:CZ	2.56	0.41
11:AA:755:LYS:HA	11:AA:755:LYS:HD2	1.86	0.41
11:AA:855:PRO:CB	16:AG:108:GLN:N	2.75	0.41
11:AA:1275:VAL:HG13	11:AA:1287:LEU:HD11	2.01	0.41
11:AA:1278:LEU:HD23	11:AA:1278:LEU:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AD:76:GLU:HB3	13:AD:80:GLU:HB3	2.01	0.41
14:AE:144:TYR:CE1	14:AE:162:GLU:OE1	2.73	0.41
14:AE:220:ARG:NH1	14:AE:220:ARG:CG	2.82	0.41
14:AE:271:ARG:HE	14:AE:271:ARG:HB2	1.58	0.41
14:AE:394:ILE:O	14:AE:394:ILE:HG13	2.19	0.41
14:AE:1350:ASN:HA	14:AE:1353:VAL:HG12	2.01	0.41
18:D:1329:A:OP1	38:X:28:THR:CA	2.67	0.41
23:I:9:GLY:HA3	33:S:89:MET:HE3	2.01	0.41
41:a:197:A:N6	41:a:2430:A:H2'	2.36	0.41
41:a:973:A:O4'	41:a:1188:U:C6	2.72	0.41
48:h:37:ASN:HB2	48:h:62:TYR:HB2	2.01	0.41
48:h:76:ALA:HB2	48:h:96:TYR:CE1	2.55	0.41
11:AA:135:THR:HG22	11:AA:144:VAL:HG22	2.02	0.41
11:AA:998:LEU:HD21	11:AA:1015:ALA:HB2	2.02	0.41
14:AE:559:ALA:HB3	14:AE:562:GLU:HB3	2.01	0.41
14:AE:797:THR:HG22	14:AE:924:GLY:HA3	2.01	0.41
18:D:216:U:H2'	18:D:217:C:C6	2.55	0.41
18:D:1225:A:H2'	18:D:1226:C:C5	2.56	0.41
22:H:110:GLY:H	22:H:153:GLU:N	2.17	0.41
40:Z:7:ILE:HD12	40:Z:7:ILE:HA	1.77	0.41
41:a:126:A:OP1	53:m:45:SER:OG	2.38	0.41
41:a:851:C:H2'	41:a:852:U:C6	2.55	0.41
41:a:1406:U:C2'	41:a:1407:G:OP2	2.69	0.41
41:a:2298:A:C5	41:a:2321:U:C4	3.09	0.41
54:n:122:PHE:CZ	54:n:167:ARG:HA	2.56	0.41
9:9:25:ALA:HA	9:9:96:PHE:HE1	1.85	0.41
9:9:67:THR:N	9:9:68:PRO:HD3	2.33	0.41
14:AE:47:ARG:NE	14:AE:47:ARG:CA	2.83	0.41
14:AE:136:GLU:OE1	14:AE:312:ARG:NH2	2.53	0.41
18:D:502:A:H2'	18:D:503:C:O4'	2.20	0.41
18:D:548:G:C6	18:D:549:C:C4	3.08	0.41
18:D:712:A:H2'	18:D:713:G:O4'	2.21	0.41
20:F:32:VAL:HG11	31:Q:89:PRO:HG3	2.01	0.41
21:G:187:VAL:HG21	21:G:199:VAL:HG23	2.02	0.41
33:S:41:ARG:O	33:S:45:VAL:HG12	2.20	0.41
39:Y:41:PHE:HA	39:Y:68:PHE:CE2	2.55	0.41
41:a:5:A:H2'	41:a:6:A:C8	2.56	0.41
41:a:548:G:H3'	41:a:549:G:O4'	2.20	0.41
41:a:2756:U:C4	41:a:2759:G:O6	2.72	0.41
48:h:119:GLY:O	48:h:130:LEU:HB3	2.20	0.41
7:6:27:DG:H1'	7:6:28:DA:C5	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-7:U:P	23:I:132:ARG:NH1	2.94	0.41
11:AA:144:VAL:HG23	11:AA:515:MET:HB2	2.02	0.41
11:AA:616:ILE:HG13	11:AA:652:TYR:HB2	2.02	0.41
11:AA:699:LEU:HG	11:AA:799:ASN:HD22	1.85	0.41
11:AA:979:LEU:HD11	11:AA:1011:LEU:HD11	2.03	0.41
10:B:7:G:O6	10:B:49:G:O6	2.39	0.41
10:B:46:G:H2'	10:B:47:U:OP2	2.21	0.41
18:D:1330:U:OP2	38:X:26:GLY:HA3	2.21	0.41
18:D:1368:A:OP1	29:O:113:ARG:NH2	2.54	0.41
21:G:38:VAL:HG23	22:H:75:VAL:HG21	1.92	0.41
22:H:33:LYS:HA	22:H:34:ASP:HA	1.60	0.41
22:H:155:LYS:O	22:H:169:SER:CB	2.68	0.41
22:H:292:CYS:SG	22:H:304:VAL:HB	2.60	0.41
29:O:55:VAL:O	29:O:57:MET:N	2.52	0.41
41:a:1169:A:H5''	41:a:1169:A:N3	2.36	0.41
41:a:1182:G:H2'	41:a:1183:U:O4'	2.21	0.41
41:a:2006:C:O2'	41:a:2823:A:N3	2.47	0.41
41:a:2803:G:H2'	41:a:2804:U:C5	2.55	0.41
9:9:118:ILE:CB	9:9:119:PRO:HD3	2.49	0.41
10:A:26:G:C2	10:A:45:G:N2	2.89	0.41
11:AA:550:VAL:HG13	14:AE:777:HIS:CD2	2.56	0.41
11:AA:1329:GLU:HA	14:AE:245:LEU:HD13	2.03	0.41
13:AC:42:ALA:HB1	13:AC:224:LEU:HD11	2.03	0.41
14:AE:390:LEU:N	14:AE:390:LEU:HD13	2.35	0.41
25:K:136:VAL:O	25:K:140:THR:HG23	2.20	0.41
28:N:11:LEU:HD22	28:N:75:ILE:HD11	2.03	0.41
42:b:59:LEU:HD12	42:b:80:ILE:HD12	2.03	0.41
53:m:12:ARG:CG	53:m:44:VAL:HG11	2.50	0.41
9:9:72:LEU:C	9:9:72:LEU:CD2	2.94	0.41
10:A:46:G:H2'	10:A:47:U:OP2	2.21	0.41
11:AA:213:LEU:HD13	11:AA:422:LYS:HG2	2.03	0.41
11:AA:987:GLU:HG2	11:AA:991:LYS:HE3	2.03	0.41
12:AB:162:VAL:CG1	12:AB:164:ILE:CG2	2.97	0.41
10:B:22:G:HO2'	10:B:23:C:P	2.44	0.41
18:D:1526:G:P	20:F:42:THR:HG23	2.61	0.41
24:J:100:ASN:OD1	24:J:111:ARG:NH1	2.54	0.41
39:Y:35:MET:O	39:Y:35:MET:SD	2.79	0.41
39:Y:116:MET:CB	39:Y:124:MET:HG2	2.46	0.41
41:a:207:A:H2'	41:a:208:C:O4'	2.21	0.41
41:a:2641:G:OP1	59:s:78:THR:HG22	2.21	0.41
63:w:29:VAL:HG11	63:w:75:ILE:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-4:U:OP1	8:7:-4:U:H4'	2.21	0.41
9:9:8:LYS:NZ	41:a:1046:A:N6	2.69	0.41
9:9:80:THR:O	41:a:1108:U:OP1	2.38	0.41
10:A:34:C:H41	27:M:83:SER:HA	1.85	0.41
11:AA:741:MET:SD	11:AA:974:ARG:NH2	2.93	0.41
11:AA:836:LEU:HD21	11:AA:921:PRO:HD3	2.02	0.41
11:AA:870:ILE:HB	11:AA:944:ARG:HD3	2.03	0.41
14:AE:109:SER:CB	14:AE:296:LYS:HG2	2.51	0.41
14:AE:137:ARG:HA	14:AE:142:GLU:HG2	2.02	0.41
14:AE:805:GLN:HG3	14:AE:1348:LYS:HD3	2.03	0.41
14:AE:820:ILE:HG12	14:AE:884:SER:HB2	2.02	0.41
14:AE:1272:SER:OG	14:AE:1273:ASP:N	2.53	0.41
10:B:8:U:H6	10:B:8:U:OP2	2.04	0.41
10:B:15:G:N2	10:B:20:U:C2	2.89	0.41
22:H:342:ILE:HG22	22:H:344:LEU:HD12	2.01	0.41
25:K:154:ALA:HA	25:K:164:ILE:HD11	2.03	0.41
39:Y:10:LEU:HD13	39:Y:10:LEU:HA	1.79	0.41
39:Y:14:ALA:HB3	39:Y:50:LYS:HA	2.03	0.41
39:Y:21:PRO:HD2	39:Y:22:PRO:HD2	2.03	0.41
39:Y:102:ARG:HD2	39:Y:103:ALA:N	2.36	0.41
41:a:476:G:H4'	41:a:502:A:N1	2.35	0.41
41:a:493:G:H2'	41:a:494:G:O4'	2.20	0.41
41:a:1082:U:N3	41:a:1086:A:C6	2.87	0.41
41:a:1406:U:O2'	41:a:1407:G:OP2	2.39	0.41
41:a:1548:A:H2'	41:a:1549:A:C8	2.55	0.41
41:a:1839:G:C4	41:a:1927:A:C5	3.08	0.41
41:a:2311:A:C2	54:n:85:ILE:HD11	2.55	0.41
41:a:2314:A:O2'	54:n:155:THR:HG22	2.21	0.41
41:a:2331:G:O2'	41:a:2336:A:N1	2.47	0.41
50:j:175:LEU:CD1	50:j:193:VAL:HG12	2.51	0.41
54:n:4:LEU:HD23	54:n:4:LEU:HA	1.96	0.41
58:r:9:VAL:HG11	58:r:12:LEU:HD21	2.02	0.41
63:w:67:PHE:O	63:w:71:ARG:HG2	2.21	0.41
2:1:92:ARG:NE	2:1:94:ASP:OD1	2.53	0.41
9:9:67:THR:H	9:9:68:PRO:CD	2.29	0.41
11:AA:176:ILE:HD12	11:AA:184:LEU:HD23	2.03	0.41
11:AA:862:LEU:HD23	11:AA:862:LEU:C	2.46	0.41
14:AE:144:TYR:CD1	14:AE:144:TYR:N	2.88	0.41
14:AE:515:ARG:HG2	14:AE:516:ASP:H	1.85	0.41
14:AE:576:ARG:HD3	14:AE:593:ASN:HA	2.03	0.41
18:D:152:A:N6	18:D:170:U:C2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:17:G:H2'	41:a:18:U:C6	2.56	0.41
41:a:2294:G:OP1	64:x:10:ARG:HD3	2.21	0.41
41:a:2572:A:N7	50:j:150:GLN:NE2	2.69	0.41
61:u:2:ARG:H	61:u:5:THR:HG1	1.66	0.41
3:2:46:ALA:O	3:2:50:LEU:HB2	2.21	0.40
8:7:-20:A:C6	8:7:-19:U:C4	3.09	0.40
8:7:-11:U:O2	8:7:-11:U:C3'	2.69	0.40
9:9:73:LYS:CB	9:9:117:LEU:HD11	2.51	0.40
10:A:7:G:O6	10:A:49:G:O6	2.39	0.40
10:A:56:C:OP1	41:a:2168:G:N3	2.53	0.40
11:AA:646:SER:OG	11:AA:647:ARG:N	2.52	0.40
12:AB:125:LYS:HB3	12:AB:126:THR:H	1.61	0.40
14:AE:279:LEU:HD13	14:AE:299:LEU:HD13	2.02	0.40
14:AE:820:ILE:HD11	14:AE:822:MET:HE2	2.02	0.40
18:D:218:U:H2'	18:D:219:U:O4'	2.21	0.40
18:D:860:A:H2'	18:D:861:G:O4'	2.21	0.40
18:D:1061:G:H5'	30:P:61:ALA:HB2	2.02	0.40
20:F:67:ARG:HD3	20:F:67:ARG:H	1.85	0.40
22:H:72:LEU:HB3	22:H:73:ASP:H	1.67	0.40
29:O:9:THR:O	29:O:85:ARG:HD2	2.22	0.40
41:a:2756:U:OP2	57:q:19:ARG:NE	2.54	0.40
48:h:175:ARG:NH1	48:h:181:MET:HE2	2.36	0.40
52:l:48:THR:HG23	52:l:86:ALA:HB3	2.02	0.40
52:l:188:MET:HE2	52:l:193:VAL:HA	2.03	0.40
9:9:61:ARG:C	9:9:65:GLU:HB2	2.45	0.40
9:9:67:THR:N	9:9:68:PRO:HD2	2.36	0.40
11:AA:678:ARG:HA	11:AA:678:ARG:HD3	1.84	0.40
11:AA:738:GLU:HA	11:AA:741:MET:HE2	2.03	0.40
11:AA:1247:SER:OG	11:AA:1248:THR:N	2.55	0.40
12:AB:140:PRO:HG2	30:P:102:LEU:CG	2.35	0.40
12:AB:141:PHE:CG	30:P:84:VAL:CG1	3.04	0.40
18:D:1189:U:OP1	33:S:98:LYS:NZ	2.55	0.40
37:W:50:ALA:HB1	37:W:57:HIS:HB3	2.04	0.40
41:a:67:U:C4	41:a:74:A:C6	3.04	0.40
41:a:244:A:OP2	55:o:8:ARG:NH2	2.50	0.40
41:a:753:A:C5	41:a:754:U:C5	3.10	0.40
41:a:1736:U:H2'	41:a:1737:G:O4'	2.22	0.40
58:r:57:LYS:O	58:r:61:VAL:HG13	2.21	0.40
61:u:74:THR:HG22	61:u:107:PHE:HB2	2.04	0.40
11:AA:310:ILE:HG21	11:AA:325:LEU:HB3	2.03	0.40
11:AA:1328:LYS:HD2	14:AE:102:MET:SD	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:103:ILE:HG13	12:AB:104:SER:H	1.85	0.40
13:AC:57:THR:HG23	13:AC:158:ARG:HH21	1.86	0.40
14:AE:1002:VAL:N	14:AE:1019:ASN:O	2.46	0.40
18:D:580:C:H2'	18:D:581:G:O4'	2.21	0.40
18:D:1370:G:C2	18:D:1371:G:C8	3.09	0.40
21:G:35:ARG:CG	22:H:10:GLU:OE2	2.63	0.40
25:K:150:PRO:HA	25:K:153:VAL:HG22	2.03	0.40
38:X:16:VAL:HG13	38:X:34:LEU:CD1	2.51	0.40
39:Y:7:TYR:HB2	39:Y:57:VAL:CG2	2.51	0.40
39:Y:128:ILE:N	39:Y:128:ILE:HD13	2.37	0.40
59:s:104:ALA:O	59:s:108:MET:HG3	2.22	0.40
63:w:9:GLN:O	63:w:17:ARG:NH2	2.51	0.40
9:9:100:ALA:HB2	9:9:125:ARG:HE	1.87	0.40
11:AA:801:ARG:HG2	11:AA:1094:VAL:HG23	2.04	0.40
11:AA:854:ILE:CG1	11:AA:855:PRO:CD	2.71	0.40
11:AA:936:ARG:HB2	11:AA:1042:LEU:HD12	2.03	0.40
13:AD:205:MET:HE1	13:AD:217:ILE:HG13	2.02	0.40
14:AE:244:VAL:HA	14:AE:269:TYR:CZ	2.57	0.40
18:D:429:U:O2	18:D:430:A:N7	2.54	0.40
18:D:579:A:O2'	34:T:54:ARG:NH1	2.54	0.40
18:D:915:A:C6	18:D:916:U:C4	3.08	0.40
18:D:1389:C:H2'	18:D:1390:U:O4'	2.22	0.40
34:T:43:PHE:CE2	34:T:56:LEU:HD22	2.56	0.40
39:Y:52:LEU:HD21	39:Y:81:LYS:HD3	2.03	0.40
39:Y:116:MET:HA	39:Y:116:MET:CE	2.50	0.40
39:Y:122:GLU:O	39:Y:122:GLU:HG2	2.21	0.40
8:7:-14:U:C6	8:7:-14:U:C5'	3.05	0.40
9:9:23:LEU:HA	9:9:118:ILE:CG1	2.51	0.40
10:A:15:G:N2	10:A:20:U:H3	2.20	0.40
14:AE:182:ALA:HB1	14:AE:238:ILE:CG2	2.52	0.40
14:AE:239:LEU:N	14:AE:239:LEU:HD23	2.36	0.40
14:AE:351:GLY:O	14:AE:467:ALA:HA	2.22	0.40
14:AE:1050:THR:HG23	14:AE:1057:SER:HB3	2.03	0.40
14:AE:1350:ASN:ND2	14:AE:1355:ARG:HD2	2.37	0.40
10:B:25:C:H2'	10:B:26:G:C5'	2.51	0.40
10:B:60:U:O3'	10:B:61:C:C6	2.75	0.40
18:D:555:U:H2'	18:D:556:C:C6	2.57	0.40
18:D:890:G:O2'	18:D:906:A:N6	2.55	0.40
18:D:915:A:C8	18:D:915:A:C3'	3.04	0.40
21:G:28:LYS:N	21:G:29:PRO:CD	2.85	0.40
22:H:110:GLY:N	22:H:153:GLU:HA	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:10:GLY:HA3	29:O:78:ALA:O	2.21	0.40
33:S:16:LEU:HD13	33:S:54:ASP:HB2	2.03	0.40
41:a:67:U:C2	41:a:74:A:N6	2.89	0.40
41:a:1365:A:O5'	43:c:28:ARG:NH2	2.52	0.40
41:a:1421:G:C2	41:a:1422:G:C8	3.09	0.40
41:a:2223:G:O2'	48:h:265:LYS:NZ	2.49	0.40
41:a:2225:A:H4'	41:a:2226:C:O5'	2.22	0.40
43:c:33:LEU:O	43:c:34:HIS:CG	2.75	0.40
56:p:52:PHE:CZ	56:p:72:LEU:HD22	2.56	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	47
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	47
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1338/1342 (100%)	1209 (90%)	126 (9%)	3 (0%)	43	78
12	AB	157/181 (87%)	134 (85%)	19 (12%)	4 (2%)	4	26
13	AC	295/329 (90%)	274 (93%)	19 (6%)	2 (1%)	18	55
13	AD	292/329 (89%)	270 (92%)	22 (8%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	121 (9%)	9 (1%)	18	55
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	490/495 (99%)	421 (86%)	51 (10%)	18 (4%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	16
23	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	24	63
24	J	203/206 (98%)	197 (97%)	6 (3%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	58
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	47
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	55
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	52
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	52
30	P	97/103 (94%)	87 (90%)	8 (8%)	2 (2%)	5	29
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	35
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	41
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6	33
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	9
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	11
42	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	67
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	63
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	45
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	49
All	All	10154/11072 (92%)	9324 (92%)	734 (7%)	96 (1%)	16	49

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
16	AG	6	LEU
16	AG	100	VAL
16	AG	400	GLU
16	AG	401	PRO
16	AG	402	THR
22	H	139	ARG
22	H	153	GLU
22	H	169	SER
22	H	306	VAL
22	H	340	ARG
29	O	56	ASP
38	X	103	LYS
39	Y	48	ILE
9	9	33	VAL

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Mol	Chain	Res	Type
9	9	119	PRO
11	AA	853	ASP
12	AB	125	LYS
12	AB	130	PRO
14	AE	175	GLU
16	AG	33	THR
16	AG	41	GLN
16	AG	109	THR
16	AG	303	HIS
22	H	108	VAL
22	H	309	MET
22	H	333	LEU
23	I	80	LYS
39	Y	93	ASN
48	h	158	ALA
52	l	142	ALA
66	z	3	ARG
9	9	48	ALA
9	9	91	ALA
9	9	118	ILE
9	9	130	PRO
14	AE	51	PRO
14	AE	805	GLN
16	AG	38	LYS
16	AG	309	VAL
16	AG	396	GLU
22	H	76	GLU
22	H	142	ARG
27	M	130	ASN
30	P	58	ASN
31	Q	119	ASN
38	X	105	ASN
39	Y	20	SER
39	Y	64	ARG
39	Y	106	GLN
9	9	69	PHE
9	9	73	LYS
9	9	108	VAL
9	9	129	LEU
9	9	133	GLU
12	AB	105	ASP
13	AC	193	GLU

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Mol	Chain	Res	Type
14	AE	174	ASP
14	AE	193	ASP
16	AG	301	ASP
16	AG	394	GLU
22	H	82	THR
30	P	90	LEU
39	Y	83	ALA
40	Z	21	GLU
54	n	40	VAL
14	AE	91	GLU
16	AG	97	ILE
16	AG	320	ARG
22	H	70	VAL
39	Y	22	PRO
39	Y	71	LYS
39	Y	89	SER
40	Z	7	ILE
4	3	39	ILE
9	9	28	ALA
12	AB	121	LYS
13	AC	192	VAL
14	AE	49	PHE
14	AE	73	GLY
14	AE	904	ALA
16	AG	105	ILE
39	Y	62	ALA
39	Y	100	ILE
26	L	96	VAL
39	Y	23	VAL
1	0	44	GLY
25	K	44	GLY
31	Q	74	VAL
35	U	64	GLY
9	9	54	VAL
11	AA	855	PRO
11	AA	1317	PRO
28	N	75	ILE
54	n	62	GLY
16	AG	290	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	25
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	33
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	44
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	39
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	51
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1135 (98%)	20 (2%)	53	68
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	6
13	AC	185/286 (65%)	184 (100%)	1 (0%)	81	82
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1047 (94%)	73 (6%)	15	37
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	71
17	C	57/65 (88%)	55 (96%)	2 (4%)	32	53
19	E	65/66 (98%)	61 (94%)	4 (6%)	16	38
20	F	60/61 (98%)	57 (95%)	3 (5%)	22	43
21	G	187/199 (94%)	174 (93%)	13 (7%)	14	36
22	H	137/461 (30%)	124 (90%)	13 (10%)	8	25
23	I	171/190 (90%)	163 (95%)	8 (5%)	23	45
24	J	172/173 (99%)	164 (95%)	8 (5%)	23	45
25	K	119/126 (94%)	111 (93%)	8 (7%)	15	37
26	L	91/116 (78%)	84 (92%)	7 (8%)	12	32
27	M	124/147 (84%)	113 (91%)	11 (9%)	9	28
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	58
29	O	105/107 (98%)	99 (94%)	6 (6%)	18	40
30	P	86/90 (96%)	73 (85%)	13 (15%)	3	13
31	Q	90/99 (91%)	88 (98%)	2 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	R	101/104 (97%)	95 (94%)	6 (6%)	18	40
33	S	83/84 (99%)	79 (95%)	4 (5%)	23	45
34	T	76/77 (99%)	65 (86%)	11 (14%)	3	14
35	U	65/65 (100%)	60 (92%)	5 (8%)	12	32
36	V	74/78 (95%)	71 (96%)	3 (4%)	27	49
37	W	72/79 (91%)	66 (92%)	6 (8%)	10	30
38	X	94/96 (98%)	87 (93%)	7 (7%)	13	33
39	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
40	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	53	68
43	c	67/68 (98%)	64 (96%)	3 (4%)	24	46
45	e	54/55 (98%)	51 (94%)	3 (6%)	19	41
46	f	48/49 (98%)	43 (90%)	5 (10%)	7	22
47	g	59/62 (95%)	55 (93%)	4 (7%)	14	36
48	h	216/218 (99%)	199 (92%)	17 (8%)	11	32
49	i	47/48 (98%)	41 (87%)	6 (13%)	4	17
50	j	164/164 (100%)	156 (95%)	8 (5%)	22	44
51	k	47/49 (96%)	44 (94%)	3 (6%)	16	38
52	l	165/165 (100%)	151 (92%)	14 (8%)	10	29
53	m	38/38 (100%)	36 (95%)	2 (5%)	20	42
54	n	148/150 (99%)	130 (88%)	18 (12%)	5	18
55	o	51/52 (98%)	47 (92%)	4 (8%)	11	32
56	p	136/138 (99%)	130 (96%)	6 (4%)	25	47
57	q	34/34 (100%)	31 (91%)	3 (9%)	9	29
58	r	114/114 (100%)	102 (90%)	12 (10%)	6	22
59	s	116/116 (100%)	106 (91%)	10 (9%)	10	29
60	t	104/104 (100%)	97 (93%)	7 (7%)	15	37
61	u	103/103 (100%)	96 (93%)	7 (7%)	14	36
62	v	109/109 (100%)	105 (96%)	4 (4%)	30	51
63	w	99/103 (96%)	91 (92%)	8 (8%)	11	31
64	x	86/87 (99%)	80 (93%)	6 (7%)	14	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	y	99/100 (99%)	91 (92%)	8 (8%)	11	31
66	z	89/90 (99%)	85 (96%)	4 (4%)	24	46
All	All	7904/8739 (90%)	7341 (93%)	563 (7%)	15	35

All (563) 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
9	9	11	ILE

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Mol	Chain	Res	Type
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
9	9	143	MET

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Mol	Chain	Res	Type
11	AA	145	ILE
11	AA	615	VAL
11	AA	851	THR
11	AA	854	ILE
11	AA	857	VAL
11	AA	859	GLU
11	AA	862	LEU
11	AA	864	LYS
11	AA	888	THR
11	AA	890	LYS
11	AA	893	THR
11	AA	894	GLN
11	AA	895	LEU
11	AA	896	THR
11	AA	898	GLU
11	AA	899	GLU
11	AA	909	LYS
11	AA	914	LYS
11	AA	1076	ILE
11	AA	1151	LEU
12	AB	104	SER
12	AB	105	ASP
12	AB	106	LYS
12	AB	114	ARG
12	AB	115	LEU
12	AB	117	GLN
12	AB	123	ARG
12	AB	125	LYS
12	AB	126	THR
12	AB	127	LEU
12	AB	132	GLU
12	AB	133	MET
12	AB	134	VAL
12	AB	135	ARG
12	AB	141	PHE
12	AB	143	ASP
12	AB	145	ASN
12	AB	150	GLU
12	AB	151	VAL
12	AB	153	TYR
12	AB	155	LYS
12	AB	157	ARG

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Mol	Chain	Res	Type
12	AB	161	SER
12	AB	162	VAL
12	AB	164	ILE
12	AB	167	ARG
12	AB	171	VAL
12	AB	172	GLU
12	AB	173	LEU
12	AB	180	LYS
13	AC	232	VAL
14	AE	40	LYS
14	AE	42	GLU
14	AE	44	ILE
14	AE	46	TYR
14	AE	47	ARG
14	AE	49	PHE
14	AE	50	LYS
14	AE	52	GLU
14	AE	53	ARG
14	AE	54	ASP
14	AE	56	LEU
14	AE	60	ARG
14	AE	66	LYS
14	AE	67	ASP
14	AE	70	CYS
14	AE	74	LYS
14	AE	76	LYS
14	AE	78	LEU
14	AE	80	HIS
14	AE	81	ARG
14	AE	88	CYS
14	AE	91	GLU
14	AE	94	GLN
14	AE	95	THR
14	AE	96	LYS
14	AE	99	ARG
14	AE	100	GLU
14	AE	114	ILE
14	AE	117	LEU
14	AE	119	SER
14	AE	123	ARG
14	AE	132	LEU
14	AE	135	ILE

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Mol	Chain	Res	Type
14	AE	142	GLU
14	AE	144	TYR
14	AE	145	VAL
14	AE	146	VAL
14	AE	147	ILE
14	AE	152	THR
14	AE	154	LEU
14	AE	157	GLN
14	AE	159	ILE
14	AE	175	GLU
14	AE	180	MET
14	AE	190	LYS
14	AE	193	ASP
14	AE	196	GLN
14	AE	210	SER
14	AE	212	THR
14	AE	216	LYS
14	AE	222	LYS
14	AE	223	LEU
14	AE	227	PHE
14	AE	233	LYS
14	AE	237	MET
14	AE	238	ILE
14	AE	239	LEU
14	AE	240	THR
14	AE	244	VAL
14	AE	271	ARG
14	AE	324	LEU
14	AE	385	LEU
14	AE	386	GLU
14	AE	387	LEU
14	AE	390	LEU
14	AE	393	THR
14	AE	394	ILE
14	AE	395	LYS
14	AE	506	VAL
14	AE	514	THR
14	AE	839	VAL
14	AE	1172	LYS
14	AE	1233	ILE
15	AF	63	ILE
17	C	33	ILE

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Mol	Chain	Res	Type
17	C	74	HIS
19	E	6	SER
19	E	10	ARG
19	E	48	GLN
19	E	64	LYS
20	F	34	ARG
20	F	62	ARG
20	F	67	ARG
21	G	8	ASP
21	G	45	LYS
21	G	59	LYS
21	G	105	LYS
21	G	108	ARG
21	G	117	LEU
21	G	128	LYS
21	G	129	LEU
21	G	132	LYS
21	G	135	LEU
21	G	161	LEU
21	G	174	LYS
21	G	208	ARG
22	H	9	PHE
22	H	31	ILE
22	H	43	LYS
22	H	54	LYS
22	H	62	ILE
22	H	70	VAL
22	H	294	VAL
22	H	305	HIS
22	H	336	ASP
22	H	337	GLU
22	H	338	GLU
22	H	339	ARG
22	H	340	ARG
23	I	14	ILE
23	I	21	THR
23	I	33	LEU
23	I	75	ILE
23	I	89	LYS
23	I	175	LEU
23	I	178	LEU
23	I	200	VAL

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Mol	Chain	Res	Type
24	J	47	ARG
24	J	48	LEU
24	J	95	GLU
24	J	104	ARG
24	J	105	MET
24	J	116	GLN
24	J	138	SER
24	J	143	VAL
25	K	10	GLU
25	K	15	LEU
25	K	60	ILE
25	K	114	VAL
25	K	115	LEU
25	K	138	ARG
25	K	141	ILE
25	K	162	GLU
26	L	7	VAL
26	L	16	GLU
26	L	24	ARG
26	L	36	ILE
26	L	38	ARG
26	L	54	LEU
26	L	86	ARG
27	M	7	ILE
27	M	17	LYS
27	M	21	GLU
27	M	23	LEU
27	M	27	VAL
27	M	50	LEU
27	M	79	ARG
27	M	91	VAL
27	M	109	ARG
27	M	130	ASN
27	M	146	GLU
28	N	96	MET
28	N	104	VAL
28	N	117	ARG
29	O	27	LYS
29	O	60	LYS
29	O	61	LEU
29	O	63	LEU
29	O	116	VAL

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Mol	Chain	Res	Type
29	O	118	LEU
30	P	17	LEU
30	P	18	ILE
30	P	24	GLU
30	P	25	ILE
30	P	27	GLU
30	P	37	ARG
30	P	87	LEU
30	P	88	MET
30	P	89	ARG
30	P	90	LEU
30	P	91	ASP
30	P	92	LEU
30	P	102	LEU
31	Q	15	GLN
31	Q	107	ILE
32	R	5	ASN
32	R	12	ARG
32	R	24	LEU
32	R	62	GLU
32	R	74	LEU
32	R	102	LEU
33	S	45	VAL
33	S	46	LEU
33	S	89	MET
33	S	92	GLU
34	T	10	LYS
34	T	22	THR
34	T	39	LEU
34	T	40	GLN
34	T	64	ARG
34	T	66	LEU
34	T	67	LEU
34	T	70	LEU
34	T	73	LYS
34	T	84	ARG
34	T	85	LEU
35	U	1	MET
35	U	2	VAL
35	U	6	LEU
35	U	19	VAL
35	U	50	THR

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Mol	Chain	Res	Type
36	V	46	VAL
36	V	75	LEU
36	V	81	LYS
37	W	21	LYS
37	W	33	THR
37	W	49	ILE
37	W	58	VAL
37	W	79	THR
37	W	81	ARG
38	X	16	VAL
38	X	25	VAL
38	X	29	ARG
38	X	59	GLU
38	X	93	ARG
38	X	101	ARG
38	X	117	LYS
39	Y	4	VAL
39	Y	10	LEU
39	Y	16	MET
39	Y	23	VAL
39	Y	27	LEU
39	Y	30	GLN
39	Y	36	GLU
39	Y	44	LYS
39	Y	45	THR
39	Y	48	ILE
39	Y	50	LYS
39	Y	52	LEU
39	Y	57	VAL
39	Y	58	ILE
39	Y	60	VAL
39	Y	61	TYR
39	Y	64	ARG
39	Y	65	SER
39	Y	67	THR
39	Y	71	LYS
39	Y	78	LEU
39	Y	80	LYS
39	Y	81	LYS
39	Y	91	LYS
39	Y	94	LYS
39	Y	95	ASP

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Mol	Chain	Res	Type
39	Y	99	LYS
39	Y	100	ILE
39	Y	102	ARG
39	Y	104	GLN
39	Y	108	ILE
39	Y	112	LYS
39	Y	116	MET
39	Y	124	MET
39	Y	125	THR
39	Y	126	ARG
39	Y	133	ARG
39	Y	135	MET
39	Y	137	LEU
39	Y	138	VAL
40	Z	1	SER
40	Z	2	ILE
40	Z	3	THR
40	Z	4	LYS
40	Z	6	GLN
40	Z	7	ILE
40	Z	8	ILE
40	Z	14	MET
40	Z	16	VAL
40	Z	17	MET
40	Z	19	VAL
40	Z	23	ILE
40	Z	26	MET
40	Z	28	GLU
40	Z	29	LYS
40	Z	30	PHE
42	b	70	GLU
43	c	33	LEU
43	c	48	THR
43	c	71	LEU
45	e	18	LEU
45	e	58	ASN
45	e	60	LYS
46	f	3	LYS
46	f	11	ARG
46	f	25	LEU
46	f	45	ARG
46	f	55	VAL

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Mol	Chain	Res	Type
47	g	3	LYS
47	g	16	CYS
47	g	24	ILE
47	g	47	LYS
48	h	51	THR
48	h	94	VAL
48	h	105	LEU
48	h	118	SER
48	h	125	LYS
48	h	130	LEU
48	h	141	VAL
48	h	156	ARG
48	h	183	LYS
48	h	187	ASP
48	h	195	VAL
48	h	202	LEU
48	h	203	ARG
48	h	204	VAL
48	h	205	LEU
48	h	242	LYS
48	h	271	ARG
49	i	9	THR
49	i	12	LYS
49	i	26	THR
49	i	27	SER
49	i	29	SER
49	i	40	ARG
50	j	13	ARG
50	j	18	ASP
50	j	91	THR
50	j	99	GLU
50	j	104	VAL
50	j	177	VAL
50	j	189	VAL
50	j	193	VAL
51	k	5	ILE
51	k	17	THR
51	k	24	THR
52	l	17	THR
52	l	22	ASP
52	l	40	ARG
52	l	48	THR

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Mol	Chain	Res	Type
52	l	57	LYS
52	l	69	ARG
52	l	77	ILE
52	l	80	SER
52	l	108	ILE
52	l	109	LEU
52	l	111	GLU
52	l	122	GLU
52	l	149	ILE
52	l	179	SER
53	m	22	MET
53	m	42	LEU
54	n	6	ASP
54	n	10	ASP
54	n	26	MET
54	n	40	VAL
54	n	47	LYS
54	n	49	LEU
54	n	57	LEU
54	n	79	ILE
54	n	80	ARG
54	n	95	ARG
54	n	105	THR
54	n	117	LEU
54	n	122	PHE
54	n	123	ASP
54	n	132	VAL
54	n	140	GLU
54	n	141	ILE
54	n	163	ASP
55	o	8	ARG
55	o	30	ARG
55	o	31	HIS
55	o	55	LEU
56	p	11	VAL
56	p	85	LYS
56	p	95	ARG
56	p	125	CYS
56	p	168	VAL
56	p	171	THR
57	q	3	VAL
57	q	26	ILE

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Mol	Chain	Res	Type
57	q	34	LYS
58	r	1	MET
58	r	9	VAL
58	r	11	ASN
58	r	12	LEU
58	r	15	LEU
58	r	41	LYS
58	r	66	ASN
58	r	72	ILE
58	r	76	GLU
58	r	94	ILE
58	r	101	ASP
58	r	127	GLU
59	s	1	MET
59	s	30	THR
59	s	31	GLU
59	s	43	GLU
59	s	57	LEU
59	s	123	LYS
59	s	124	VAL
59	s	139	VAL
59	s	140	LEU
59	s	142	ILE
60	t	7	MET
60	t	35	VAL
60	t	49	ARG
60	t	67	LYS
60	t	70	ARG
60	t	80	ASP
60	t	104	THR
61	u	5	THR
61	u	27	LEU
61	u	59	ARG
61	u	73	ILE
61	u	76	GLU
61	u	78	ARG
61	u	84	LYS
62	v	110	GLU
62	v	126	ILE
62	v	127	LYS
62	v	128	THR
63	w	2	ARG

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Mol	Chain	Res	Type
63	w	20	MET
63	w	24	MET
63	w	51	LEU
63	w	65	LEU
63	w	69	ARG
63	w	95	THR
63	w	116	VAL
64	x	13	ARG
64	x	31	THR
64	x	47	VAL
64	x	48	LEU
64	x	91	SER
64	x	116	GLN
65	y	8	LEU
65	y	10	GLN
65	y	27	GLU
65	y	40	LEU
65	y	81	VAL
65	y	85	SER
65	y	102	GLU
65	y	114	LEU
66	z	18	LEU
66	z	51	ARG
66	z	109	LEU
66	z	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) 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	314	ASN
11	AA	330	HIS
11	AA	343	HIS
11	AA	513	GLN

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Mol	Chain	Res	Type
11	AA	554	HIS
11	AA	688	GLN
11	AA	808	ASN
11	AA	1008	GLN
11	AA	1237	HIS
11	AA	1268	GLN
11	AA	1313	HIS
12	AB	117	GLN
12	AB	145	ASN
12	AB	177	GLN
13	AC	23	HIS
13	AD	66	HIS
13	AD	84	ASN
13	AD	117	HIS
13	AD	128	HIS
13	AD	227	GLN
14	AE	196	GLN
14	AE	294	ASN
14	AE	469	HIS
14	AE	865	HIS
14	AE	1195	GLN
14	AE	1238	GLN
14	AE	1249	ASN
15	AF	7	GLN
15	AF	31	GLN
19	E	3	ASN
19	E	55	GLN
19	E	61	GLN
21	G	18	HIS
21	G	58	ASN
21	G	94	HIS
23	I	6	HIS
23	I	123	GLN
24	J	36	GLN
24	J	40	GLN
24	J	41	HIS
25	K	97	GLN
26	L	11	HIS
26	L	63	ASN
26	L	94	HIS
27	M	97	ASN
27	M	148	ASN

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Mol	Chain	Res	Type
29	O	81	HIS
30	P	58	ASN
32	R	6	GLN
32	R	72	HIS
34	T	40	GLN
35	U	59	HIS
38	X	12	HIS
38	X	105	ASN
47	g	33	ASN
47	g	41	HIS
48	h	70	ASN
50	j	173	GLN
51	k	26	ASN
54	n	63	GLN
55	o	28	ASN
56	p	88	GLN
58	r	18	GLN
58	r	20	ASN
58	r	133	GLN
60	t	88	ASN
65	y	15	GLN
65	y	66	ASN
66	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%)
18	D	1514/1542 (98%)	291 (19%)	34 (2%)
41	a	2859/2904 (98%)	540 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	32/44 (72%)	20 (62%)	4 (12%)
All	All	4674/4762 (98%)	932 (19%)	50 (1%)

All (932) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-18	G
8	7	-17	U
8	7	-16	U

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Mol	Chain	Res	Type
8	7	-14	U
8	7	-13	U
8	7	-12	U
8	7	-11	U
8	7	-10	U
8	7	-9	U
8	7	-8	U
8	7	-7	U
8	7	-6	U
8	7	-5	U
8	7	-3	U
8	7	-1	U
8	7	0	U
8	7	1	U
8	7	2	U
8	7	12	G
8	7	13	G
10	A	2	G
10	A	6	G
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

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Mol	Chain	Res	Type
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
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
18	D	4	U
18	D	5	U
18	D	9	G

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Mol	Chain	Res	Type
18	D	22	G
18	D	29	U
18	D	32	A
18	D	39	G
18	D	41	G
18	D	47	C
18	D	48	C
18	D	50	A
18	D	51	A
18	D	52	C
18	D	54	C
18	D	69	G
18	D	70	U
18	D	71	A
18	D	72	A
18	D	74	A
18	D	76	G
18	D	82	G
18	D	83	C
18	D	84	U
18	D	87	C
18	D	90	C
18	D	94	G
18	D	95	C
18	D	96	U
18	D	108	G
18	D	120	A
18	D	122	G
18	D	128	G
18	D	131	A
18	D	141	G
18	D	144	G
18	D	148	G
18	D	149	A
18	D	160	A
18	D	164	G
18	D	173	U
18	D	181	A
18	D	182	A
18	D	197	A
18	D	198	G
18	D	204	G

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Mol	Chain	Res	Type
18	D	208	U
18	D	209	U
18	D	210	C
18	D	211	G
18	D	212	G
18	D	216	U
18	D	226	G
18	D	245	U
18	D	247	G
18	D	251	G
18	D	253	A
18	D	258	G
18	D	262	A
18	D	266	G
18	D	267	C
18	D	271	C
18	D	279	A
18	D	289	G
18	D	299	G
18	D	306	A
18	D	321	A
18	D	328	C
18	D	329	A
18	D	332	G
18	D	347	G
18	D	352	C
18	D	353	A
18	D	354	G
18	D	355	C
18	D	367	U
18	D	372	C
18	D	373	A
18	D	376	G
18	D	382	A
18	D	384	G
18	D	392	C
18	D	393	A
18	D	397	A
18	D	398	U
18	D	406	G
18	D	412	A
18	D	413	G

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Mol	Chain	Res	Type
18	D	414	A
18	D	421	U
18	D	422	C
18	D	424	G
18	D	429	U
18	D	446	G
18	D	451	A
18	D	457	G
18	D	458	U
18	D	460	A
18	D	463	U
18	D	464	U
18	D	467	U
18	D	468	A
18	D	469	C
18	D	478	A
18	D	479	U
18	D	481	G
18	D	484	G
18	D	485	U
18	D	486	U
18	D	505	G
18	D	509	A
18	D	511	C
18	D	518	C
18	D	519	C
18	D	526	C
18	D	531	U
18	D	532	A
18	D	533	A
18	D	542	G
18	D	547	A
18	D	559	A
18	D	562	U
18	D	568	G
18	D	572	A
18	D	573	A
18	D	576	C
18	D	577	G
18	D	579	A
18	D	596	A
18	D	628	G

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Mol	Chain	Res	Type
18	D	633	G
18	D	641	U
18	D	642	A
18	D	649	A
18	D	650	G
18	D	653	U
18	D	665	A
18	D	666	G
18	D	687	A
18	D	700	G
18	D	723	U
18	D	724	G
18	D	731	G
18	D	734	G
18	D	747	A
18	D	748	G
18	D	755	G
18	D	760	G
18	D	777	A
18	D	793	U
18	D	794	A
18	D	815	A
18	D	817	C
18	D	828	U
18	D	829	G
18	D	832	G
18	D	841	C
18	D	844	G
18	D	845	A
18	D	849	G
18	D	874	G
18	D	887	G
18	D	902	G
18	D	914	A
18	D	916	U
18	D	926	G
18	D	934	C
18	D	935	A
18	D	954	G
18	D	960	U
18	D	963	G
18	D	969	A

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Mol	Chain	Res	Type
18	D	972	C
18	D	975	A
18	D	976	G
18	D	991	U
18	D	992	U
18	D	993	G
18	D	996	A
18	D	999	C
18	D	1004	A
18	D	1008	U
18	D	1009	U
18	D	1017	U
18	D	1018	G
18	D	1021	A
18	D	1024	G
18	D	1026	G
18	D	1028	C
18	D	1030	U
18	D	1031	C
18	D	1037	C
18	D	1043	G
18	D	1044	A
18	D	1046	A
18	D	1065	U
18	D	1085	U
18	D	1086	U
18	D	1094	G
18	D	1095	U
18	D	1099	G
18	D	1101	A
18	D	1124	G
18	D	1133	G
18	D	1135	U
18	D	1136	C
18	D	1137	C
18	D	1139	G
18	D	1140	C
18	D	1141	C
18	D	1142	G
18	D	1143	G
18	D	1145	A
18	D	1146	A

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Mol	Chain	Res	Type
18	D	1151	A
18	D	1152	A
18	D	1158	C
18	D	1159	U
18	D	1167	A
18	D	1171	A
18	D	1174	G
18	D	1175	G
18	D	1176	A
18	D	1184	G
18	D	1196	A
18	D	1197	A
18	D	1206	G
18	D	1211	U
18	D	1212	U
18	D	1213	A
18	D	1214	C
18	D	1215	G
18	D	1226	C
18	D	1227	A
18	D	1228	C
18	D	1238	A
18	D	1256	A
18	D	1257	A
18	D	1260	G
18	D	1275	A
18	D	1276	G
18	D	1278	G
18	D	1279	G
18	D	1280	A
18	D	1285	A
18	D	1286	U
18	D	1287	A
18	D	1299	A
18	D	1300	G
18	D	1302	C
18	D	1305	G
18	D	1312	G
18	D	1317	C
18	D	1320	C
18	D	1323	G
18	D	1329	A

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Mol	Chain	Res	Type
18	D	1338	G
18	D	1340	A
18	D	1346	A
18	D	1347	G
18	D	1353	G
18	D	1363	A
18	D	1370	G
18	D	1378	C
18	D	1379	G
18	D	1381	U
18	D	1391	U
18	D	1396	A
18	D	1397	C
18	D	1398	A
18	D	1404	C
18	D	1419	G
18	D	1429	A
18	D	1441	A
18	D	1446	A
18	D	1447	A
18	D	1448	C
18	D	1452	C
18	D	1453	G
18	D	1475	G
18	D	1487	G
18	D	1492	A
18	D	1493	A
18	D	1494	G
18	D	1495	U
18	D	1497	G
18	D	1503	A
18	D	1506	U
18	D	1517	G
18	D	1529	G
18	D	1530	G
18	D	1534	A
41	a	10	A
41	a	15	G
41	a	34	U
41	a	35	G
41	a	46	G
41	a	58	G

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Mol	Chain	Res	Type
41	a	60	G
41	a	63	A
41	a	71	A
41	a	74	A
41	a	75	G
41	a	83	A
41	a	84	A
41	a	85	G
41	a	93	G
41	a	96	C
41	a	102	U
41	a	103	A
41	a	110	G
41	a	114	U
41	a	118	A
41	a	119	A
41	a	120	U
41	a	122	G
41	a	131	A
41	a	136	G
41	a	139	U
41	a	140	C
41	a	141	G
41	a	145	C
41	a	163	C
41	a	165	A
41	a	181	A
41	a	196	A
41	a	199	A
41	a	200	U
41	a	215	G
41	a	216	A
41	a	222	A
41	a	225	C
41	a	248	G
41	a	249	C
41	a	261	G
41	a	264	C
41	a	265	A
41	a	266	G
41	a	267	C
41	a	271	G

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Mol	Chain	Res	Type
41	a	272	A
41	a	275	C
41	a	276	U
41	a	278	A
41	a	285	G
41	a	311	A
41	a	324	A
41	a	329	G
41	a	330	A
41	a	353	C
41	a	359	G
41	a	361	G
41	a	362	A
41	a	371	A
41	a	372	G
41	a	373	U
41	a	375	G
41	a	383	C
41	a	386	G
41	a	396	G
41	a	405	U
41	a	411	G
41	a	412	A
41	a	420	C
41	a	424	G
41	a	435	C
41	a	451	U
41	a	456	C
41	a	457	A
41	a	477	A
41	a	481	G
41	a	491	G
41	a	501	A
41	a	503	A
41	a	504	A
41	a	505	A
41	a	509	C
41	a	522	A
41	a	529	A
41	a	532	A
41	a	543	G
41	a	546	U

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Mol	Chain	Res	Type
41	a	547	A
41	a	548	G
41	a	549	G
41	a	551	G
41	a	563	A
41	a	569	U
41	a	573	U
41	a	575	A
41	a	588	U
41	a	603	A
41	a	609	A
41	a	613	A
41	a	614	A
41	a	615	U
41	a	616	A
41	a	618	G
41	a	620	G
41	a	621	A
41	a	627	A
41	a	637	A
41	a	645	C
41	a	647	G
41	a	654	A
41	a	664	G
41	a	668	A
41	a	685	A
41	a	686	U
41	a	710	U
41	a	717	C
41	a	730	A
41	a	738	G
41	a	757	G
41	a	764	A
41	a	765	C
41	a	775	G
41	a	776	G
41	a	782	A
41	a	784	G
41	a	785	G
41	a	800	A
41	a	802	A
41	a	805	G

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Mol	Chain	Res	Type
41	a	812	C
41	a	819	A
41	a	827	U
41	a	828	U
41	a	845	A
41	a	846	U
41	a	858	G
41	a	859	G
41	a	869	G
41	a	878	A
41	a	881	G
41	a	883	G
41	a	884	U
41	a	885	C
41	a	888	C
41	a	891	G
41	a	892	A
41	a	893	C
41	a	895	U
41	a	896	A
41	a	897	C
41	a	899	A
41	a	907	G
41	a	910	A
41	a	914	G
41	a	915	C
41	a	931	U
41	a	941	A
41	a	945	A
41	a	946	C
41	a	953	G
41	a	961	C
41	a	974	G
41	a	983	A
41	a	984	A
41	a	985	C
41	a	995	C
41	a	996	A
41	a	999	U
41	a	1005	C
41	a	1012	U
41	a	1013	C

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Mol	Chain	Res	Type
41	a	1022	G
41	a	1023	U
41	a	1026	G
41	a	1033	U
41	a	1041	G
41	a	1042	G
41	a	1045	C
41	a	1046	A
41	a	1047	G
41	a	1060	U
41	a	1061	U
41	a	1062	G
41	a	1063	G
41	a	1064	C
41	a	1065	U
41	a	1066	U
41	a	1067	A
41	a	1068	G
41	a	1069	A
41	a	1070	A
41	a	1071	G
41	a	1073	A
41	a	1074	G
41	a	1076	C
41	a	1079	C
41	a	1080	A
41	a	1081	U
41	a	1082	U
41	a	1083	U
41	a	1084	A
41	a	1087	G
41	a	1088	A
41	a	1090	A
41	a	1095	A
41	a	1096	A
41	a	1107	G
41	a	1110	G
41	a	1111	A
41	a	1112	G
41	a	1119	U
41	a	1122	G
41	a	1132	U

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Mol	Chain	Res	Type
41	a	1134	A
41	a	1135	C
41	a	1142	A
41	a	1143	A
41	a	1169	A
41	a	1170	C
41	a	1173	U
41	a	1174	U
41	a	1175	A
41	a	1176	U
41	a	1177	G
41	a	1178	C
41	a	1179	G
41	a	1180	U
41	a	1186	G
41	a	1238	G
41	a	1248	G
41	a	1253	A
41	a	1256	G
41	a	1266	G
41	a	1271	G
41	a	1272	A
41	a	1273	U
41	a	1301	A
41	a	1321	A
41	a	1345	C
41	a	1352	U
41	a	1365	A
41	a	1368	G
41	a	1378	A
41	a	1379	U
41	a	1380	G
41	a	1383	A
41	a	1387	A
41	a	1395	A
41	a	1406	U
41	a	1407	G
41	a	1408	G
41	a	1411	U
41	a	1414	C
41	a	1415	U
41	a	1416	G

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Mol	Chain	Res	Type
41	a	1417	C
41	a	1419	A
41	a	1420	A
41	a	1428	C
41	a	1452	G
41	a	1453	A
41	a	1460	U
41	a	1478	G
41	a	1482	G
41	a	1490	A
41	a	1491	G
41	a	1497	U
41	a	1503	A
41	a	1508	A
41	a	1509	A
41	a	1510	G
41	a	1515	A
41	a	1529	G
41	a	1534	U
41	a	1535	A
41	a	1536	C
41	a	1537	G
41	a	1554	U
41	a	1559	U
41	a	1566	A
41	a	1569	A
41	a	1578	U
41	a	1580	A
41	a	1581	G
41	a	1582	C
41	a	1583	A
41	a	1584	U
41	a	1589	U
41	a	1590	A
41	a	1608	A
41	a	1609	A
41	a	1610	A
41	a	1647	U
41	a	1648	U
41	a	1649	G
41	a	1651	G
41	a	1674	G

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Mol	Chain	Res	Type
41	a	1677	A
41	a	1703	G
41	a	1714	U
41	a	1715	G
41	a	1718	G
41	a	1729	U
41	a	1730	C
41	a	1732	C
41	a	1738	G
41	a	1750	G
41	a	1755	A
41	a	1758	U
41	a	1764	C
41	a	1773	A
41	a	1791	A
41	a	1800	C
41	a	1808	A
41	a	1811	G
41	a	1816	C
41	a	1829	A
41	a	1833	C
41	a	1847	A
41	a	1848	A
41	a	1858	A
41	a	1859	U
41	a	1862	G
41	a	1864	U
41	a	1869	G
41	a	1870	C
41	a	1872	A
41	a	1873	G
41	a	1905	C
41	a	1906	G
41	a	1907	G
41	a	1913	A
41	a	1914	C
41	a	1919	A
41	a	1920	C
41	a	1922	G
41	a	1923	U
41	a	1924	C
41	a	1925	C

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Mol	Chain	Res	Type
41	a	1926	U
41	a	1928	A
41	a	1929	G
41	a	1930	G
41	a	1936	A
41	a	1938	A
41	a	1955	U
41	a	1965	C
41	a	1967	C
41	a	1970	A
41	a	1971	U
41	a	1972	G
41	a	1987	A
41	a	1991	U
41	a	1992	G
41	a	1993	U
41	a	1997	C
41	a	2002	G
41	a	2022	U
41	a	2023	C
41	a	2027	G
41	a	2033	A
41	a	2043	C
41	a	2051	A
41	a	2052	A
41	a	2055	C
41	a	2056	G
41	a	2060	A
41	a	2061	G
41	a	2062	A
41	a	2063	C
41	a	2077	A
41	a	2093	G
41	a	2097	A
41	a	2099	U
41	a	2100	G
41	a	2108	A
41	a	2110	G
41	a	2111	U
41	a	2113	U
41	a	2115	G
41	a	2116	G

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Mol	Chain	Res	Type
41	a	2117	A
41	a	2118	U
41	a	2121	G
41	a	2122	U
41	a	2124	G
41	a	2125	G
41	a	2126	A
41	a	2127	G
41	a	2128	G
41	a	2131	U
41	a	2132	U
41	a	2133	G
41	a	2134	A
41	a	2139	U
41	a	2141	G
41	a	2146	C
41	a	2147	A
41	a	2154	A
41	a	2157	G
41	a	2158	A
41	a	2159	G
41	a	2162	G
41	a	2163	A
41	a	2164	C
41	a	2165	C
41	a	2169	A
41	a	2171	A
41	a	2172	U
41	a	2178	C
41	a	2182	U
41	a	2183	A
41	a	2185	U
41	a	2188	U
41	a	2189	U
41	a	2190	G
41	a	2191	A
41	a	2193	G
41	a	2194	U
41	a	2198	A
41	a	2204	G
41	a	2210	U
41	a	2211	A

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Mol	Chain	Res	Type
41	a	2212	A
41	a	2213	U
41	a	2225	A
41	a	2226	C
41	a	2229	U
41	a	2238	G
41	a	2239	G
41	a	2244	U
41	a	2250	G
41	a	2268	A
41	a	2278	A
41	a	2283	C
41	a	2287	A
41	a	2297	A
41	a	2305	U
41	a	2308	G
41	a	2309	A
41	a	2315	G
41	a	2322	A
41	a	2325	G
41	a	2327	A
41	a	2333	A
41	a	2339	C
41	a	2345	G
41	a	2347	C
41	a	2350	C
41	a	2361	G
41	a	2372	U
41	a	2376	A
41	a	2383	G
41	a	2385	C
41	a	2402	U
41	a	2403	C
41	a	2406	A
41	a	2423	U
41	a	2424	C
41	a	2425	A
41	a	2426	A
41	a	2429	G
41	a	2430	A
41	a	2431	U
41	a	2434	A

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Mol	Chain	Res	Type
41	a	2435	A
41	a	2441	U
41	a	2447	G
41	a	2448	A
41	a	2470	G
41	a	2474	U
41	a	2476	A
41	a	2478	A
41	a	2484	G
41	a	2491	U
41	a	2502	G
41	a	2506	U
41	a	2507	C
41	a	2512	C
41	a	2513	A
41	a	2518	A
41	a	2520	C
41	a	2525	G
41	a	2529	G
41	a	2535	G
41	a	2547	A
41	a	2554	U
41	a	2566	A
41	a	2567	G
41	a	2572	A
41	a	2573	C
41	a	2574	G
41	a	2585	U
41	a	2586	U
41	a	2602	A
41	a	2603	G
41	a	2609	U
41	a	2610	C
41	a	2611	C
41	a	2613	U
41	a	2629	U
41	a	2663	G
41	a	2669	G
41	a	2671	G
41	a	2689	U
41	a	2690	U
41	a	2714	G

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Mol	Chain	Res	Type
41	a	2722	G
41	a	2726	A
41	a	2744	G
41	a	2748	A
41	a	2757	A
41	a	2758	A
41	a	2765	A
41	a	2777	G
41	a	2778	A
41	a	2791	G
41	a	2793	C
41	a	2796	U
41	a	2797	U
41	a	2798	U
41	a	2799	A
41	a	2801	G
41	a	2818	U
41	a	2820	A
41	a	2823	A
41	a	2825	G
41	a	2849	U
41	a	2850	A
41	a	2859	G
41	a	2861	U
41	a	2867	G
41	a	2880	C
41	a	2884	U
41	a	2885	G
41	a	2891	U
41	a	2902	C
44	d	2	G
44	d	9	G
44	d	13	G
44	d	16	G
44	d	17	C
44	d	35	C
44	d	36	C
44	d	45	A
44	d	51	G
44	d	56	G
44	d	64	G
44	d	66	A

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Mol	Chain	Res	Type
44	d	88	C
44	d	89	U
44	d	90	C
44	d	99	A
44	d	109	A

All (50) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	7	-17	U
8	7	-14	U
8	7	-11	U
8	7	11	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
10	B	9	G
10	B	22	G
10	B	37	A
10	B	60	U
18	D	7	A
18	D	70	U
18	D	121	U
18	D	181	A
18	D	183	C
18	D	197	A
18	D	209	U
18	D	305	G
18	D	328	C
18	D	428	G
18	D	496	A
18	D	517	G
18	D	531	U
18	D	532	A
18	D	562	U
18	D	641	U
18	D	722	G

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Mol	Chain	Res	Type
18	D	793	U
18	D	991	U
18	D	992	U
18	D	1145	A
18	D	1196	A
18	D	1211	U
18	D	1212	U
18	D	1213	A
18	D	1214	C
18	D	1225	A
18	D	1299	A
18	D	1396	A
18	D	1432	G
18	D	1447	A
18	D	1491	G
18	D	1492	A
18	D	1493	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

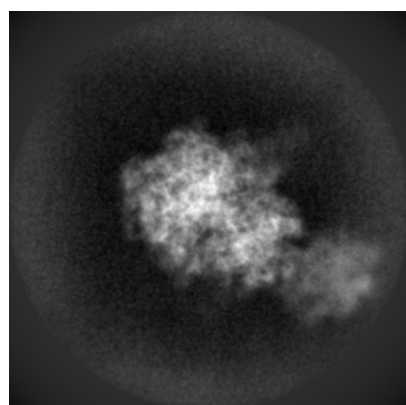
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22107. These allow visual inspection of the internal detail of the map and identification of artifacts.

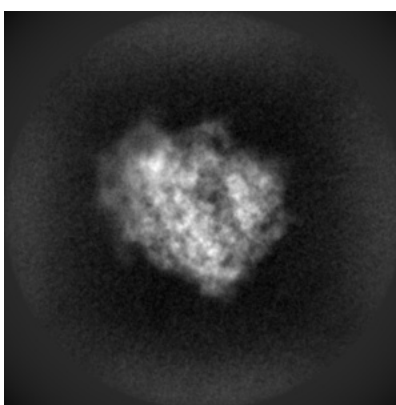
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

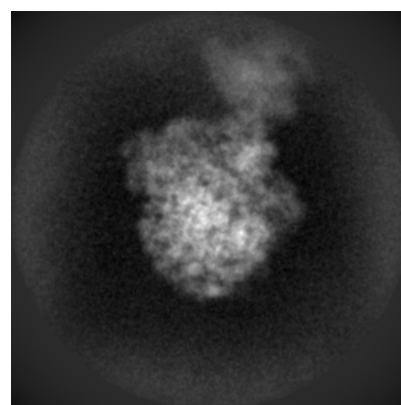
6.1.1 Primary map



X



Y

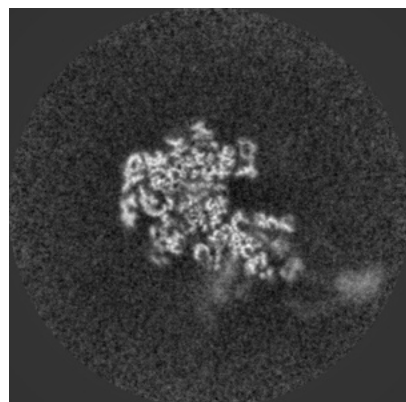


Z

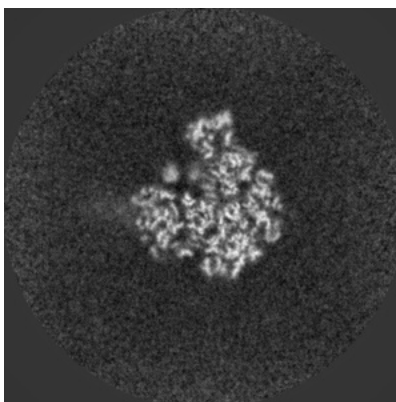
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

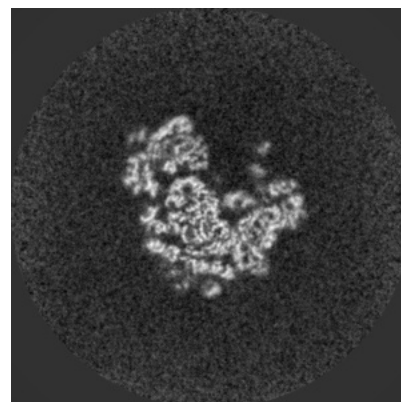
6.2.1 Primary map



X Index: 256



Y Index: 256

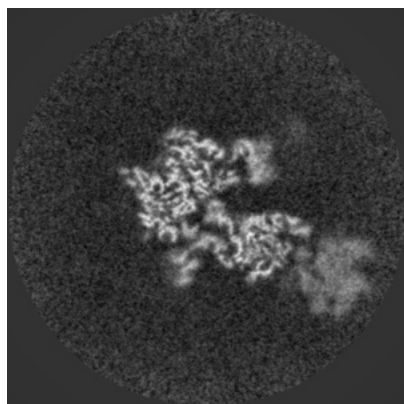


Z Index: 256

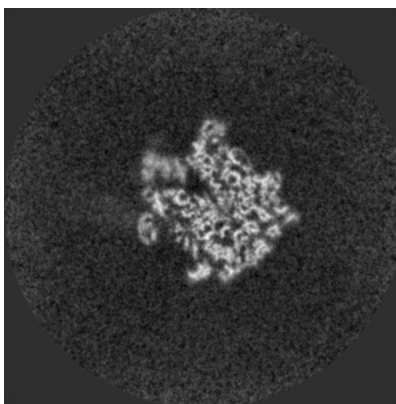
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

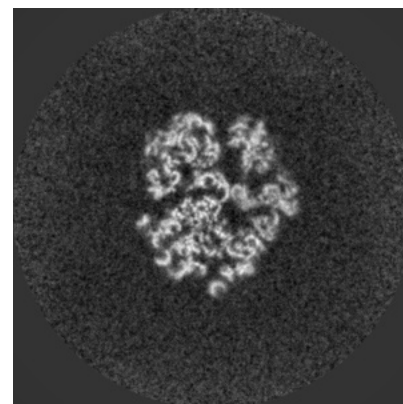
6.3.1 Primary map



X Index: 296



Y Index: 240

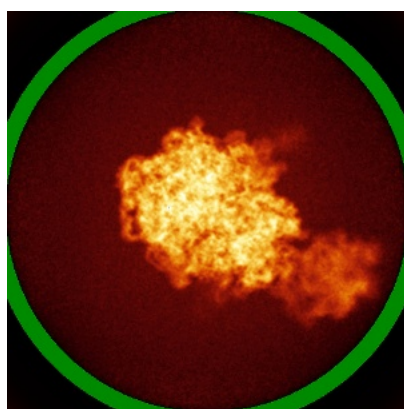


Z Index: 243

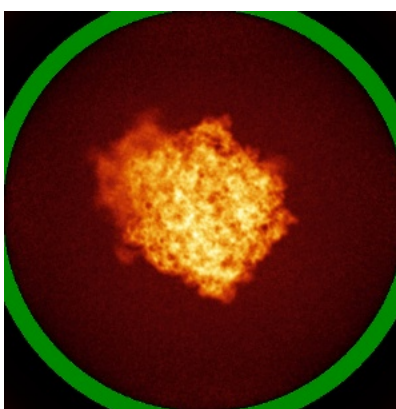
The images above show the largest variance slices of the map in three orthogonal directions.

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

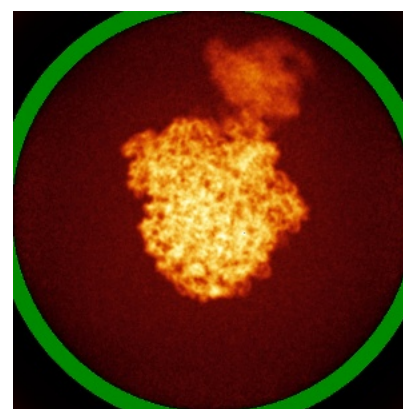
6.4.1 Primary map



X



Y

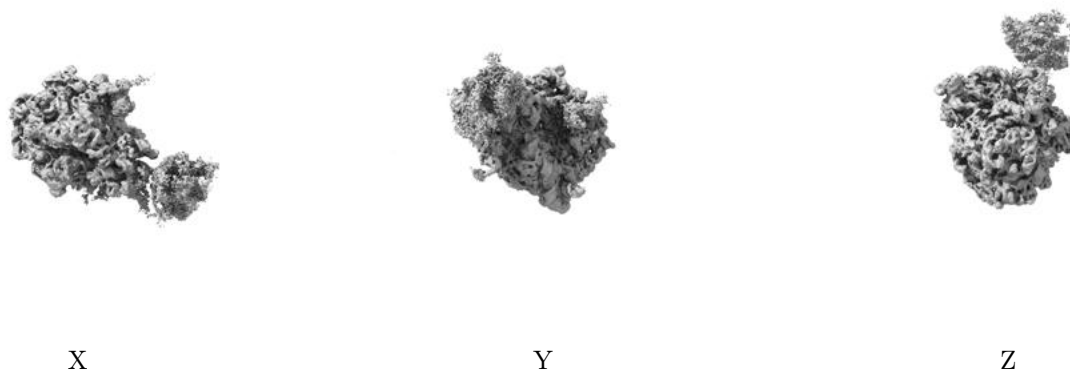


Z

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 0.00868. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

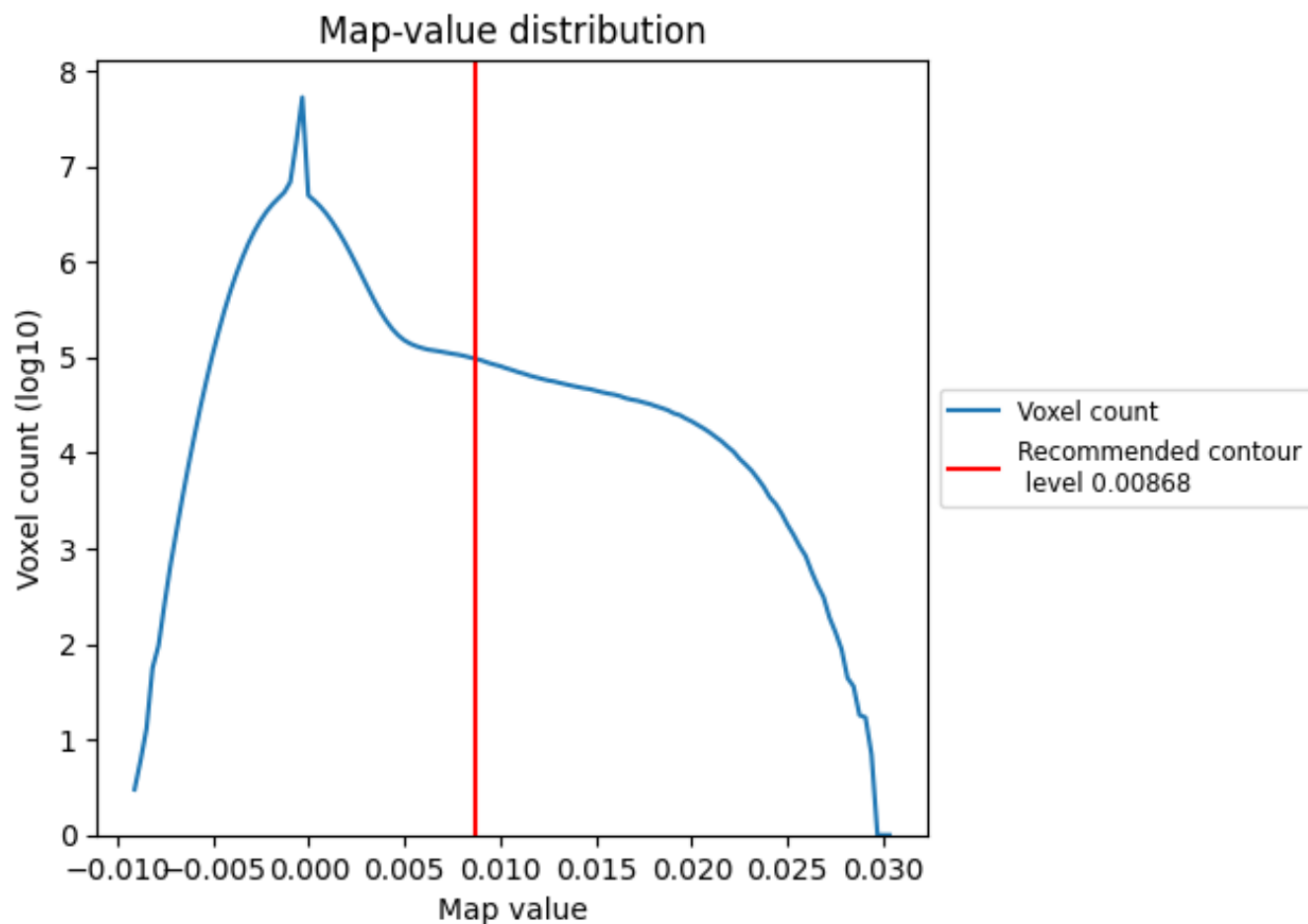
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

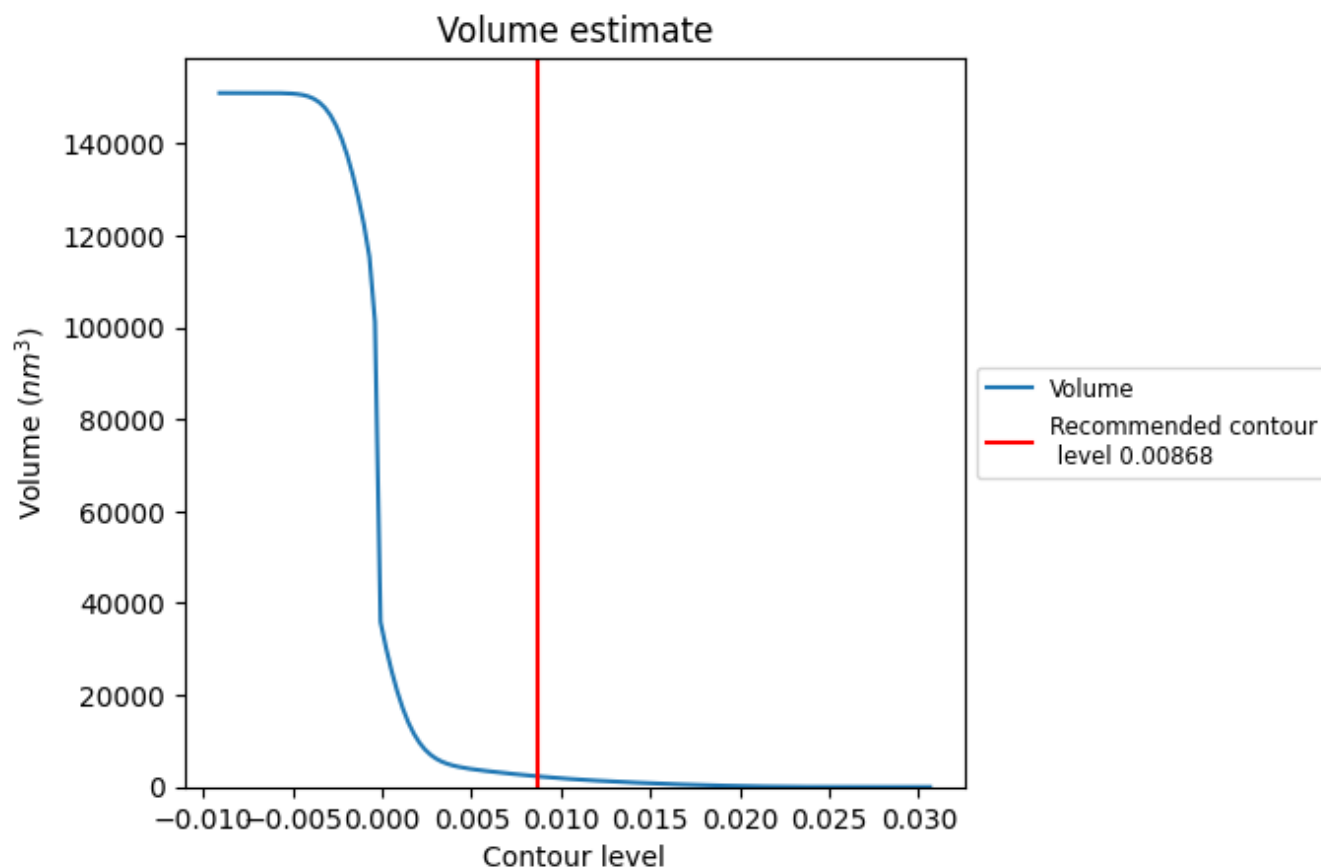
This section contains the results of statistical analysis of the map.

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.

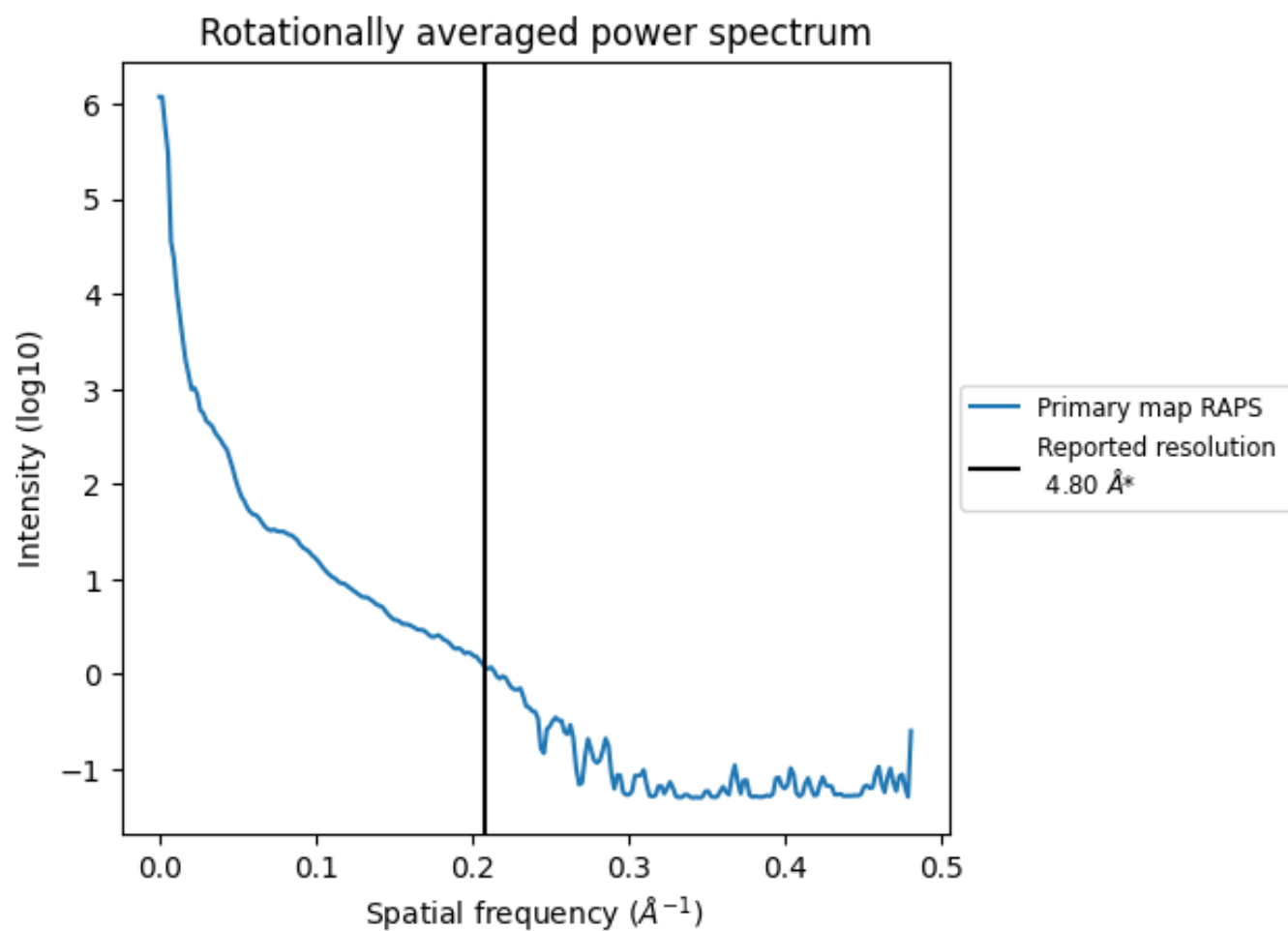
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2318 nm^3 ; this corresponds to an approximate mass of 2094 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 0.208 Å⁻¹

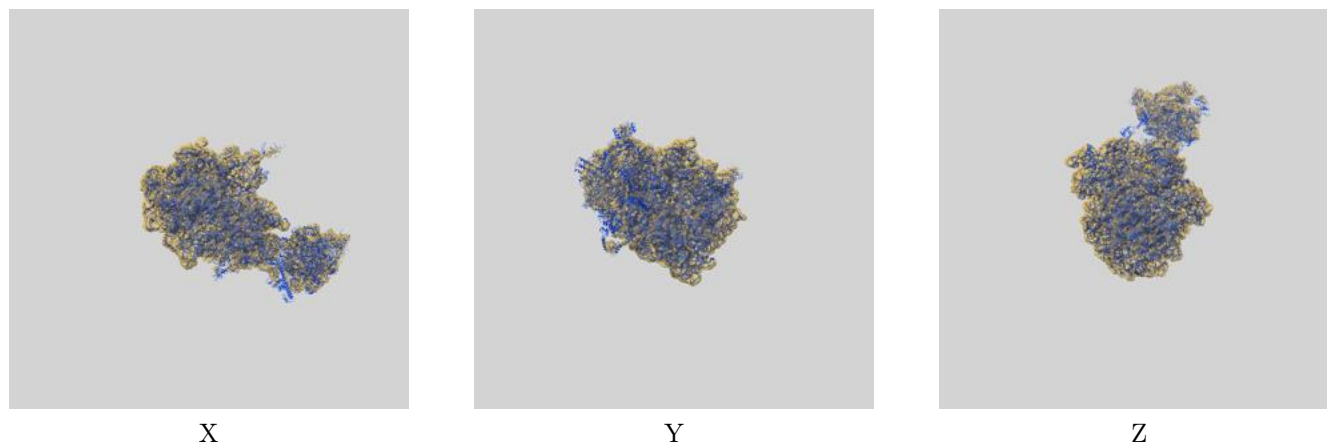
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

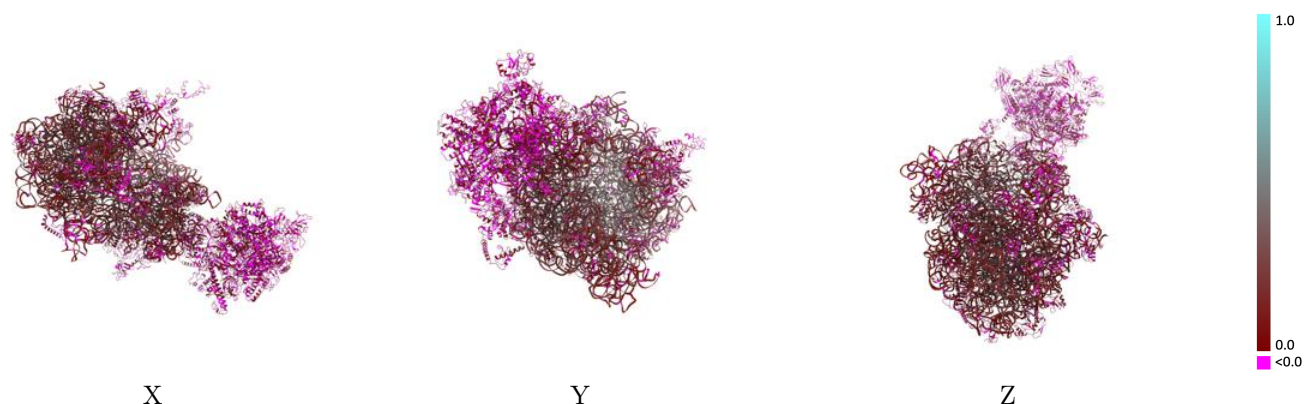
This section contains information regarding the fit between EMDB map EMD-22107 and PDB model 6X9Q. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



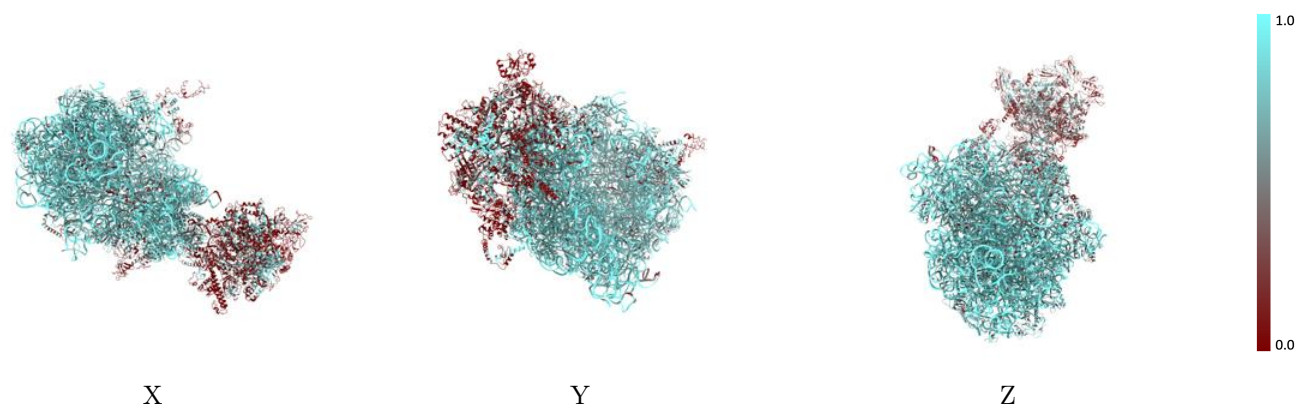
The images above show the 3D surface view of the map at the recommended contour level 0.00868 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



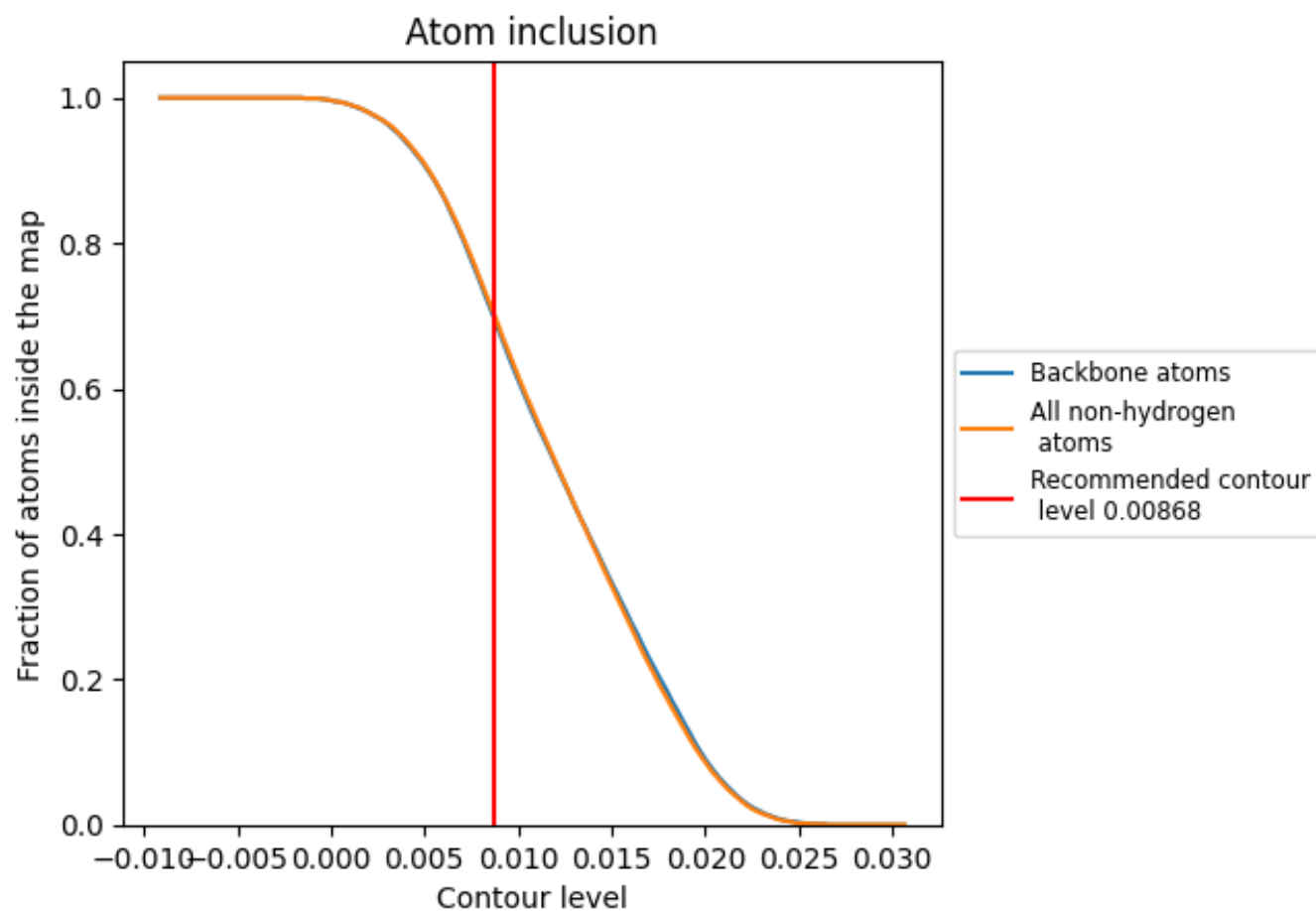
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00868).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 70% 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 (0.00868) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7050	 0.1560
0	 0.7290	 0.1450
1	 0.7240	 0.2060
2	 0.6630	 0.1170
3	 0.6950	 0.1010
4	 0.7150	 0.0980
5	 0.3710	 0.0370
6	 0.3840	 0.0290
7	 0.4960	 0.0750
9	 0.4420	 0.0440
A	 0.8150	 0.1630
AA	 0.2700	 0.0210
AB	 0.2820	 0.0420
AC	 0.1910	 0.0290
AD	 0.2200	 0.0160
AE	 0.3440	 0.0230
AF	 0.0470	 0.0300
AG	 0.4020	 0.1000
B	 0.6630	 0.0810
C	 0.6600	 0.1380
D	 0.9280	 0.2220
E	 0.7030	 0.1120
F	 0.6150	 0.1830
G	 0.6670	 0.1480
H	 0.1230	 0.0340
I	 0.6920	 0.1870
J	 0.6960	 0.1490
K	 0.7430	 0.2470
L	 0.6590	 0.0980
M	 0.6590	 0.1380
N	 0.7310	 0.1770
O	 0.6580	 0.0940
P	 0.6040	 0.1140
Q	 0.7060	 0.1570
R	 0.7280	 0.2390



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Chain	Atom inclusion	Q-score
S	 0.7110	 0.1220
T	 0.7130	 0.1610
U	 0.6760	 0.0900
V	 0.7250	 0.1650
W	 0.6090	 0.0770
X	 0.5800	 0.0810
Y	 0.2990	 0.0340
Z	 0.0350	 -0.0040
a	 0.9190	 0.2100
b	 0.6750	 0.0980
c	 0.7060	 0.1780
d	 0.8750	 0.1350
e	 0.6890	 0.0870
f	 0.7340	 0.1300
g	 0.5200	 0.0530
h	 0.7110	 0.1540
i	 0.7410	 0.1910
j	 0.7060	 0.1260
k	 0.6480	 0.0810
l	 0.6680	 0.1530
m	 0.7800	 0.2390
n	 0.6150	 0.0640
o	 0.6540	 0.1480
p	 0.6500	 0.0570
q	 0.6810	 0.0730
r	 0.3860	 0.0590
s	 0.7120	 0.1160
t	 0.6510	 0.1450
u	 0.7010	 0.1470
v	 0.6950	 0.1480
w	 0.7500	 0.1490
x	 0.6670	 0.0560
y	 0.6290	 0.1060
z	 0.7570	 0.1550