Full wwPDB EM Validation Report

Mar 28, 2026 – 10:24 PM UTC

PDB ID	:	6VYR / pdb_00006vyr
EMDB ID	:	EMD-21469
Title	:	Escherichia coli transcription-translation complex A1 (TTC-A1) containing an 18 nt long mRNA spacer, NusG, and fMet-tRNAs at E-site and P-site
Authors	:	Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on	:	2020-02-27
Resolution	:	3.80 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:

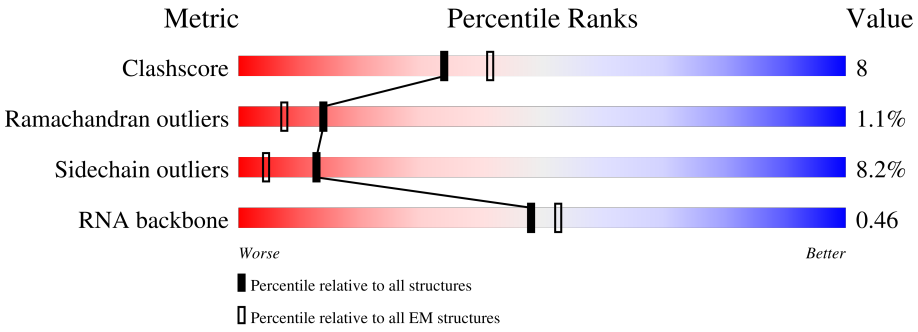
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

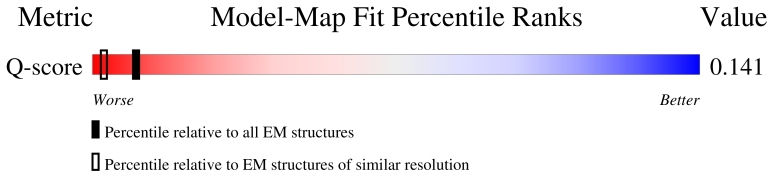
1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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 <=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	38% 84% 15% •
2	1	110	19% 77% 23%
3	2	100	52% 86% 6% • 6%

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Mol	Chain	Length	Quality of chain
4	3	104	54% 84% 14%
5	4	94	48% 97%
6	5	36	64% 25% 36% 36%
7	6	36	75% 39% 36% 25%
8	7	35	97% 57% 37%
9	9	165	85% 27% 36% 24% 10%
10	A	76	64% 12% 47% 36% 5%
10	B	76	80% 12% 46% 37% 5%
11	AA	1342	98% 69% 22% 6%
12	AB	181	54% 49% 5% 46%
13	AC	329	70% 51% 15% 30%
13	AD	329	69% 52% 16% 31%
14	AE	1407	95% 67% 24% 5%
15	C	75	45% 72% 15% 12%
16	D	1542	6% 70% 25%
17	E	87	61% 87% 10%
18	F	71	56% 87% 10%
19	G	241	53% 80% 12% 7%
20	H	557	46% 25% 16% 54%
21	I	233	50% 79% 9% 11%
22	J	206	52% 90% 9%
23	K	167	20% 75% 14% 7%
24	L	135	47% 67% 10% 23%
25	M	179	50% 71% 12% 16%
26	N	130	32% 90% 8%

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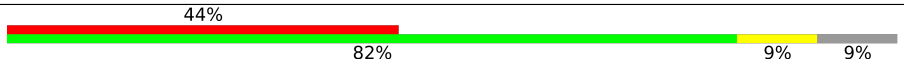
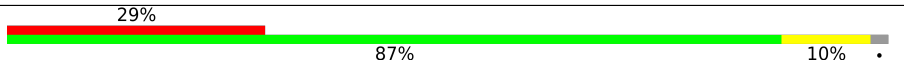
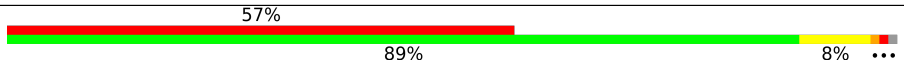
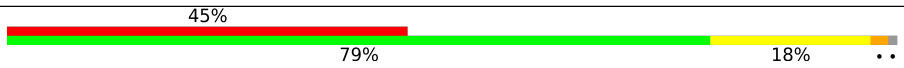
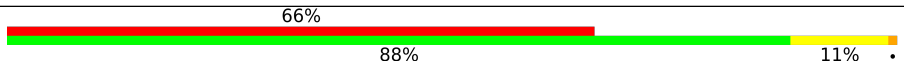
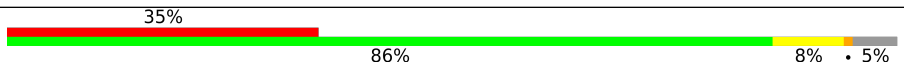
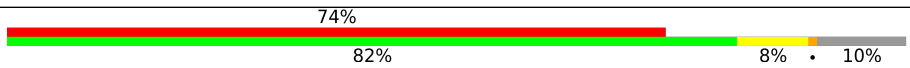
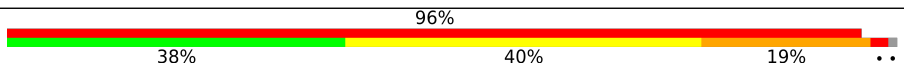
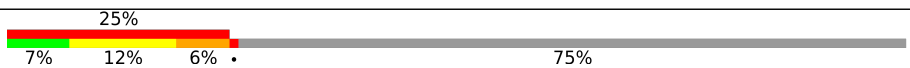
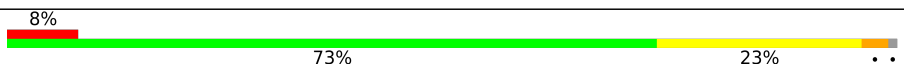
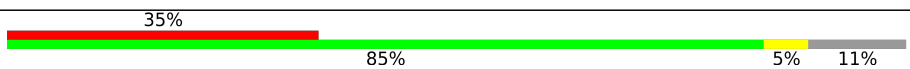
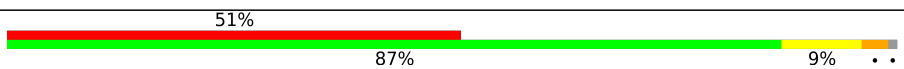
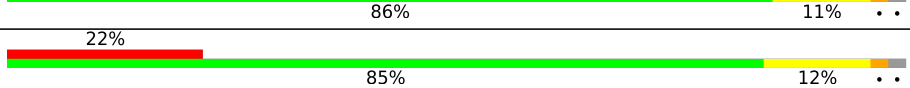
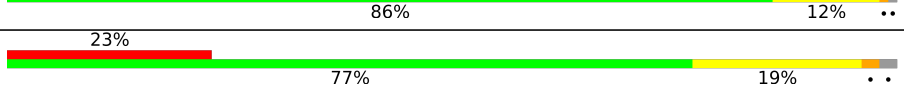
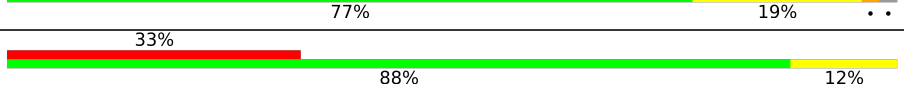
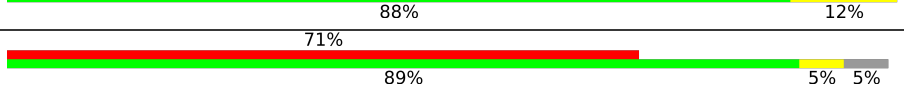
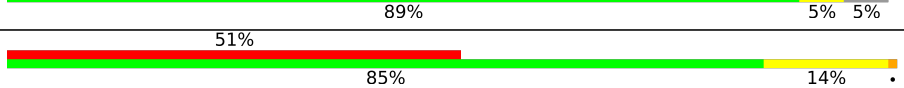
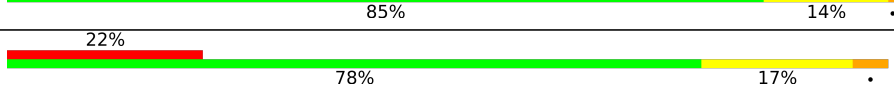
Mol	Chain	Length	Quality of chain
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	
32	T	89	
33	U	82	
34	V	84	
35	W	92	
36	X	118	
37	Y	142	
38	Z	121	
39	a	2904	
40	b	85	
41	c	78	
42	d	120	
43	e	63	
44	f	59	
45	g	70	
46	h	273	
47	i	57	
48	j	209	
49	k	55	
50	l	201	
51	m	46	

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Mol	Chain	Length	Quality of chain
52	n	179	68% 76% 20%
53	o	65	51% 88% 8%
54	p	177	69% 90% 8%
55	q	38	45% 89% 8%
56	r	149	89% 89% 10%
57	s	142	34% 83% 15%
58	t	123	43% 80% 19%
59	u	144	48% 90% 10%
60	v	136	43% 91% 8%
61	w	127	28% 74% 20% 6%
62	x	117	68% 82% 16%
63	y	115	61% 89% 10%
64	z	118	27% 84% 15%

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300728 atoms, of which 124723 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 18 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	35	Total	C	H	N	O	P	0	0
			829	327	97	106	264	35		

- 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	1322	Total	C	H	N	O	S	0	0
			20851	6539	10426	1817	2026	43		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

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

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

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Mol	Chain	Residues	Atoms						AltConf	Trace
13	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	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 30S ribosomal protein S18.

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

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

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

- Molecule 17 is a protein called 30S ribosomal protein S20.

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

- Molecule 18 is a protein called 30S ribosomal protein S21.

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

- Molecule 19 is a protein called 30S ribosomal protein S2.

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

- Molecule 20 is a protein called 30S ribosomal protein S1.

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

- Molecule 21 is a protein called 30S ribosomal protein S3.

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

- Molecule 22 is a protein called 30S ribosomal protein S4.

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

- Molecule 23 is a protein called 30S ribosomal protein S5.

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

- Molecule 24 is a protein called 30S ribosomal protein S6.

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

- Molecule 25 is a protein called 30S ribosomal protein S7.

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

- Molecule 26 is a protein called 30S ribosomal protein S8.

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

- Molecule 27 is a protein called 30S ribosomal protein S9.

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

- Molecule 28 is a protein called 30S ribosomal protein S10.

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

- Molecule 29 is a protein called 30S ribosomal protein S11.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S14.

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

- Molecule 32 is a protein called 30S ribosomal protein S15.

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

- Molecule 33 is a protein called 30S ribosomal protein S16.

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

- Molecule 34 is a protein called 30S ribosomal protein S17.

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

- Molecule 35 is a protein called 30S ribosomal protein S19.

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

- Molecule 36 is a protein called 30S ribosomal protein S13.

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

- Molecule 37 is a protein called 50S ribosomal protein L11.

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

- Molecule 38 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 39 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	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 40 is a protein called 50S ribosomal protein L27.

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

- Molecule 41 is a protein called 50S ribosomal protein L28.

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

- Molecule 42 is a RNA chain called 5S rRNA.

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

- Molecule 43 is a protein called 50S ribosomal protein L29.

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

- Molecule 44 is a protein called 50S ribosomal protein L30.

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

- Molecule 45 is a protein called 50S ribosomal protein L31.

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

- Molecule 46 is a protein called 50S ribosomal protein L2.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L3.

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

- Molecule 49 is a protein called 50S ribosomal protein L33.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L5.

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

- Molecule 53 is a protein called 50S ribosomal protein L35.

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

- Molecule 54 is a protein called 50S ribosomal protein L6.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is a protein called 50S ribosomal protein L9.

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

- Molecule 57 is a protein called 50S ribosomal protein L13.

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

- Molecule 58 is a protein called 50S ribosomal protein L14.

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

- Molecule 59 is a protein called 50S ribosomal protein L15.

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

- Molecule 60 is a protein called 50S ribosomal protein L16.

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

- Molecule 61 is a protein called 50S ribosomal protein L17.

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

- Molecule 62 is a protein called 50S ribosomal protein L18.

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

- Molecule 63 is a protein called 50S ribosomal protein L19.

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

- Molecule 64 is a protein called 50S ribosomal protein L20.

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

- Molecule 65 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 66 is ZINC ION (CCD ID: ZN) (formula: Zn).

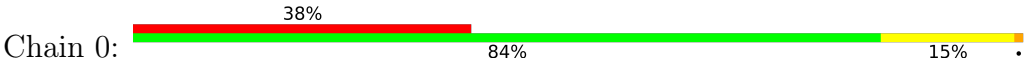
Mol	Chain	Residues	Atoms		AltConf
66	AE	2	Total	Zn	0
			2	2	

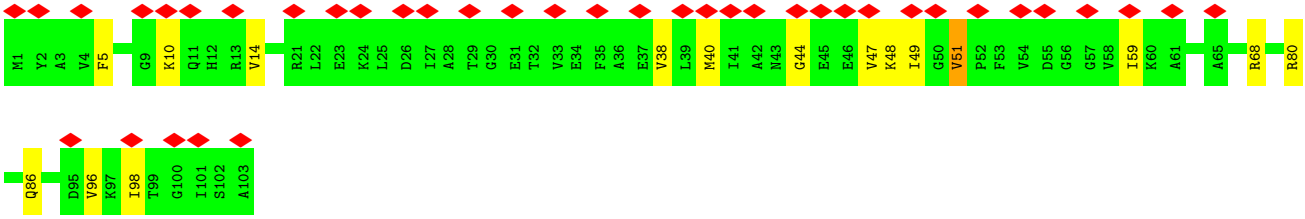
3 Residue-property plots (i)

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

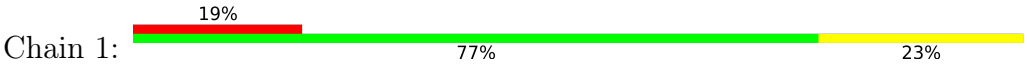
Chain 0:

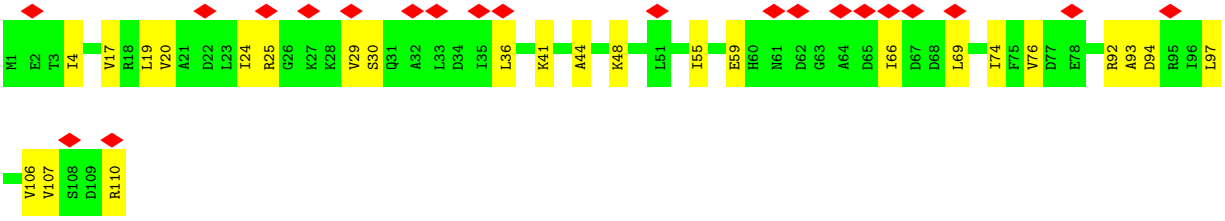




• Molecule 2: 50S ribosomal protein L22

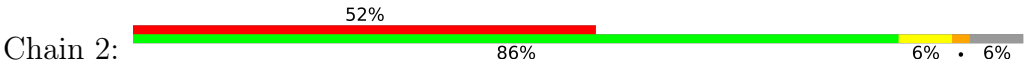
Chain 1:

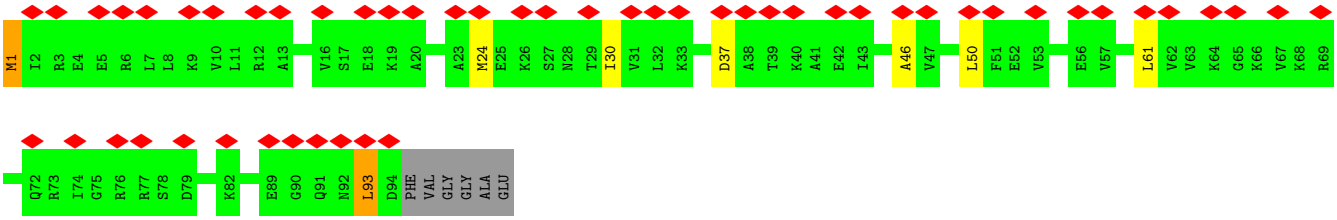




• Molecule 3: 50S ribosomal protein L23

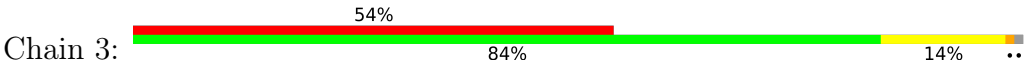
Chain 2:

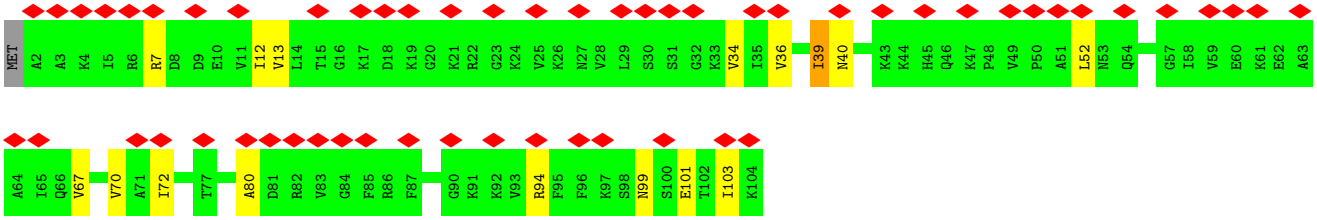




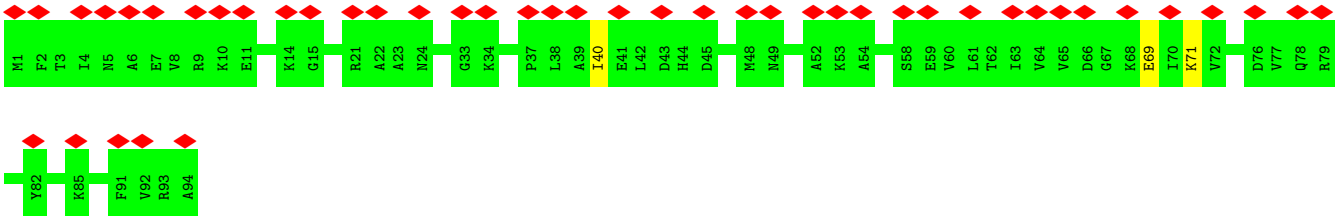
• Molecule 4: 50S ribosomal protein L24

Chain 3:

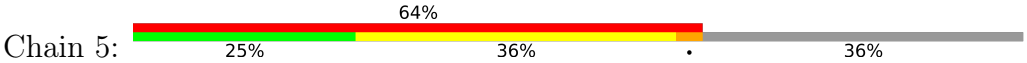


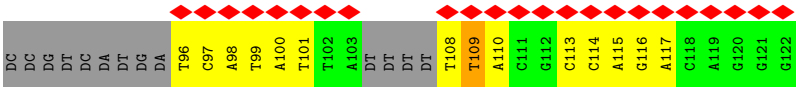


• Molecule 5: 50S ribosomal protein L25

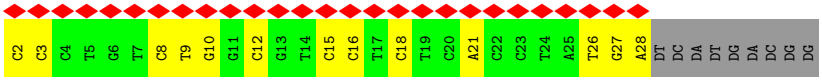


• Molecule 6: NT DNA



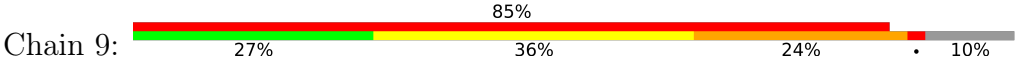


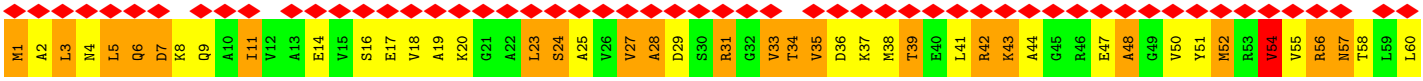
• Molecule 7: T DNA

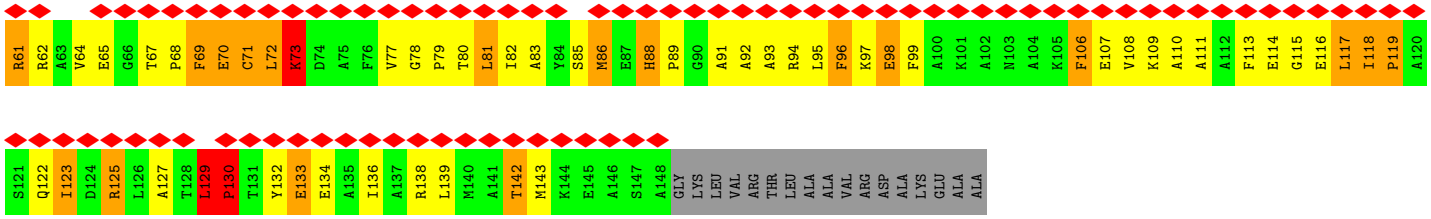


• Molecule 8: mRNA with 18 nt long spacer

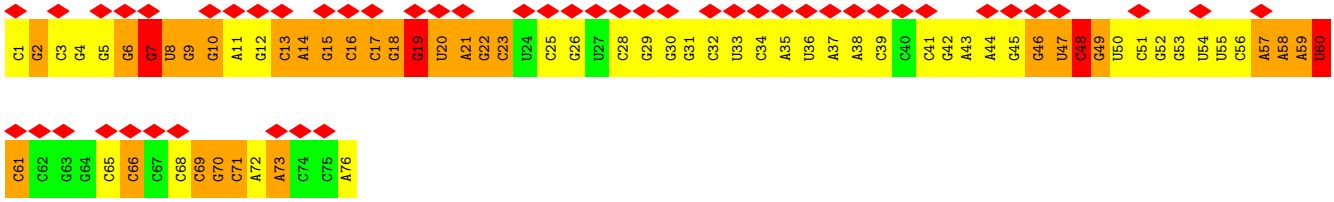
• Molecule 9: 50S ribosomal protein L10



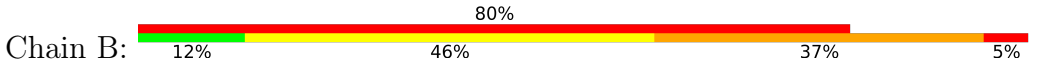


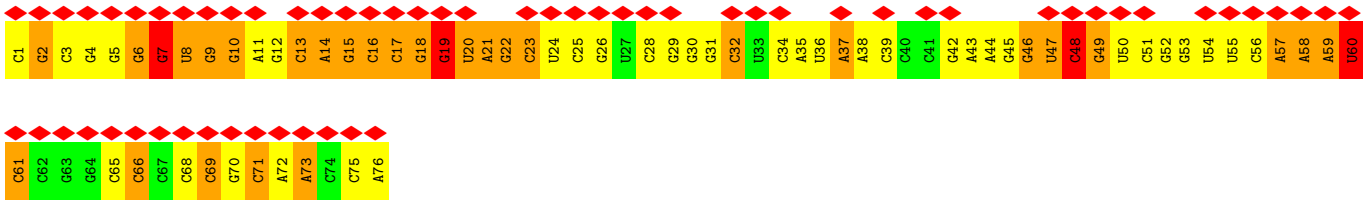


• Molecule 10: E-site and P-site tRNA (fMet)

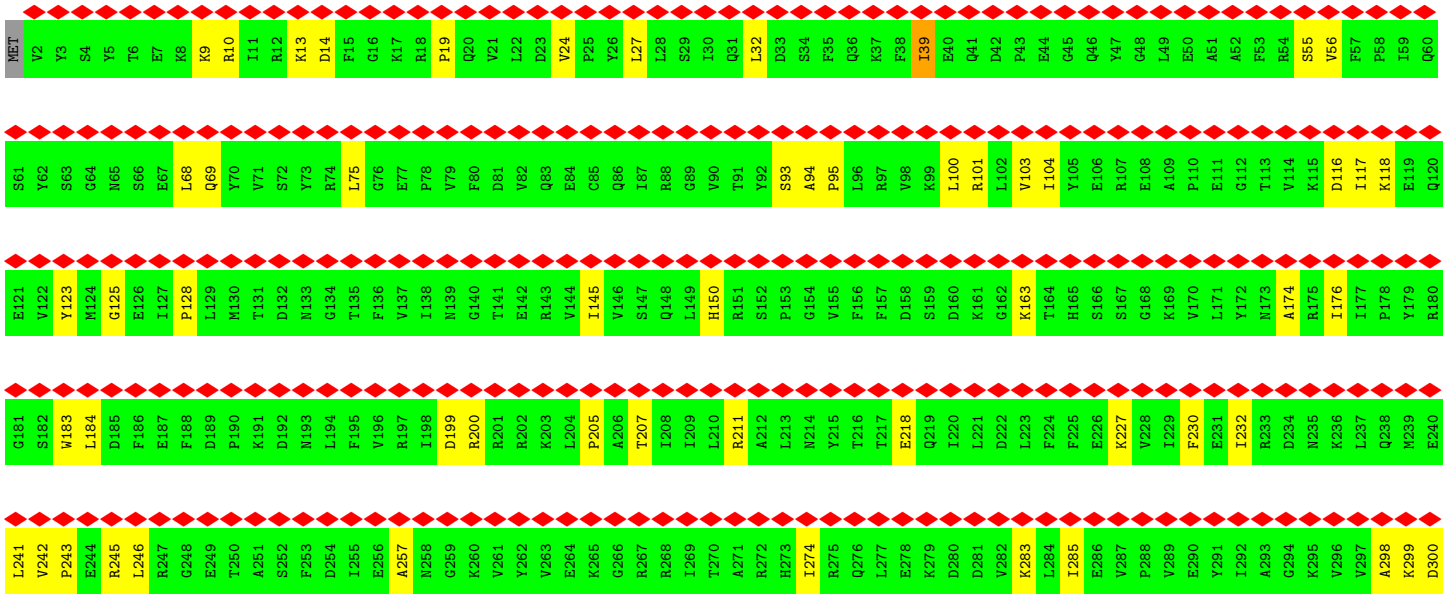


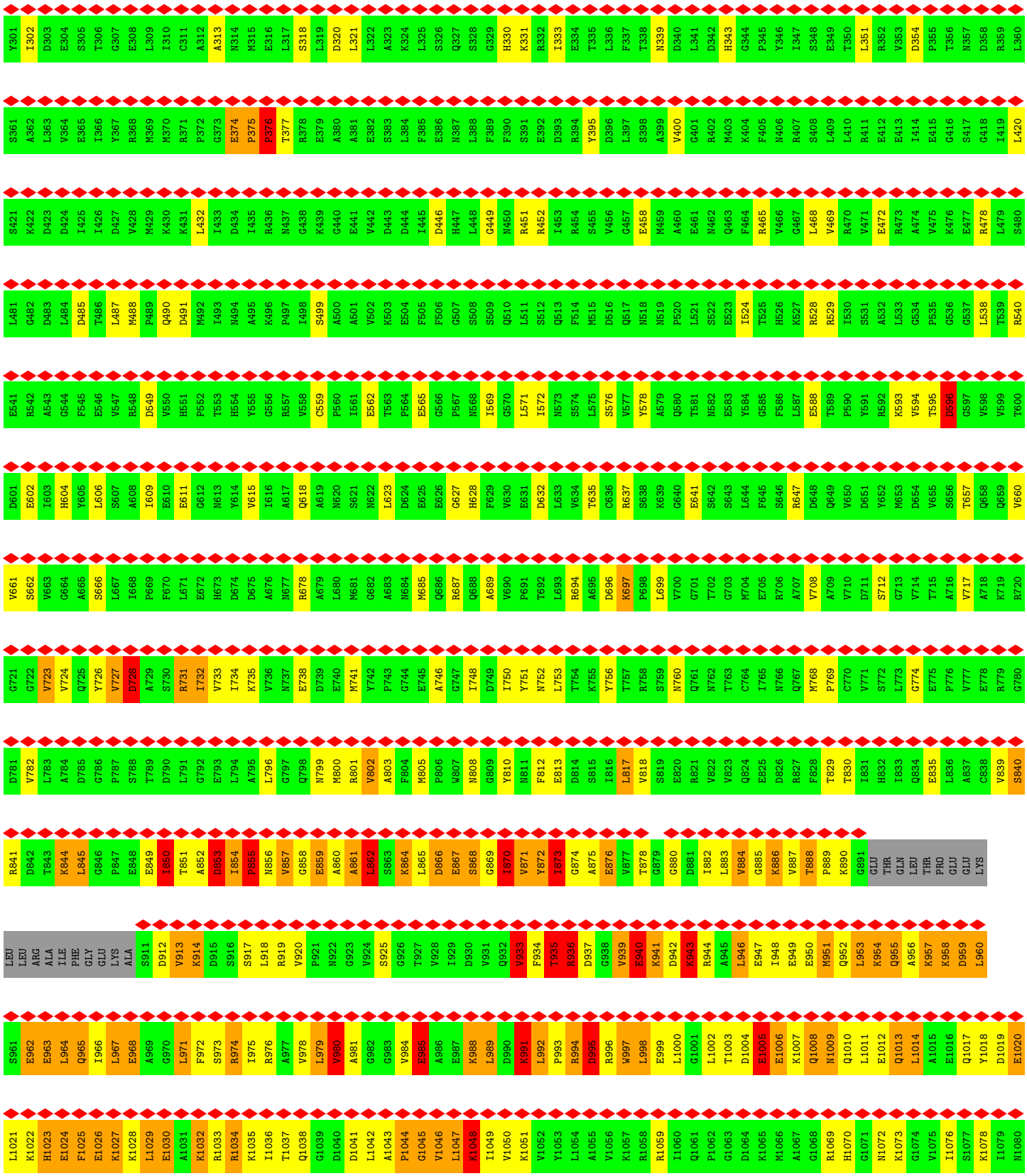
• Molecule 10: E-site and P-site tRNA (fMet)

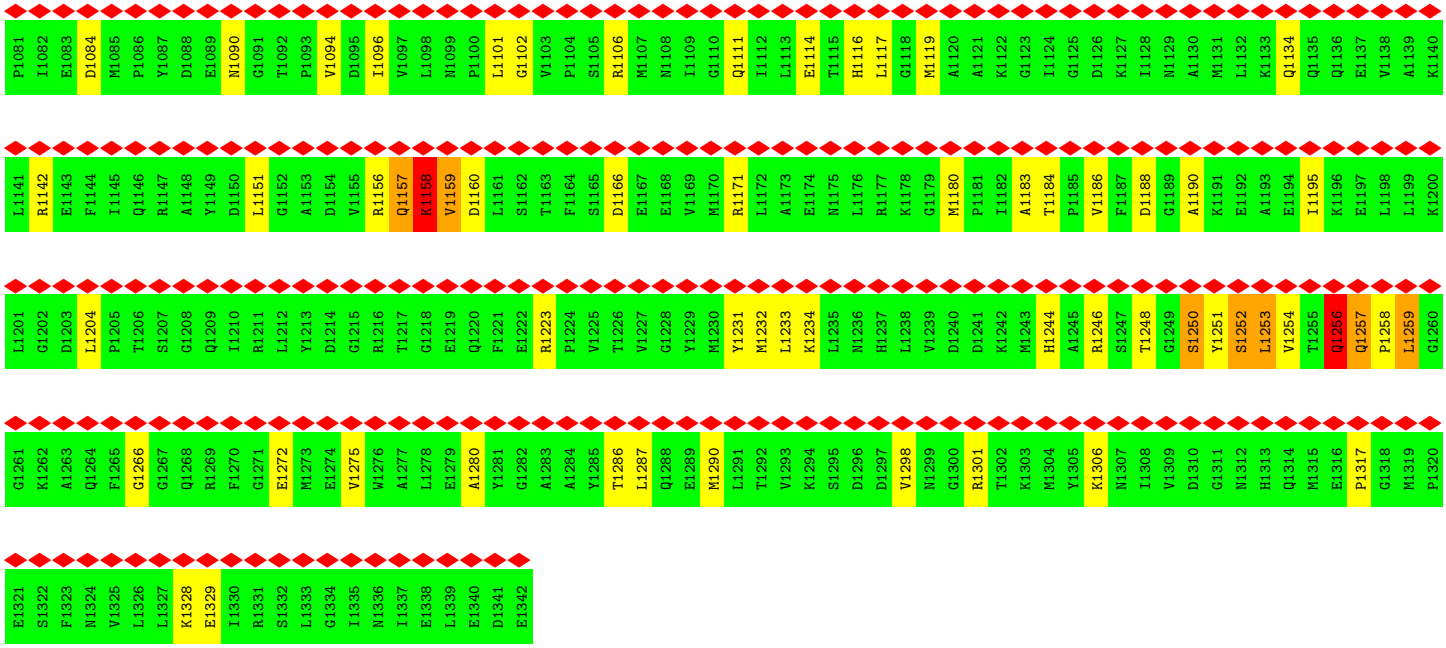




• Molecule 11: DNA-directed RNA polymerase subunit beta

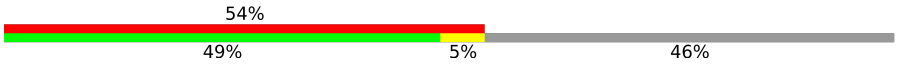


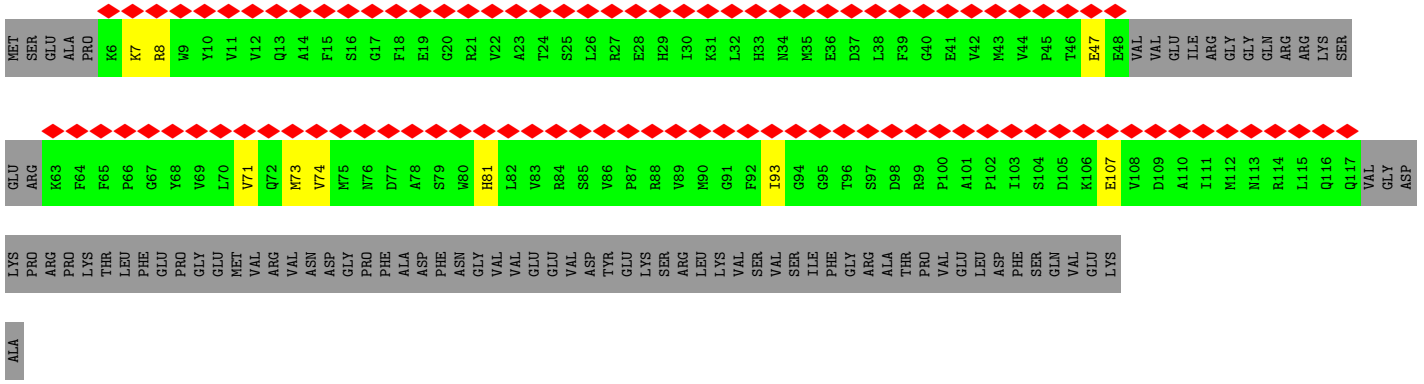

Y301 I302 D303 E304 S305 T306 G307 E308 L309 I310 C311 A312 A313 N314 M315 E316 L317 S318 L319 D320 L321 L322 A323 K324 L325 S326 Q327 S328 G329 H330 K331 R332 I333 E334 T335 L336 F337 T338 N339 D340 L341 D342 H343 G344 P345 Y346 I347 S348 E349 T350 L351 R352 V353 D354 P355 T356 N357 D358 R359 L360
S361 A362 L363 V364 E365 I366 Y367 R368 M369 M370 R371 P372 G373 E374 P375 P376 T377 R378 E379 A380 A381 E382 S383 L384 F385 E386 N387 L388 F389 F390 S391 E392 D393 R394 Y395 D396 L397 S398 A399 V400 G401 R402 M403 K404 F405 N406 R407 S408 L409 L410 R411 E412 E413 I414 E415 G416 S417 G418 I419 L420
S421 K422 D423 D424 I425 I426 D427 V428 M429 K430 K431 L432 I433 D434 I435 R436 N437 G438 K439 G440 E441 V442 D443 D444 I445 D446 H447 L448 G449 N450 R451 R452 I453 R454 S455 V456 G457 E458 M459 A460 E461 N462 Q463 F464 R465 V466 G467 L468 V469 R470 V471 E472 R473 A474 V475 K476 E477 R478 L479 S480
L481 G482 D483 L484 D485 T486 L487 M488 P489 Q490 D491 M492 I493 N494 A495 K496 P497 I498 S499 A500 A501 V502 K503 E504 F505 P506 G507 S508 S509 Q510 L511 S512 Q513 F514 M515 D516 Q517 N518 N519 P520 L521 S522 E523 I524 T525 H526 K527 R528 R529 I530 S531 A532 L533 G534 P535 G536 G537 L538 T539 R540
E541 R542 A543 G544 F545 E546 V547 R548 D549 V550 H551 P552 T553 H554 Y555 G556 R557 V558 C559 P560 I561 E562 T563 P564 E565 G566 P567 N568 I569 G570 L571 I572 N573 S574 L575 S576 V577 Y578 A579 Q580 T581 N582 E583 Y584 G585 F586 L587 E588 T589 P590 Y591 R592 K593 V594 T595 D596 G597 V598 V599 T600
D601 E602 I603 H604 Y605 L606 S607 A608 I609 E610 E611 G612 N613 Y614 V615 I616 A617 Q618 A619 N620 S621 N622 L623 D624 E625 E626 G627 H628 F629 V630 E631 D632 L633 V634 T635 C636 R637 S638 K639 G640 E641 S642 S643 L644 F645 S646 R647 D648 Q649 V650 D651 Y652 M653 D654 V655 S656 T657 Q658 Q659 V660
V661 S662 V663 G664 A665 S666 L667 I668 P669 F670 L671 E672 H673 D674 D675 A676 N677 R678 A679 L680 M681 G682 A683 N684 M685 Q686 R687 Q688 A689 V690 P691 T692 L693 R694 A695 D696 K697 P698 L699 V700 G701 T702 G703 M704 E705 R706 A707 V708 A709 V710 D711 S712 G713 V714 T715 A716 V717 A718 K719 R720
G721 G722 V723 V724 Q725 Y726 V727 D728 A729 S730 R731 I732 V733 I734 K735 V736 N737 E738 D739 E740 M741 Y742 P743 G744 E745 A746 G747 I748 D749 I750 Y751 N752 L753 T754 K755 Y756 T757 R758 S759 N760 Q761 N762 T763 C764 I765 N766 Q767 M768 P769 C770 V771 S772 L773 G774 E775 P776 V777 E778 R779 G780
D781 V782 L783 A784 D785 G786 P787 S788 T789 D790 L791 G792 E793 L794 A795 L796 G797 Q798 N799 M800 R801 V802 A803 F804 M805 P806 W807 N808 G809 Y810 N811 F812 E813 D814 S815 I816 L817 V818 S819 E820 R821 V822 V823 Q824 E825 D826 R827 F828 T829 T830 I831 H832 I833 Q834 E835 L836 A837 C838 V839 S840
R841 D842 T843 K844 L845 G846 P847 E848 E849 I850 T851 A852 D853 I854 P855 N856 V857 G858 E859 A860 A861 L862 S863 K864 L865 D866 E867 S868 G869 I870 V871 Y872 I873 G874 A875 E876 V877 T878 G879 G880 D881 I882 L883 V884 G885 K886 V887 T888 P889 K890 G891 GLU THR GLN LEU THR PRO GLU GLU LYS
LEU LEU ARG ALA ILE PHE GLY GLU LYS ALA S911 D912 V913 K914 D915 S916 S917 L918 R919 V920 P921 N922 G923 V924 S925 G926 T927 V928 I929 D930 V931 Q932 V933 F934 T935 R936 D937 G938 V939 E940 K941 D942 K943 R944 A945 L946 E947 I948 E949 E950 M951 Q952 L953 K954 Q955 A956 K957 K958 D959 L960
S961 E962 E963 L964 Q965 I966 L967 E968 A969 G970 L971 F972 S973 R974 I975 R976 A977 V978 L979 V980 A981 G982 G983 V984 E985 A986 E987 K988 L989 D990 K991 L992 P993 R994 D995 R996 W997 L998 E999 L1000 G1001 L1002 T1003 D1004 E1005 E1006 K1007 Q1008 N1009 Q1010 L1011 E1012 Q1013 L1014 A1015 E1016 Q1017 Y1018 D1019 E1020
L1021 K1022 H1023 E1024 F1025 E1026 K1027 K1028 L1029 E1030 A1031 K1032 R1033 R1034 K1035 I1036 T1037 Q1038 G1039 D1040 D1041 L1042 A1043 P1044 G1045 V1046 L1047 K1048 I1049 V1050 K1051 V1052 Y1053 L1054 A1055 V1056 K1057 R1058 R1059 I1060 Q1061 P1062 G1063 D1064 K1065 M1066 A1067 G1068 R1069 H1070 G1071 N1072 K1073 G1074 V1075 I1076 S1077 K1078 I1079 N1080



• Molecule 12: Transcription termination/antitermination protein NusG

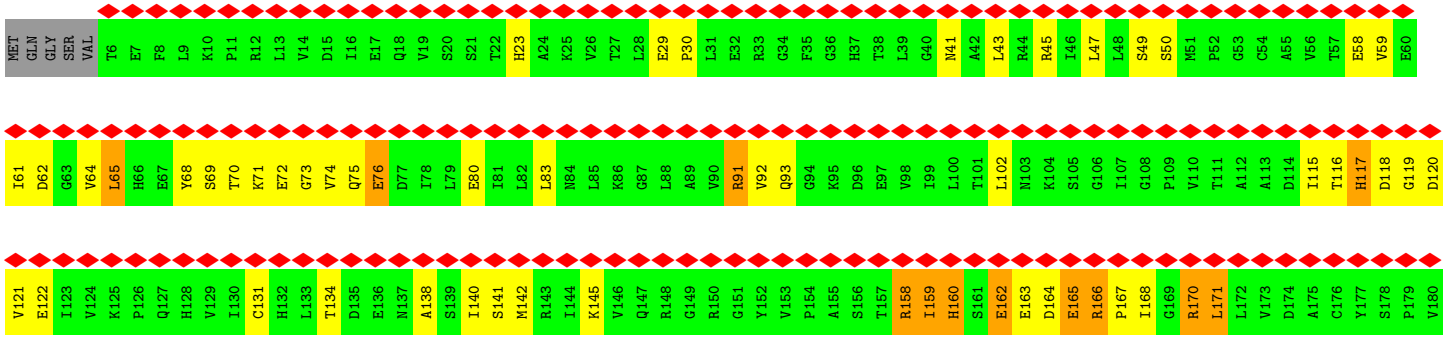
Chain AB:

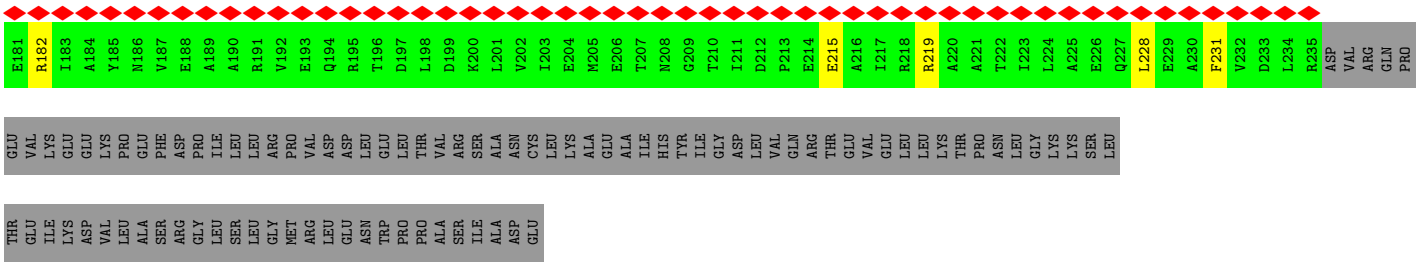




• Molecule 13: DNA-directed RNA polymerase subunit alpha

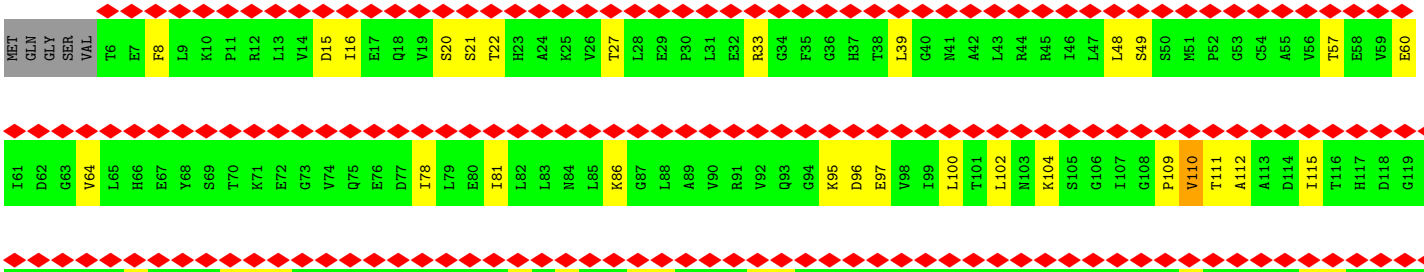
Chain AC:





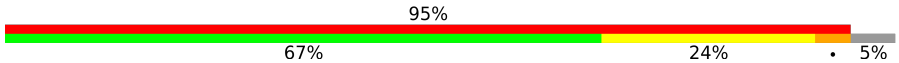
• Molecule 13: DNA-directed RNA polymerase subunit alpha

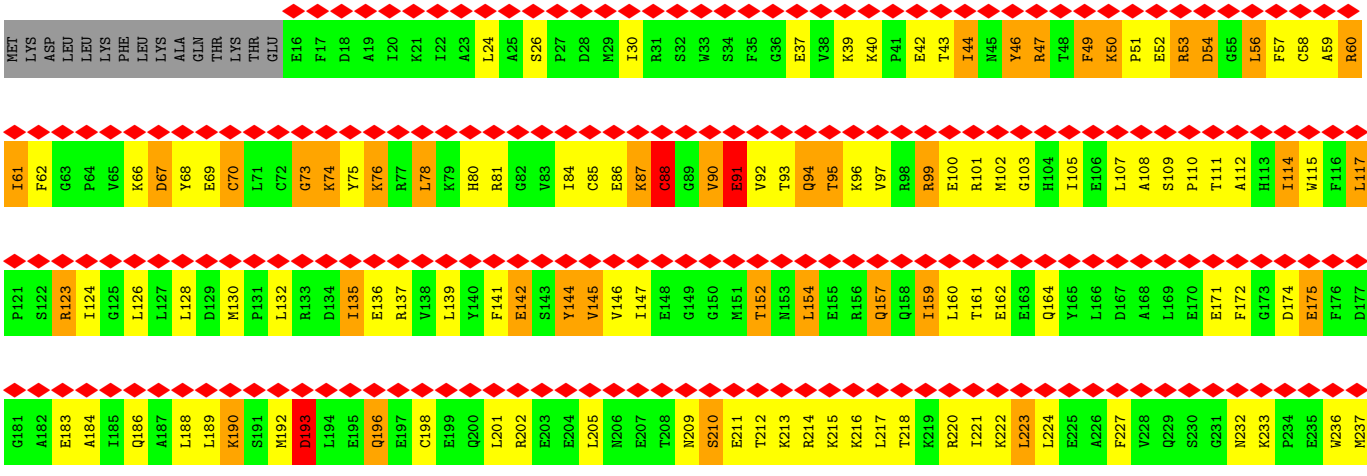
Chain AD:

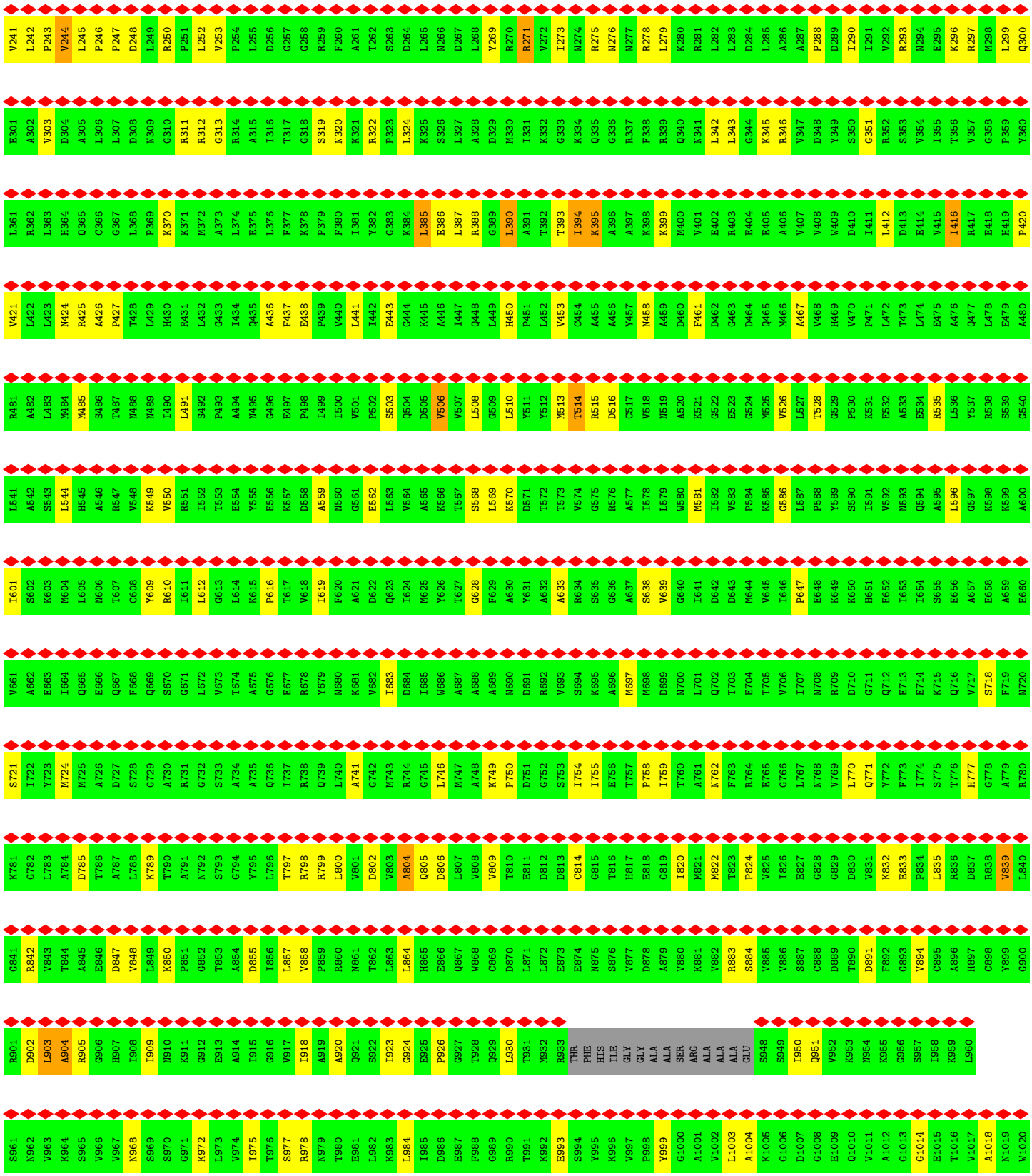


• Molecule 14: DNA-directed RNA polymerase subunit beta'

Chain AE:



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E301 A302 V303 D304 A305 L306 L307 D308 N309 G310 R311 R312 G313 R314 A315 I316 T317 G318 S319 N320 K321 R322 P323 L324 K325 S326 L327 A328 D329 M330 I331 K332 G333 K334 Q335 G336 R337 F338 R339 Q340 N341 L342 L343 G344 K345 R346 V347 D348 Y349 S350 G351 R352 S353 V354 I355 T356 V357 G358 P359 Y360
L361 R362 L363 H364 Q365 C366 G367 L368 P369 K370 K371 M372 A373 L374 E375 L376 F377 K378 P379 F380 I381 Y382 G383 K384 L385 E386 L387 R388 G389 L390 A391 T392 T393 I394 K395 A396 A397 K398 K399 M400 V401 E402 R403 E404 E405 A406 V407 V408 W409 D410 I411 L412 D413 E414 V415 I416 R417 E418 H419 P420
V421 L422 L423 N424 R425 A426 P427 T428 L429 H430 R431 L432 G433 I434 Q435 A436 F437 E438 P439 V440 L441 I442 E443 G444 K445 A446 I447 Q448 L449 H450 P451 L452 V453 C454 A455 A456 Y457 N458 A459 D460 F461 D462 G463 D464 Q465 M466 A467 V468 H469 V470 P471 L472 T473 L474 E475 A476 Q477 L478 E479 A480
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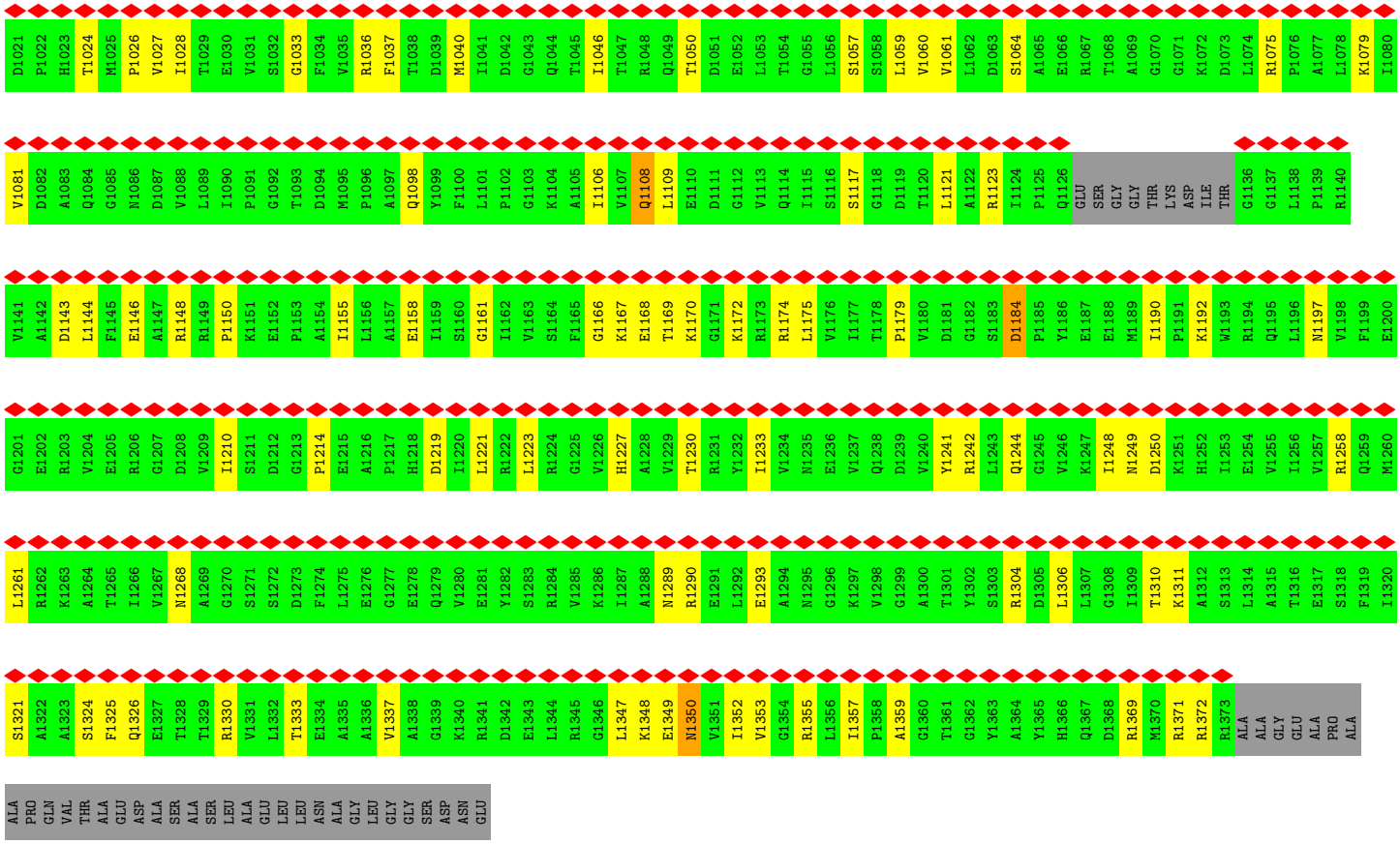
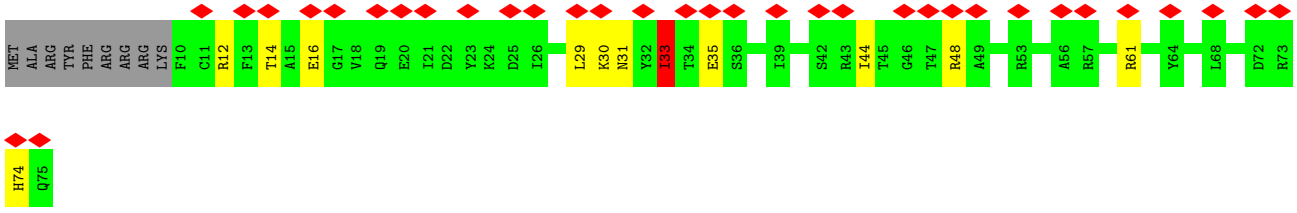
L541 A542 S543 L544 H545 A546 R547 V548 K549 V550 R551 I552 T553 E554 Y555 E556 K557 D558 A559 N560 G561 E562 L563 V564 A565 K566 T567 S568 L569 K570 D571 T572 T573 V574 G575 R576 A577 I578 L579 W580 M581 I582 V583 P584 K585 G586 L587 P588 Y589 S590 I591 V592 N593 Q594 A595 L596 G597 K598 K599 A600
I601 S602 K603 M604 L605 N606 T607 C608 Y609 R610 I611 L612 G613 L614 K615 P616 T617 V618 I619 F620 A621 D622 Q623 I624 M625 Y626 T627 G628 F629 A630 Y631 A632 A633 R634 S635 G636 A637 S638 V639 G640 I641 D642 D643 M644 V645 I646 P647 E648 K649 K650 H651 E652 I653 I654 S655 E656 A657 E658 A659 E660
V661 A662 E663 I664 Q665 E666 Q667 F668 Q669 S670 G671 L672 V673 T674 A675 G676 E677 R678 Y679 N680 K681 V682 I683 D684 I685 W686 A687 A688 A689 N690 D691 R692 V693 S694 K695 A696 M697 M698 D699 N700 L701 Q702 T703 E704 T705 V706 I707 N708 R709 D710 G711 Q712 E713 I774 S775 T776 H777 G778 A779 R780
S721 I722 Y723 M724 M725 A726 D727 S728 G729 A730 R731 G732 S733 A734 A735 Q736 I737 R738 Q739 L740 A741 G742 M743 R744 G745 L746 M747 A748 K749 P750 D751 G752 S753 I754 I755 E756 T757 P758 I759 T760 A761 N762 F763 R764 E765 G766 L767 N768 V769 L770 Q771 Y772 F773 I774 S775 T776 H777 G778 A779 R780
K781 G782 L783 A784 D785 T786 A787 L788 K789 T790 A791 N792 S793 G794 Y795 L796 T797 R798 R799 L800 V801 D802 V803 A804 Q805 D806 L807 V808 V809 T810 E811 D812 D813 C814 G815 T816 H817 E818 G819 I820 M821 M822 T823 P824 V825 I826 E827 G828 G829 D830 V831 K832 E833 P834 L835 R836 D837 R838 V839 L840
G841 R842 V843 T844 A845 E846 D847 V848 L849 K850 P851 G852 T853 A854 D855 I856 L857 V858 P859 R860 N861 T862 L863 L864 H865 E866 Q867 W868 C869 D870 L871 L872 E873 E874 N875 S876 V877 D878 A879 V880 K881 V882 R883 S884 V885 V886 S887 C888 D889 T890 D891 F892 G893 V894 C895 A896 H897 C898 Y899 G900
R901 D902 L903 A904 R905 G906 H907 I908 I909 N910 K911 G912 E913 A914 I915 G916 V917 I918 A919 A920 Q921 S922 I923 G924 E925 P926 G927 T928 Q929 L930 T931 R932 R933 THR PHE HIS ILE GLY GLY ALA ALA SER ARG ALA ALA ALA GLU S948 S949 I950 Q951 V952 K953 N954 K955 G956 S957 I958 K959 L960
S961 N962 V963 K964 S965 V966 V967 N968 S969 S970 G971 K972 L973 V974 I975 T976 S977 R978 N979 T980 E981 L982 K983 L984 I985 D986 E987 F988 G989 R990 T991 K992 E993 S994 Y995 K996 V997 P998 Y999 G1000 A1001 V1002 L1003 A1004 K1005 G1006 D1007 G1008 E1009 Q1010 V1011 A1012 G1013 G1014 E1015 T1016 V1017 A1018 N1019 W1020



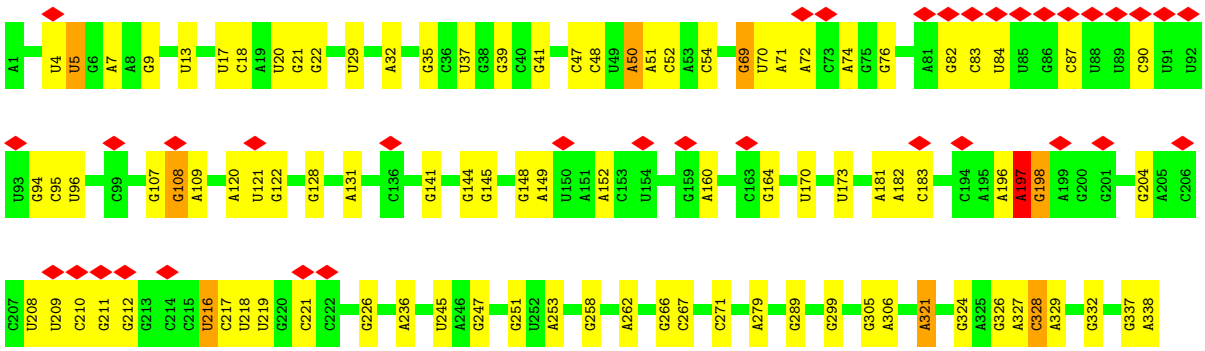
• Molecule 15: 30S ribosomal protein S18

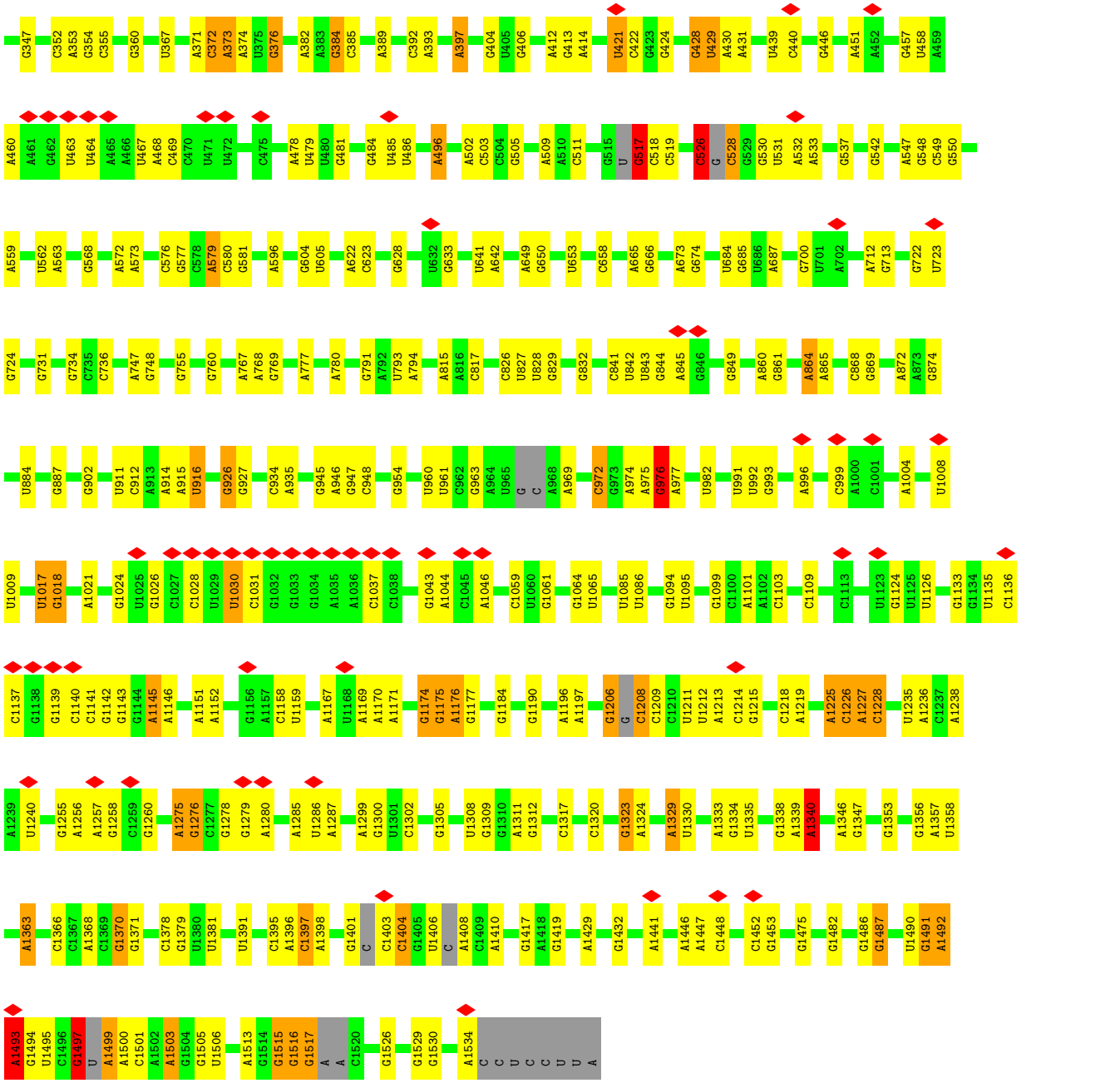
Chain C:



• Molecule 16: 16S rRNA

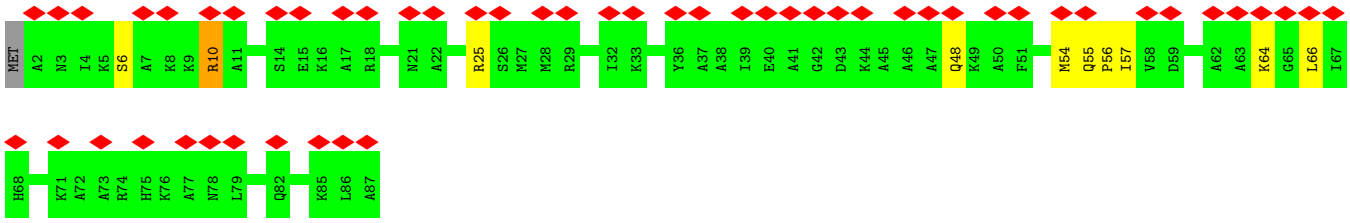
Chain D:





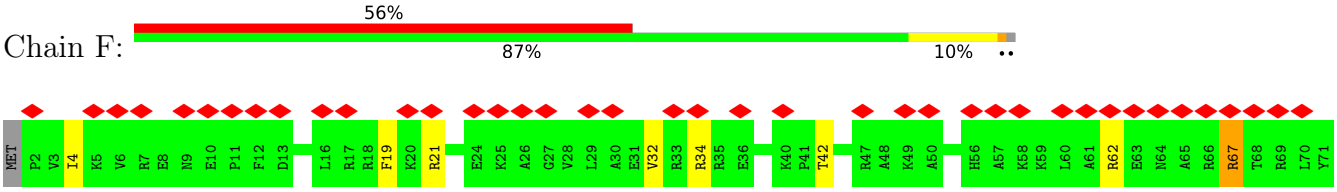
• Molecule 17: 30S ribosomal protein S20

Chain E:



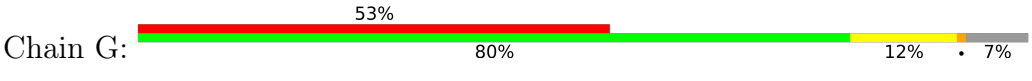
• Molecule 18: 30S ribosomal protein S21

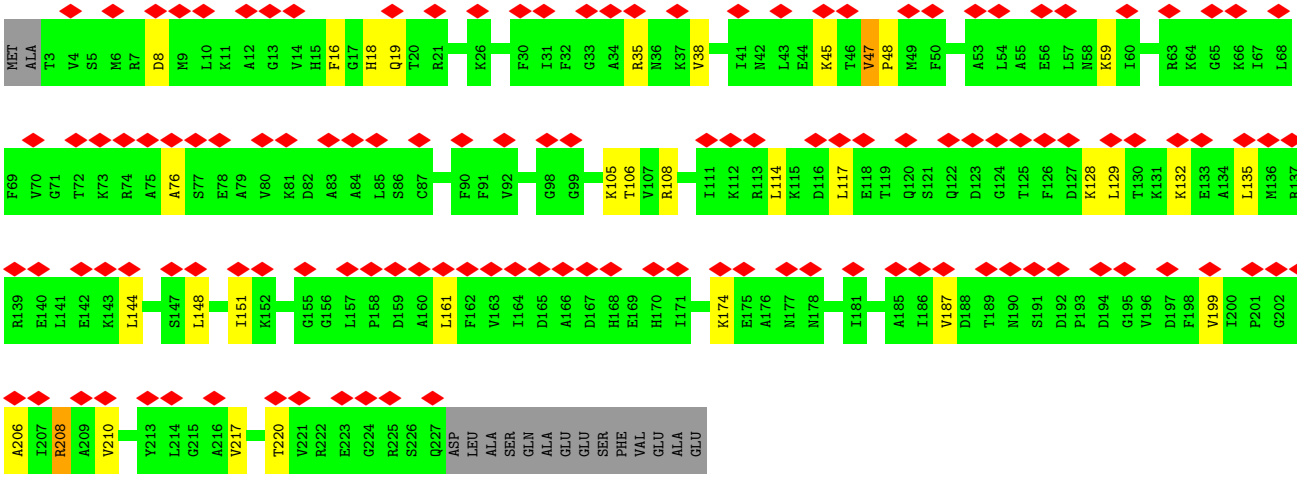
Chain F:



• Molecule 19: 30S ribosomal protein S2

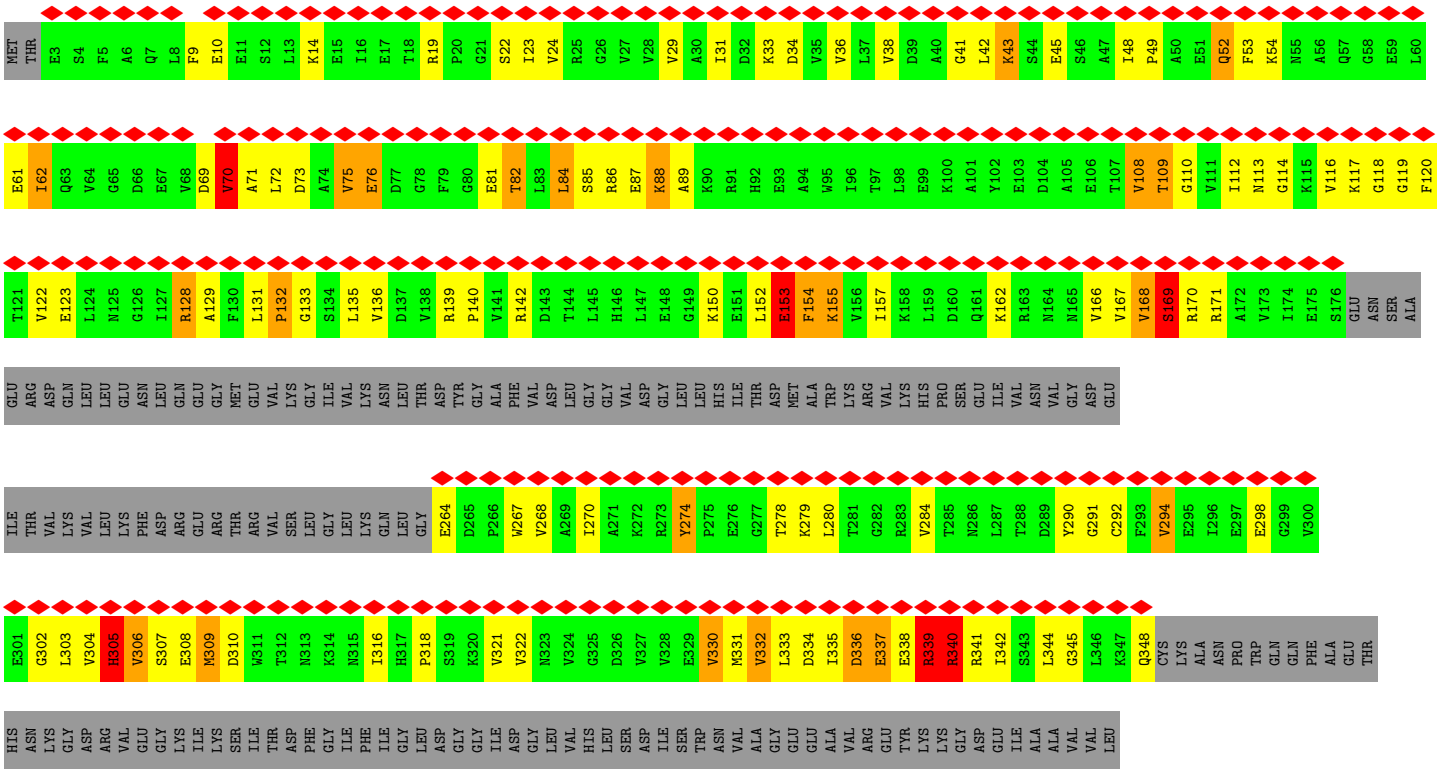
Chain G:

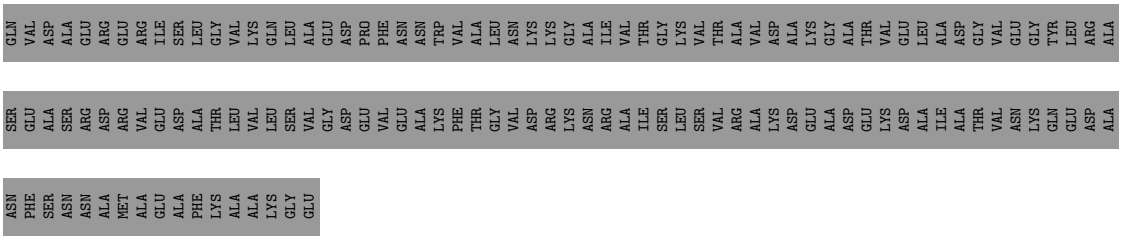




• Molecule 20: 30S ribosomal protein S1

Chain H:



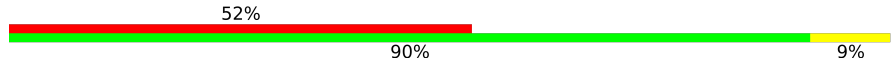


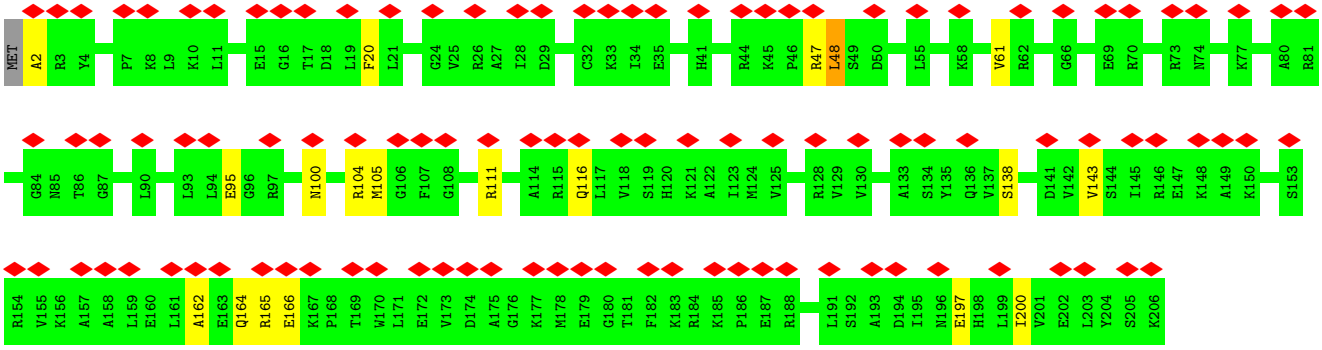
• Molecule 21: 30S ribosomal protein S3

Chain I:

• Molecule 22: 30S ribosomal protein S4

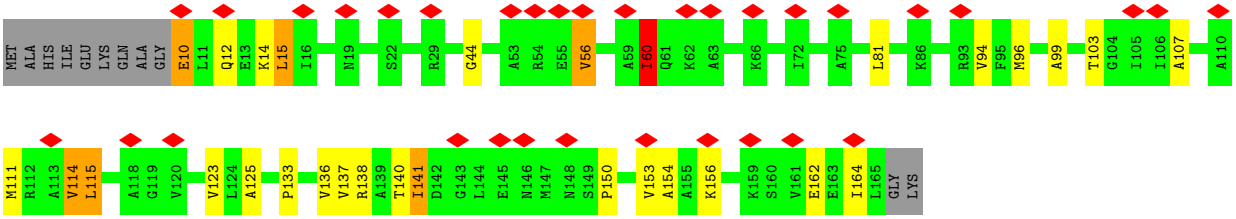
Chain J:





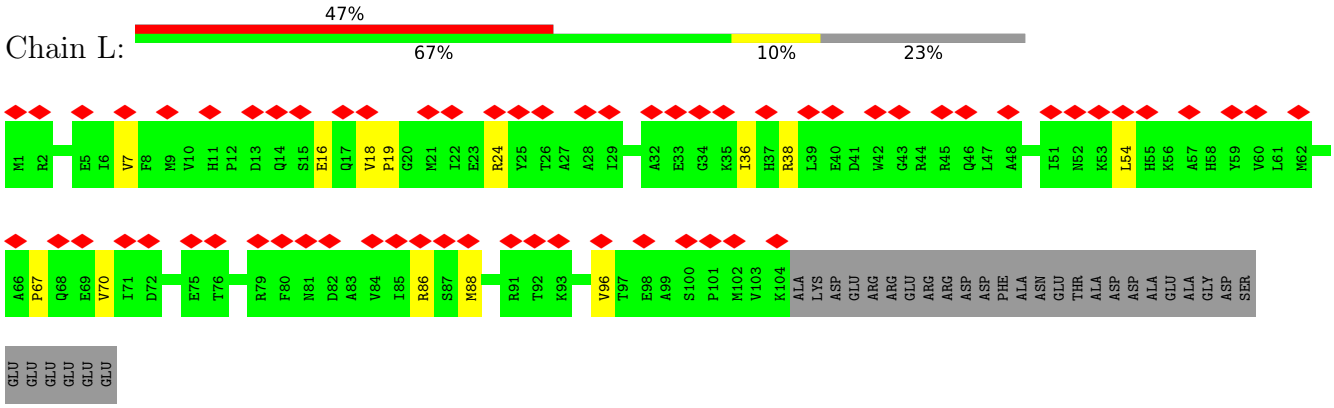
• Molecule 23: 30S ribosomal protein S5

Chain K:



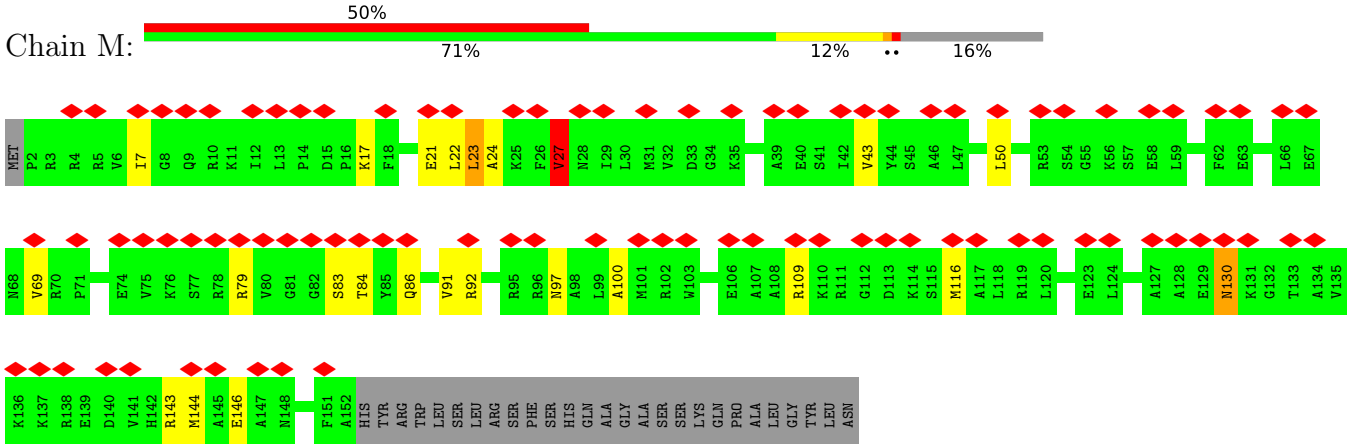
• Molecule 24: 30S ribosomal protein S6

Chain L:



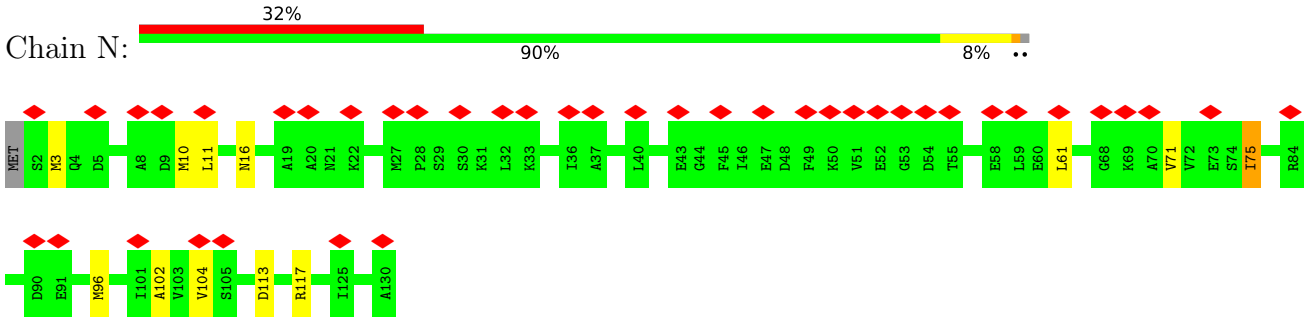
• Molecule 25: 30S ribosomal protein S7

Chain M:



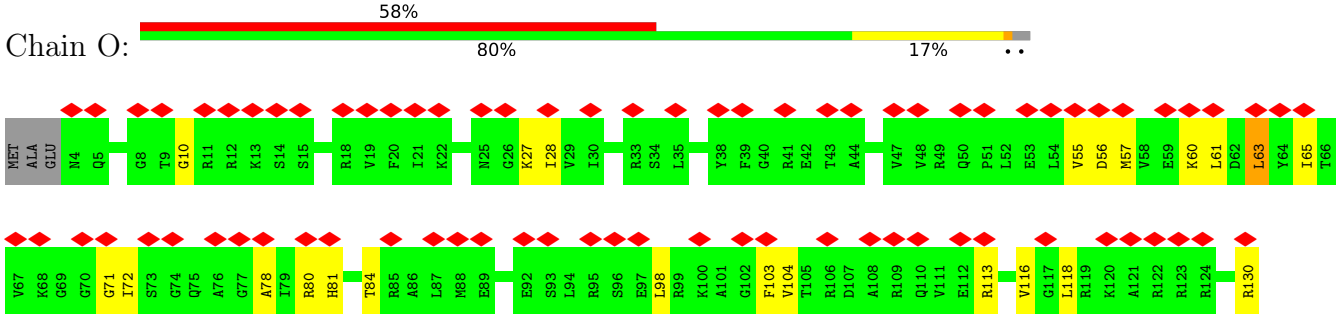
• Molecule 26: 30S ribosomal protein S8

Chain N:



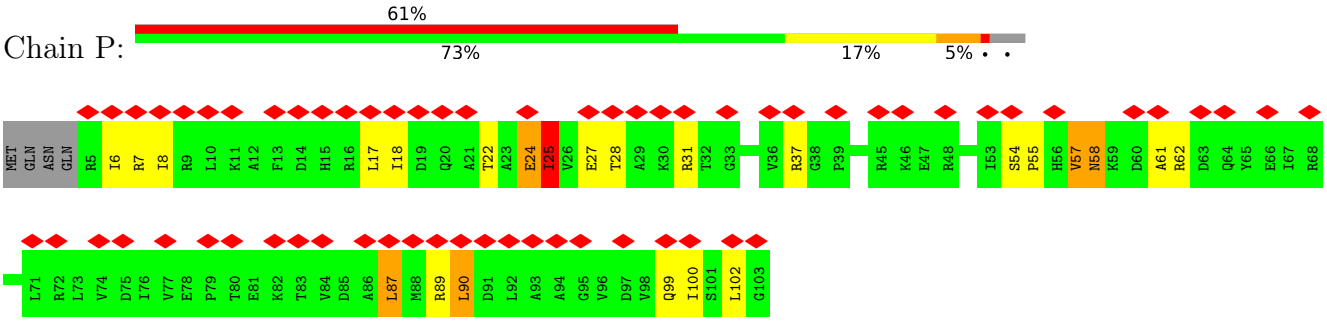
• Molecule 27: 30S ribosomal protein S9

Chain O:



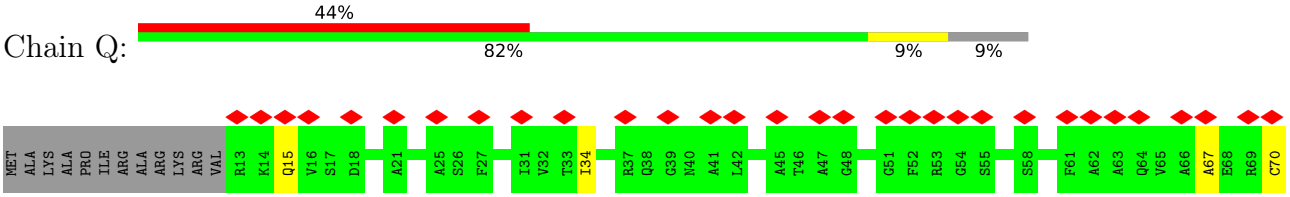
• Molecule 28: 30S ribosomal protein S10

Chain P:



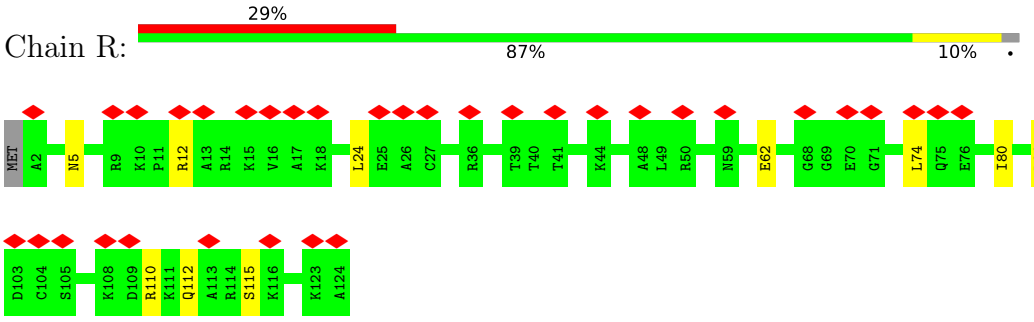
• Molecule 29: 30S ribosomal protein S11

Chain Q:



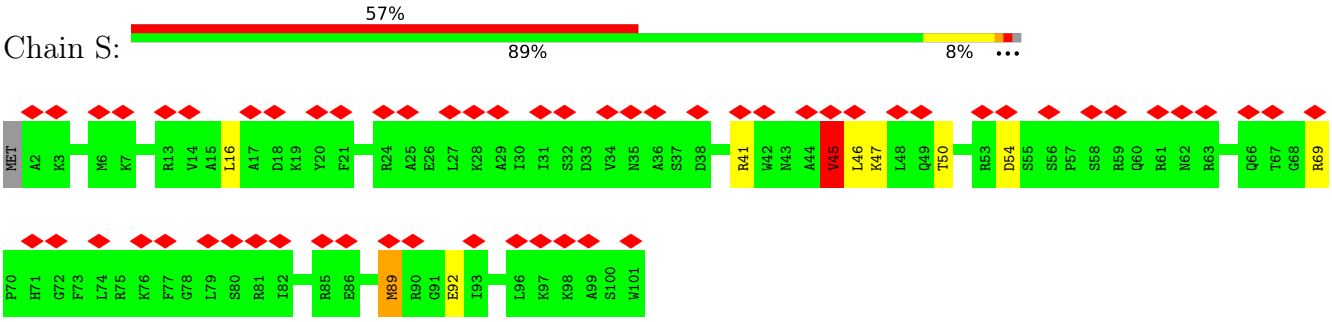
• Molecule 30: 30S ribosomal protein S12

Chain R:



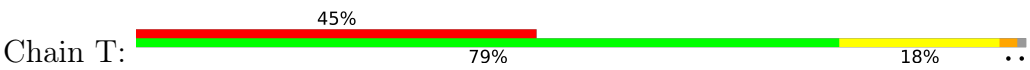
• Molecule 31: 30S ribosomal protein S14

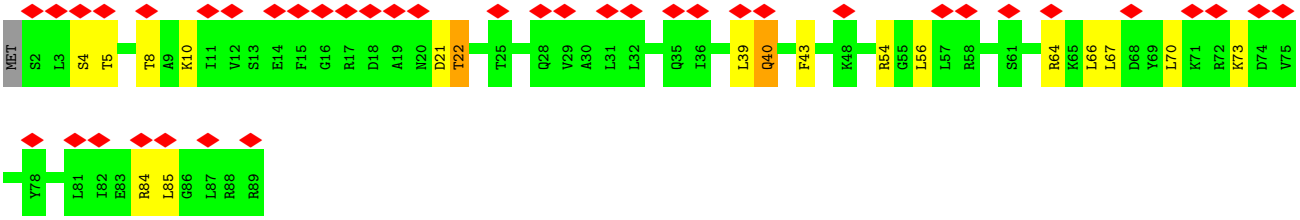
Chain S:



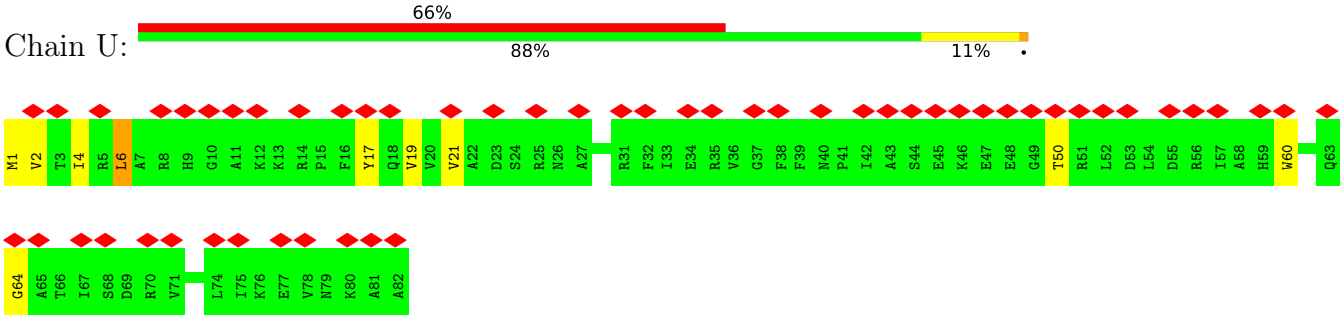
• Molecule 32: 30S ribosomal protein S15

Chain T:

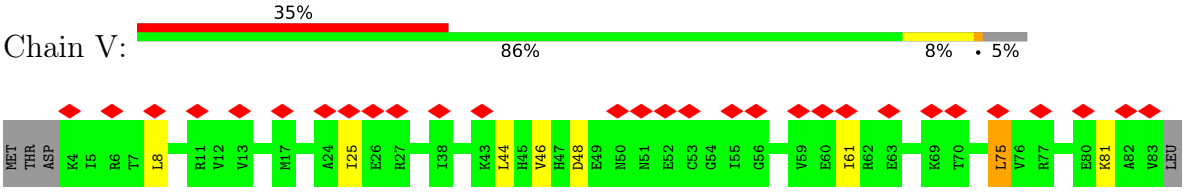




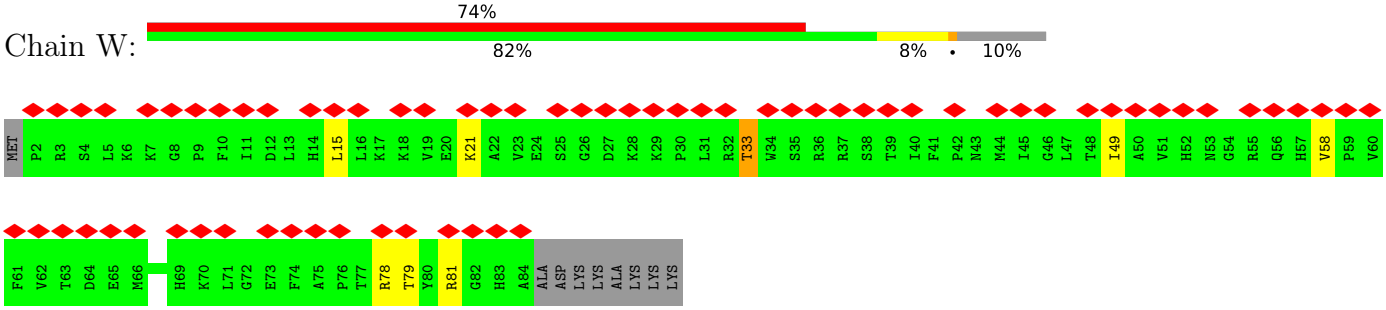
• Molecule 33: 30S ribosomal protein S16



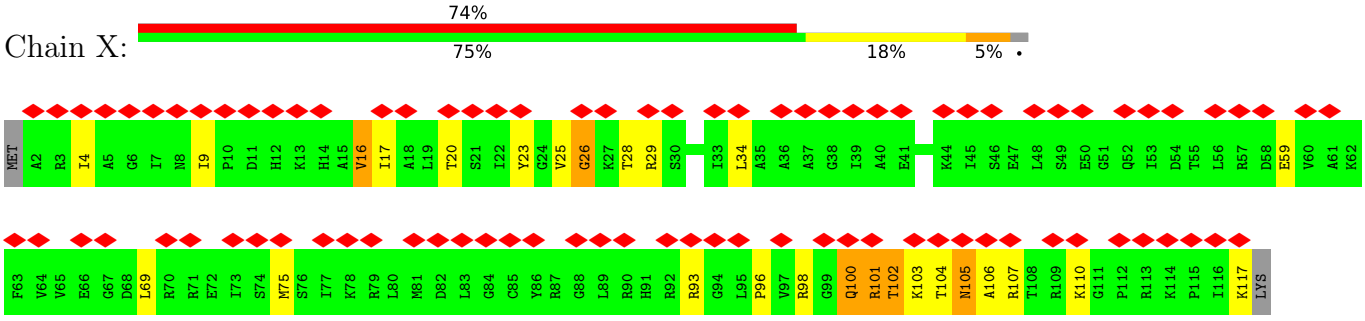
• Molecule 34: 30S ribosomal protein S17



• Molecule 35: 30S ribosomal protein S19



• Molecule 36: 30S ribosomal protein S13

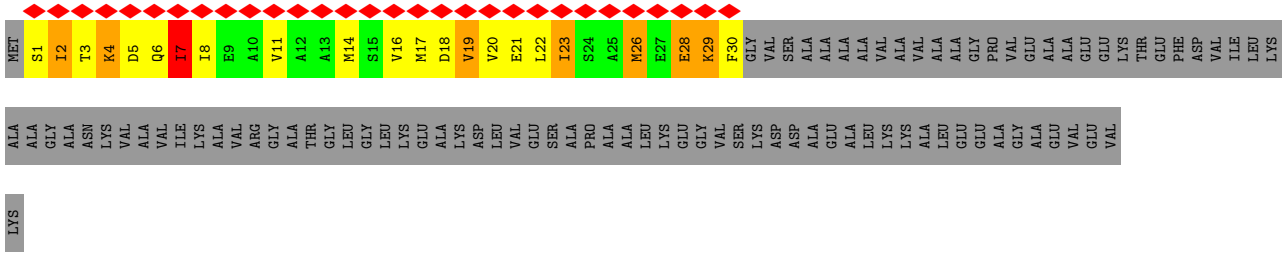


• Molecule 37: 50S ribosomal protein L11

Chain Y:

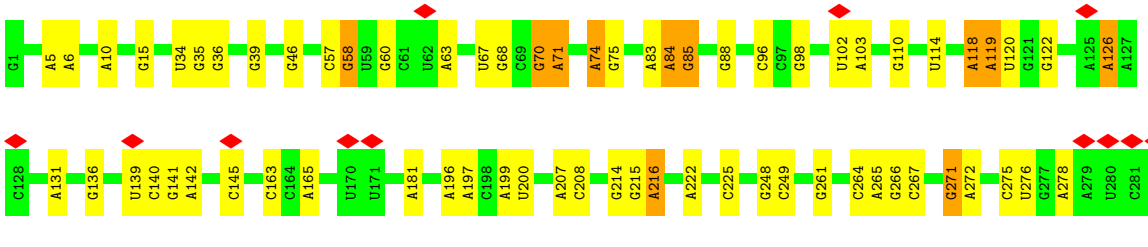
• Molecule 38: 50S ribosomal protein L7/L12

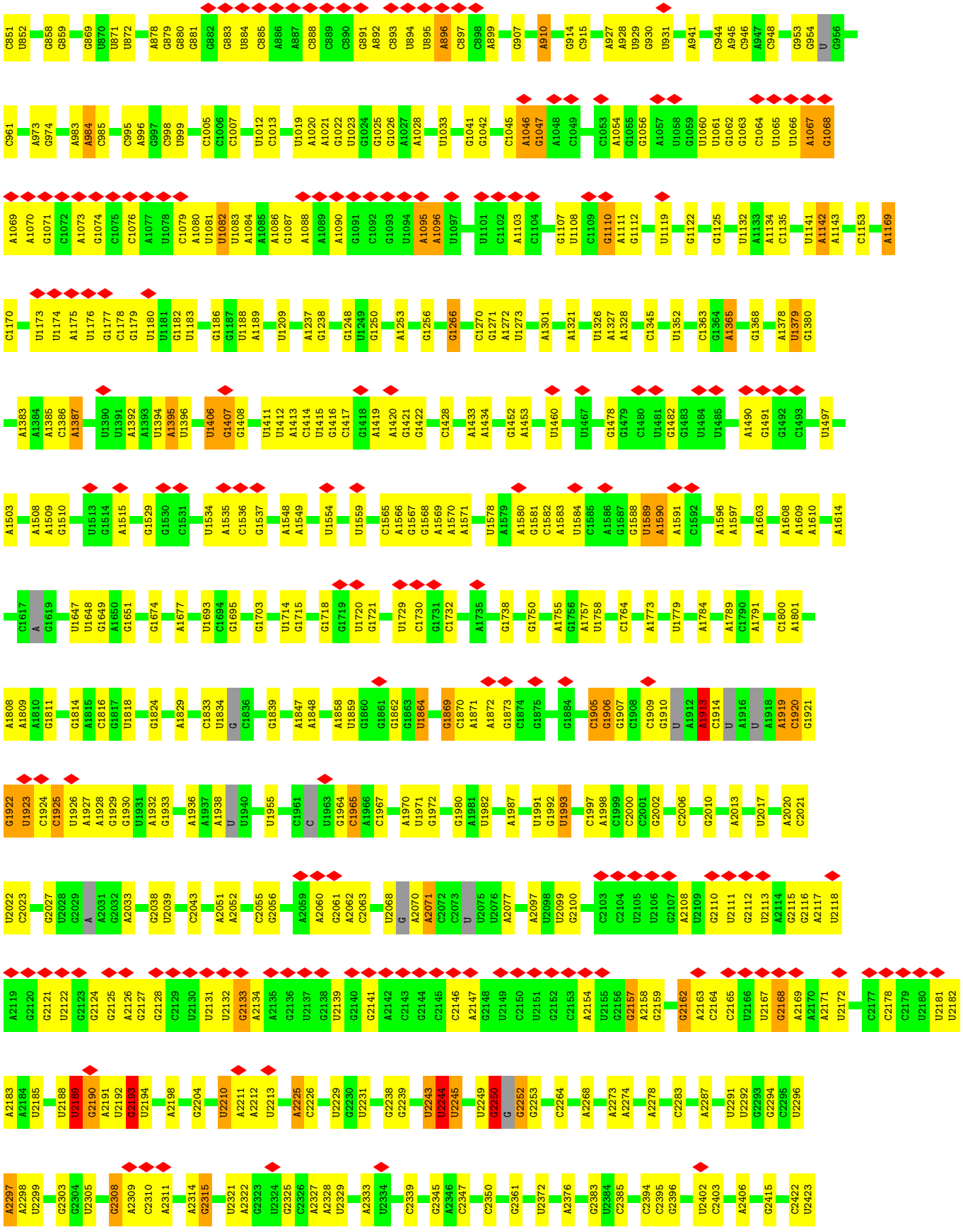
Chain Z:

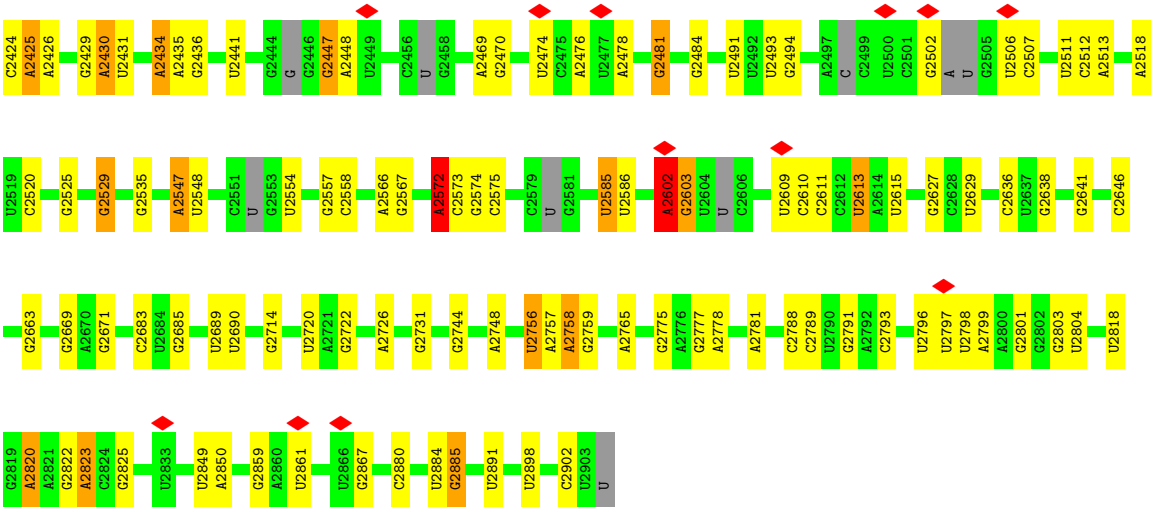


• Molecule 39: 23S rRNA

Chain a:

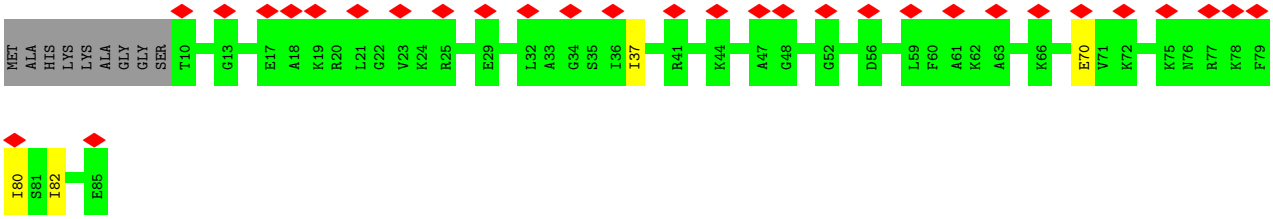






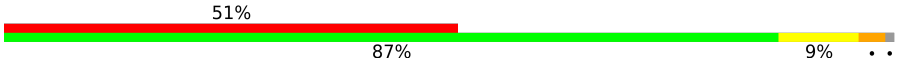
• Molecule 40: 50S ribosomal protein L27

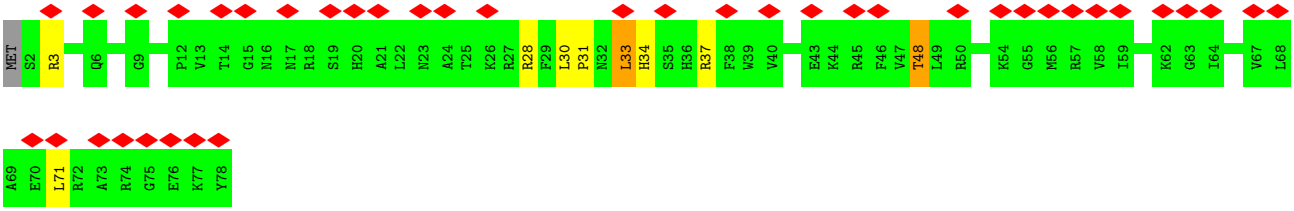
Chain b:



• Molecule 41: 50S ribosomal protein L28

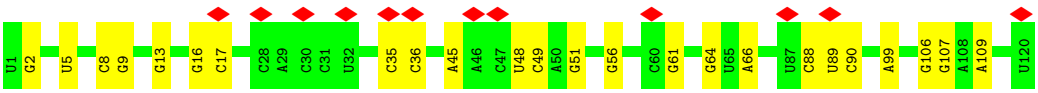
Chain c:





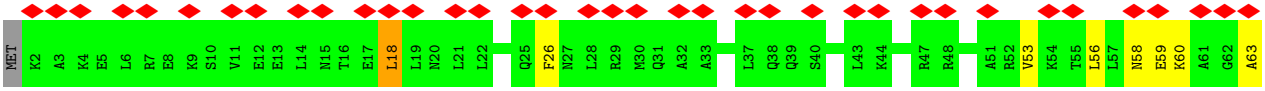
• Molecule 42: 5S rRNA

Chain d:

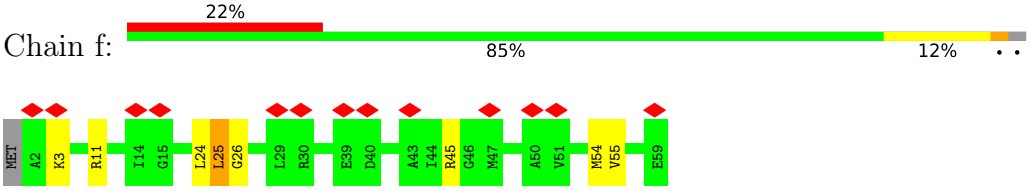


• Molecule 43: 50S ribosomal protein L29

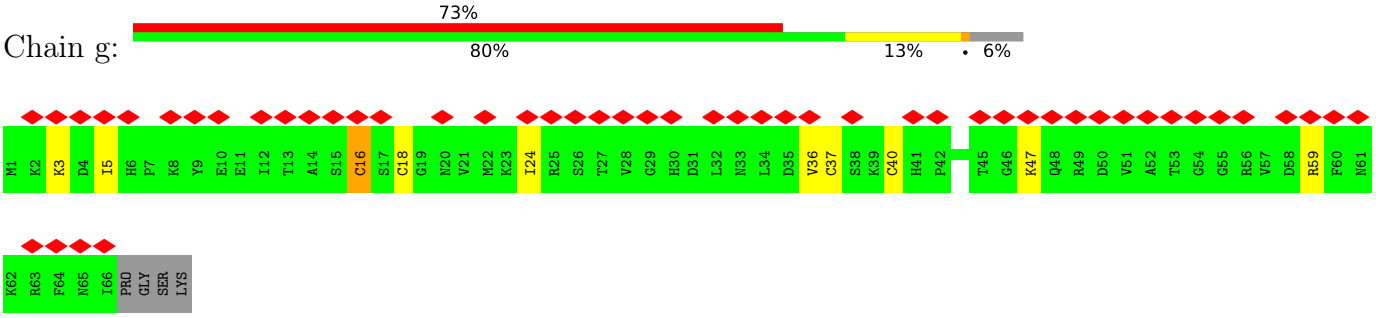
Chain e:



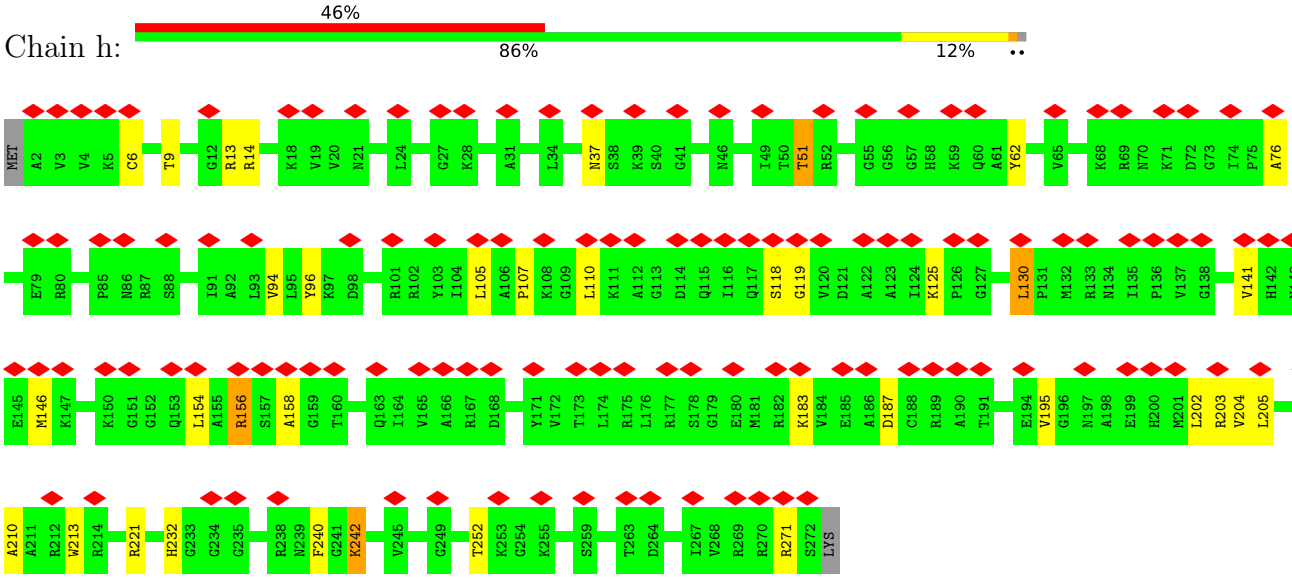
• Molecule 44: 50S ribosomal protein L30



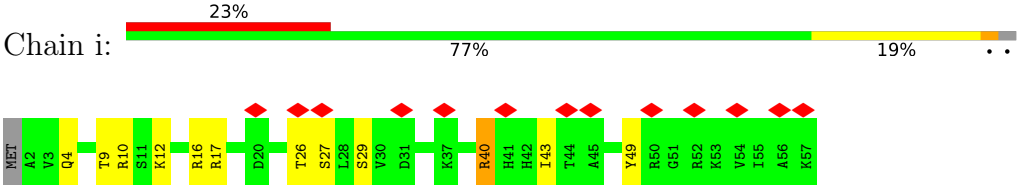
• Molecule 45: 50S ribosomal protein L31



• Molecule 46: 50S ribosomal protein L2

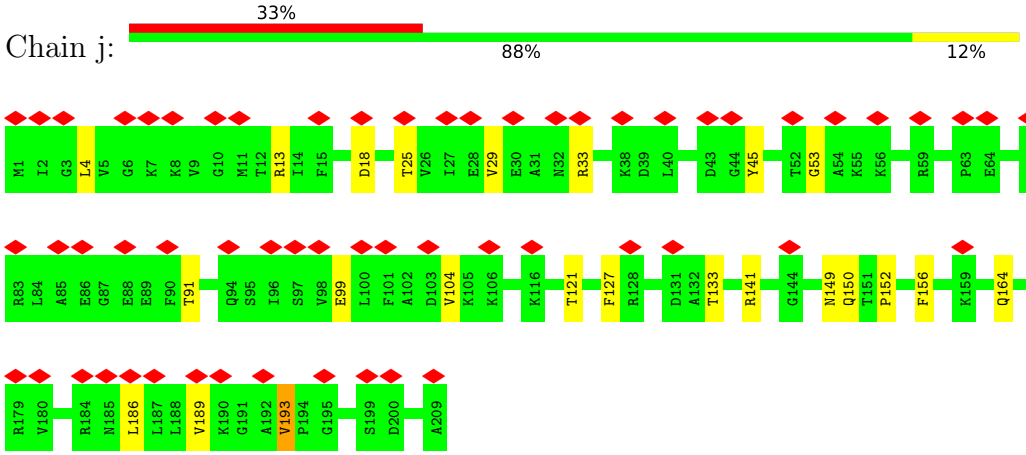


• Molecule 47: 50S ribosomal protein L32



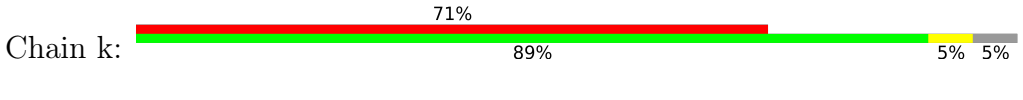
• Molecule 48: 50S ribosomal protein L3

Chain j:



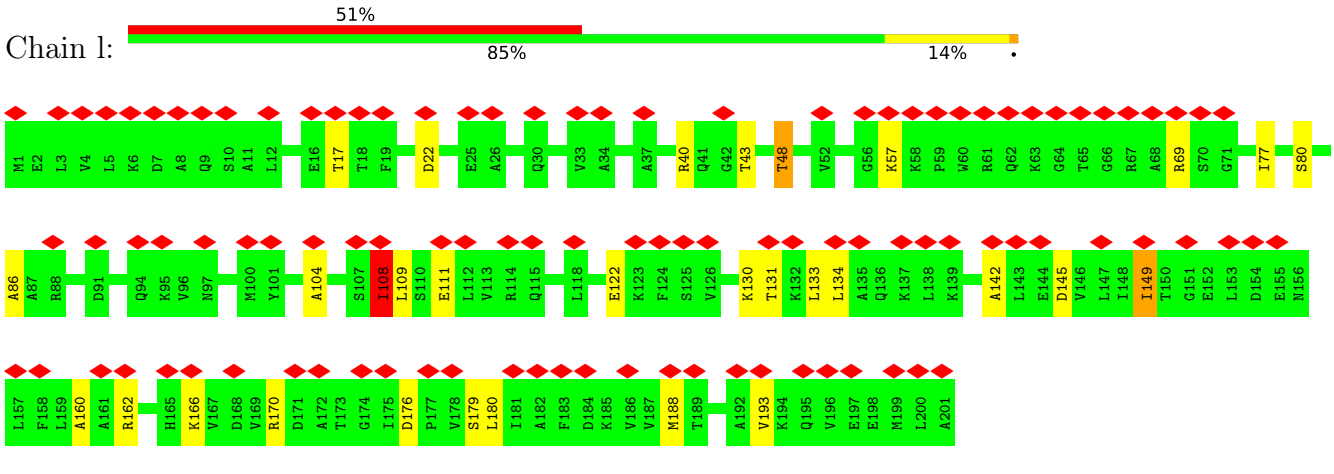
• Molecule 49: 50S ribosomal protein L33

Chain k:



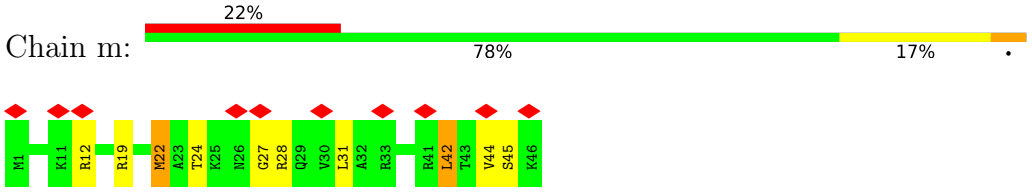
• Molecule 50: 50S ribosomal protein L4

Chain l:



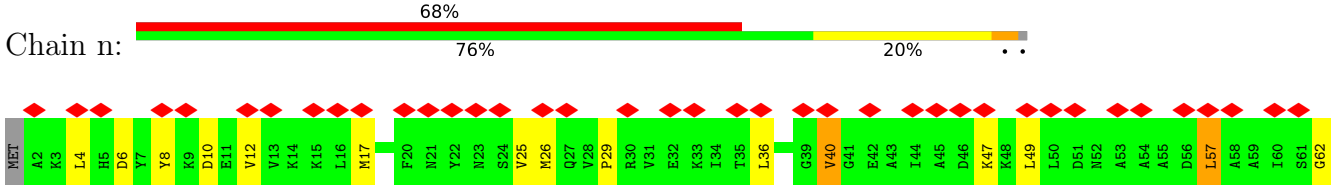
• Molecule 51: 50S ribosomal protein L34

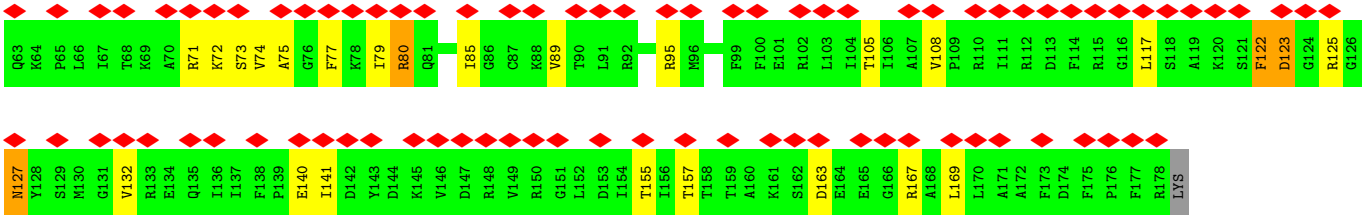
Chain m:



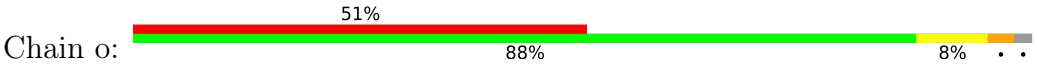
• Molecule 52: 50S ribosomal protein L5

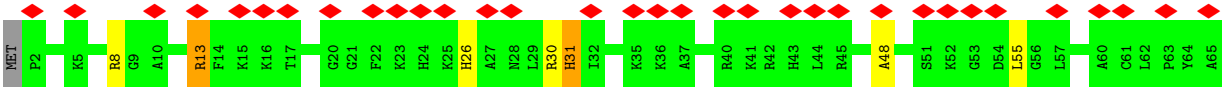
Chain n:



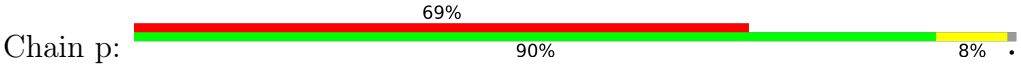


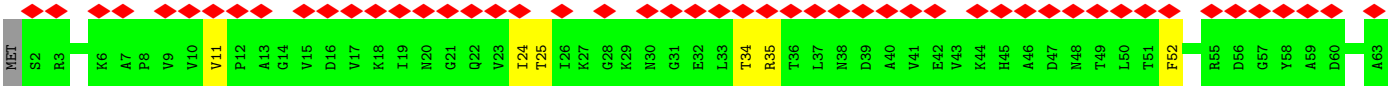
• Molecule 53: 50S ribosomal protein L35

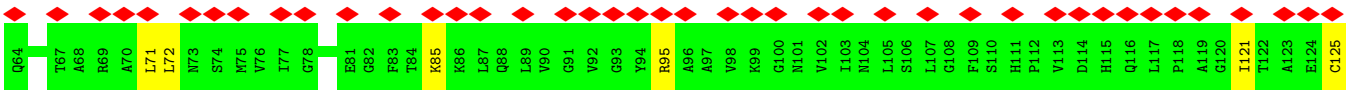


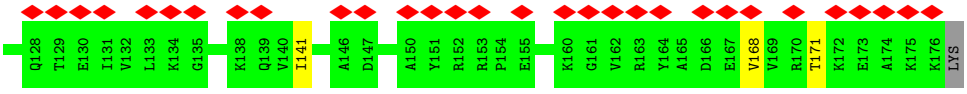


• Molecule 54: 50S ribosomal protein L6

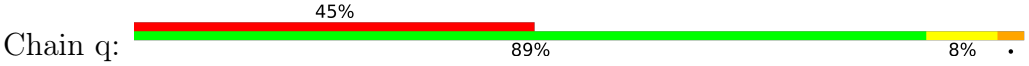


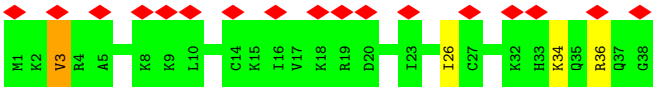




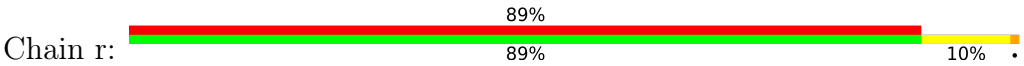


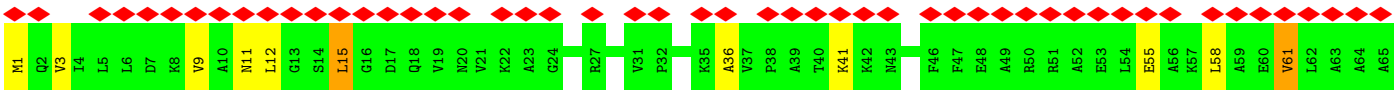
• Molecule 55: 50S ribosomal protein L36

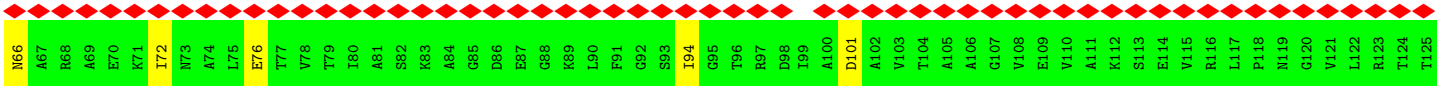


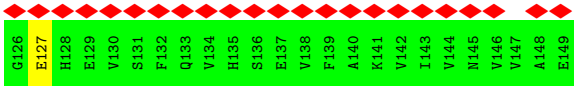


• Molecule 56: 50S ribosomal protein L9



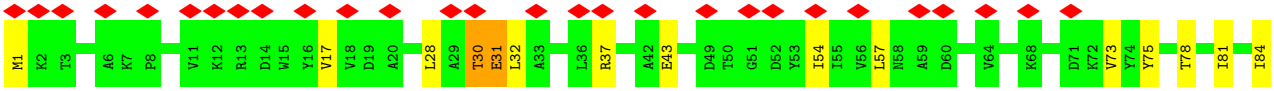


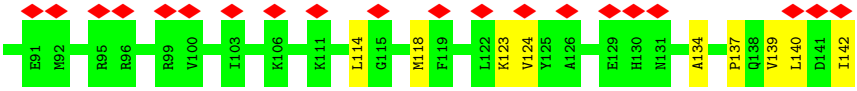




• Molecule 57: 50S ribosomal protein L13

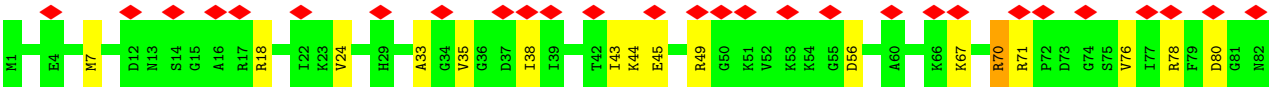
Chain s:

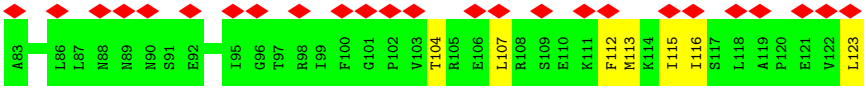




• Molecule 58: 50S ribosomal protein L14

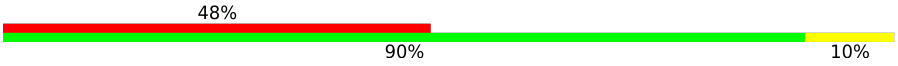
Chain t:

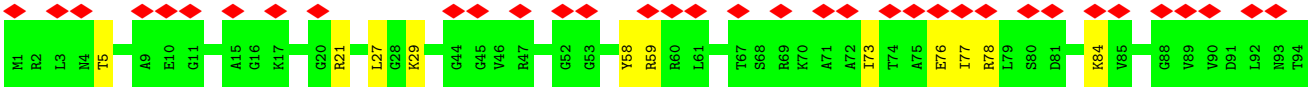


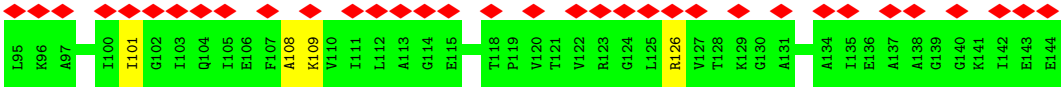


• Molecule 59: 50S ribosomal protein L15

Chain u:

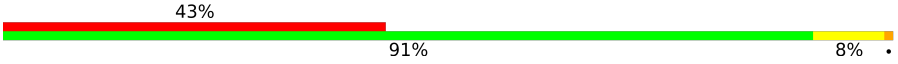


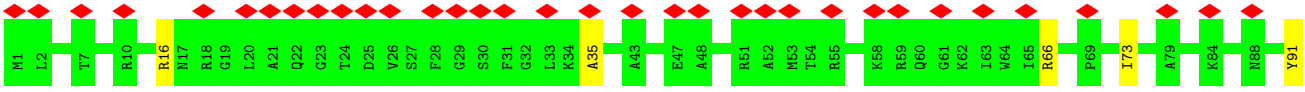


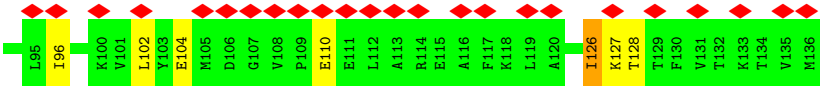


• Molecule 60: 50S ribosomal protein L16

Chain v:

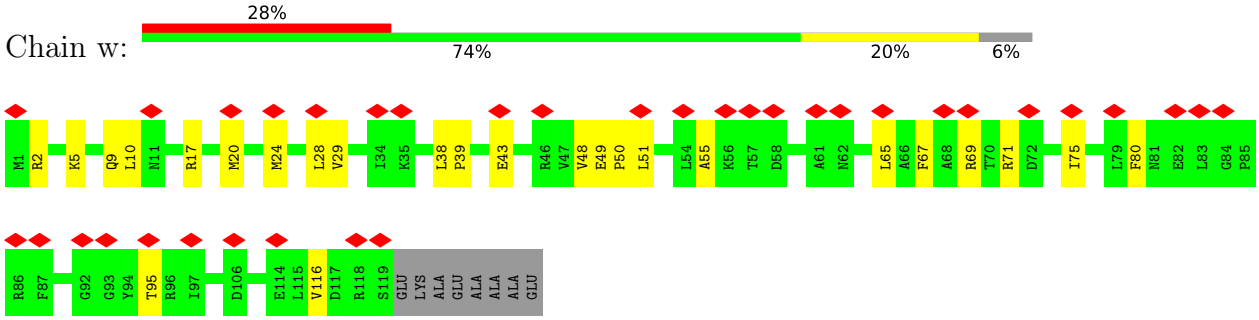






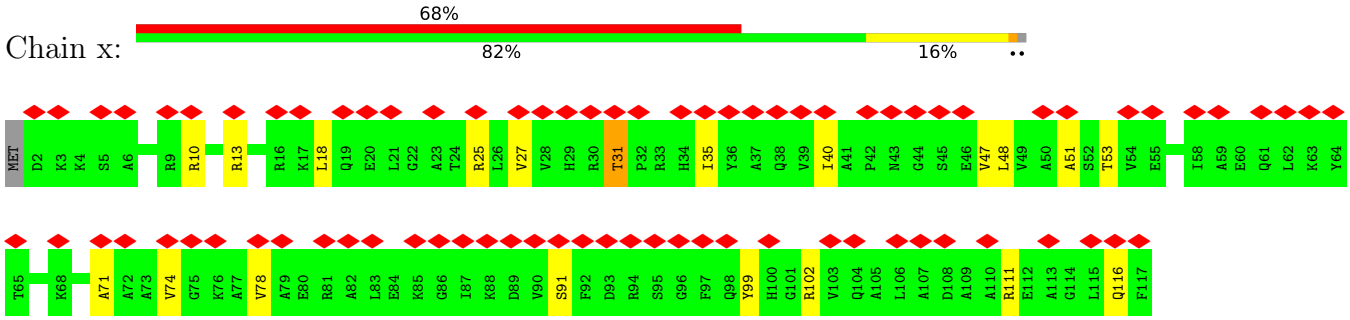
• Molecule 61: 50S ribosomal protein L17

Chain w:



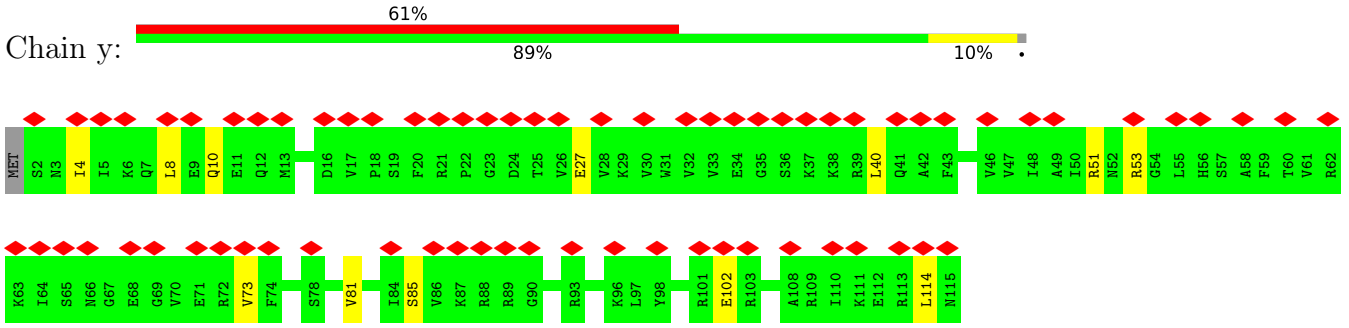
• Molecule 62: 50S ribosomal protein L18

Chain x:



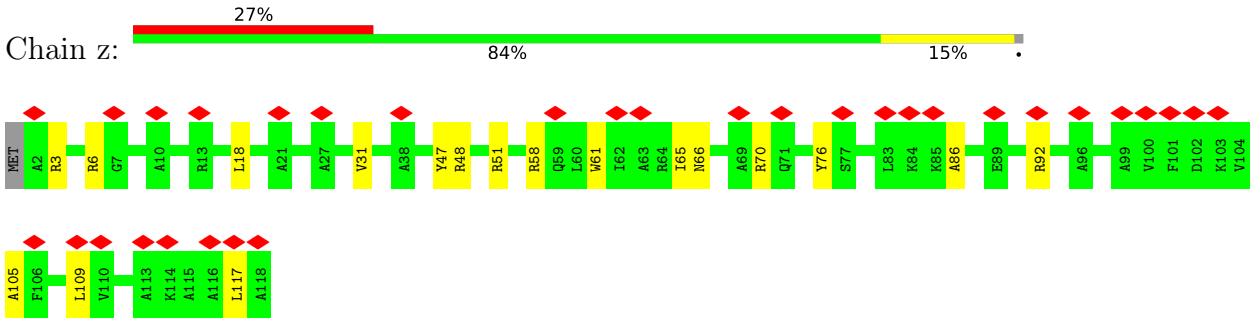
• Molecule 63: 50S ribosomal protein L19

Chain y:



• Molecule 64: 50S ribosomal protein L20

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24582	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	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	0.069	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.56	2/813 (0.2%)	0.80	2/1262 (0.2%)
9	9	1.15	2/1131 (0.2%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.67	12/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AB	0.43	1/808 (0.1%)	0.70	2/1088 (0.2%)
13	AC	0.60	4/1808 (0.2%)	0.73	9/2450 (0.4%)
13	AD	0.39	0/1789	0.55	0/2425
14	AE	0.54	9/10545 (0.1%)	0.74	23/14236 (0.2%)
15	C	0.66	0/553	1.14	2/743 (0.3%)
16	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.72	0/597	1.20	0/792
19	G	0.65	0/1791	1.08	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.58	0/1663	0.97	0/2241
22	J	0.63	0/1665	1.08	0/2227
23	K	0.64	1/1165 (0.1%)	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.68	0/1195	1.19	3/1602 (0.2%)
26	N	0.55	0/989	0.91	0/1326
27	O	0.58	0/1034	1.02	1/1375 (0.1%)
28	P	0.60	0/800	1.10	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.68	0/722	1.21	0/964
33	U	0.57	0/659	0.99	0/884
34	V	0.46	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	1.04	0/1046	1.09	1/1410 (0.1%)
38	Z	1.02	0/227	1.13	0/304
39	a	0.40	3/69247 (0.0%)	0.75	56/107985 (0.1%)
40	b	0.51	0/589	0.76	0/779
41	c	0.63	0/635	0.97	0/848
42	d	0.37	0/2872	0.69	0/4478
43	e	0.69	0/502	1.19	0/667
44	f	0.62	0/452	1.02	0/605
45	g	0.55	0/531	0.99	1/709 (0.1%)
46	h	0.54	0/2121	0.85	0/2852
47	i	0.52	0/450	0.94	0/599
48	j	0.60	0/1586	0.87	0/2134
49	k	0.47	0/433	0.80	0/576
50	l	0.61	0/1571	1.03	1/2113 (0.0%)
51	m	0.68	0/380	1.22	0/498
52	n	0.62	0/1434	1.18	10/1926 (0.5%)
53	o	0.64	0/513	1.10	1/676 (0.1%)
54	p	0.58	0/1333	0.89	0/1805
55	q	0.50	0/303	0.88	0/397
56	r	0.63	0/1122	0.97	1/1515 (0.1%)
57	s	0.68	0/1152	1.02	2/1551 (0.1%)
58	t	0.57	0/955	0.88	0/1279
59	u	0.55	0/1062	0.96	1/1413 (0.1%)
60	v	0.59	0/1093	0.97	0/1460
61	w	0.67	0/964	1.13	0/1289
62	x	0.61	0/902	1.09	0/1209
63	y	0.52	0/929	0.79	0/1242
64	z	0.80	0/960	1.25	0/1278
All	All	0.50	49/189246 (0.0%)	0.84	268/278938 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
14	AE	0	5
20	H	0	3
36	X	0	1
All	All	0	23

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.29	1.70	1.47
11	AA	374	GLU	C-N	17.43	1.53	1.33
11	AA	850	ILE	N-CA	-13.12	1.29	1.46
14	AE	93	THR	CA-C	12.23	1.69	1.52
20	H	169	SER	N-CA	11.82	1.61	1.46
16	D	1516	G	O3'-P	-10.68	1.45	1.61
14	AE	70	CYS	CA-CB	-8.66	1.41	1.53
16	D	1339	A	O3'-P	8.45	1.73	1.61
8	7	19	G	C1'-N9	-7.43	1.36	1.48
8	7	-13	U	C1'-N1	7.10	1.59	1.48
20	H	88	LYS	N-CA	7.04	1.55	1.46
6	5	109	DT	O3'-P	6.98	1.71	1.61
13	AC	76	GLU	N-CA	-6.92	1.37	1.46
16	D	145	G	O3'-P	6.72	1.71	1.61
16	D	196	A	O3'-P	6.64	1.71	1.61
20	H	168	VAL	C-N	6.39	1.42	1.33
16	D	1275	A	O3'-P	6.23	1.70	1.61
13	AC	75	GLN	CA-C	-6.14	1.45	1.53
39	a	2434	A	O3'-P	6.05	1.70	1.61
16	D	1515	G	O3'-P	-5.83	1.52	1.61
20	H	88	LYS	CA-C	5.78	1.60	1.52
14	AE	90	VAL	CA-C	5.76	1.60	1.52
16	D	1395	C	O3'-P	5.72	1.69	1.61
11	AA	885	GLY	C-O	-5.57	1.16	1.23
16	D	1490	U	O3'-P	5.49	1.69	1.61
7	6	10	DG	C1'-N9	-5.43	1.35	1.46
11	AA	604	HIS	ND1-CE1	5.37	1.38	1.32
39	a	1905	C	O3'-P	5.29	1.69	1.61
16	D	1492	A	O3'-P	5.27	1.69	1.61
11	AA	996	ARG	N-CA	-5.24	1.38	1.45
11	AA	1116	HIS	ND1-CE1	5.22	1.37	1.32
39	a	2167	U	O3'-P	5.21	1.69	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	AE	1350	ASN	CG-ND2	-5.21	1.22	1.33
13	AC	160	HIS	CD2-NE2	-5.21	1.32	1.37
11	AA	1116	HIS	CD2-NE2	-5.14	1.32	1.37
11	AA	1257	GLN	CD-OE1	5.14	1.33	1.23
11	AA	1157	GLN	CD-NE2	-5.14	1.22	1.33
14	AE	424	ASN	CG-ND2	-5.12	1.22	1.33
12	AB	81	HIS	ND1-CE1	5.12	1.37	1.32
9	9	129	LEU	C-N	5.11	1.45	1.33
14	AE	777	HIS	ND1-CE1	5.11	1.37	1.32
23	K	56	VAL	CA-CB	5.11	1.57	1.54
14	AE	1108	GLN	CD-OE1	5.10	1.33	1.23
14	AE	450	HIS	CD2-NE2	-5.10	1.32	1.37
11	AA	604	HIS	CD2-NE2	-5.08	1.32	1.37
11	AA	760	ASN	CG-ND2	-5.07	1.22	1.33
11	AA	1256	GLN	CD-OE1	5.07	1.33	1.23
14	AE	1268	ASN	CG-OD1	5.05	1.33	1.23
13	AC	41	ASN	CG-ND2	-5.00	1.22	1.33

All (268) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	D	1516	G	O3'-P-O5'	17.49	130.24	104.00
11	AA	727	VAL	N-CA-C	-17.18	95.10	110.74
20	H	88	LYS	CA-C-N	16.94	143.58	120.38
20	H	88	LYS	C-N-CA	16.94	143.58	120.38
10	B	29	G	C3'-C2'-O2'	15.97	134.66	110.70
9	9	129	LEU	CA-C-N	15.83	139.63	119.84
9	9	129	LEU	C-N-CA	15.83	139.63	119.84
16	D	1516	G	P-O3'-C3'	-15.54	96.89	120.20
11	AA	374	GLU	CA-C-N	15.04	135.87	120.38
11	AA	374	GLU	C-N-CA	15.04	135.87	120.38
11	AA	1250	SER	CA-C-N	14.90	149.53	123.01
11	AA	1250	SER	C-N-CA	14.90	149.53	123.01
20	H	332	VAL	N-CA-C	13.62	124.52	110.62
20	H	169	SER	N-CA-C	12.72	137.90	110.80
20	H	330	VAL	N-CA-C	12.18	126.92	109.51
20	H	305	HIS	N-CA-C	11.93	131.05	111.37
14	AE	90	VAL	N-CA-C	9.92	122.23	107.75
11	AA	995	ASP	O-C-N	-9.82	109.53	122.59
39	a	2244	U	C1'-C2'-O2'	-9.77	93.75	108.40
11	AA	375	PRO	CA-N-CD	-9.71	98.40	112.00
16	D	1206	G	C4'-C3'-O3'	9.57	127.36	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
52	n	73	SER	N-CA-CB	-9.56	94.60	110.47
11	AA	935	THR	CA-CB-OG1	-9.42	95.47	109.60
28	P	54	SER	CA-C-N	9.32	129.01	118.85
28	P	54	SER	C-N-CA	9.32	129.01	118.85
39	a	2250	G	C4'-C3'-O3'	-9.24	95.54	109.40
11	AA	376	PRO	N-CA-CB	-9.13	93.67	103.25
11	AA	943	LYS	CA-C-O	-9.00	107.64	120.51
16	D	1401	G	C4'-C3'-O3'	8.87	126.30	113.00
16	D	428	G	C4'-C3'-O3'	8.69	122.43	109.40
9	9	130	PRO	CA-N-CD	-8.62	99.94	112.00
8	7	-14	A	O3'-P-O5'	-8.60	91.10	104.00
20	H	339	ARG	CA-C-N	8.54	137.85	121.54
20	H	339	ARG	C-N-CA	8.54	137.85	121.54
16	D	1515	G	O3'-P-O5'	-8.47	91.29	104.00
31	S	45	VAL	N-CA-CB	8.43	120.41	110.55
39	a	2296	U	C4'-C3'-O3'	8.42	122.02	109.40
11	AA	375	PRO	N-CA-C	8.38	120.93	110.70
39	a	404	A	C2'-C3'-O3'	8.36	122.04	109.50
8	7	-11	U	C2'-C3'-O3'	8.34	122.00	109.50
11	AA	849	GLU	CA-C-N	8.34	136.98	121.97
11	AA	849	GLU	C-N-CA	8.34	136.98	121.97
28	P	57	VAL	N-CA-C	8.28	120.03	107.77
16	D	197	A	C2'-C3'-O3'	8.19	121.79	109.50
39	a	2252	G	N9-C1'-C2'	-8.15	99.78	112.00
11	AA	1048	LYS	CA-C-N	-8.02	115.35	122.96
11	AA	1048	LYS	C-N-CA	-8.02	115.35	122.96
16	D	1401	G	N9-C1'-C2'	-7.96	100.06	112.00
11	AA	855	PRO	N-CA-CB	-7.83	95.03	103.25
39	a	2425	A	C2'-C3'-O3'	7.83	121.24	109.50
20	H	155	LYS	CA-C-N	-7.80	110.89	121.66
20	H	155	LYS	C-N-CA	-7.80	110.89	121.66
39	a	2071	A	C4'-C3'-O3'	-7.74	101.39	113.00
20	H	168	VAL	CA-C-N	7.66	136.17	121.54
20	H	168	VAL	C-N-CA	7.66	136.17	121.54
20	H	52	GLN	N-CA-C	-7.64	104.10	113.50
16	D	1493	A	C2'-C3'-O3'	7.63	125.14	113.70
20	H	84	LEU	N-CA-C	7.63	121.00	110.24
52	n	75	ALA	CA-C-N	7.60	129.65	120.14
52	n	75	ALA	C-N-CA	7.60	129.65	120.14
14	AE	903	LEU	CA-C-N	7.60	136.06	121.54
14	AE	903	LEU	C-N-CA	7.60	136.06	121.54
16	D	1499	A	N9-C1'-C2'	-7.60	100.61	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	D	1339	A	P-O3'-C3'	7.58	131.57	120.20
36	X	102	THR	CB-CA-C	7.55	123.38	110.84
23	K	60	ILE	N-CA-CB	7.54	119.37	110.55
16	D	528	C	N1-C1'-C2'	-7.51	100.73	112.00
11	AA	864	LYS	N-CA-C	-7.47	102.39	112.26
20	H	336	ASP	CB-CA-C	-7.46	98.63	110.79
52	n	108	VAL	O-C-N	7.41	125.33	120.07
23	K	56	VAL	O-C-N	7.41	125.16	120.42
52	n	73	SER	CB-CA-C	7.40	122.86	110.79
10	B	28	C	P-O3'-C3'	7.38	131.26	120.20
39	a	2602	A	C4'-C3'-O3'	7.29	120.34	109.40
39	a	783	A	C4'-C3'-O3'	7.26	123.89	113.00
11	AA	751	TYR	CA-C-N	7.24	132.22	121.72
11	AA	751	TYR	C-N-CA	7.24	132.22	121.72
19	G	47	VAL	O-C-N	7.21	125.04	120.42
10	B	29	G	N9-C1'-C2'	-7.17	101.25	112.00
16	D	1497	G	C1'-C2'-O2'	-7.15	97.68	108.40
16	D	196	A	P-O3'-C3'	7.14	130.92	120.20
11	AA	375	PRO	CB-CA-C	-7.13	102.22	110.92
39	a	2162	G	C4'-C3'-O3'	7.12	120.08	109.40
39	a	896	A	C4'-C3'-O3'	7.00	119.91	109.40
25	M	27	VAL	N-CA-CB	7.00	118.74	110.55
39	a	1379	U	C2'-C3'-O3'	6.98	124.16	113.70
39	a	2225	A	C4'-C3'-O3'	6.96	119.84	109.40
39	a	2244	U	C4'-C3'-O3'	6.89	123.33	113.00
20	H	140	PRO	N-CA-CB	6.85	110.44	103.25
20	H	340	ARG	CA-C-N	-6.80	112.55	123.23
20	H	340	ARG	C-N-CA	-6.80	112.55	123.23
11	AA	604	HIS	CB-CG-CD2	-6.79	122.37	131.20
11	AA	728	ASP	N-CA-C	6.79	125.26	110.80
13	AC	160	HIS	CB-CG-CD2	-6.79	122.38	131.20
39	a	2252	G	C4'-C3'-O3'	6.76	123.14	113.00
52	n	71	ARG	CA-C-N	6.75	133.99	122.37
52	n	71	ARG	C-N-CA	6.75	133.99	122.37
11	AA	855	PRO	CB-CA-C	-6.69	100.52	111.56
39	a	2243	U	C4'-C3'-O3'	6.67	123.01	113.00
16	D	517	G	C5'-C4'-C3'	6.66	125.19	115.20
20	H	170	ARG	N-CA-C	6.63	119.60	110.24
20	H	87	GLU	N-CA-C	-6.63	104.06	111.28
20	H	303	LEU	N-CA-C	6.62	121.19	112.13
13	AC	117	HIS	CB-CA-C	-6.61	97.94	109.64
39	a	2189	U	C1'-C2'-O2'	-6.59	101.91	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	AA	1116	HIS	CB-CG-CD2	-6.58	122.65	131.20
20	H	132	PRO	N-CA-CB	6.55	110.25	103.38
27	O	72	ILE	N-CA-C	-6.55	105.33	111.48
16	D	526	C	C4'-C3'-O3'	6.54	122.81	113.00
39	a	894	U	C2'-C3'-O3'	6.53	119.29	109.50
20	H	155	LYS	N-CA-C	-6.52	98.28	108.90
39	a	2167	U	P-O3'-C3'	6.52	129.98	120.20
52	n	127	ASN	CB-CA-C	6.52	121.65	110.77
20	H	112	ILE	N-CA-C	6.51	117.06	106.72
56	r	61	VAL	N-CA-CB	6.48	118.14	110.55
16	D	1340	A	C1'-C2'-O2'	6.47	118.11	108.40
16	D	526	C	N1-C1'-C2'	-6.47	102.30	112.00
53	o	13	ARG	N-CA-C	6.46	120.99	113.18
52	n	127	ASN	CA-CB-CG	-6.44	106.16	112.60
12	AB	81	HIS	CB-CG-CD2	-6.41	122.86	131.20
14	AE	450	HIS	CB-CG-CD2	-6.41	122.87	131.20
39	a	754	U	N1-C1'-C2'	6.41	121.61	112.00
13	AC	23	HIS	CB-CG-CD2	-6.40	122.88	131.20
14	AE	61	ILE	CA-C-N	-6.37	114.00	121.64
14	AE	61	ILE	C-N-CA	-6.37	114.00	121.64
14	AE	93	THR	CA-C-N	6.35	133.00	121.06
14	AE	93	THR	C-N-CA	6.35	133.00	121.06
16	D	69	G	C4'-C3'-O3'	-6.33	103.51	113.00
16	D	1208	C	N1-C1'-C2'	-6.30	102.55	112.00
11	AA	150	HIS	CB-CG-CD2	-6.28	123.04	131.20
14	AE	777	HIS	CB-CG-CD2	-6.27	123.05	131.20
39	a	2434	A	P-O3'-C3'	6.26	129.59	120.20
11	AA	888	THR	CB-CA-C	-6.25	99.35	108.91
20	H	153	GLU	N-CA-C	-6.23	97.52	110.80
15	C	33	ILE	CA-C-O	-6.23	114.95	121.93
11	AA	850	ILE	N-CA-CB	6.21	121.48	111.23
39	a	2425	A	C4'-C3'-O3'	6.21	118.71	109.40
10	B	28	C	O3'-P-O5'	-6.20	94.71	104.00
16	D	1206	G	N9-C1'-C2'	-6.15	102.78	112.00
14	AE	70	CYS	CB-CA-C	6.12	120.33	110.29
20	H	113	ASN	N-CA-C	6.11	118.02	111.36
11	AA	861	ALA	CA-C-N	6.10	133.19	121.54
11	AA	861	ALA	C-N-CA	6.10	133.19	121.54
16	D	1516	G	OP1-P-O3'	-6.06	89.82	108.00
39	a	271	G	C4'-C3'-O3'	6.05	118.48	109.40
11	AA	869	GLY	CA-C-O	-6.05	117.74	122.52
11	AA	1004	ASP	CB-CA-C	6.02	122.40	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
39	a	2820	A	C4'-C3'-O3'	-6.00	104.00	113.00
16	D	1408	A	C4'-C3'-O3'	5.99	121.98	113.00
39	a	2210	U	C4'-C3'-O3'	5.99	118.38	109.40
16	D	550	G	C3'-C2'-O2'	5.96	119.65	110.70
13	AC	74	VAL	N-CA-C	5.96	117.42	108.96
39	a	1913	A	C2'-C3'-O3'	5.96	118.44	109.50
14	AE	90	VAL	CA-C-O	-5.95	114.20	120.39
13	AC	75	GLN	N-CA-CB	5.94	119.39	110.19
25	M	92	ARG	CA-C-N	5.89	125.37	119.24
25	M	92	ARG	C-N-CA	5.89	125.37	119.24
11	AA	604	HIS	CB-CG-ND1	5.88	131.51	122.70
39	a	2308	G	C2'-C3'-O3'	-5.87	104.90	113.70
20	H	150	LYS	N-CA-C	5.85	118.25	110.53
20	H	109	THR	N-CA-C	-5.85	99.12	109.06
50	l	108	ILE	N-CA-CB	5.83	118.47	110.54
39	a	1905	C	P-O3'-C3'	5.82	128.93	120.20
11	AA	732	ILE	CB-CA-C	-5.82	103.59	111.15
52	n	72	LYS	N-CA-C	-5.82	99.17	109.06
39	a	2756	U	C4'-C3'-O3'	5.81	118.12	109.40
10	B	29	G	O5'-C5'-C4'	-5.81	102.78	111.50
11	AA	1116	HIS	CB-CG-ND1	5.81	131.41	122.70
13	AC	76	GLU	N-CA-C	-5.80	101.70	110.28
11	AA	936	ARG	CA-C-O	-5.79	114.04	120.70
36	X	26	GLY	N-CA-C	-5.79	104.37	112.13
20	H	75	VAL	N-CA-C	5.79	116.45	108.12
39	a	70	G	C4'-C3'-O3'	5.78	118.07	109.40
16	D	1275	A	P-O3'-C3'	5.78	128.87	120.20
14	AE	91	GLU	N-CA-C	5.76	123.08	110.80
13	AC	160	HIS	CB-CG-ND1	5.74	131.31	122.70
10	A	48	C	N1-C1'-C2'	5.74	120.61	112.00
16	D	1490	U	P-O3'-C3'	5.73	128.79	120.20
16	D	976	G	C4'-C3'-O3'	-5.71	104.44	113.00
16	D	1406	U	N1-C1'-C2'	-5.71	103.44	112.00
39	a	2168	G	C4'-C3'-O3'	-5.70	104.45	113.00
16	D	1340	A	C5'-C4'-C3'	5.69	124.54	116.00
10	B	48	C	N1-C1'-C2'	5.69	120.54	112.00
16	D	1492	A	P-O3'-C3'	5.68	128.73	120.20
39	a	2017	U	C2'-C3'-O3'	-5.66	105.20	113.70
39	a	1757	A	C4'-C3'-O3'	-5.66	104.51	113.00
11	AA	996	ARG	N-CA-C	-5.64	101.23	109.63
20	H	114	GLY	N-CA-C	5.61	121.23	111.14
12	AB	81	HIS	CB-CG-ND1	5.60	131.10	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	AC	23	HIS	CB-CG-ND1	5.55	131.03	122.70
11	AA	942	ASP	N-CA-C	-5.55	106.67	113.50
14	AE	450	HIS	CB-CG-ND1	5.55	131.02	122.70
16	D	780	A	C4'-C3'-O3'	-5.54	104.69	113.00
11	AA	853	ASP	CA-C-N	5.53	130.32	120.70
11	AA	853	ASP	C-N-CA	5.53	130.32	120.70
39	a	1568	G	C4'-C3'-O3'	-5.53	104.71	113.00
11	AA	940	GLU	CA-C-O	-5.52	112.62	120.51
39	a	2447	G	C2'-C3'-O3'	-5.51	101.23	109.50
39	a	2731	G	C4'-C3'-O3'	-5.49	104.76	113.00
11	AA	872	TYR	CA-C-N	5.45	131.78	121.97
11	AA	872	TYR	C-N-CA	5.45	131.78	121.97
11	AA	150	HIS	CB-CG-ND1	5.45	130.87	122.70
11	AA	375	PRO	N-CA-CB	5.40	108.32	103.08
16	D	1145	A	C4'-C3'-O3'	-5.40	104.90	113.00
16	D	1499	A	C4'-C3'-O3'	5.40	121.09	113.00
39	a	2572	A	C4'-C3'-O3'	-5.40	101.31	109.40
14	AE	93	THR	CB-CA-C	5.39	121.16	110.42
14	AE	69	GLU	CA-C-N	-5.37	113.93	121.72
14	AE	69	GLU	C-N-CA	-5.37	113.93	121.72
16	D	864	A	N9-C1'-C2'	5.37	120.06	112.00
39	a	944	C	C4'-C3'-O3'	-5.37	104.95	113.00
39	a	375	G	C2'-C3'-O3'	5.37	121.75	113.70
16	D	517	G	C4'-C3'-O3'	-5.36	101.36	109.40
14	AE	777	HIS	CB-CG-ND1	5.36	130.74	122.70
10	B	35	A	P-O3'-C3'	5.36	128.24	120.20
39	a	2068	U	C4'-C3'-O3'	-5.36	104.96	113.00
39	a	2481	G	C4'-C3'-O3'	-5.35	104.97	113.00
16	D	145	G	P-O3'-C3'	5.33	128.19	120.20
39	a	2231	U	C1'-C2'-O2'	5.33	116.39	108.40
14	AE	70	CYS	N-CA-C	-5.31	101.12	109.25
45	g	5	ILE	N-CA-C	5.31	117.68	111.05
11	AA	1158	LYS	CA-C-N	5.30	131.52	121.97
11	AA	1158	LYS	C-N-CA	5.30	131.52	121.97
39	a	1270	C	C2'-C3'-O3'	-5.30	105.75	113.70
39	a	2529	G	C4'-C3'-O3'	-5.29	105.06	113.00
39	a	2020	A	C4'-C3'-O3'	-5.27	105.09	113.00
14	AE	73	GLY	N-CA-C	5.27	125.67	113.18
36	X	102	THR	CA-C-O	-5.26	114.87	121.02
11	AA	732	ILE	N-CA-CB	5.26	116.26	110.53
11	AA	1030	GLU	N-CA-C	-5.25	105.23	111.69
14	AE	90	VAL	O-C-N	-5.24	117.64	123.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	D	1395	C	P-O3'-C3'	5.24	128.05	120.20
11	AA	934	PHE	N-CA-C	-5.21	103.78	111.81
37	Y	5	GLN	O-C-N	5.21	124.69	120.83
11	AA	870	ILE	CA-C-N	5.19	128.27	120.69
11	AA	870	ILE	C-N-CA	5.19	128.27	120.69
14	AE	88	CYS	N-CA-C	5.19	120.26	113.88
39	a	423	A	C2'-C3'-O3'	-5.19	105.91	113.70
39	a	2245	U	N1-C1'-C2'	-5.18	104.23	112.00
10	B	60	U	C2'-C3'-O3'	5.18	117.27	109.50
20	H	128	ARG	CA-C-N	-5.18	114.11	122.81
20	H	128	ARG	C-N-CA	-5.18	114.11	122.81
10	A	60	U	C2'-C3'-O3'	5.16	117.24	109.50
39	a	1834	U	C4'-C3'-O3'	-5.15	105.27	113.00
20	H	154	PHE	N-CA-C	-5.14	100.32	109.06
39	a	528	A	C4'-C3'-O3'	-5.14	105.28	113.00
59	u	101	ILE	N-CA-C	5.14	116.43	112.12
16	D	1335	U	C4'-C3'-O3'	-5.13	105.30	113.00
39	a	328	U	C4'-C3'-O3'	-5.10	105.35	113.00
39	a	479	A	C4'-C3'-O3'	5.10	117.05	109.40
28	P	25	ILE	N-CA-CB	5.09	117.46	110.54
14	AE	61	ILE	CA-C-O	-5.09	115.66	120.95
15	C	35	GLU	N-CA-C	-5.07	105.94	111.82
39	a	126	A	C4'-C3'-O3'	-5.07	105.39	113.00
39	a	1864	U	C4'-C3'-O3'	-5.07	105.39	113.00
57	s	28	LEU	CA-C-N	5.07	127.03	120.44
57	s	28	LEU	C-N-CA	5.07	127.03	120.44
9	9	115	GLY	CA-C-O	-5.06	118.19	122.29
14	AE	1184	ASP	N-CA-C	5.06	121.00	109.81
39	a	2193	G	C2'-C3'-O3'	5.05	121.28	113.70
11	AA	943	LYS	N-CA-C	5.05	121.55	110.80
13	AC	117	HIS	N-CA-C	5.04	116.80	110.24
20	H	108	VAL	N-CA-C	-5.04	98.86	109.34
10	B	19	G	N9-C1'-C2'	5.04	119.56	112.00
11	AA	377	THR	CA-C-N	5.03	126.98	120.44
11	AA	377	THR	C-N-CA	5.03	126.98	120.44
39	a	614	A	C2'-C3'-O3'	5.03	117.04	109.50
39	a	1025	G	C4'-C3'-O3'	5.02	116.93	109.40

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	1134	GLN	Peptide
11	AA	1157	GLN	Peptide
11	AA	1158	LYS	Peptide
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide
11	AA	595	THR	Peptide
11	AA	596	ASP	Mainchain
11	AA	696	ASP	Peptide
11	AA	746	ALA	Peptide
11	AA	853	ASP	Mainchain
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
10	B	19	G	Sidechain
10	B	7	G	Sidechain
20	H	274	TYR	Peptide
20	H	81	GLU	Peptide
20	H	82	THR	Peptide
36	X	100	GLN	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	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	10	0
5	4	753	780	780	0	0
6	5	472	260	261	24	0
7	6	542	305	306	23	0
8	7	732	97	362	85	0
9	9	1117	0	1153	163	0
10	A	1620	826	826	173	0
10	B	1620	813	827	139	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	AA	10425	10426	10428	398	0
12	AB	790	783	783	8	0
13	AC	1786	1813	1813	90	0
13	AD	1767	1789	1789	47	0
14	AE	10388	10612	10611	368	0
15	C	544	559	560	23	0
16	D	32703	16423	16459	222	0
17	E	669	719	719	4	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	212	0
21	I	1636	1710	1710	53	0
22	J	1643	1707	1707	31	0
23	K	1152	1196	1196	32	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	32	0
26	N	979	1031	1031	6	0
27	O	1022	1070	1070	11	0
28	P	790	831	831	52	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	7	0
31	S	805	844	844	5	0
32	T	714	734	734	8	0
33	U	649	666	666	3	0
34	V	648	691	691	5	0
35	W	663	688	688	2	0
36	X	900	964	964	58	0
37	Y	1032	0	1088	81	0
38	Z	227	0	237	19	0
39	a	61841	31077	31123	301	0
40	b	582	599	599	2	0
41	c	625	652	652	5	0
42	d	2569	1301	1301	4	0
43	e	501	531	531	5	0
44	f	448	488	488	5	0
45	g	522	520	520	11	0
46	h	2082	2154	2154	19	0
47	i	444	459	458	6	0
48	j	1565	1617	1616	16	0
49	k	426	464	464	0	0
50	l	1552	1619	1619	14	0
51	m	377	418	418	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	n	1410	1443	1444	28	0
53	o	504	572	572	3	0
54	p	1313	1358	1358	7	0
55	q	302	343	343	1	0
56	r	1111	1148	1148	4	0
57	s	1129	1162	1162	13	0
58	t	946	1023	1023	12	0
59	u	1053	1129	1129	7	0
60	v	1074	1157	1157	5	0
61	w	951	994	994	10	0
62	x	892	923	923	10	0
63	y	917	962	962	4	0
64	z	947	1020	1019	12	0
65	AE	1	0	0	0	0
66	AE	2	0	0	0	0
All	All	176005	124723	127564	2459	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 (2459) 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)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.62
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.60
11:AA:1026:GLU:HG3	16:D:1030:U:C2	1.47	1.49
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.47
9:9:130:PRO:N	9:9:130:PRO:CA	1.70	1.45
9:9:31:ARG:NE	39:a:1054:A:H5'	1.31	1.39
20:H:71:ALA:C	20:H:72:LEU:HD12	1.49	1.37
20:H:118:GLY:O	20:H:133:GLY:CA	1.74	1.35
9:9:57:ASN:OD1	9:9:62:ARG:CG	1.75	1.35
16:D:1358:U:O4	16:D:1363:A:N1	1.60	1.33
8:7:0:U:C5	23:K:12:GLN:HB2	1.62	1.32
39:a:1839:G:H1'	39:a:1927:A:C8	1.62	1.32
39:a:1021:A:N1	39:a:1141:U:O4	1.63	1.30
16:D:1308:U:H2'	36:X:98:ARG:NH2	1.48	1.27
14:AE:87:LYS:HG3	22:J:20:PHE:CE1	1.69	1.26
9:9:31:ARG:CZ	39:a:1054:A:H5'	1.63	1.26
8:7:17:G:OP2	11:AA:540:ARG:NH1	1.68	1.25
15:C:12:ARG:CG	20:H:264:GLU:CB	2.15	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:118:GLY:O	20:H:133:GLY:HA3	1.27	1.23
10:A:18:G:N7	10:A:57:A:N6	1.87	1.23
10:A:32:C:O4'	25:M:144:MET:HE1	1.09	1.23
16:D:948:C:OP2	36:X:105:ASN:OD1	1.53	1.23
20:H:267:TRP:CZ2	20:H:340:ARG:HG2	1.75	1.22
9:9:88:HIS:HB3	9:9:89:PRO:CD	1.70	1.21
16:D:1227:A:OP2	36:X:110:LYS:HE3	1.35	1.21
16:D:1308:U:C2'	36:X:98:ARG:NH2	2.03	1.21
16:D:563:A:N1	16:D:884:U:O4	1.73	1.20
10:B:18:G:N7	10:B:57:A:N6	1.87	1.19
9:9:142:THR:HG21	38:Z:7:ILE:HG12	1.21	1.18
8:7:6:U:OP2	11:AA:1306:LYS:NZ	1.77	1.16
9:9:31:ARG:NE	39:a:1054:A:C5'	2.07	1.16
10:B:70:G:H2'	10:B:71:C:H5"	1.23	1.16
13:AC:65:LEU:HB3	21:I:80:LYS:HB2	1.29	1.13
16:D:1329:A:OP1	36:X:28:THR:HB	1.47	1.13
20:H:119:GLY:HA2	20:H:133:GLY:HA2	1.15	1.13
10:A:32:C:O4'	25:M:144:MET:CE	1.97	1.12
20:H:267:TRP:CE2	20:H:340:ARG:HG2	1.84	1.12
10:A:70:G:H2'	10:A:71:C:H5"	1.22	1.12
8:7:0:U:H5	23:K:12:GLN:CB	1.62	1.11
15:C:44:ILE:HD13	20:H:339:ARG:CG	1.78	1.11
16:D:1308:U:H3'	36:X:98:ARG:CZ	1.43	1.11
20:H:135:LEU:CB	20:H:167:VAL:CB	2.27	1.11
9:9:129:LEU:N	9:9:130:PRO:HD3	1.66	1.10
8:7:0:U:H3	23:K:14:LYS:NZ	1.48	1.10
39:a:1839:G:C8	39:a:1927:A:H1'	1.87	1.10
9:9:50:VAL:HG22	37:Y:119:ALA:CB	1.82	1.09
19:G:19:GLN:CD	20:H:76:GLU:CB	2.19	1.09
16:D:1308:U:C3'	36:X:98:ARG:CZ	2.31	1.09
20:H:267:TRP:CH2	20:H:340:ARG:HG2	1.87	1.09
15:C:44:ILE:HD13	20:H:339:ARG:HG2	1.18	1.08
20:H:71:ALA:O	20:H:72:LEU:HD12	1.53	1.08
16:D:1308:U:C3'	36:X:98:ARG:NH2	2.16	1.08
22:J:162:ALA:HA	22:J:165:ARG:CZ	1.83	1.07
19:G:19:GLN:CG	20:H:75:VAL:HG22	1.84	1.07
8:7:-12:G:H5"	16:D:1500:A:N6	1.70	1.06
9:9:88:HIS:CB	9:9:89:PRO:HD3	1.82	1.06
11:AA:1030:GLU:CD	16:D:1030:U:O4	1.97	1.06
19:G:19:GLN:CD	20:H:76:GLU:HB3	1.67	1.06
9:9:57:ASN:OD1	9:9:62:ARG:HG3	1.44	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:56:C:H2'	10:B:57:A:H5"	1.39	1.05
20:H:162:LYS:CB	20:H:298:GLU:CD	2.30	1.05
10:A:18:G:N2	10:A:55:U:O2	1.90	1.04
19:G:19:GLN:HG3	20:H:75:VAL:HG22	1.38	1.04
14:AE:24:LEU:HG	14:AE:232:ASN:HD21	1.17	1.03
10:B:56:C:O4'	52:n:80:ARG:NH2	1.91	1.03
20:H:19:ARG:O	20:H:72:LEU:HB2	1.58	1.03
13:AC:118:ASP:HA	28:P:89:ARG:CB	1.86	1.03
10:B:18:G:N2	10:B:55:U:O2	1.90	1.03
16:D:1308:U:C2'	36:X:98:ARG:HH21	1.63	1.03
10:A:70:G:C2'	10:A:71:C:H5"	1.89	1.02
9:9:129:LEU:H	9:9:130:PRO:HD3	0.90	1.02
9:9:93:ALA:O	9:9:129:LEU:HD12	1.60	1.01
16:D:1227:A:OP2	36:X:110:LYS:CE	2.06	1.01
20:H:290:TYR:O	20:H:305:HIS:O	1.77	1.01
10:B:56:C:H5'	52:n:80:ARG:CZ	1.90	1.01
10:B:70:G:C2'	10:B:71:C:H5"	1.89	1.01
14:AE:86:GLU:HA	22:J:166:GLU:CB	1.90	1.01
19:G:38:VAL:CG2	20:H:75:VAL:HG21	1.90	1.01
14:AE:111:THR:HG23	14:AE:300:GLN:CD	1.86	1.01
16:D:13:U:N3	16:D:915:A:C6	2.29	1.01
16:D:1329:A:OP1	36:X:28:THR:CB	2.07	1.01
16:D:13:U:O4	16:D:20:U:O4	1.79	1.00
11:AA:1026:GLU:CG	16:D:1030:U:C2	2.44	1.00
10:A:56:C:H2'	10:A:57:A:H5"	1.39	1.00
11:AA:992:LEU:HD22	11:AA:992:LEU:H	1.21	1.00
13:AC:65:LEU:HA	21:I:80:LYS:HB3	1.41	1.00
39:a:2297:A:N1	39:a:2321:U:C4	2.29	1.00
20:H:131:LEU:CB	20:H:167:VAL:CB	2.40	0.99
13:AC:118:ASP:HA	28:P:89:ARG:HB2	1.43	0.99
19:G:38:VAL:HG22	20:H:75:VAL:HG21	1.44	0.98
10:A:32:C:C4'	25:M:144:MET:HE1	1.93	0.98
10:A:32:C:O2'	25:M:86:GLN:CG	2.12	0.98
8:7:0:U:O4	23:K:12:GLN:NE2	1.97	0.97
9:9:31:ARG:CD	39:a:1054:A:H5'	1.94	0.97
39:a:1839:G:C1'	39:a:1927:A:C8	2.46	0.97
9:9:129:LEU:H	9:9:130:PRO:CD	1.77	0.97
8:7:-13:U:P	16:D:1505:G:H8	1.87	0.97
16:D:1308:U:H3'	36:X:98:ARG:NH2	1.76	0.97
9:9:142:THR:HG21	38:Z:7:ILE:CG1	1.95	0.96
39:a:1839:G:O4'	39:a:1927:A:O4'	1.82	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:57:ASN:OD1	9:9:62:ARG:HG2	1.64	0.95
20:H:118:GLY:O	20:H:133:GLY:HA2	1.63	0.95
10:A:72:A:H2'	10:A:73:A:H5"	1.49	0.95
14:AE:68:TYR:O	14:AE:75:TYR:CE2	2.20	0.95
11:AA:1026:GLU:CG	16:D:1030:U:N1	2.28	0.95
20:H:119:GLY:CA	20:H:133:GLY:HA2	1.95	0.95
39:a:67:U:N3	39:a:74:A:C6	2.35	0.94
13:AC:119:GLY:H	28:P:90:LEU:HD23	1.30	0.94
14:AE:53:ARG:NH2	22:J:164:GLN:O	2.01	0.94
16:D:13:U:C4	16:D:915:A:N6	2.36	0.94
39:a:1839:G:O4'	39:a:1927:A:C1'	2.15	0.94
11:AA:878:THR:O	11:AA:920:VAL:HG11	1.68	0.94
20:H:135:LEU:HA	20:H:157:ILE:CB	1.98	0.94
16:D:1308:U:H2'	36:X:98:ARG:HH21	1.06	0.94
10:B:68:C:H2'	10:B:69:C:H5"	1.50	0.94
20:H:119:GLY:HA3	20:H:131:LEU:O	1.68	0.93
7:6:15:DC:N4	7:6:16:DC:N4	2.15	0.93
9:9:88:HIS:CB	9:9:89:PRO:CD	2.41	0.93
16:D:13:U:N3	16:D:915:A:N6	2.16	0.93
10:A:32:C:O2'	25:M:86:GLN:HG3	1.68	0.93
20:H:71:ALA:C	20:H:72:LEU:CD1	2.42	0.93
11:AA:768:MET:CE	13:AC:80:GLU:OE1	2.17	0.93
10:B:72:A:H2'	10:B:73:A:H5"	1.49	0.92
10:A:68:C:H2'	10:A:69:C:H5"	1.51	0.92
10:B:75:C:OP1	39:a:2602:A:C8	2.23	0.92
14:AE:202:ARG:HG2	14:AE:202:ARG:HH11	1.35	0.92
9:9:88:HIS:HB3	9:9:89:PRO:HD3	0.92	0.91
39:a:2013:A:N6	39:a:2613:U:H3	1.68	0.91
39:a:1406:U:O2'	39:a:1407:G:C5'	2.19	0.91
8:7:0:U:H3	23:K:14:LYS:HZ3	0.96	0.91
11:AA:868:SER:OG	11:AA:941:LYS:HG2	1.69	0.91
13:AC:158:ARG:HB3	13:AC:158:ARG:HH11	1.32	0.91
8:7:-13:U:P	16:D:1505:G:C8	2.64	0.91
8:7:-11:U:O2'	16:D:1403:C:O2	1.87	0.91
16:D:13:U:C4	16:D:20:U:O4	2.23	0.91
10:A:56:C:H1'	39:a:2112:G:C6	2.06	0.91
6:5:113:DC:OP2	11:AA:163:LYS:HD3	1.71	0.91
9:9:50:VAL:HG22	37:Y:119:ALA:HB1	1.50	0.91
11:AA:1026:GLU:HG3	16:D:1030:U:N1	1.53	0.91
9:9:93:ALA:O	9:9:129:LEU:CD1	2.19	0.90
37:Y:104:GLN:HG2	37:Y:108:ILE:HD11	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:86:GLU:HA	22:J:166:GLU:HB2	1.52	0.90
14:AE:136:GLU:OE1	14:AE:312:ARG:NH1	2.04	0.90
20:H:279:LYS:HA	20:H:331:MET:HB3	1.54	0.90
6:5:114:DC:H5"	14:AE:1148:ARG:NH2	1.87	0.90
8:7:-12:G:C5'	16:D:1500:A:H62	1.85	0.90
14:AE:24:LEU:HB2	14:AE:232:ASN:OD1	1.72	0.89
10:A:18:G:N2	10:A:58:A:N7	2.19	0.89
20:H:162:LYS:N	20:H:298:GLU:OE2	2.06	0.89
11:AA:728:ASP:OD1	11:AA:769:PRO:HG2	1.71	0.89
9:9:142:THR:CG2	38:Z:7:ILE:HG12	2.02	0.89
10:B:18:G:N2	10:B:58:A:N7	2.19	0.89
14:AE:68:TYR:C	14:AE:75:TYR:HE2	1.80	0.89
6:5:109:DT:H2"	11:AA:200:ARG:HG3	1.53	0.88
12:AB:107:GLU:OE1	14:AE:288:PRO:HB3	1.72	0.88
9:9:31:ARG:CZ	39:a:1054:A:C5'	2.49	0.88
9:9:50:VAL:CG2	37:Y:119:ALA:HB3	2.04	0.88
12:AB:107:GLU:CD	14:AE:288:PRO:HB3	1.99	0.88
39:a:2314:A:H1'	52:n:155:THR:HG21	1.54	0.88
10:A:33:U:H5"	25:M:84:THR:HG21	1.55	0.88
20:H:131:LEU:CB	20:H:167:VAL:N	2.37	0.88
8:7:17:G:OP2	11:AA:540:ARG:CZ	2.21	0.88
20:H:119:GLY:HA2	20:H:133:GLY:CA	2.01	0.88
15:C:31:ASN:OD1	20:H:268:VAL:HG22	1.74	0.88
9:9:129:LEU:N	9:9:130:PRO:CD	2.34	0.87
37:Y:21:PRO:HB2	37:Y:22:PRO:HD3	1.54	0.87
39:a:783:A:N3	39:a:783:A:H2'	1.89	0.87
19:G:18:HIS:HA	20:H:43:LYS:HD2	1.55	0.87
13:AC:91:ARG:NE	13:AC:122:GLU:OE2	2.07	0.87
6:5:110:DA:N7	11:AA:183:TRP:CH2	2.43	0.87
20:H:162:LYS:CA	20:H:298:GLU:OE2	2.17	0.86
11:AA:1008:GLN:NE2	11:AA:1008:GLN:O	2.07	0.86
11:AA:1090:ASN:O	13:AC:182:ARG:NH1	2.08	0.86
14:AE:24:LEU:HG	14:AE:232:ASN:ND2	1.90	0.86
20:H:348:GLN:N	20:H:348:GLN:OE1	2.08	0.86
9:9:52:MET:C	9:9:52:MET:HE3	2.00	0.86
14:AE:86:GLU:HA	22:J:166:GLU:HB3	1.55	0.86
22:J:61:VAL:HG21	22:J:200:ILE:HD11	1.57	0.86
22:J:162:ALA:HB2	22:J:165:ARG:NH2	1.90	0.86
9:9:31:ARG:CD	39:a:1054:A:H4'	2.06	0.86
45:g:16:CYS:CB	45:g:37:CYS:HB3	2.05	0.86
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:967:LEU:O	11:AA:967:LEU:HD12	1.76	0.85
10:A:18:G:N7	10:A:57:A:C6	2.44	0.85
14:AE:425:ARG:NH1	14:AE:458:ASN:O	2.09	0.85
10:B:18:G:N7	10:B:57:A:C6	2.44	0.85
11:AA:981:ALA:HB3	11:AA:1008:GLN:HG3	1.57	0.85
20:H:267:TRP:CD2	20:H:340:ARG:HG2	2.12	0.85
20:H:332:VAL:HG11	20:H:335:ILE:HG13	1.57	0.85
11:AA:872:TYR:HD2	21:I:78:GLY:O	1.58	0.85
16:D:197:A:C6	16:D:221:C:H4'	2.11	0.85
37:Y:81:LYS:O	37:Y:81:LYS:HE3	1.75	0.85
11:AA:975:ILE:HG13	11:AA:1014:LEU:HD23	1.57	0.85
20:H:267:TRP:CZ3	20:H:340:ARG:HG2	2.12	0.85
9:9:125:ARG:NH1	9:9:125:ARG:HA	1.92	0.84
39:a:67:U:N3	39:a:74:A:N6	2.25	0.84
15:C:12:ARG:HH22	20:H:268:VAL:CG2	1.90	0.84
39:a:2303:G:C2	39:a:2314:A:C2	2.66	0.84
8:7:-12:G:H5"	16:D:1500:A:H62	1.40	0.84
20:H:135:LEU:CB	20:H:167:VAL:C	2.50	0.84
14:AE:68:TYR:HB3	14:AE:75:TYR:OH	1.76	0.84
11:AA:980:VAL:HA	11:AA:984:VAL:HB	1.58	0.84
14:AE:26:SER:HB2	14:AE:236:TRP:CZ2	2.12	0.84
7:6:21:DA:N1	8:7:15:G:N2	2.26	0.84
14:AE:68:TYR:O	14:AE:75:TYR:HE2	1.58	0.84
23:K:111:MET:HE2	23:K:125:ALA:HB1	1.59	0.84
20:H:131:LEU:CB	20:H:166:VAL:O	2.26	0.83
9:9:31:ARG:HH11	9:9:31:ARG:HG3	1.41	0.83
9:9:28:ALA:H	9:9:110:ALA:HA	1.44	0.83
10:A:68:C:C2'	10:A:69:C:H5"	2.08	0.83
19:G:16:PHE:HB3	20:H:43:LYS:HA	1.60	0.83
9:9:62:ARG:HG2	9:9:62:ARG:HH21	1.43	0.83
10:A:72:A:C2'	10:A:73:A:H5"	2.09	0.83
10:A:16:C:O2	39:a:2181:U:H5'	1.76	0.83
16:D:1227:A:H5'	36:X:110:LYS:NZ	1.93	0.83
37:Y:60:VAL:HG13	37:Y:66:PHE:HB3	1.58	0.83
13:AC:117:HIS:N	28:P:89:ARG:HD2	1.92	0.83
8:7:-13:U:OP1	16:D:1505:G:C8	2.32	0.83
13:AC:120:ASP:HA	28:P:31:ARG:NH2	1.94	0.83
10:B:56:C:H5'	52:n:80:ARG:NE	1.93	0.83
10:B:72:A:C2'	10:B:73:A:H5"	2.09	0.83
8:7:-12:G:C5'	16:D:1500:A:N6	2.42	0.82
9:9:31:ARG:CD	39:a:1054:A:C4'	2.56	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AC:119:GLY:N	28:P:90:LEU:HD23	1.94	0.82
10:B:68:C:C2'	10:B:69:C:H5"	2.08	0.82
11:AA:953:LEU:HA	11:AA:1036:ILE:HD13	1.59	0.82
11:AA:1043:ALA:HB1	11:AA:1044:PRO:HD2	1.61	0.82
37:Y:20:SER:HB3	37:Y:21:PRO:HD3	1.59	0.82
20:H:267:TRP:CH2	20:H:340:ARG:CG	2.60	0.82
9:9:57:ASN:OD1	9:9:62:ARG:CD	2.27	0.82
11:AA:883:LEU:HD11	11:AA:920:VAL:HG22	1.59	0.82
13:AD:86:LYS:CE	14:AE:528:THR:HB	2.09	0.82
39:a:1406:U:O2'	39:a:1407:G:H5"	1.79	0.82
11:AA:872:TYR:CD2	21:I:78:GLY:O	2.31	0.82
14:AE:141:PHE:HE2	14:AE:296:LYS:HB2	1.44	0.82
39:a:1021:A:N6	39:a:1141:U:H3	1.77	0.82
13:AC:118:ASP:HB3	28:P:90:LEU:CD2	2.10	0.82
20:H:267:TRP:CZ3	20:H:340:ARG:CG	2.63	0.82
9:9:3:LEU:HD13	9:9:5:LEU:HG	1.62	0.82
39:a:1839:G:C1'	39:a:1927:A:N9	2.43	0.82
8:7:-13:U:OP2	16:D:1505:G:C8	2.32	0.82
9:9:50:VAL:HG22	37:Y:119:ALA:HB3	1.60	0.82
10:A:54:U:H3	10:A:58:A:N6	1.77	0.82
10:A:56:C:C2'	10:A:57:A:H5"	2.11	0.81
20:H:305:HIS:CD2	20:H:306:VAL:H	1.98	0.81
14:AE:141:PHE:CE2	14:AE:296:LYS:HB2	2.15	0.81
16:D:1397:C:OP1	16:D:1397:C:H2'	1.81	0.81
20:H:155:LYS:CB	20:H:169:SER:CB	2.58	0.81
9:9:43:LYS:HD2	9:9:43:LYS:C	2.05	0.81
14:AE:1169:THR:OG1	14:AE:1192:LYS:NZ	2.13	0.81
10:B:54:U:H3	10:B:58:A:N6	1.77	0.81
37:Y:102:ARG:HB3	37:Y:141:ASP:HA	1.61	0.81
11:AA:611:GLU:OE2	11:AA:637:ARG:NH2	2.13	0.81
10:B:56:C:C2'	10:B:57:A:H5"	2.11	0.81
16:D:972:C:O2'	28:P:57:VAL:CG2	2.29	0.81
39:a:585:G:N7	64:z:6:ARG:NH1	2.29	0.81
39:a:1019:U:H3	39:a:1142:A:N6	1.77	0.81
9:9:50:VAL:CG2	37:Y:119:ALA:CB	2.59	0.81
11:AA:724:VAL:CG1	11:AA:774:GLY:H	1.93	0.81
16:D:37:U:N3	16:D:397:A:N6	2.28	0.81
6:5:110:DA:N7	11:AA:183:TRP:HH2	1.77	0.81
8:7:-13:U:OP1	16:D:1505:G:H8	1.62	0.81
11:AA:862:LEU:HD12	21:I:72:ARG:NH2	1.95	0.81
7:6:18:DC:H42	8:7:17:G:H1	1.27	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:J:162:ALA:CA	22:J:165:ARG:NH2	2.44	0.80
37:Y:72:THR:OG1	37:Y:73:PRO:HD2	1.81	0.80
9:9:3:LEU:H	9:9:3:LEU:HD12	1.47	0.80
10:A:58:A:O2'	10:A:59:A:H3'	1.81	0.80
10:A:22:G:H2'	10:A:23:C:C6	2.16	0.80
10:B:76:A:H1'	39:a:2494:G:P	2.20	0.80
20:H:123:GLU:HA	20:H:128:ARG:HA	1.63	0.80
11:AA:118:LYS:NZ	11:AA:487:LEU:O	2.14	0.80
45:g:16:CYS:HB2	45:g:37:CYS:HB3	1.63	0.80
15:C:12:ARG:CB	20:H:264:GLU:CB	2.59	0.80
10:A:18:G:N2	10:A:58:A:C5	2.50	0.80
10:B:22:G:H2'	10:B:23:C:C6	2.16	0.80
10:B:58:A:O2'	10:B:59:A:H3'	1.81	0.80
39:a:2298:A:C4	39:a:2321:U:C5	2.70	0.80
45:g:18:CYS:HB3	45:g:40:CYS:CB	2.12	0.80
9:9:39:THR:HA	9:9:42:ARG:HD2	1.64	0.80
37:Y:27:LEU:HD12	37:Y:27:LEU:O	1.81	0.80
7:6:21:DA:N1	8:7:15:G:C2	2.49	0.80
9:9:31:ARG:HD2	39:a:1054:A:H4'	1.62	0.80
10:B:18:G:N2	10:B:58:A:C5	2.50	0.80
22:J:162:ALA:HA	22:J:165:ARG:NH2	1.95	0.80
22:J:162:ALA:CB	22:J:165:ARG:NH2	2.44	0.79
39:a:2189:U:OP1	39:a:2189:U:O4'	2.00	0.79
8:7:0:U:H5	23:K:12:GLN:HB2	0.70	0.79
11:AA:886:LYS:HE3	11:AA:886:LYS:O	1.80	0.79
14:AE:111:THR:HG23	14:AE:300:GLN:OE1	1.81	0.79
16:D:1329:A:P	36:X:28:THR:HB	2.22	0.79
52:n:125:ARG:O	52:n:127:ASN:ND2	2.14	0.79
39:a:2297:A:N1	39:a:2321:U:O4	2.14	0.79
14:AE:186:GLN:HG3	14:AE:238:ILE:HG13	1.65	0.79
39:a:1021:A:H61	39:a:1141:U:H3	1.29	0.79
20:H:122:VAL:O	20:H:129:ALA:N	2.13	0.79
20:H:270:ILE:CG2	20:H:337:GLU:HB3	2.12	0.79
39:a:1019:U:H3	39:a:1142:A:H61	1.28	0.79
9:9:78:GLY:N	9:9:79:PRO:HD2	1.97	0.79
14:AE:37:GLU:O	14:AE:61:ILE:HD11	1.81	0.79
10:A:33:U:O3'	25:M:84:THR:OG1	2.01	0.79
10:A:76:A:H2'	39:a:2394:C:H42	1.48	0.79
11:AA:1257:GLN:HE22	14:AE:345:LYS:HA	1.48	0.79
22:J:162:ALA:HB2	22:J:165:ARG:HH22	1.47	0.79
9:9:11:ILE:HD11	9:9:62:ARG:HA	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:31:ARG:CD	39:a:1054:A:C5’	2.58	0.78
13:AC:167:PRO:HB3	21:I:103:ILE:O	1.83	0.78
19:G:16:PHE:CZ	20:H:41:GLY:O	2.36	0.78
48:j:4:LEU:HD23	48:j:29:VAL:HG11	1.65	0.78
14:AE:87:LYS:HA	14:AE:87:LYS:HE3	1.64	0.78
14:AE:90:VAL:HG13	14:AE:90:VAL:O	1.82	0.78
10:B:7:G:H4’	10:B:8:U:OP1	1.81	0.78
14:AE:144:TYR:HE1	14:AE:162:GLU:OE2	1.64	0.78
11:AA:964:LEU:HD12	11:AA:964:LEU:O	1.84	0.78
11:AA:1257:GLN:OE1	14:AE:345:LYS:CG	2.32	0.78
10:A:7:G:H4’	10:A:8:U:OP1	1.81	0.78
13:AC:118:ASP:HB3	28:P:90:LEU:HD22	1.65	0.78
37:Y:32:VAL:HG13	37:Y:60:VAL:HG21	1.66	0.78
14:AE:1075:ARG:NH2	14:AE:1168:GLU:OE2	2.17	0.78
10:B:15:G:N1	10:B:20:U:O2	2.17	0.78
39:a:1406:U:O2’	39:a:1407:G:P	2.41	0.78
19:G:35:ARG:HD2	20:H:14:LYS:HD3	1.66	0.78
13:AC:76:GLU:CD	13:AC:131:CYS:HA	2.09	0.78
10:B:5:G:H2’	10:B:6:G:H5’	1.66	0.77
10:B:18:G:C5	10:B:57:A:C6	2.72	0.77
11:AA:1007:LYS:O	11:AA:1007:LYS:HD2	1.83	0.77
39:a:2756:U:N3	39:a:2758:A:N6	2.32	0.77
11:AA:1024:GLU:HA	11:AA:1027:LYS:HE3	1.66	0.77
10:B:70:G:H2’	10:B:71:C:C5’	2.11	0.77
20:H:305:HIS:CD2	20:H:306:VAL:N	2.53	0.77
11:AA:1026:GLU:HA	11:AA:1026:GLU:OE2	1.84	0.77
10:A:5:G:H2’	10:A:6:G:H5’	1.66	0.77
10:B:68:C:C3’	10:B:69:C:H5”	2.15	0.77
14:AE:123:ARG:HG3	14:AE:1337:VAL:HG11	1.67	0.77
39:a:1406:U:O2’	39:a:1407:G:O5’	2.01	0.77
7:6:18:DC:N3	8:7:17:G:N2	2.31	0.77
8:7:8:A:H2’	8:7:8:A:N3	1.99	0.77
9:9:27:VAL:HG23	9:9:83:ALA:HB3	1.67	0.77
20:H:19:ARG:HD3	20:H:73:ASP:CG	2.09	0.77
39:a:2756:U:N3	39:a:2758:A:C6	2.53	0.77
10:A:15:G:N1	10:A:20:U:O2	2.17	0.77
10:A:70:G:H2’	10:A:71:C:C5’	2.11	0.77
16:D:1358:U:C4	16:D:1363:A:N1	2.52	0.76
10:A:18:G:C5	10:A:57:A:C6	2.72	0.76
11:AA:955:GLN:OE1	11:AA:955:GLN:HA	1.83	0.76
13:AC:167:PRO:HA	21:I:103:ILE:O	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:60:LEU:HD23	9:9:64:VAL:HG21	1.67	0.76
10:A:68:C:C3'	10:A:69:C:H5"	2.15	0.76
7:6:15:DC:C4	7:6:16:DC:N4	2.53	0.76
11:AA:871:VAL:N	11:AA:883:LEU:O	2.18	0.76
9:9:31:ARG:NE	39:a:1054:A:C4'	2.48	0.76
9:9:97:LYS:HD3	9:9:127:ALA:HA	1.68	0.76
11:AA:1246:ARG:HH11	11:AA:1266:GLY:HA2	1.50	0.75
19:G:35:ARG:HG3	20:H:10:GLU:OE2	1.86	0.75
37:Y:74:PRO:HG2	37:Y:77:VAL:HB	1.67	0.75
4:3:36:VAL:HG11	4:3:39:ILE:HD12	1.69	0.75
10:A:32:C:C1'	25:M:144:MET:HE1	2.16	0.75
13:AC:118:ASP:CA	28:P:89:ARG:HB2	2.16	0.75
11:AA:1272:GLU:OE2	14:AE:798:ARG:NH1	2.20	0.75
10:A:41:C:O4'	25:M:143:ARG:NH1	2.20	0.75
14:AE:86:GLU:CA	22:J:166:GLU:HB3	2.16	0.75
10:A:41:C:H1'	25:M:143:ARG:HH12	1.52	0.75
11:AA:954:LYS:HZ2	11:AA:954:LYS:C	1.93	0.75
11:AA:985:GLU:HG2	11:AA:988:LYS:HE3	1.69	0.75
11:AA:992:LEU:H	11:AA:992:LEU:CD2	1.95	0.75
45:g:18:CYS:CB	45:g:40:CYS:HB3	2.16	0.75
6:5:108:DT:H72	11:AA:199:ASP:HB3	1.68	0.75
13:AC:65:LEU:CB	21:I:80:LYS:HB2	2.15	0.75
14:AE:87:LYS:HG3	22:J:20:PHE:HE1	1.42	0.75
16:D:197:A:N6	16:D:221:C:H4'	2.01	0.75
8:7:-6:U:C5	16:D:528:C:P	2.80	0.74
20:H:131:LEU:CB	20:H:166:VAL:C	2.60	0.74
14:AE:110:PRO:HG2	14:AE:183:GLU:HG3	1.68	0.74
10:B:70:G:C3'	10:B:71:C:H5"	2.17	0.74
23:K:137:VAL:O	23:K:140:THR:OG1	2.04	0.74
62:x:31:THR:O	62:x:102:ARG:NH1	2.19	0.74
10:A:70:G:C3'	10:A:71:C:H5"	2.18	0.74
9:9:78:GLY:N	9:9:79:PRO:CD	2.51	0.74
13:AD:196:THR:HB	14:AE:443:GLU:HG3	1.68	0.74
14:AE:44:ILE:HD12	14:AE:252:LEU:CD2	2.18	0.74
39:a:2013:A:N6	39:a:2613:U:N3	2.33	0.74
9:9:52:MET:HG3	9:9:95:LEU:HD11	1.68	0.74
11:AA:991:LYS:HD2	11:AA:991:LYS:N	2.03	0.74
11:AA:1034:ARG:HG2	11:AA:1034:ARG:HH11	1.52	0.74
19:G:19:GLN:CD	20:H:76:GLU:HB2	2.08	0.74
8:7:14:U:H4'	14:AE:322:ARG:CD	2.18	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)
20:H:109:THR:HA	20:H:153:GLU:HA	1.69	0.74
10:A:18:G:H1'	10:A:58:A:C2	2.23	0.74
11:AA:956:ALA:HB1	11:AA:1032:LYS:HG3	1.70	0.74
11:AA:979:LEU:HD21	11:AA:998:LEU:HD23	1.70	0.74
10:B:76:A:H1'	39:a:2494:G:OP1	1.88	0.74
16:D:1228:C:OP1	36:X:107:ARG:NH1	2.21	0.74
11:AA:964:LEU:HD12	11:AA:964:LEU:C	2.13	0.73
10:B:18:G:H1'	10:B:58:A:C2	2.23	0.73
11:AA:859:GLU:HB3	21:I:109:PRO:HG3	1.67	0.73
10:B:18:G:O2'	10:B:60:U:C2	2.41	0.73
39:a:2298:A:C4	39:a:2321:U:H5	2.04	0.73
10:A:6:G:O2'	10:A:7:G:O5'	2.05	0.73
13:AC:158:ARG:HB3	13:AC:158:ARG:NH1	2.02	0.73
14:AE:1143:ASP:OD1	14:AE:1148:ARG:NH1	2.21	0.73
15:C:44:ILE:CD1	20:H:339:ARG:CG	2.62	0.73
19:G:19:GLN:CG	20:H:76:GLU:HB2	2.18	0.73
20:H:109:THR:CA	20:H:153:GLU:HA	2.18	0.73
20:H:304:VAL:HG12	20:H:309:MET:SD	2.28	0.73
14:AE:210:SER:HB3	14:AE:213:LYS:HB2	1.71	0.73
19:G:19:GLN:OE1	20:H:75:VAL:O	1.85	0.73
10:A:18:G:O2'	10:A:60:U:C2	2.41	0.73
13:AC:61:ILE:HB	13:AC:64:VAL:HG21	1.71	0.73
14:AE:107:LEU:HD11	14:AE:242:LEU:HB2	1.70	0.73
14:AE:120:LEU:O	14:AE:1330:ARG:NH1	2.21	0.73
10:B:76:A:H2'	10:B:76:A:N3	2.03	0.73
6:5:115:DA:OP1	14:AE:1148:ARG:NE	2.21	0.73
11:AA:1047:LEU:O	11:AA:1049:ILE:HD12	1.89	0.73
28:P:24:GLU:OE2	28:P:90:LEU:HD11	1.87	0.73
11:AA:870:ILE:HG12	11:AA:884:VAL:HG12	1.70	0.73
20:H:19:ARG:HB2	20:H:73:ASP:OD2	1.88	0.73
11:AA:998:LEU:HD13	11:AA:998:LEU:C	2.13	0.73
20:H:110:GLY:CA	20:H:153:GLU:O	2.36	0.73
14:AE:68:TYR:C	14:AE:75:TYR:CE2	2.65	0.73
13:AC:65:LEU:HB3	21:I:80:LYS:CB	2.16	0.72
7:6:21:DA:C6	8:7:15:G:N2	2.57	0.72
11:AA:1253:LEU:HD12	14:AE:253:VAL:CG1	2.19	0.72
14:AE:157:GLN:OE1	14:AE:157:GLN:HA	1.89	0.72
39:a:1913:A:OP2	39:a:1913:A:H3'	1.89	0.72
10:A:33:U:H5"	25:M:84:THR:CG2	2.19	0.72
20:H:70:VAL:HA	20:H:85:SER:CB	2.20	0.72
20:H:267:TRP:CE3	20:H:340:ARG:HG2	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:D:827:U:H3	16:D:872:A:N6	1.87	0.72
27:O:84:THR:HG21	27:O:103:PHE:HB3	1.71	0.72
11:AA:972:PHE:HA	11:AA:975:ILE:HD12	1.71	0.72
11:AA:1043:ALA:HB1	11:AA:1044:PRO:CD	2.19	0.72
11:AA:1257:GLN:OE1	14:AE:345:LYS:HD3	1.89	0.72
10:A:72:A:C3'	10:A:73:A:H5"	2.20	0.72
19:G:16:PHE:CB	20:H:43:LYS:HA	2.20	0.72
10:A:46:G:H1'	10:A:47:U:C5	2.25	0.72
14:AE:44:ILE:HD12	14:AE:252:LEU:HD21	1.71	0.72
14:AE:211:GLU:HG2	14:AE:215:LYS:HE3	1.70	0.72
10:B:76:A:H2'	39:a:2493:U:H5"	1.72	0.72
16:D:517:G:O2'	16:D:530:G:H4'	1.89	0.72
15:C:12:ARG:HB2	20:H:264:GLU:CB	2.20	0.72
15:C:44:ILE:HD13	20:H:339:ARG:HG3	1.69	0.72
37:Y:36:GLU:OE1	37:Y:36:GLU:HA	1.88	0.72
14:AE:105:ILE:HD12	14:AE:242:LEU:HD22	1.71	0.71
10:B:72:A:C3'	10:B:73:A:H5"	2.20	0.71
9:9:18:VAL:HA	9:9:86:MET:HE2	1.71	0.71
13:AC:118:ASP:CA	28:P:89:ARG:CB	2.67	0.71
30:R:86:ARG:HG3	30:R:86:ARG:O	1.89	0.71
11:AA:839:VAL:O	11:AA:886:LYS:HD3	1.90	0.71
14:AE:220:ARG:HG2	14:AE:220:ARG:HH11	1.55	0.71
39:a:67:U:C4	39:a:74:A:N6	2.57	0.71
20:H:267:TRP:CE3	20:H:340:ARG:CG	2.72	0.71
36:X:96:PRO:HG2	36:X:102:THR:CG2	2.21	0.71
45:g:18:CYS:CB	45:g:40:CYS:CB	2.69	0.71
37:Y:85:ILE:H	37:Y:85:ILE:HD12	1.52	0.71
13:AD:86:LYS:HE3	14:AE:528:THR:HB	1.72	0.71
10:B:18:G:C5	10:B:57:A:N6	2.59	0.71
39:a:1021:A:N1	39:a:1141:U:C4	2.55	0.71
39:a:1839:G:C1'	39:a:1927:A:C1'	2.67	0.71
9:9:3:LEU:HD12	9:9:3:LEU:N	2.05	0.71
9:9:77:VAL:HG12	9:9:82:ILE:HG21	1.71	0.71
14:AE:54:ASP:OD1	14:AE:54:ASP:N	2.24	0.71
10:A:32:C:C1'	25:M:144:MET:CE	2.69	0.71
11:AA:878:THR:HA	11:AA:925:SER:HA	1.73	0.71
14:AE:142:GLU:HG3	14:AE:142:GLU:O	1.89	0.71
11:AA:19:PRO:HA	11:AA:1156:ARG:HD3	1.73	0.71
13:AC:117:HIS:CA	28:P:89:ARG:HD2	2.20	0.71
16:D:1309:G:H8	36:X:98:ARG:NH2	1.89	0.71
8:7:14:U:H4'	14:AE:322:ARG:HD2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:839:VAL:HA	11:AA:1048:LYS:O	1.91	0.70
10:B:15:G:H2'	10:B:15:G:N3	2.06	0.70
16:D:1227:A:H5'	36:X:110:LYS:HZ2	1.53	0.70
10:A:18:G:C5	10:A:57:A:N6	2.59	0.70
13:AC:65:LEU:HA	21:I:80:LYS:CB	2.19	0.70
9:9:58:THR:HG21	9:9:81:LEU:HG	1.74	0.70
14:AE:202:ARG:HG2	14:AE:202:ARG:NH1	1.99	0.70
10:B:46:G:H1'	10:B:47:U:C5	2.25	0.70
39:a:2314:A:C1'	52:n:155:THR:HG21	2.21	0.70
10:A:32:C:C4'	25:M:144:MET:CE	2.66	0.70
11:AA:878:THR:O	11:AA:920:VAL:CG1	2.40	0.70
8:7:16:A:P	11:AA:540:ARG:HH21	2.14	0.70
11:AA:207:THR:OG1	11:AA:354:ASP:OD2	2.09	0.70
16:D:1308:U:O5'	36:X:98:ARG:HG3	1.90	0.70
16:D:915:A:N6	16:D:916:U:C4	2.60	0.70
20:H:19:ARG:HD3	20:H:73:ASP:OD1	1.92	0.70
10:A:41:C:C1'	25:M:143:ARG:NH1	2.55	0.69
20:H:86:ARG:O	20:H:89:ALA:HB3	1.91	0.69
39:a:742:A:H2'	39:a:743:A:C8	2.26	0.69
46:h:146:MET:HE3	46:h:154:LEU:HD21	1.74	0.69
10:A:15:G:H2'	10:A:15:G:N3	2.06	0.69
10:A:16:C:O2	39:a:2181:U:C5'	2.40	0.69
14:AE:86:GLU:CB	22:J:166:GLU:HB3	2.22	0.69
16:D:972:C:O2'	28:P:57:VAL:HG23	1.92	0.69
39:a:2310:C:O2'	52:n:74:VAL:CG1	2.40	0.69
9:9:73:LYS:HB2	9:9:117:LEU:HD21	1.75	0.69
11:AA:883:LEU:HD11	11:AA:920:VAL:CG2	2.21	0.69
20:H:19:ARG:HD3	20:H:73:ASP:OD2	1.92	0.69
11:AA:1009:ASN:O	11:AA:1009:ASN:ND2	2.24	0.69
39:a:1596:A:H2'	39:a:1597:A:C8	2.28	0.69
39:a:1839:G:C4	39:a:1927:A:C4	2.81	0.69
14:AE:87:LYS:CG	22:J:20:PHE:CE1	2.64	0.69
20:H:70:VAL:HA	20:H:85:SER:CA	2.22	0.69
11:AA:339:ASN:HB3	11:AA:343:HIS:H	1.58	0.69
11:AA:1047:LEU:O	11:AA:1049:ILE:CD1	2.40	0.69
13:AC:118:ASP:HA	28:P:89:ARG:HB3	1.72	0.69
14:AE:128:LEU:HD11	14:AE:189:LEU:HG	1.73	0.69
10:A:11:A:H2'	10:A:12:G:O4'	1.92	0.69
11:AA:1005:GLU:OE1	11:AA:1005:GLU:HA	1.92	0.69
20:H:110:GLY:HA3	20:H:153:GLU:O	1.93	0.69
36:X:96:PRO:CG	36:X:102:THR:CG2	2.71	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:a:927:A:H2'	39:a:928:A:C8	2.28	0.69
14:AE:94:GLN:HB2	14:AE:97:VAL:HG23	1.75	0.68
37:Y:21:PRO:CB	37:Y:22:PRO:HD3	2.22	0.68
9:9:31:ARG:HD2	39:a:1054:A:C5'	2.22	0.68
13:AC:76:GLU:OE1	13:AC:131:CYS:HA	1.92	0.68
14:AE:161:THR:HG22	14:AE:164:GLN:HB2	1.75	0.68
39:a:1021:A:H3'	39:a:1021:A:N3	2.07	0.68
8:7:0:U:N3	23:K:14:LYS:NZ	2.30	0.68
11:AA:875:ALA:H	21:I:80:LYS:HE3	1.59	0.68
20:H:267:TRP:CD2	20:H:340:ARG:CG	2.76	0.68
9:9:50:VAL:HG13	37:Y:119:ALA:CB	2.22	0.68
11:AA:868:SER:OG	11:AA:941:LYS:CG	2.41	0.68
16:D:37:U:H3	16:D:397:A:N6	1.90	0.68
1:0:80:ARG:NH2	39:a:572:A:OP2	2.25	0.68
14:AE:832:LYS:C	14:AE:1242:ARG:HH12	2.01	0.68
16:D:13:U:O4	16:D:21:G:C2	2.46	0.68
39:a:1153:C:OP1	64:z:92:ARG:NH1	2.27	0.68
9:9:43:LYS:HD2	9:9:43:LYS:O	1.94	0.68
11:AA:859:GLU:HB3	21:I:109:PRO:CG	2.23	0.68
10:B:11:A:H2'	10:B:12:G:O4'	1.92	0.68
9:9:118:ILE:HB	9:9:119:PRO:HD3	1.76	0.68
11:AA:935:THR:HA	11:AA:1049:ILE:HD12	1.74	0.68
19:G:16:PHE:HZ	20:H:41:GLY:O	1.77	0.68
9:9:11:ILE:CD1	9:9:62:ARG:HD3	2.24	0.68
13:AC:167:PRO:CB	21:I:103:ILE:O	2.42	0.68
14:AE:39:LYS:O	14:AE:273:ILE:CG2	2.41	0.68
7:6:8:DC:C6	7:6:9:DT:H72	2.29	0.67
10:A:5:G:H2'	10:A:6:G:C5'	2.24	0.67
14:AE:141:PHE:CD2	14:AE:293:ARG:O	2.47	0.67
20:H:117:LYS:CB	20:H:279:LYS:O	2.41	0.67
7:6:21:DA:C2	8:7:15:G:N2	2.61	0.67
11:AA:728:ASP:OD1	11:AA:769:PRO:CG	2.41	0.67
11:AA:768:MET:HE1	13:AC:80:GLU:CD	2.19	0.67
11:AA:802:VAL:HA	11:AA:1096:ILE:O	1.93	0.67
39:a:2310:C:O2'	52:n:74:VAL:HG12	1.94	0.67
39:a:2756:U:C4	39:a:2758:A:N6	2.61	0.67
39:a:1779:U:H5	39:a:1784:A:N7	1.93	0.67
13:AC:76:GLU:OE2	13:AC:131:CYS:HA	1.95	0.67
14:AE:1355:ARG:NH1	14:AE:1369:ARG:HH12	1.93	0.67
15:C:44:ILE:CD1	20:H:339:ARG:HG2	2.12	0.67
39:a:1920:C:O5'	39:a:1920:C:H6	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:p:24:ILE:HD13	54:p:72:LEU:HD21	1.77	0.67
10:A:66:C:H6	10:A:66:C:H5'	1.60	0.67
11:AA:1253:LEU:HD12	14:AE:253:VAL:HG11	1.77	0.67
36:X:96:PRO:CG	36:X:102:THR:HG22	2.25	0.67
11:AA:958:LYS:HB3	11:AA:958:LYS:NZ	2.08	0.67
14:AE:108:ALA:HB3	14:AE:279:LEU:HD22	1.77	0.67
20:H:118:GLY:C	20:H:133:GLY:CA	2.67	0.67
13:AC:167:PRO:CA	21:I:103:ILE:O	2.42	0.67
11:AA:963:GLU:HA	11:AA:966:ILE:HD12	1.77	0.67
14:AE:111:THR:CG2	14:AE:300:GLN:CD	2.66	0.67
14:AE:117:LEU:HD12	14:AE:117:LEU:O	1.94	0.67
20:H:110:GLY:H	20:H:153:GLU:CA	2.08	0.67
37:Y:14:ALA:HB2	37:Y:54:ILE:HD12	1.76	0.66
37:Y:58:ILE:HD13	37:Y:58:ILE:N	2.09	0.66
8:7:-6:U:C5	16:D:528:C:OP1	2.49	0.66
9:9:67:THR:N	9:9:68:PRO:CD	2.58	0.66
11:AA:768:MET:HE1	13:AC:80:GLU:OE1	1.94	0.66
10:A:19:G:N2	39:a:2112:G:C8	2.62	0.66
11:AA:768:MET:HE3	13:AC:80:GLU:OE1	1.95	0.66
10:B:21:A:H4'	10:B:21:A:OP1	1.95	0.66
16:D:563:A:N1	16:D:884:U:C4	2.60	0.66
20:H:70:VAL:HA	20:H:85:SER:HA	1.77	0.66
9:9:50:VAL:CG1	37:Y:119:ALA:HB3	2.26	0.66
10:B:5:G:H2'	10:B:6:G:C5'	2.24	0.66
10:B:66:C:H5'	10:B:66:C:H6	1.60	0.66
20:H:19:ARG:O	20:H:72:LEU:CB	2.41	0.66
20:H:110:GLY:N	20:H:153:GLU:C	2.53	0.66
9:9:60:LEU:HA	9:9:64:VAL:HB	1.77	0.66
39:a:1839:G:C8	39:a:1927:A:C1'	2.74	0.66
8:7:-1:U:OP1	23:K:15:LEU:HD21	1.94	0.66
14:AE:108:ALA:CB	14:AE:279:LEU:HD22	2.25	0.66
11:AA:852:ALA:O	11:AA:854:ILE:N	2.28	0.66
11:AA:1251:TYR:C	11:AA:1259:LEU:CD1	2.69	0.66
14:AE:978:ARG:HG2	14:AE:1197:ASN:HD21	1.60	0.66
8:7:-1:U:H4'	23:K:15:LEU:CD2	2.26	0.66
11:AA:839:VAL:O	11:AA:886:LYS:CD	2.44	0.66
11:AA:1030:GLU:OE1	16:D:1030:U:O4	2.12	0.66
16:D:1227:A:OP2	36:X:110:LYS:NZ	2.29	0.66
10:A:21:A:H4'	10:A:21:A:OP1	1.95	0.66
13:AC:120:ASP:CA	28:P:31:ARG:NH2	2.58	0.66
10:A:56:C:C5	39:a:2168:G:C6	2.83	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AC:167:PRO:HB3	21:I:103:ILE:C	2.22	0.65
11:AA:858:GLY:C	11:AA:860:ALA:H	2.03	0.65
20:H:162:LYS:CB	20:H:298:GLU:OE1	2.44	0.65
11:AA:9:LYS:HG2	11:AA:1171:ARG:NH1	2.11	0.65
11:AA:1257:GLN:OE1	14:AE:345:LYS:CD	2.44	0.65
10:B:56:C:H5'	52:n:80:ARG:NH2	2.10	0.65
37:Y:116:MET:HB3	37:Y:124:MET:HG2	1.76	0.65
11:AA:1257:GLN:HE22	14:AE:345:LYS:CA	2.09	0.65
14:AE:1037:PHE:HB3	14:AE:1040:MET:HB2	1.78	0.65
21:I:75:ILE:O	21:I:75:ILE:HD13	1.95	0.65
9:9:11:ILE:HG13	9:9:65:GLU:HB3	1.79	0.65
9:9:57:ASN:CG	9:9:62:ARG:CG	2.68	0.65
14:AE:984:LEU:HB3	14:AE:993:GLU:HB2	1.77	0.65
10:B:6:G:HO2'	10:B:7:G:H8	1.42	0.65
9:9:61:ARG:NH1	39:a:1047:G:N7	2.44	0.65
13:AD:86:LYS:HE3	14:AE:528:THR:CG2	2.26	0.65
14:AE:193:ASP:HB3	14:AE:196:GLN:HB2	1.78	0.65
10:B:76:A:H1'	39:a:2493:U:O3'	1.97	0.65
9:9:142:THR:HG21	38:Z:7:ILE:CD1	2.26	0.65
11:AA:960:LEU:HD13	11:AA:1029:LEU:HB2	1.77	0.65
12:AB:93:ILE:HG22	14:AE:290:ILE:CG2	2.27	0.65
13:AD:102:LEU:HB2	13:AD:115:ILE:HG13	1.77	0.65
14:AE:141:PHE:HD2	14:AE:293:ARG:O	1.80	0.65
16:D:1308:U:O5'	36:X:98:ARG:CG	2.45	0.65
16:D:1329:A:P	36:X:28:THR:HG1	2.19	0.65
36:X:96:PRO:HG3	36:X:102:THR:HG22	1.78	0.65
37:Y:116:MET:HE2	37:Y:116:MET:HA	1.79	0.65
11:AA:859:GLU:CB	21:I:109:PRO:HG2	2.27	0.65
11:AA:962:GLU:OE1	11:AA:962:GLU:HA	1.97	0.65
11:AA:964:LEU:HD21	11:AA:1022:LYS:HD2	1.77	0.65
16:D:1308:U:H5"	36:X:98:ARG:HG2	1.78	0.65
7:6:16:DC:H1'	14:AE:426:ALA:HB1	1.76	0.65
10:A:22:G:H2'	10:A:23:C:H6	1.62	0.65
14:AE:84:ILE:O	14:AE:84:ILE:HG13	1.96	0.65
11:AA:992:LEU:HD22	11:AA:992:LEU:N	2.04	0.65
14:AE:68:TYR:HB3	14:AE:75:TYR:CE2	2.32	0.65
20:H:267:TRP:CZ2	20:H:340:ARG:CG	2.68	0.65
34:V:25:ILE:HD11	34:V:61:ILE:HD11	1.77	0.65
53:o:26:HIS:CE1	53:o:48:ALA:HB2	2.32	0.65
57:s:114:LEU:HG	57:s:118:MET:HE3	1.78	0.65
10:A:3:C:H2'	10:A:4:G:H8	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:41:C:C4'	25:M:143:ARG:NH1	2.60	0.64
11:AA:1026:GLU:HG3	16:D:1030:U:N3	2.08	0.64
20:H:85:SER:O	20:H:88:LYS:CB	2.45	0.64
8:7:-6:U:C5	16:D:528:C:OP2	2.49	0.64
16:D:1358:U:O4	16:D:1363:A:C2	2.47	0.64
16:D:1358:U:N3	16:D:1363:A:N6	2.46	0.64
14:AE:395:LYS:HZ2	14:AE:399:LYS:CD	2.09	0.64
16:D:827:U:N3	16:D:872:A:N6	2.45	0.64
19:G:19:GLN:CG	20:H:75:VAL:CG2	2.70	0.64
39:a:1923:U:H2'	39:a:1923:U:OP2	1.96	0.64
11:AA:9:LYS:HG2	11:AA:1171:ARG:HH12	1.61	0.64
10:B:18:G:C8	10:B:57:A:C6	2.85	0.64
10:B:37:A:H3'	10:B:37:A:OP2	1.96	0.64
16:D:197:A:C6	16:D:221:C:C4'	2.80	0.64
20:H:162:LYS:CB	20:H:298:GLU:OE2	2.45	0.64
11:AA:995:ASP:OD1	11:AA:995:ASP:N	2.29	0.64
39:a:1909:C:O5'	39:a:1909:C:H6	1.81	0.64
39:a:2303:G:N3	39:a:2314:A:C2	2.66	0.64
2:1:36:LEU:HD13	2:1:48:LYS:HA	1.80	0.64
10:A:18:G:C8	10:A:57:A:C6	2.85	0.64
13:AC:71:LYS:HZ1	13:AC:140:ILE:HB	1.62	0.64
14:AE:67:ASP:OD1	14:AE:95:THR:OG1	2.15	0.64
16:D:1308:U:C3'	36:X:98:ARG:HH21	1.92	0.64
16:D:1358:U:H3	16:D:1363:A:N6	1.96	0.64
39:a:1082:U:N3	39:a:1086:A:N6	2.45	0.64
39:a:1839:G:H8	39:a:1927:A:H1'	1.54	0.64
10:A:50:U:H2'	10:A:51:C:C6	2.33	0.64
10:B:3:C:H2'	10:B:4:G:H8	1.62	0.64
10:B:75:C:OP1	39:a:2602:A:N9	2.30	0.64
20:H:267:TRP:CE3	20:H:340:ARG:HG3	2.32	0.64
7:6:15:DC:N4	7:6:16:DC:H41	1.96	0.64
11:AA:118:LYS:NZ	11:AA:485:ASP:OD1	2.25	0.64
14:AE:975:ILE:HG22	14:AE:977:SER:H	1.62	0.64
54:p:121:ILE:HD12	54:p:141:ILE:HG22	1.79	0.64
9:9:29:ASP:HB2	9:9:56:ARG:HD3	1.79	0.64
14:AE:87:LYS:HG3	22:J:20:PHE:CD1	2.29	0.64
14:AE:136:GLU:CD	14:AE:312:ARG:HH22	2.06	0.64
9:9:11:ILE:HD12	9:9:62:ARG:HD3	1.80	0.64
9:9:57:ASN:OD1	9:9:62:ARG:HD2	1.98	0.64
11:AA:529:ARG:HH11	11:AA:572:ILE:HG22	1.62	0.64
22:J:162:ALA:CB	22:J:165:ARG:HH22	2.08	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AC:120:ASP:HA	28:P:31:ARG:HH22	1.63	0.63
10:B:22:G:H2'	10:B:23:C:H6	1.62	0.63
19:G:18:HIS:HA	20:H:43:LYS:CD	2.27	0.63
20:H:52:GLN:O	20:H:53:PHE:CD1	2.50	0.63
39:a:2885:G:N7	47:i:40:ARG:NH2	2.46	0.63
1:0:40:MET:HE1	64:z:105:ALA:HB1	1.80	0.63
6:5:101:DT:OP2	14:AE:275:ARG:NH2	2.31	0.63
10:A:31:G:O2'	25:M:144:MET:SD	2.56	0.63
11:AA:978:VAL:HG21	11:AA:1010:GLN:HG3	1.79	0.63
11:AA:1257:GLN:OE1	14:AE:345:LYS:HG2	1.96	0.63
16:D:13:U:O4	16:D:20:U:C4	2.52	0.63
9:9:78:GLY:H	9:9:79:PRO:CD	2.10	0.63
10:B:69:C:H2'	10:B:70:G:O4'	1.99	0.63
20:H:270:ILE:HG23	20:H:337:GLU:HB3	1.77	0.63
31:S:47:LYS:O	31:S:50:THR:OG1	2.12	0.63
39:a:1839:G:H1'	39:a:1927:A:N9	2.03	0.63
19:G:35:ARG:HH21	20:H:10:GLU:HG2	1.62	0.63
10:A:69:C:H2'	10:A:70:G:O4'	1.99	0.63
14:AE:245:LEU:HG	14:AE:246:PRO:HD2	1.79	0.63
16:D:1329:A:P	36:X:28:THR:CB	2.83	0.63
16:D:1059:C:O2	28:P:55:PRO:HG3	1.99	0.63
20:H:135:LEU:CA	20:H:157:ILE:CB	2.74	0.63
20:H:332:VAL:HG12	20:H:334:ASP:H	1.62	0.63
39:a:2189:U:O4'	39:a:2189:U:P	2.57	0.63
14:AE:162:GLU:OE1	14:AE:162:GLU:HA	1.97	0.63
16:D:37:U:O2	16:D:548:G:C2	2.52	0.63
39:a:2297:A:C2	39:a:2321:U:C4	2.86	0.63
14:AE:128:LEU:HA	14:AE:192:MET:HE1	1.81	0.63
19:G:18:HIS:CA	20:H:43:LYS:HD2	2.29	0.63
13:AC:120:ASP:HB3	28:P:31:ARG:HH21	1.63	0.62
14:AE:44:ILE:CD1	14:AE:252:LEU:HD21	2.29	0.62
19:G:19:GLN:HG3	20:H:75:VAL:CG2	2.23	0.62
19:G:38:VAL:HG22	20:H:75:VAL:CG2	2.24	0.62
39:a:1021:A:C2	39:a:1141:U:O4	2.51	0.62
39:a:1998:A:OP2	48:j:141:ARG:NH2	2.32	0.62
8:7:16:A:P	11:AA:540:ARG:NH2	2.72	0.62
10:A:37:A:O2'	10:A:38:A:H5'	1.99	0.62
11:AA:858:GLY:O	11:AA:860:ALA:N	2.17	0.62
13:AC:120:ASP:OD1	28:P:90:LEU:HD21	1.99	0.62
14:AE:92:VAL:O	14:AE:92:VAL:HG12	1.99	0.62
10:B:50:U:H2'	10:B:51:C:C6	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:119:GLY:CA	20:H:131:LEU:O	2.46	0.62
6:5:98:DA:C2'	6:5:99:DT:H72	2.28	0.62
11:AA:992:LEU:N	11:AA:992:LEU:HD13	2.14	0.62
13:AC:118:ASP:HB3	28:P:90:LEU:HD23	1.81	0.62
16:D:1309:G:C8	36:X:98:ARG:NH2	2.66	0.62
19:G:19:GLN:CG	20:H:76:GLU:CB	2.76	0.62
11:AA:988:LYS:NZ	11:AA:988:LYS:HB3	2.13	0.62
20:H:270:ILE:CG2	20:H:337:GLU:CB	2.77	0.62
9:9:23:LEU:HB3	9:9:92:ALA:HA	1.81	0.62
11:AA:724:VAL:HG23	11:AA:734:ILE:HD13	1.80	0.62
39:a:1839:G:O4'	39:a:1927:A:H1'	1.97	0.62
6:5:108:DT:O4	11:AA:199:ASP:OD2	2.18	0.62
9:9:57:ASN:CG	9:9:62:ARG:HG2	2.25	0.62
11:AA:1251:TYR:C	11:AA:1259:LEU:HD13	2.24	0.62
14:AE:111:THR:CG2	14:AE:300:GLN:NE2	2.63	0.62
10:A:56:C:O2	39:a:2112:G:C4	2.52	0.62
10:A:65:C:H2'	10:A:66:C:H5'	1.82	0.62
11:AA:850:ILE:O	11:AA:850:ILE:HG22	1.98	0.62
11:AA:868:SER:CB	11:AA:941:LYS:HG2	2.29	0.62
20:H:49:PRO:CD	20:H:84:LEU:HD11	2.29	0.62
20:H:110:GLY:N	20:H:153:GLU:O	2.32	0.62
20:H:270:ILE:HG21	20:H:337:GLU:HB3	1.80	0.62
36:X:101:ARG:O	36:X:101:ARG:HD3	2.00	0.62
39:a:754:U:H2'	39:a:755:U:C6	2.35	0.62
10:A:41:C:C1'	25:M:143:ARG:HH12	2.12	0.62
14:AE:201:LEU:HB2	14:AE:221:ILE:HD13	1.80	0.62
28:P:57:VAL:O	28:P:58:ASN:CG	2.43	0.62
39:a:1789:A:OP2	46:h:221:ARG:NH1	2.32	0.62
10:A:54:U:N3	10:A:58:A:N6	2.48	0.62
14:AE:395:LYS:NZ	14:AE:399:LYS:HD3	2.15	0.62
39:a:1839:G:N9	39:a:1927:A:N9	2.48	0.62
8:7:-6:U:C6	16:D:528:C:OP1	2.53	0.61
14:AE:68:TYR:HB3	14:AE:75:TYR:CZ	2.35	0.61
15:C:29:LEU:O	15:C:33:ILE:HG23	2.00	0.61
19:G:19:GLN:HG3	20:H:76:GLU:HB2	1.82	0.61
20:H:305:HIS:O	20:H:306:VAL:HB	2.00	0.61
11:AA:981:ALA:HB3	11:AA:1008:GLN:CG	2.28	0.61
11:AA:954:LYS:O	11:AA:954:LYS:NZ	2.33	0.61
11:AA:1328:LYS:HD2	14:AE:102:MET:SD	2.40	0.61
19:G:19:GLN:CD	20:H:75:VAL:HG22	2.25	0.61
11:AA:13:LYS:HB2	11:AA:1180:MET:HE2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AC:167:PRO:HB3	21:I:103:ILE:H	1.66	0.61
13:AD:176:CYS:SG	14:AE:535:ARG:NH2	2.72	0.61
10:B:65:C:H2'	10:B:66:C:H5'	1.82	0.61
25:M:23:LEU:O	25:M:27:VAL:HG13	1.99	0.61
37:Y:32:VAL:HA	37:Y:60:VAL:HG11	1.81	0.61
9:9:18:VAL:HG13	9:9:71:CYS:HB2	1.81	0.61
10:A:42:G:H2'	10:A:43:A:H8	1.65	0.61
38:Z:7:ILE:HG23	38:Z:7:ILE:O	2.01	0.61
39:a:1406:U:HO2'	39:a:1407:G:C5'	2.11	0.61
7:6:15:DC:C4	7:6:16:DC:C4	2.89	0.61
14:AE:1355:ARG:NH1	14:AE:1369:ARG:NH1	2.47	0.61
16:D:13:U:C5	16:D:20:U:O4	2.53	0.61
10:A:3:C:H2'	10:A:4:G:C8	2.36	0.61
14:AE:1161:GLY:HA3	14:AE:1179:PRO:HA	1.83	0.61
20:H:267:TRP:CE2	20:H:340:ARG:CG	2.73	0.61
3:2:50:LEU:HD23	43:e:26:PHE:CE1	2.35	0.61
10:B:3:C:H2'	10:B:4:G:C8	2.36	0.61
10:B:54:U:N3	10:B:58:A:N6	2.47	0.61
15:C:44:ILE:CD1	20:H:339:ARG:HG3	2.28	0.61
20:H:84:LEU:HD22	20:H:84:LEU:N	2.16	0.61
10:A:33:U:H4'	25:M:84:THR:HB	1.82	0.61
14:AE:395:LYS:HZ2	14:AE:399:LYS:HD3	1.65	0.61
39:a:2683:C:OP1	63:y:51:ARG:NH2	2.32	0.61
9:9:92:ALA:HB3	9:9:129:LEU:HB2	1.82	0.61
11:AA:374:GLU:HG3	11:AA:374:GLU:O	2.01	0.61
11:AA:660:VAL:HG13	11:AA:661:VAL:HG13	1.82	0.61
8:7:-8:U:H5"	8:7:-8:U:H6	1.65	0.60
14:AE:154:LEU:HD21	14:AE:160:LEU:HD21	1.83	0.60
16:D:658:C:H1'	32:T:22:THR:HG21	1.83	0.60
9:9:77:VAL:HG12	9:9:77:VAL:O	2.01	0.60
9:9:136:ILE:HD12	9:9:139:LEU:HD12	1.83	0.60
10:A:34:C:P	25:M:84:THR:OG1	2.60	0.60
11:AA:979:LEU:HD11	11:AA:998:LEU:HD23	1.83	0.60
33:U:21:VAL:HG21	33:U:60:TRP:CD1	2.36	0.60
37:Y:21:PRO:HB2	37:Y:22:PRO:CD	2.30	0.60
11:AA:1223:ARG:NH2	14:AE:721:SER:OG	2.34	0.60
10:B:42:G:H2'	10:B:43:A:H8	1.65	0.60
10:B:56:C:C4'	52:n:80:ARG:NH2	2.64	0.60
20:H:305:HIS:CD2	20:H:307:SER:H	2.20	0.60
39:a:2720:U:OP1	63:y:53:ARG:NH2	2.34	0.60
44:f:24:LEU:HD11	44:f:54:MET:HE2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:978:VAL:HG11	11:AA:1010:GLN:HB3	1.82	0.60
14:AE:144:TYR:CE1	14:AE:162:GLU:OE2	2.51	0.60
20:H:304:VAL:HG12	20:H:304:VAL:O	1.99	0.60
23:K:107:ALA:HB2	23:K:125:ALA:HB3	1.83	0.60
9:9:6:GLN:OE1	9:9:6:GLN:HA	2.00	0.60
9:9:47:GLU:HG3	9:9:95:LEU:HD21	1.83	0.60
11:AA:861:ALA:HA	11:AA:882:ILE:HD13	1.83	0.60
11:AA:967:LEU:HD12	11:AA:967:LEU:C	2.25	0.60
14:AE:201:LEU:HD11	14:AE:220:ARG:HH11	1.67	0.60
14:AE:342:LEU:HD23	14:AE:1352:ILE:HG23	1.83	0.60
20:H:331:MET:N	20:H:331:MET:SD	2.75	0.60
25:M:69:VAL:HG23	25:M:100:ALA:HB1	1.83	0.60
39:a:2297:A:C2	39:a:2321:U:C5	2.89	0.60
10:A:41:C:H4’	25:M:143:ARG:CZ	2.31	0.60
14:AE:370:LYS:HG2	14:AE:441:LEU:HD23	1.84	0.60
20:H:117:LYS:CB	20:H:278:THR:HG23	2.32	0.60
11:AA:981:ALA:CB	11:AA:1008:GLN:HG3	2.31	0.60
16:D:1308:U:C5’	36:X:98:ARG:HG2	2.32	0.60
19:G:217:VAL:O	19:G:220:THR:HG22	2.02	0.60
20:H:270:ILE:HG21	20:H:337:GLU:CB	2.32	0.60
37:Y:54:ILE:O	37:Y:54:ILE:HG22	2.00	0.60
39:a:84:A:N1	39:a:98:G:O2’	2.33	0.60
11:AA:963:GLU:HA	11:AA:963:GLU:OE1	2.01	0.60
14:AE:24:LEU:CG	14:AE:232:ASN:ND2	2.63	0.60
14:AE:118:LYS:HD2	14:AE:312:ARG:NH2	2.17	0.60
14:AE:514:THR:HG21	14:AE:596:LEU:HD12	1.84	0.60
16:D:1218:C:H2’	16:D:1219:A:C8	2.36	0.60
11:AA:888:THR:OG1	11:AA:889:PRO:HD2	2.02	0.60
14:AE:926:PRO:HG2	14:AE:1248:ILE:HD11	1.84	0.60
14:AE:951:GLN:NE2	14:AE:1014:GLY:O	2.34	0.60
16:D:404:G:N7	22:J:2:ALA:HB3	2.17	0.60
20:H:280:LEU:N	20:H:330:VAL:O	2.32	0.60
8:7:-1:U:H4’	23:K:15:LEU:HD23	1.83	0.59
10:B:47:U:O2’	10:B:50:U:P	2.60	0.59
20:H:118:GLY:C	20:H:133:GLY:HA2	2.27	0.59
4:3:36:VAL:CG1	4:3:39:ILE:HD12	2.33	0.59
16:D:1227:A:H5’	36:X:110:LYS:HZ1	1.66	0.59
38:Z:20:VAL:O	38:Z:20:VAL:HG12	2.02	0.59
39:a:1921:G:O5’	39:a:1921:G:H8	1.84	0.59
14:AE:223:LEU:HG	14:AE:223:LEU:O	2.00	0.59
20:H:36:VAL:HB	20:H:48:ILE:HB	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:0:U:H5”	8:7:0:U:O2	2.01	0.59
9:9:19:ALA:HA	9:9:70:GLU:HG2	1.84	0.59
16:D:1225:A:H4’	35:W:78:ARG:NH1	2.17	0.59
20:H:284:VAL:HG12	20:H:294:VAL:HB	1.84	0.59
11:AA:870:ILE:HG12	11:AA:884:VAL:CG1	2.33	0.59
11:AA:914:LYS:H	11:AA:914:LYS:HD3	1.68	0.59
14:AE:412:LEU:HD22	14:AE:441:LEU:HD21	1.84	0.59
16:D:13:U:C2	16:D:915:A:N6	2.70	0.59
10:A:47:U:O2’	10:A:50:U:P	2.61	0.59
13:AD:81:ILE:HD13	13:AD:131:CYS:HB2	1.83	0.59
14:AE:90:VAL:O	14:AE:90:VAL:CG1	2.48	0.59
18:F:4:ILE:CD1	18:F:19:PHE:HA	2.33	0.59
9:9:52:MET:HE3	9:9:52:MET:O	2.03	0.59
11:AA:478:ARG:NH1	11:AA:491:ASP:O	2.34	0.59
14:AE:275:ARG:NH1	14:AE:278:ARG:NH1	2.51	0.59
14:AE:416:ILE:HG13	14:AE:441:LEU:HD11	1.83	0.59
37:Y:112:LYS:HZ2	37:Y:112:LYS:HB3	1.68	0.59
11:AA:376:PRO:O	11:AA:376:PRO:HG2	2.02	0.59
13:AC:76:GLU:OE1	13:AC:131:CYS:CA	2.50	0.59
10:B:58:A:H1’	10:B:60:U:C5	2.38	0.59
17:E:25:ARG:HA	17:E:66:LEU:HD21	1.85	0.59
37:Y:78:LEU:HD13	37:Y:108:ILE:HG22	1.85	0.59
39:a:2572:A:C8	48:j:149:ASN:OD1	2.56	0.59
10:A:76:A:H2’	39:a:2394:C:N4	2.11	0.59
11:AA:528:ARG:NH2	11:AA:576:SER:O	2.34	0.59
13:AD:86:LYS:HE3	14:AE:528:THR:CB	2.32	0.59
9:9:31:ARG:HH11	9:9:31:ARG:CG	2.14	0.58
9:9:31:ARG:HG3	9:9:31:ARG:NH1	2.17	0.58
10:A:35:A:H2’	10:A:36:U:C6	2.38	0.58
14:AE:161:THR:HG23	14:AE:164:GLN:H	1.68	0.58
33:U:4:ILE:HG12	33:U:21:VAL:HG22	1.84	0.58
7:6:18:DC:N4	8:7:17:G:H1	1.99	0.58
11:AA:1014:LEU:HA	11:AA:1017:GLN:HG2	1.85	0.58
12:AB:93:ILE:HG22	14:AE:290:ILE:HG22	1.85	0.58
14:AE:802:ASP:OD1	14:AE:1348:LYS:NZ	2.31	0.58
11:AA:976:ARG:HG3	11:AA:989:LEU:HD13	1.85	0.58
20:H:119:GLY:HA3	20:H:132:PRO:C	2.28	0.58
14:AE:67:ASP:OD1	14:AE:67:ASP:N	2.34	0.58
19:G:35:ARG:HD2	20:H:14:LYS:CD	2.32	0.58
11:AA:859:GLU:CB	21:I:109:PRO:CG	2.81	0.58
14:AE:241:VAL:HG12	14:AE:241:VAL:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:D:496:A:N3	16:D:496:A:H2'	2.19	0.58
20:H:110:GLY:H	20:H:153:GLU:C	2.12	0.58
39:a:2245:U:O2'	39:a:2436:G:OP2	2.22	0.58
48:j:33:ARG:NH1	48:j:53:GLY:O	2.36	0.58
9:9:34:THR:HG22	9:9:38:MET:HE3	1.85	0.58
11:AA:1008:GLN:HE21	11:AA:1008:GLN:C	2.11	0.58
14:AE:97:VAL:HG11	14:AE:101:ARG:NH2	2.18	0.58
14:AE:638:SER:OG	14:AE:639:VAL:N	2.36	0.58
16:D:439:U:O2	16:D:440:C:C6	2.56	0.58
16:D:563:A:N6	16:D:884:U:N3	2.51	0.58
39:a:1590:A:H2'	39:a:1591:A:C8	2.38	0.58
51:m:31:LEU:HD22	51:m:42:LEU:HD13	1.84	0.58
9:9:61:ARG:CZ	39:a:1047:G:N7	2.67	0.58
11:AA:979:LEU:HD13	11:AA:1011:LEU:HD21	1.84	0.58
11:AA:1184:THR:HG23	11:AA:1190:ALA:H	1.67	0.58
20:H:72:LEU:HD12	20:H:72:LEU:N	2.11	0.58
20:H:291:GLY:HA2	20:H:305:HIS:HA	1.86	0.58
37:Y:7:TYR:HB2	37:Y:57:VAL:HG22	1.86	0.58
6:5:115:DA:OP2	14:AE:1148:ARG:HG3	2.04	0.58
10:A:58:A:H1'	10:A:60:U:C5	2.38	0.58
11:AA:1034:ARG:NH1	11:AA:1034:ARG:O	2.37	0.58
6:5:99:DT:H2"	6:5:100:DA:H5"	1.85	0.58
9:9:54:VAL:O	9:9:54:VAL:HG22	2.03	0.58
11:AA:867:GLU:HB3	21:I:75:ILE:HG13	1.84	0.58
20:H:330:VAL:HB	20:H:344:LEU:HD23	1.86	0.58
39:a:1839:G:N9	39:a:1927:A:C4	2.72	0.58
14:AE:99:ARG:HG3	14:AE:99:ARG:NH1	2.18	0.58
11:AA:1072:ASN:ND2	11:AA:1111:GLN:OE1	2.37	0.57
11:AA:1142:ARG:NH2	11:AA:1166:ASP:OD1	2.36	0.57
14:AE:124:ILE:HG22	14:AE:124:ILE:O	2.04	0.57
14:AE:438:GLU:HG3	14:AE:485:MET:HE1	1.85	0.57
16:D:1526:G:OP2	18:F:42:THR:HG23	2.04	0.57
10:A:60:U:P	10:A:61:C:H41	2.27	0.57
11:AA:400:VAL:HG11	11:AA:452:ARG:HD2	1.86	0.57
11:AA:1084:ASP:OD1	13:AC:45:ARG:NH1	2.32	0.57
16:D:1329:A:P	36:X:28:THR:OG1	2.62	0.57
20:H:267:TRP:CH2	20:H:340:ARG:CB	2.86	0.57
37:Y:137:LEU:N	37:Y:137:LEU:HD23	2.19	0.57
11:AA:10:ARG:NH1	11:AA:697:LYS:HD3	2.19	0.57
13:AD:15:ASP:HB3	13:AD:27:THR:HB	1.86	0.57
10:B:11:A:H2'	10:B:12:G:C8	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Y:59:THR:HG22	37:Y:61:TYR:HE1	1.69	0.57
13:AC:120:ASP:CB	28:P:31:ARG:NH2	2.67	0.57
13:AD:81:ILE:HD11	13:AD:130:ILE:HG22	1.87	0.57
14:AE:99:ARG:HH11	14:AE:99:ARG:CG	2.18	0.57
39:a:2314:A:O2'	52:n:155:THR:CG2	2.52	0.57
8:7:-8:U:H5"	8:7:-8:U:C6	2.39	0.57
11:AA:218:GLU:OE2	11:AA:300:ASP:N	2.28	0.57
36:X:17:ILE:O	36:X:20:THR:OG1	2.22	0.57
11:AA:1256:GLN:OE1	11:AA:1256:GLN:HA	2.03	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:510:LEU:HD22	14:AE:601:ILE:HD12	1.86	0.57
20:H:290:TYR:C	20:H:305:HIS:O	2.47	0.57
36:X:104:THR:O	36:X:104:THR:HG22	2.03	0.57
2:1:20:VAL:HG11	2:1:44:ALA:HA	1.86	0.57
10:B:50:U:H2'	10:B:51:C:H6	1.69	0.57
20:H:119:GLY:CA	20:H:133:GLY:CA	2.74	0.57
39:a:70:G:H4'	39:a:71:A:OP1	2.02	0.57
9:9:17:GLU:HB3	9:9:86:MET:HB2	1.87	0.57
11:AA:818:VAL:HG22	11:AA:1096:ILE:HG12	1.87	0.57
11:AA:855:PRO:O	11:AA:855:PRO:HG2	2.04	0.57
11:AA:974:ARG:HD2	11:AA:1014:LEU:HD11	1.85	0.57
2:1:93:ALA:HB2	39:a:1614:A:C2	2.40	0.57
14:AE:86:GLU:CG	22:J:166:GLU:HB3	2.34	0.57
26:N:10:MET:HE3	26:N:61:LEU:HD11	1.87	0.57
10:A:11:A:H2'	10:A:12:G:C8	2.40	0.57
11:AA:840:SER:O	11:AA:840:SER:OG	2.19	0.57
10:B:60:U:P	10:B:61:C:H41	2.27	0.57
13:AC:69:SER:OG	13:AC:70:THR:N	2.39	0.56
13:AC:162:GLU:HG2	13:AC:162:GLU:O	2.04	0.56
14:AE:86:GLU:HG3	22:J:166:GLU:HB3	1.86	0.56
23:K:56:VAL:O	23:K:60:ILE:HG23	2.04	0.56
8:7:-6:U:C4	16:D:528:C:OP2	2.58	0.56
10:B:60:U:O2'	10:B:61:C:OP1	2.23	0.56
20:H:110:GLY:N	20:H:153:GLU:CA	2.67	0.56
45:g:16:CYS:HB3	45:g:37:CYS:HB3	1.86	0.56
8:7:-14:A:H2'	8:7:-13:U:H6	1.70	0.56
9:9:78:GLY:H	9:9:79:PRO:HD2	1.68	0.56
11:AA:449:GLY:HA3	11:AA:609:ILE:HG23	1.87	0.56
11:AA:1257:GLN:OE1	14:AE:345:LYS:HB3	2.05	0.56
13:AC:65:LEU:CA	21:I:80:LYS:HB3	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:343:LEU:HD11	14:AE:1324:SER:HB3	1.87	0.56
14:AE:491:LEU:HB2	14:AE:904:ALA:HA	1.86	0.56
14:AE:741:ALA:O	14:AE:762:ASN:ND2	2.38	0.56
10:B:32:C:OP2	27:O:130:ARG:NH2	2.38	0.56
39:a:1818:U:OP2	46:h:156:ARG:NH1	2.38	0.56
14:AE:130:MET:HE2	14:AE:135:ILE:HG12	1.87	0.56
14:AE:903:LEU:HD21	14:AE:1249:ASN:HD22	1.70	0.56
10:A:50:U:H2'	10:A:51:C:H6	1.69	0.56
11:AA:227:LYS:NZ	11:AA:298:ALA:HB1	2.21	0.56
11:AA:241:LEU:HD21	11:AA:246:LEU:HD11	1.88	0.56
11:AA:855:PRO:CB	11:AA:913:VAL:HG21	2.36	0.56
11:AA:875:ALA:N	21:I:80:LYS:HE3	2.21	0.56
14:AE:198:CYS:HA	14:AE:221:ILE:HD11	1.86	0.56
10:B:56:C:C5'	52:n:80:ARG:NH2	2.67	0.56
9:9:35:VAL:HA	9:9:38:MET:HB2	1.88	0.56
10:A:6:G:HO2'	10:A:7:G:H8	1.53	0.56
11:AA:862:LEU:O	21:I:72:ARG:HB3	2.05	0.56
14:AE:74:LYS:HD2	14:AE:85:CYS:SG	2.45	0.56
19:G:148:LEU:HD22	19:G:151:ILE:HD11	1.86	0.56
11:AA:39:ILE:HD12	11:AA:75:LEU:HD22	1.88	0.56
11:AA:1006:GLU:OE1	11:AA:1006:GLU:HA	2.04	0.56
11:AA:1008:GLN:C	11:AA:1010:GLN:H	2.12	0.56
11:AA:1069:ARG:NH2	11:AA:1114:GLU:OE2	2.30	0.56
11:AA:1246:ARG:NH1	11:AA:1266:GLY:HA2	2.20	0.56
14:AE:1046:ILE:HD12	14:AE:1059:LEU:HB3	1.86	0.56
16:D:321:A:N7	16:D:328:C:O2'	2.35	0.56
28:P:6:ILE:HG23	28:P:100:ILE:HG23	1.87	0.56
37:Y:96:LYS:HE3	37:Y:136:GLY:HA3	1.87	0.56
59:u:77:ILE:HD11	59:u:108:ALA:HB1	1.87	0.56
50:l:104:ALA:O	50:l:108:ILE:HG23	2.05	0.56
1:0:51:VAL:HG23	64:z:86:ALA:O	2.05	0.56
11:AA:1251:TYR:C	11:AA:1259:LEU:HD11	2.31	0.56
19:G:19:GLN:NE2	20:H:75:VAL:HG22	2.19	0.56
39:a:404:A:O2'	39:a:405:U:OP2	2.22	0.56
39:a:2249:U:H3'	39:a:2250:G:C5'	2.36	0.56
8:7:6:U:OP2	11:AA:1306:LYS:CE	2.54	0.56
11:AA:801:ARG:HG2	11:AA:1094:VAL:HG23	1.87	0.56
11:AA:880:GLY:O	11:AA:919:ARG:HD3	2.06	0.56
39:a:580:U:O3'	64:z:31:VAL:HG13	2.05	0.56
41:c:31:PRO:HG2	41:c:33:LEU:HD13	1.87	0.56
13:AC:91:ARG:HD2	13:AC:122:GLU:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:18:G:C8	10:B:57:A:N6	2.69	0.55
16:D:1227:A:P	36:X:110:LYS:HZ2	2.29	0.55
29:Q:67:ALA:HB2	29:Q:96:THR:HG23	1.86	0.55
10:A:56:C:C6	39:a:2168:G:C6	2.94	0.55
14:AE:144:TYR:HE1	14:AE:162:GLU:CD	2.14	0.55
14:AE:833:GLU:HB2	14:AE:1242:ARG:NH1	2.22	0.55
14:AE:1166:GLY:HA3	14:AE:1174:ARG:HB2	1.88	0.55
10:B:11:A:H8	10:B:11:A:O5'	1.89	0.55
20:H:49:PRO:HD3	20:H:84:LEU:HD11	1.87	0.55
35:W:15:LEU:HD13	35:W:33:THR:HG21	1.88	0.55
39:a:2000:C:OP1	61:w:5:LYS:NZ	2.36	0.55
60:v:66:ARG:NH1	60:v:104:GLU:OE1	2.39	0.55
8:7:-12:G:H5"	16:D:1501:C:N4	2.21	0.55
8:7:-5:U:H5"	8:7:-5:U:O2	2.07	0.55
11:AA:1257:GLN:NE2	14:AE:346:ARG:H	2.04	0.55
13:AC:120:ASP:HB3	28:P:31:ARG:NH2	2.21	0.55
14:AE:102:MET:HG2	14:AE:246:PRO:HG3	1.87	0.55
16:D:528:C:H6	16:D:528:C:H5"	1.71	0.55
20:H:267:TRP:CH2	20:H:340:ARG:HB3	2.41	0.55
11:AA:1030:GLU:CG	16:D:1030:U:O4	2.55	0.55
7:6:21:DA:N6	8:7:15:G:H1	2.04	0.55
11:AA:867:GLU:N	21:I:75:ILE:CG1	2.70	0.55
13:AD:196:THR:HB	14:AE:443:GLU:CG	2.36	0.55
7:6:26:DT:H2"	7:6:27:DG:H5'	1.89	0.55
10:A:38:A:H2'	10:A:39:C:H5'	1.89	0.55
11:AA:1046:VAL:HG22	11:AA:1049:ILE:HG13	1.88	0.55
14:AE:86:GLU:CA	22:J:166:GLU:CB	2.73	0.55
16:D:563:A:N6	16:D:884:U:H3	2.05	0.55
20:H:84:LEU:HD22	20:H:84:LEU:H	1.72	0.55
20:H:154:PHE:CB	20:H:168:VAL:CB	2.85	0.55
20:H:305:HIS:HD2	20:H:306:VAL:H	1.49	0.55
39:a:2303:G:C4	39:a:2314:A:C2	2.95	0.55
10:A:11:A:O5'	10:A:11:A:H8	1.89	0.55
10:A:72:A:H2'	10:A:73:A:C5'	2.32	0.55
11:AA:724:VAL:CG1	11:AA:774:GLY:N	2.68	0.55
14:AE:1175:LEU:HD22	14:AE:1190:ILE:HD11	1.88	0.55
9:9:31:ARG:HD2	39:a:1054:A:H5'	1.80	0.55
13:AC:140:ILE:HD11	13:AC:142:MET:HE3	1.89	0.55
14:AE:759:ILE:HG23	14:AE:771:GLN:HB3	1.89	0.55
38:Z:2:ILE:HB	38:Z:5:ASP:HB3	1.89	0.55
11:AA:872:TYR:OH	21:I:80:LYS:NZ	2.27	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:1246:ARG:NH1	11:AA:1258:PRO:HB3	2.22	0.55
14:AE:39:LYS:O	14:AE:273:ILE:HG21	2.06	0.55
14:AE:1155:ILE:HG13	14:AE:1210:ILE:HB	1.88	0.55
20:H:332:VAL:O	20:H:334:ASP:N	2.40	0.55
32:T:5:THR:O	32:T:8:THR:OG1	2.18	0.55
37:Y:116:MET:HG3	37:Y:124:MET:HB3	1.89	0.55
50:l:108:ILE:HD11	50:l:180:LEU:HD13	1.89	0.55
9:9:51:TYR:CD1	9:9:51:TYR:C	2.85	0.55
14:AE:145:VAL:HG23	14:AE:159:ILE:HG22	1.89	0.55
14:AE:171:GLU:HA	14:AE:171:GLU:OE1	2.05	0.55
10:B:56:C:C5'	52:n:80:ARG:CZ	2.76	0.55
37:Y:77:VAL:O	37:Y:77:VAL:HG12	2.05	0.55
39:a:2314:A:O2'	52:n:155:THR:HG21	2.06	0.55
11:AA:976:ARG:HG3	11:AA:976:ARG:HH11	1.71	0.54
11:AA:1252:SER:N	11:AA:1259:LEU:CD1	2.70	0.54
13:AD:142:MET:N	13:AD:142:MET:SD	2.80	0.54
20:H:52:GLN:OE1	20:H:86:ARG:CB	2.55	0.54
7:6:2:DC:H2"	7:6:3:DC:C5	2.43	0.54
8:7:-14:A:C4	8:7:-13:U:C5	2.95	0.54
11:AA:174:ALA:HB2	11:AA:432:LEU:HD13	1.88	0.54
11:AA:840:SER:HA	11:AA:886:LYS:HD2	1.89	0.54
11:AA:991:LYS:HB2	11:AA:992:LEU:HD22	1.88	0.54
11:AA:1034:ARG:HH11	11:AA:1034:ARG:CG	2.20	0.54
11:AA:1287:LEU:HD13	14:AE:1357:ILE:HD11	1.89	0.54
13:AC:65:LEU:CA	21:I:80:LYS:CB	2.85	0.54
16:D:961:U:O4	16:D:974:A:N1	2.40	0.54
28:P:8:ILE:HD12	28:P:25:ILE:HD11	1.89	0.54
8:7:-12:G:C3'	16:D:1500:A:N6	2.71	0.54
9:9:31:ARG:HD2	39:a:1054:A:C4'	2.29	0.54
10:A:76:A:C2'	39:a:2394:C:H42	2.16	0.54
11:AA:724:VAL:HG12	11:AA:774:GLY:H	1.72	0.54
14:AE:26:SER:HB2	14:AE:236:TRP:CE2	2.42	0.54
10:B:72:A:H2'	10:B:73:A:C5'	2.33	0.54
20:H:71:ALA:O	20:H:72:LEU:CD1	2.42	0.54
56:r:58:LEU:O	56:r:61:VAL:HG22	2.08	0.54
62:x:35:ILE:HG21	62:x:71:ALA:HA	1.90	0.54
14:AE:58:CYS:SG	14:AE:59:ALA:N	2.80	0.54
14:AE:746:LEU:HG	14:AE:758:PRO:HG3	1.90	0.54
10:B:12:G:H2'	10:B:13:C:OP1	2.08	0.54
16:D:1515:G:H2'	16:D:1516:G:H8	1.72	0.54
20:H:116:VAL:C	20:H:279:LYS:HB2	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:332:VAL:CG1	20:H:335:ILE:HG13	2.33	0.54
14:AE:136:GLU:OE1	14:AE:312:ARG:CZ	2.55	0.54
30:R:80:ILE:HD12	30:R:97:THR:HG22	1.89	0.54
37:Y:33:ASN:H	37:Y:66:PHE:HE1	1.56	0.54
2:1:59:GLU:CG	2:1:66:ILE:HD11	2.38	0.54
14:AE:37:GLU:O	14:AE:61:ILE:CD1	2.52	0.54
16:D:1308:U:H2'	36:X:98:ARG:HH22	1.61	0.54
20:H:22:SER:N	20:H:69:ASP:OD2	2.40	0.54
10:A:12:G:H2'	10:A:13:C:OP1	2.08	0.54
13:AD:215:GLU:OE1	13:AD:218:ARG:NH1	2.40	0.54
14:AE:804:ALA:O	14:AE:806:ASP:N	2.41	0.54
16:D:945:G:C2	16:D:946:A:C8	2.96	0.54
37:Y:12:VAL:HG12	37:Y:23:VAL:HG21	1.90	0.54
3:2:50:LEU:HD23	43:e:26:PHE:CZ	2.42	0.54
11:AA:452:ARG:HH12	11:AA:458:GLU:CD	2.15	0.54
11:AA:1253:LEU:HD12	14:AE:253:VAL:HG13	1.90	0.54
14:AE:30:ILE:HG21	14:AE:241:VAL:O	2.08	0.54
14:AE:785:ASP:O	14:AE:789:LYS:HB2	2.08	0.54
37:Y:109:ALA:HB2	37:Y:128:ILE:HG13	1.89	0.54
8:7:-12:G:H3'	16:D:1500:A:N6	2.23	0.54
9:9:139:LEU:HD11	38:Z:11:VAL:HG13	1.90	0.54
10:A:18:G:C8	10:A:57:A:N6	2.69	0.54
13:AC:215:GLU:OE2	13:AC:219:ARG:NH2	2.41	0.54
16:D:439:U:O2	16:D:440:C:C5	2.61	0.54
45:g:18:CYS:HB3	45:g:40:CYS:HB2	1.88	0.54
50:l:130:LYS:HB2	50:l:133:LEU:HD12	1.89	0.54
11:AA:699:LEU:HG	11:AA:799:ASN:HD22	1.72	0.53
11:AA:870:ILE:HG23	11:AA:884:VAL:HG13	1.90	0.53
23:K:99:ALA:HB1	23:K:103:THR:HG21	1.89	0.53
40:b:37:ILE:HD11	40:b:82:ILE:HD11	1.90	0.53
13:AD:22:THR:OG1	13:AD:207:THR:O	2.26	0.53
39:a:811:U:H2'	59:u:21:ARG:HA	1.89	0.53
8:7:-5:U:O4	16:D:1397:C:C5	2.62	0.53
9:9:58:THR:HG21	9:9:81:LEU:HA	1.90	0.53
11:AA:738:GLU:HA	11:AA:741:MET:HE2	1.90	0.53
14:AE:46:TYR:CD1	14:AE:46:TYR:C	2.85	0.53
8:7:15:G:H2'	8:7:16:A:C8	2.43	0.53
10:A:6:G:O2'	10:A:7:G:H8	1.92	0.53
10:A:18:G:C2	10:A:58:A:C5	2.96	0.53
11:AA:867:GLU:H	21:I:75:ILE:HG12	1.74	0.53
11:AA:953:LEU:HD13	11:AA:1036:ILE:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:107:GLU:OE1	14:AE:288:PRO:CB	2.52	0.53
13:AD:100:LEU:O	13:AD:144:ILE:N	2.39	0.53
14:AE:814:CYS:SG	14:AE:883:ARG:NH2	2.81	0.53
10:B:18:G:C2	10:B:58:A:C5	2.97	0.53
16:D:769:G:H4'	16:D:1513:A:H4'	1.88	0.53
20:H:19:ARG:O	20:H:72:LEU:HD22	2.09	0.53
37:Y:116:MET:HE2	37:Y:117:THR:H	1.74	0.53
37:Y:138:VAL:HG12	37:Y:138:VAL:O	2.08	0.53
39:a:2192:U:H2'	39:a:2193:G:C8	2.43	0.53
62:x:27:VAL:HG21	62:x:40:ILE:HD12	1.89	0.53
8:7:17:G:H2'	8:7:18:A:C8	2.44	0.53
9:9:43:LYS:HG2	9:9:98:GLU:HG2	1.90	0.53
10:A:56:C:H2'	10:A:57:A:C5'	2.27	0.53
39:a:2315:G:O2'	52:n:125:ARG:HD3	2.09	0.53
11:AA:958:LYS:HB3	11:AA:958:LYS:HZ1	1.72	0.53
13:AD:33:ARG:HD3	13:AD:197:ASP:HB2	1.91	0.53
16:D:673:A:H2'	16:D:674:G:C8	2.44	0.53
37:Y:57:VAL:O	37:Y:57:VAL:HG12	2.07	0.53
9:9:123:ILE:O	9:9:123:ILE:HG12	2.08	0.53
9:9:125:ARG:HA	9:9:125:ARG:CZ	2.38	0.53
10:A:16:C:O2	10:A:16:C:H2'	2.08	0.53
11:AA:884:VAL:HG11	11:AA:1050:VAL:HG11	1.90	0.53
11:AA:1257:GLN:OE1	14:AE:345:LYS:CB	2.57	0.53
14:AE:39:LYS:O	14:AE:273:ILE:HG23	2.08	0.53
14:AE:67:ASP:CG	14:AE:95:THR:HG1	2.17	0.53
14:AE:99:ARG:HG3	14:AE:99:ARG:HH11	1.74	0.53
10:B:16:C:O2	10:B:16:C:H2'	2.08	0.53
16:D:1228:C:OP2	36:X:110:LYS:NZ	2.41	0.53
20:H:45:GLU:OE1	20:H:45:GLU:N	2.40	0.53
20:H:84:LEU:H	20:H:84:LEU:CD2	2.21	0.53
22:J:61:VAL:HG21	22:J:200:ILE:CD1	2.35	0.53
37:Y:37:PHE:CZ	37:Y:56:VAL:HG11	2.44	0.53
52:n:8:TYR:HA	52:n:12:VAL:HB	1.91	0.53
4:3:13:VAL:CG2	4:3:39:ILE:HD13	2.39	0.53
11:AA:726:TYR:HD2	11:AA:726:TYR:O	1.92	0.53
13:AC:171:LEU:HD23	13:AC:171:LEU:N	2.24	0.53
14:AE:112:ALA:HA	14:AE:238:ILE:HA	1.91	0.53
16:D:13:U:C2	16:D:915:A:C6	2.95	0.53
20:H:135:LEU:CB	20:H:157:ILE:CB	2.87	0.53
11:AA:835:GLU:OE2	11:AA:1051:LYS:HD3	2.08	0.53
14:AE:56:LEU:CD1	14:AE:273:ILE:HD12	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:215:LYS:HA	14:AE:218:THR:HG22	1.91	0.53
16:D:13:U:C4	16:D:21:G:C2	2.96	0.53
16:D:767:A:H2'	16:D:768:A:O4'	2.08	0.53
20:H:24:VAL:HG12	20:H:69:ASP:H	1.74	0.53
20:H:321:VAL:HG13	20:H:322:VAL:HG23	1.90	0.53
23:K:94:VAL:HG13	23:K:111:MET:HE1	1.91	0.53
39:a:1056:G:O2'	39:a:1103:A:N6	2.41	0.53
8:7:-12:G:C4'	16:D:1500:A:H62	2.21	0.53
11:AA:862:LEU:HD23	11:AA:862:LEU:H	1.74	0.53
13:AC:119:GLY:H	28:P:90:LEU:CD2	2.14	0.53
14:AE:78:LEU:O	14:AE:78:LEU:HD13	2.08	0.53
37:Y:19:PRO:HG2	37:Y:24:GLY:H	1.73	0.53
45:g:16:CYS:CB	45:g:37:CYS:CB	2.82	0.53
50:l:131:THR:HG22	50:l:160:ALA:O	2.08	0.53
8:7:-5:U:O2'	21:I:162:ILE:HG13	2.09	0.52
10:A:12:G:C2'	10:A:13:C:OP1	2.58	0.52
11:AA:628:HIS:HB3	11:AA:647:ARG:HH21	1.73	0.52
11:AA:946:LEU:HD23	11:AA:946:LEU:N	2.23	0.52
11:AA:1275:VAL:HG13	11:AA:1287:LEU:HD11	1.90	0.52
13:AD:182:ARG:CD	14:AE:581:MET:HE1	2.39	0.52
14:AE:124:ILE:HG23	14:AE:128:LEU:HD12	1.89	0.52
14:AE:209:ASN:HA	14:AE:214:ARG:HH21	1.74	0.52
20:H:49:PRO:HD2	20:H:84:LEU:CD1	2.39	0.52
39:a:1906:G:H5"	39:a:1906:G:H8	1.73	0.52
58:t:7:MET:HE1	58:t:44:LYS:HD2	1.91	0.52
10:A:56:C:C2	39:a:2112:G:C8	2.96	0.52
11:AA:242:VAL:HB	11:AA:245:ARG:NH1	2.24	0.52
11:AA:994:ARG:HD2	11:AA:994:ARG:O	2.09	0.52
11:AA:998:LEU:HD21	11:AA:1011:LEU:HD13	1.90	0.52
10:B:12:G:C2'	10:B:13:C:OP1	2.57	0.52
10:B:22:G:O2'	10:B:23:C:P	2.67	0.52
10:B:76:A:N3	39:a:2493:U:H4'	2.24	0.52
10:A:22:G:O2'	10:A:23:C:P	2.68	0.52
13:AD:109:PRO:HA	13:AD:132:HIS:HA	1.91	0.52
14:AE:68:TYR:CA	14:AE:75:TYR:HE2	2.22	0.52
15:C:61:ARG:NH2	16:D:736:C:OP1	2.43	0.52
16:D:1329:A:OP1	36:X:28:THR:N	2.42	0.52
19:G:35:ARG:NH2	20:H:10:GLU:HG2	2.25	0.52
28:P:24:GLU:OE2	28:P:90:LEU:CD1	2.56	0.52
10:A:15:G:N3	10:A:15:G:C2'	2.73	0.52
11:AA:808:ASN:H	14:AE:633:ALA:HB2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:960:LEU:HB3	11:AA:1025:PHE:CE1	2.45	0.52
11:AA:984:VAL:O	11:AA:984:VAL:HG22	2.10	0.52
11:AA:985:GLU:HB2	11:AA:988:LYS:HB2	1.90	0.52
14:AE:205:LEU:HG	14:AE:217:LEU:HB3	1.90	0.52
10:A:38:A:C2'	10:A:39:C:H5'	2.39	0.52
14:AE:201:LEU:HD12	14:AE:224:LEU:HD12	1.91	0.52
14:AE:832:LYS:HB3	14:AE:1242:ARG:NH1	2.24	0.52
27:O:81:HIS:O	27:O:84:THR:OG1	2.23	0.52
4:3:94:ARG:HB3	4:3:103:ILE:HD12	1.91	0.52
8:7:20:G:O2'	14:AE:425:ARG:NH2	2.40	0.52
9:9:71:CYS:HA	9:9:117:LEU:HD13	1.91	0.52
10:B:6:G:O2'	10:B:7:G:H8	1.92	0.52
20:H:135:LEU:CB	20:H:167:VAL:CA	2.86	0.52
39:a:1910:G:O5'	39:a:1910:G:H8	1.93	0.52
10:A:17:C:O2	10:A:17:C:H2'	2.08	0.52
11:AA:813:GLU:HB2	14:AE:461:PHE:HD2	1.74	0.52
11:AA:876:GLU:HG2	13:AC:159:ILE:HD11	1.92	0.52
14:AE:144:TYR:CE1	14:AE:162:GLU:CD	2.88	0.52
10:B:17:C:O2	10:B:17:C:H2'	2.08	0.52
16:D:1308:U:P	36:X:98:ARG:HG3	2.50	0.52
20:H:267:TRP:CZ3	20:H:340:ARG:HG3	2.43	0.52
37:Y:27:LEU:HD12	37:Y:27:LEU:C	2.35	0.52
39:a:639:U:H2'	39:a:640:C:C6	2.45	0.52
39:a:1209:U:O2'	39:a:1237:A:N1	2.40	0.52
39:a:1693:U:O2'	46:h:14:ARG:NH2	2.43	0.52
39:a:2298:A:C5	39:a:2321:U:O4	2.62	0.52
39:a:2328:A:H2'	39:a:2329:U:C6	2.44	0.52
9:9:62:ARG:CG	9:9:62:ARG:HH21	2.14	0.52
11:AA:524:ILE:HG21	11:AA:708:VAL:HG13	1.91	0.52
16:D:927:G:O2'	16:D:1503:A:N7	2.36	0.52
27:O:98:LEU:HB3	27:O:104:VAL:HG13	1.92	0.52
9:9:3:LEU:HD13	9:9:5:LEU:H	1.75	0.52
10:A:60:U:O2'	10:A:61:C:OP1	2.23	0.52
11:AA:862:LEU:HD23	11:AA:862:LEU:N	2.25	0.52
14:AE:111:THR:HG22	14:AE:300:GLN:NE2	2.23	0.52
37:Y:100:ILE:HB	37:Y:105:LEU:HD11	1.92	0.52
39:a:523:C:O2	39:a:554:U:O2'	2.25	0.52
8:7:16:A:H2'	8:7:17:G:C8	2.45	0.52
14:AE:390:LEU:N	14:AE:390:LEU:CD1	2.73	0.52
20:H:308:GLU:O	20:H:310:ASP:N	2.43	0.52
37:Y:59:THR:HG22	37:Y:61:TYR:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:a:1266:G:OP2	47:i:17:ARG:NE	2.43	0.52
64:z:58:ARG:HA	64:z:61:TRP:CE3	2.45	0.52
14:AE:975:ILE:HD11	14:AE:1003:LEU:HD11	1.91	0.51
10:B:56:C:C3'	10:B:57:A:H5"	2.40	0.51
16:D:1308:U:OP1	36:X:100:GLN:OE1	2.23	0.51
21:I:77:ILE:HA	21:I:84:VAL:HG23	1.91	0.51
14:AE:850:LYS:HB2	14:AE:857:LEU:HB2	1.91	0.51
39:a:929:U:H1'	44:f:26:GLY:O	2.10	0.51
8:7:-13:U:H2'	8:7:-12:G:C8	2.45	0.51
9:9:23:LEU:HA	9:9:118:ILE:HG13	1.93	0.51
9:9:93:ALA:O	9:9:129:LEU:HD13	2.06	0.51
9:9:125:ARG:HG3	9:9:125:ARG:O	2.10	0.51
10:A:56:C:H1'	39:a:2112:G:C5	2.46	0.51
11:AA:1007:LYS:HD2	11:AA:1007:LYS:C	2.35	0.51
16:D:1228:C:OP1	36:X:107:ARG:CZ	2.58	0.51
37:Y:112:LYS:NZ	37:Y:112:LYS:CB	2.73	0.51
39:a:587:C:OP2	59:u:21:ARG:NH1	2.43	0.51
42:d:106:G:H2'	42:d:107:G:O4'	2.10	0.51
61:w:38:LEU:N	61:w:39:PRO:CD	2.73	0.51
10:A:76:A:O2'	39:a:2395:C:C2	2.64	0.51
11:AA:1045:GLY:O	11:AA:1047:LEU:HD13	2.10	0.51
13:AD:182:ARG:HD3	14:AE:581:MET:HE1	1.91	0.51
14:AE:99:ARG:HA	14:AE:248:ASP:HB2	1.92	0.51
14:AE:683:ILE:HD12	14:AE:754:ILE:HG21	1.93	0.51
10:B:18:G:C2	10:B:58:A:C6	2.99	0.51
10:B:24:U:O2'	39:a:1922:G:O3'	2.29	0.51
16:D:1404:C:H2'	16:D:1404:C:O2	2.10	0.51
16:D:1499:A:O2'	16:D:1500:A:H5'	2.10	0.51
54:p:121:ILE:HD12	54:p:141:ILE:CG2	2.41	0.51
10:A:34:C:P	25:M:84:THR:HG1	2.34	0.51
10:A:56:C:C3'	10:A:57:A:H5"	2.40	0.51
13:AC:118:ASP:HA	28:P:89:ARG:C	2.34	0.51
10:B:15:G:N3	10:B:15:G:C2'	2.73	0.51
16:D:864:A:C2	16:D:865:A:C2	2.98	0.51
20:H:49:PRO:HD2	20:H:84:LEU:HD11	1.92	0.51
39:a:118:A:C8	39:a:119:A:C8	2.99	0.51
9:9:11:ILE:CD1	9:9:11:ILE:N	2.73	0.51
14:AE:88:CYS:HB3	14:AE:90:VAL:HG12	1.92	0.51
15:C:30:LYS:HA	15:C:33:ILE:HD13	1.91	0.51
39:a:1980:G:O2'	39:a:1982:U:OP2	2.28	0.51
42:d:5:U:OP1	42:d:61:G:O2'	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:93:ALA:HB2	39:a:1614:A:N1	2.25	0.51
14:AE:275:ARG:HH12	14:AE:278:ARG:NH1	2.09	0.51
28:P:57:VAL:O	28:P:57:VAL:HG13	2.11	0.51
39:a:1141:U:O2	39:a:1142:A:N6	2.44	0.51
39:a:1814:G:H4'	46:h:51:THR:HG21	1.92	0.51
58:t:113:MET:O	58:t:116:ILE:HG13	2.11	0.51
11:AA:657:THR:HG21	11:AA:1188:ASP:HB2	1.92	0.51
16:D:1410:A:C2	16:D:1491:G:C2	2.99	0.51
32:T:40:GLN:CA	32:T:40:GLN:HE21	2.23	0.51
8:7:15:G:H2'	8:7:16:A:H8	1.75	0.51
10:A:48:C:H2'	10:A:48:C:O2	2.11	0.51
11:AA:876:GLU:HA	11:AA:876:GLU:OE2	2.11	0.51
11:AA:880:GLY:C	11:AA:919:ARG:HD3	2.36	0.51
11:AA:1252:SER:CA	11:AA:1259:LEU:HD11	2.41	0.51
10:B:5:G:C2'	10:B:6:G:H5'	2.40	0.51
23:K:81:LEU:HD13	23:K:123:VAL:HG12	1.92	0.51
51:m:31:LEU:HD22	51:m:42:LEU:CD1	2.40	0.51
2:1:59:GLU:HG3	2:1:66:ILE:HD11	1.92	0.51
8:7:-12:G:C4'	16:D:1500:A:N6	2.73	0.51
9:9:41:LEU:HD12	37:Y:117:THR:HG22	1.92	0.51
11:AA:694:ARG:NH2	13:AC:83:LEU:HD13	2.26	0.51
11:AA:817:LEU:HD12	11:AA:1078:LYS:HB3	1.93	0.51
11:AA:862:LEU:HD12	21:I:72:ARG:HH22	1.72	0.51
19:G:38:VAL:CG2	20:H:75:VAL:CG2	2.77	0.51
37:Y:80:LYS:HG3	37:Y:86:LYS:HA	1.93	0.51
39:a:1839:G:N9	39:a:1927:A:H1'	2.23	0.51
11:AA:991:LYS:N	11:AA:991:LYS:CD	2.73	0.50
14:AE:972:LYS:HD2	14:AE:1004:ALA:HA	1.93	0.50
20:H:332:VAL:C	20:H:334:ASP:H	2.18	0.50
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.93	0.50
4:3:12:ILE:HG21	4:3:80:ALA:HB2	1.92	0.50
10:A:18:G:C2	10:A:58:A:C6	2.99	0.50
11:AA:988:LYS:NZ	11:AA:988:LYS:CB	2.73	0.50
10:B:34:C:O2	10:B:34:C:H2'	2.11	0.50
39:a:523:C:H4'	39:a:540:C:O2	2.10	0.50
39:a:1824:G:O2'	46:h:252:THR:HG21	2.11	0.50
39:a:1964:G:H4'	39:a:1965:C:OP2	2.11	0.50
61:w:55:ALA:HA	61:w:80:PHE:CE1	2.47	0.50
64:z:47:TYR:CD1	64:z:47:TYR:C	2.90	0.50
2:1:55:ILE:HG23	2:1:66:ILE:HD12	1.93	0.50
6:5:98:DA:N9	6:5:99:DT:H72	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:733:VAL:HG22	11:AA:750:ILE:HG12	1.93	0.50
10:B:15:G:H22	10:B:20:U:H3	1.59	0.50
10:B:48:C:O2	10:B:48:C:H2'	2.11	0.50
16:D:13:U:C4	16:D:915:A:C6	2.92	0.50
16:D:1276:G:O5'	16:D:1276:G:H8	1.93	0.50
57:s:30:THR:HG22	57:s:31:GLU:N	2.27	0.50
2:1:24:ILE:HD13	2:1:36:LEU:HD11	1.93	0.50
10:A:56:C:C5	39:a:2168:G:O6	2.64	0.50
11:AA:689:ALA:HB2	11:AA:1233:LEU:HD23	1.92	0.50
11:AA:859:GLU:HG3	21:I:109:PRO:HG2	1.92	0.50
8:7:0:U:OP2	23:K:15:LEU:HD23	2.11	0.50
11:AA:1032:LYS:HZ1	11:AA:1036:ILE:HD11	1.76	0.50
11:AA:1252:SER:HA	11:AA:1259:LEU:HD11	1.93	0.50
14:AE:1167:LYS:HZ2	14:AE:1170:LYS:HB2	1.75	0.50
16:D:108:G:H5"	16:D:108:G:N3	2.27	0.50
18:F:4:ILE:HD12	18:F:19:PHE:HA	1.93	0.50
26:N:3:MET:HA	26:N:3:MET:HE3	1.94	0.50
39:a:1869:G:N2	39:a:1871:A:O2'	2.44	0.50
54:p:35:ARG:HD3	54:p:71:LEU:HD13	1.93	0.50
6:5:101:DT:H72	14:AE:271:ARG:CZ	2.41	0.50
9:9:52:MET:HE3	9:9:52:MET:CA	2.42	0.50
13:AC:71:LYS:NZ	13:AC:140:ILE:HB	2.27	0.50
10:B:39:C:O5'	10:B:39:C:H6	1.95	0.50
46:h:107:PRO:HD2	46:h:110:LEU:HD22	1.94	0.50
57:s:32:LEU:CD2	57:s:54:ILE:HG21	2.42	0.50
58:t:71:ARG:NH2	58:t:123:LEU:O	2.42	0.50
10:A:41:C:H4'	25:M:143:ARG:NH1	2.25	0.50
12:AB:71:VAL:HG12	12:AB:73:MET:HB2	1.93	0.50
16:D:1366:C:O2'	28:P:62:ARG:NH2	2.44	0.50
10:A:15:G:H22	10:A:20:U:H3	1.59	0.50
11:AA:14:ASP:HA	11:AA:1183:ALA:HB3	1.93	0.50
11:AA:867:GLU:OE1	21:I:49:LYS:HG2	2.12	0.50
11:AA:935:THR:HA	11:AA:1049:ILE:CD1	2.41	0.50
16:D:1208:C:H2'	16:D:1209:C:C6	2.47	0.50
16:D:1356:G:H2'	16:D:1357:A:C8	2.47	0.50
20:H:117:LYS:CB	20:H:278:THR:CG2	2.90	0.50
32:T:21:ASP:O	32:T:22:THR:HG22	2.12	0.50
34:V:48:ASP:HB3	34:V:75:LEU:HD23	1.94	0.50
39:a:2243:U:H2'	39:a:2244:U:C6	2.46	0.50
48:j:25:THR:HG21	48:j:193:VAL:HG22	1.94	0.50
8:7:0:U:H3	23:K:14:LYS:HZ2	1.52	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:62:ARG:HG2	9:9:62:ARG:NH2	2.20	0.50
10:A:37:A:H2'	10:A:38:A:H8	1.77	0.50
14:AE:145:VAL:HG12	14:AE:184:ALA:HB1	1.94	0.50
32:T:4:SER:O	32:T:8:THR:HG23	2.12	0.50
39:a:2557:G:H2'	39:a:2558:C:C6	2.47	0.50
58:t:43:ILE:HD12	58:t:56:ASP:HB2	1.93	0.50
6:5:96:DT:H2"	6:5:97:DC:C5	2.46	0.49
9:9:31:ARG:NH1	9:9:31:ARG:CG	2.73	0.49
9:9:51:TYR:CG	9:9:89:PRO:HD2	2.47	0.49
13:AC:158:ARG:NH1	13:AC:158:ARG:CB	2.73	0.49
39:a:560:C:O2	64:z:48:ARG:NH1	2.41	0.49
39:a:2297:A:C6	39:a:2321:U:O4	2.65	0.49
62:x:51:ALA:HB3	62:x:78:VAL:HB	1.94	0.49
10:A:11:A:C2'	10:A:12:G:O4'	2.60	0.49
11:AA:125:GLY:HA2	11:AA:499:SER:HB2	1.94	0.49
57:s:17:VAL:HG23	57:s:137:PRO:HB2	1.93	0.49
9:9:62:ARG:CG	9:9:62:ARG:NH2	2.73	0.49
11:AA:632:ASP:HA	11:AA:647:ARG:HB2	1.94	0.49
11:AA:1070:HIS:NE2	11:AA:1114:GLU:OE1	2.36	0.49
13:AD:60:GLU:OE2	13:AD:170:ARG:NE	2.44	0.49
13:AD:95:LYS:O	13:AD:148:ARG:NH2	2.42	0.49
14:AE:437:PHE:HZ	14:AE:453:VAL:HG11	1.76	0.49
39:a:464:U:O3'	51:m:12:ARG:NH2	2.45	0.49
9:9:44:ALA:HB1	9:9:52:MET:HB3	1.93	0.49
10:A:28:C:H2'	10:A:29:G:H8	1.76	0.49
11:AA:958:LYS:NZ	11:AA:958:LYS:CB	2.73	0.49
14:AE:102:MET:HG2	14:AE:246:PRO:HD3	1.95	0.49
14:AE:421:VAL:O	14:AE:436:ALA:HA	2.11	0.49
10:B:25:C:H2'	10:B:26:G:H5'	1.94	0.49
16:D:872:A:H2'	16:D:872:A:N3	2.27	0.49
20:H:72:LEU:CD1	20:H:72:LEU:N	2.73	0.49
39:a:2303:G:C6	39:a:2314:A:N1	2.81	0.49
11:AA:867:GLU:N	21:I:75:ILE:HG13	2.27	0.49
20:H:132:PRO:N	20:H:167:VAL:CB	2.75	0.49
24:L:18:VAL:N	24:L:19:PRO:CD	2.76	0.49
39:a:2298:A:N3	39:a:2321:U:C5	2.80	0.49
39:a:2646:C:O5'	39:a:2646:C:H6	1.95	0.49
39:a:742:A:C2	39:a:743:A:C6	3.00	0.49
39:a:2038:G:H2'	39:a:2039:U:O4'	2.13	0.49
51:m:24:THR:HG23	51:m:27:GLY:H	1.78	0.49
10:A:11:A:H2'	10:A:12:G:C1'	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:1008:GLN:C	11:AA:1010:GLN:N	2.70	0.49
13:AC:65:LEU:HD22	21:I:80:LYS:O	2.12	0.49
13:AD:20:SER:OG	13:AD:21:SER:N	2.46	0.49
16:D:50:A:O2'	16:D:360:G:N2	2.45	0.49
16:D:1311:A:OP1	45:g:59:ARG:NH1	2.46	0.49
20:H:120:PHE:CB	20:H:136:VAL:CB	2.91	0.49
8:7:-9:U:C2	16:D:1493:A:H2	2.31	0.49
11:AA:1013:GLN:N	11:AA:1013:GLN:NE2	2.60	0.49
16:D:1499:A:H3'	16:D:1499:A:OP2	2.12	0.49
48:j:4:LEU:HD23	48:j:29:VAL:CG1	2.39	0.49
7:6:21:DA:N6	8:7:15:G:N1	2.61	0.49
8:7:-13:U:OP2	16:D:926:G:N2	2.45	0.49
8:7:-9:U:C2	16:D:1493:A:C2	3.00	0.49
11:AA:845:LEU:HD23	11:AA:845:LEU:N	2.28	0.49
14:AE:114:ILE:HG12	14:AE:311:ARG:HD2	1.95	0.49
14:AE:1371:ARG:HE	14:AE:1372:ARG:NH1	2.10	0.49
10:B:42:G:H2'	10:B:43:A:C8	2.47	0.49
20:H:52:GLN:O	20:H:53:PHE:HD1	1.95	0.49
37:Y:21:PRO:CB	37:Y:22:PRO:CD	2.90	0.49
52:n:127:ASN:ND2	52:n:127:ASN:N	2.60	0.49
10:A:49:G:H8	10:A:49:G:O5'	1.96	0.49
11:AA:728:ASP:HA	11:AA:731:ARG:O	2.12	0.49
11:AA:1102:GLY:HA2	11:AA:1106:ARG:NH1	2.28	0.49
13:AC:167:PRO:HB3	21:I:103:ILE:N	2.27	0.49
14:AE:115:TRP:O	14:AE:1333:THR:HG21	2.13	0.49
14:AE:201:LEU:HD11	14:AE:220:ARG:HG2	1.94	0.49
14:AE:749:LYS:HB3	14:AE:755:ILE:HD11	1.93	0.49
14:AE:809:VAL:HG21	14:AE:909:ILE:HG12	1.95	0.49
10:B:18:G:C5	10:B:57:A:C5	3.01	0.49
20:H:318:PRO:HA	20:H:321:VAL:HG12	1.95	0.49
39:a:1412:U:C4	39:a:1413:A:N7	2.81	0.49
39:a:1433:A:H2'	39:a:1434:A:O4'	2.13	0.49
46:h:210:ALA:HA	46:h:213:TRP:CE3	2.48	0.49
1:0:14:VAL:CG2	1:0:98:ILE:HG13	2.43	0.48
9:9:57:ASN:CG	9:9:62:ARG:HG3	2.30	0.48
10:A:18:G:C5	10:A:57:A:C5	3.01	0.48
10:A:19:G:C5	39:a:2112:G:H4'	2.44	0.48
10:A:47:U:H2'	10:A:48:C:H4'	1.94	0.48
10:A:59:A:H2'	10:A:60:U:H5'	1.94	0.48
11:AA:103:VAL:HG12	11:AA:117:ILE:HG22	1.94	0.48
11:AA:318:SER:OG	11:AA:320:ASP:OD1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:857:VAL:CG1	11:AA:861:ALA:HB2	2.43	0.48
11:AA:988:LYS:HB3	11:AA:988:LYS:HZ2	1.77	0.48
11:AA:1244:HIS:NE2	11:AA:1266:GLY:O	2.34	0.48
13:AC:118:ASP:CB	28:P:90:LEU:CD2	2.87	0.48
14:AE:799:ARG:HG2	14:AE:1325:PHE:HZ	1.78	0.48
8:7:3:U:H1'	23:K:10:GLU:OE2	2.13	0.48
9:9:23:LEU:HD22	9:9:92:ALA:HB1	1.95	0.48
10:A:15:G:C2	10:A:20:U:O2	2.66	0.48
11:AA:24:VAL:HG22	11:AA:578:TYR:HE1	1.78	0.48
11:AA:232:ILE:HD12	11:AA:331:LYS:HA	1.94	0.48
13:AC:71:LYS:NZ	13:AC:140:ILE:CG1	2.76	0.48
14:AE:550:VAL:O	14:AE:569:LEU:HA	2.13	0.48
16:D:1017:U:O2'	16:D:1018:G:O4'	2.31	0.48
28:P:6:ILE:HG23	28:P:100:ILE:CG2	2.43	0.48
41:c:3:ARG:HD2	41:c:30:LEU:HD22	1.94	0.48
61:w:67:PHE:O	61:w:71:ARG:N	2.45	0.48
2:1:25:ARG:NH1	2:1:74:ILE:O	2.46	0.48
14:AE:117:LEU:HG	14:AE:118:LYS:HG3	1.95	0.48
10:B:15:G:C2	10:B:20:U:O2	2.66	0.48
10:B:47:U:H2'	10:B:48:C:H4'	1.94	0.48
16:D:5:U:O2	16:D:5:U:O4'	2.29	0.48
16:D:974:A:OP1	31:S:69:ARG:NH1	2.46	0.48
28:P:6:ILE:CG2	28:P:100:ILE:HG23	2.43	0.48
56:r:3:VAL:HG22	56:r:36:ALA:HB1	1.95	0.48
10:A:5:G:C2'	10:A:6:G:H5'	2.40	0.48
11:AA:914:LYS:NZ	11:AA:914:LYS:HB2	2.29	0.48
10:B:59:A:H2'	10:B:60:U:H5'	1.94	0.48
16:D:13:U:O4	16:D:21:G:N3	2.46	0.48
16:D:1329:A:OP1	36:X:28:THR:OG1	2.31	0.48
23:K:114:VAL:HG21	23:K:141:ILE:HD12	1.94	0.48
37:Y:77:VAL:HG13	37:Y:80:LYS:CE	2.44	0.48
37:Y:77:VAL:HG13	37:Y:80:LYS:HE3	1.95	0.48
43:e:18:LEU:HB2	43:e:53:VAL:HG11	1.95	0.48
10:B:11:A:H2'	10:B:12:G:C1'	2.43	0.48
16:D:1169:A:H2'	16:D:1170:A:C8	2.48	0.48
48:j:156:PHE:CE1	57:s:81:ILE:HD13	2.48	0.48
51:m:22:MET:O	51:m:28:ARG:NH1	2.45	0.48
13:AD:48:LEU:HD22	14:AE:535:ARG:HG3	1.95	0.48
14:AE:1027:VAL:HB	14:AE:1121:LEU:HB2	1.96	0.48
14:AE:1347:LEU:HG	14:AE:1357:ILE:HG23	1.96	0.48
19:G:35:ARG:CD	20:H:14:LYS:HD3	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:V:75:LEU:C	34:V:75:LEU:HD12	2.38	0.48
39:a:2685:G:OP1	58:t:78:ARG:NH2	2.47	0.48
8:7:-8:U:C6	8:7:-8:U:C3'	2.97	0.48
10:A:18:G:N3	10:A:58:A:C6	2.82	0.48
11:AA:991:LYS:HA	11:AA:991:LYS:HE3	1.95	0.48
13:AD:96:ASP:OD1	13:AD:96:ASP:N	2.46	0.48
14:AE:53:ARG:HA	14:AE:54:ASP:HA	1.55	0.48
14:AE:152:THR:HB	14:AE:172:PHE:CZ	2.48	0.48
14:AE:1261:LEU:HD12	14:AE:1304:ARG:HH21	1.79	0.48
39:a:1588:G:C6	39:a:1589:U:O4	2.67	0.48
39:a:1839:G:N9	39:a:1927:A:C1'	2.77	0.48
1:0:40:MET:HE3	1:0:49:ILE:CD1	2.43	0.48
10:A:76:A:N6	39:a:2422:C:O4'	2.46	0.48
14:AE:103:GLY:H	14:AE:244:VAL:HG22	1.79	0.48
10:B:49:G:O5'	10:B:49:G:H8	1.96	0.48
10:B:56:C:H2'	10:B:57:A:C5'	2.27	0.48
10:B:68:C:C4	10:B:69:C:C5	3.02	0.48
39:a:565:C:H2'	39:a:566:U:O4'	2.13	0.48
9:9:17:GLU:HG2	9:9:88:HIS:NE2	2.29	0.48
11:AA:867:GLU:HB3	21:I:75:ILE:CG1	2.43	0.48
11:AA:964:LEU:C	11:AA:964:LEU:CD1	2.86	0.48
13:AC:102:LEU:HB2	13:AC:115:ILE:HG12	1.95	0.48
14:AE:395:LYS:NZ	14:AE:399:LYS:CD	2.74	0.48
16:D:1174:G:H2'	16:D:1175:G:H5'	1.95	0.48
39:a:2636:C:HO2'	48:j:45:TYR:HH	1.57	0.48
2:1:4:ILE:HG12	2:1:106:VAL:HG22	1.95	0.48
10:A:25:C:H2'	10:A:26:G:H5'	1.95	0.48
10:A:37:A:H2'	10:A:38:A:C8	2.48	0.48
11:AA:1101:LEU:HD21	14:AE:508:LEU:HD22	1.95	0.48
40:b:37:ILE:HG21	40:b:80:ILE:HG21	1.95	0.48
2:1:29:VAL:HB	2:1:55:ILE:HD11	1.95	0.47
9:9:50:VAL:CG1	37:Y:119:ALA:CB	2.88	0.47
10:A:58:A:OP2	10:A:58:A:C8	2.67	0.47
11:AA:618:GLN:HG3	14:AE:770:LEU:HD13	1.95	0.47
14:AE:800:LEU:HB3	14:AE:920:ALA:HB1	1.95	0.47
23:K:111:MET:CE	23:K:125:ALA:HB1	2.39	0.47
39:a:2168:G:H8	39:a:2168:G:OP1	1.97	0.47
39:a:2303:G:C2	39:a:2314:A:N3	2.82	0.47
44:f:24:LEU:HD11	44:f:54:MET:CE	2.42	0.47
48:j:121:THR:HB	48:j:127:PHE:CD2	2.49	0.47
9:9:8:LYS:NZ	39:a:1046:A:H61	2.11	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:51:TYR:CD1	9:9:88:HIS:HB2	2.49	0.47
10:A:41:C:H5'	25:M:143:ARG:HD2	1.96	0.47
11:AA:866:ASP:HA	21:I:75:ILE:HA	1.95	0.47
13:AC:43:LEU:O	13:AC:47:LEU:HB2	2.14	0.47
13:AD:191:ARG:NH2	13:AD:193:GLU:O	2.47	0.47
14:AE:1221:LEU:HD22	14:AE:1306:LEU:HB2	1.97	0.47
16:D:13:U:O2	16:D:915:A:N7	2.47	0.47
16:D:371:A:H2'	16:D:372:C:O4'	2.14	0.47
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.47
8:7:16:A:H2'	8:7:17:G:H8	1.80	0.47
11:AA:529:ARG:HH22	11:AA:687:ARG:NH1	2.11	0.47
14:AE:1146:GLU:OE2	14:AE:1310:THR:HG22	2.14	0.47
10:B:11:A:C2'	10:B:12:G:O4'	2.60	0.47
10:B:14:A:N3	10:B:14:A:H2'	2.29	0.47
20:H:330:VAL:HG12	20:H:345:GLY:O	2.14	0.47
10:A:9:G:H5"	10:A:10:G:OP2	2.14	0.47
11:AA:800:MET:HE3	11:AA:800:MET:HB2	1.60	0.47
13:AC:116:THR:C	28:P:89:ARG:CD	2.88	0.47
14:AE:1321:SER:OG	14:AE:1349:GLU:OE2	2.21	0.47
10:B:9:G:H5"	10:B:10:G:OP2	2.14	0.47
16:D:911:U:H2'	16:D:912:C:C6	2.49	0.47
23:K:99:ALA:CB	23:K:103:THR:HG21	2.43	0.47
11:AA:1010:GLN:C	11:AA:1010:GLN:NE2	2.73	0.47
13:AC:118:ASP:HB3	28:P:90:LEU:HA	1.96	0.47
13:AD:104:LYS:HG2	13:AD:110:VAL:HB	1.96	0.47
14:AE:24:LEU:CB	14:AE:232:ASN:OD1	2.54	0.47
14:AE:47:ARG:CZ	14:AE:47:ARG:HB2	2.44	0.47
14:AE:128:LEU:HD21	14:AE:188:LEU:HB3	1.97	0.47
14:AE:141:PHE:HE2	14:AE:296:LYS:CB	2.22	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
10:B:60:U:H4'	10:B:61:C:OP2	2.14	0.47
39:a:686:U:O4	51:m:12:ARG:HB2	2.14	0.47
9:9:118:ILE:HB	9:9:119:PRO:CD	2.45	0.47
10:A:33:U:H2'	10:A:35:A:OP2	2.14	0.47
10:A:60:U:H4'	10:A:61:C:OP2	2.14	0.47
11:AA:976:ARG:HG3	11:AA:976:ARG:NH1	2.30	0.47
11:AA:1029:LEU:C	11:AA:1029:LEU:HD23	2.39	0.47
11:AA:1032:LYS:CA	11:AA:1032:LYS:CE	2.92	0.47
14:AE:833:GLU:N	14:AE:1242:ARG:HH12	2.12	0.47
14:AE:1150:PRO:HG3	14:AE:1214:PRO:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:D:526:C:P	30:R:88:LYS:HE3	2.55	0.47
22:J:162:ALA:O	22:J:165:ARG:O	2.33	0.47
62:x:27:VAL:CG2	62:x:40:ILE:HD12	2.44	0.47
1:0:51:VAL:HG22	1:0:51:VAL:O	2.15	0.47
4:3:7:ARG:HB2	39:a:85:G:OP2	2.13	0.47
9:9:67:THR:H	9:9:68:PRO:HD3	1.80	0.47
10:A:42:G:H2'	10:A:43:A:C8	2.47	0.47
10:A:60:U:OP2	10:A:61:C:N4	2.45	0.47
11:AA:318:SER:H	11:AA:321:LEU:HD12	1.80	0.47
11:AA:559:CYS:HB2	11:AA:662:SER:HB3	1.97	0.47
11:AA:841:ARG:HB2	11:AA:841:ARG:NH1	2.30	0.47
11:AA:1034:ARG:NH1	11:AA:1034:ARG:C	2.73	0.47
11:AA:1047:LEU:O	11:AA:1049:ILE:HD11	2.13	0.47
14:AE:420:PRO:HA	14:AE:437:PHE:O	2.15	0.47
14:AE:968:ASN:HA	14:AE:1117:SER:HB2	1.96	0.47
10:B:18:G:N3	10:B:58:A:C6	2.82	0.47
16:D:526:C:OP2	30:R:88:LYS:HE3	2.15	0.47
16:D:1308:U:P	36:X:98:ARG:CG	3.03	0.47
26:N:102:ALA:HB3	26:N:113:ASP:HB3	1.96	0.47
58:t:18:ARG:HB2	58:t:45:GLU:HB3	1.97	0.47
9:9:48:ALA:HB3	9:9:51:TYR:CD2	2.50	0.47
10:A:14:A:H2'	10:A:14:A:N3	2.29	0.47
11:AA:756:TYR:CD2	13:AC:68:TYR:O	2.68	0.47
11:AA:948:ILE:HA	11:AA:951:MET:SD	2.55	0.47
13:AC:118:ASP:CB	28:P:90:LEU:HD23	2.43	0.47
14:AE:53:ARG:NH2	22:J:164:GLN:C	2.73	0.47
20:H:23:ILE:N	20:H:69:ASP:OD2	2.47	0.47
24:L:67:PRO:O	24:L:70:VAL:HG22	2.15	0.47
28:P:89:ARG:HH21	28:P:89:ARG:HG3	1.79	0.47
37:Y:133:ARG:O	37:Y:133:ARG:HG2	2.14	0.47
39:a:2756:U:C4	39:a:2759:G:C6	3.03	0.47
4:3:94:ARG:CB	4:3:103:ILE:HD12	2.45	0.47
6:5:109:DT:H2"	11:AA:200:ARG:CG	2.37	0.47
9:9:58:THR:HB	9:9:82:ILE:H	1.80	0.47
9:9:132:TYR:CE1	38:Z:19:VAL:HG22	2.50	0.47
10:A:76:A:C2'	39:a:2394:C:N4	2.75	0.47
11:AA:685:MET:SD	11:AA:1073:LYS:HG2	2.55	0.47
11:AA:829:THR:HG23	11:AA:1059:ARG:HA	1.97	0.47
13:AC:166:ARG:HB3	13:AC:166:ARG:NH1	2.30	0.47
13:AD:109:PRO:HB3	13:AD:132:HIS:CD2	2.50	0.47
14:AE:108:ALA:HB1	14:AE:279:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:1219:ASP:O	14:AE:1223:LEU:HB2	2.15	0.47
20:H:309:MET:HE2	20:H:318:PRO:HB3	1.97	0.47
39:a:1020:A:C6	39:a:1141:U:O2	2.68	0.47
48:j:152:PRO:HG3	48:j:156:PHE:CZ	2.50	0.47
9:9:1:MET:SD	9:9:2:ALA:N	2.88	0.47
9:9:139:LEU:HD21	38:Z:11:VAL:HG22	1.97	0.47
10:A:18:G:C8	10:A:57:A:N1	2.84	0.47
11:AA:1257:GLN:CD	14:AE:345:LYS:HB3	2.40	0.47
14:AE:842:ARG:HH22	14:AE:1250:ASP:HB2	1.80	0.47
16:D:1064:G:O2'	16:D:1190:G:N2	2.47	0.47
38:Z:18:ASP:HB3	38:Z:22:LEU:CD1	2.45	0.47
39:a:742:A:C2	39:a:755:U:N3	2.80	0.47
3:2:30:ILE:HD13	3:2:93:LEU:HD12	1.97	0.46
8:7:17:G:H2'	8:7:18:A:H8	1.80	0.46
10:A:68:C:C4	10:A:69:C:C5	3.02	0.46
11:AA:855:PRO:HB3	11:AA:913:VAL:HG21	1.97	0.46
10:B:5:G:C2'	10:B:6:G:C5'	2.93	0.46
10:B:76:A:N3	10:B:76:A:C2'	2.74	0.46
16:D:915:A:C8	16:D:915:A:H3'	2.51	0.46
16:D:1103:C:O2	19:G:106:THR:HG21	2.15	0.46
45:g:18:CYS:HB2	45:g:40:CYS:HB3	1.96	0.46
53:o:13:ARG:HD3	59:u:58:TYR:O	2.14	0.46
10:A:6:G:O2'	10:A:7:G:C5'	2.64	0.46
11:AA:549:ASP:OD2	14:AE:750:PRO:HB3	2.15	0.46
11:AA:618:GLN:OE1	11:AA:635:THR:OG1	2.32	0.46
11:AA:867:GLU:CB	21:I:75:ILE:HG13	2.44	0.46
11:AA:1280:ALA:HB1	14:AE:918:ILE:HG22	1.96	0.46
13:AD:49:SER:O	13:AD:49:SER:OG	2.32	0.46
14:AE:526:VAL:HG12	14:AE:549:LYS:HB2	1.96	0.46
14:AE:902:ASP:OD2	14:AE:905:ARG:HB2	2.15	0.46
14:AE:1167:LYS:NZ	14:AE:1170:LYS:HB2	2.30	0.46
10:B:18:G:C6	10:B:57:A:N7	2.83	0.46
18:F:67:ARG:HD3	18:F:67:ARG:N	2.31	0.46
39:a:299:A:N1	39:a:322:A:O2'	2.47	0.46
39:a:2822:G:OP1	48:j:164:GLN:NE2	2.47	0.46
52:n:36:LEU:HB3	52:n:57:LEU:HD21	1.97	0.46
57:s:84:ILE:HG23	57:s:84:ILE:O	2.14	0.46
11:AA:227:LYS:HZ2	11:AA:298:ALA:HB1	1.79	0.46
11:AA:641:GLU:OE2	14:AE:749:LYS:NZ	2.47	0.46
11:AA:735:LYS:HA	11:AA:748:ILE:HG22	1.96	0.46
11:AA:936:ARG:O	11:AA:936:ARG:HD3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:974:ARG:HD2	11:AA:1014:LEU:CD1	2.46	0.46
11:AA:978:VAL:HG11	11:AA:1010:GLN:CB	2.45	0.46
11:AA:1018:TYR:CD1	11:AA:1018:TYR:C	2.94	0.46
11:AA:1046:VAL:CG2	11:AA:1049:ILE:HG13	2.46	0.46
13:AC:117:HIS:N	28:P:89:ARG:CD	2.72	0.46
14:AE:43:THR:HG22	14:AE:57:PHE:HE1	1.80	0.46
15:C:33:ILE:O	15:C:33:ILE:HG12	2.15	0.46
16:D:373:A:C2	16:D:374:A:C8	3.03	0.46
16:D:604:G:H2'	16:D:605:U:O4'	2.14	0.46
16:D:1175:G:N3	16:D:1176:A:C8	2.83	0.46
16:D:1517:G:H1'	39:a:1919:A:O2'	2.16	0.46
20:H:316:ILE:HD11	20:H:321:VAL:HG11	1.97	0.46
28:P:8:ILE:HD12	28:P:25:ILE:CD1	2.46	0.46
36:X:16:VAL:HG23	36:X:17:ILE:HD12	1.97	0.46
39:a:1814:G:C4'	46:h:51:THR:HG21	2.44	0.46
39:a:2315:G:H5'	52:n:157:THR:HG23	1.97	0.46
39:a:2585:U:O2	39:a:2585:U:O4'	2.32	0.46
11:AA:588:GLU:HA	11:AA:606:LEU:O	2.15	0.46
11:AA:933:VAL:O	11:AA:933:VAL:HG12	2.16	0.46
11:AA:1023:HIS:ND1	11:AA:1023:HIS:C	2.73	0.46
13:AC:141:SER:O	13:AC:141:SER:OG	2.33	0.46
14:AE:141:PHE:CE2	14:AE:296:LYS:CB	2.94	0.46
14:AE:1060:VAL:HG13	14:AE:1106:ILE:HG12	1.96	0.46
16:D:429:U:N3	16:D:431:A:N6	2.64	0.46
16:D:1225:A:OP1	36:X:101:ARG:HB2	2.16	0.46
19:G:114:LEU:HA	19:G:144:LEU:HD13	1.98	0.46
20:H:84:LEU:N	20:H:84:LEU:CD2	2.78	0.46
20:H:279:LYS:HA	20:H:331:MET:CB	2.33	0.46
20:H:291:GLY:HA2	20:H:305:HIS:O	2.15	0.46
20:H:332:VAL:HG13	20:H:342:ILE:HG23	1.98	0.46
39:a:1067:A:O2'	39:a:1068:G:O4'	2.31	0.46
39:a:1993:U:H4'	48:j:133:THR:HG22	1.96	0.46
39:a:2298:A:C6	39:a:2299:U:C2	3.04	0.46
9:9:18:VAL:HA	9:9:86:MET:CE	2.44	0.46
9:9:60:LEU:HB2	9:9:61:ARG:NH2	2.31	0.46
9:9:67:THR:H	9:9:68:PRO:CD	2.29	0.46
10:A:29:G:H2'	10:A:30:G:O4'	2.15	0.46
19:G:16:PHE:CD2	20:H:42:LEU:O	2.69	0.46
39:a:631:A:N3	39:a:2415:G:O2'	2.48	0.46
45:g:37:CYS:N	45:g:40:CYS:SG	2.78	0.46
7:6:18:DC:C2	8:7:17:G:N2	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:31:ARG:HD3	39:a:1054:A:H4'	1.96	0.46
10:A:5:G:C2'	10:A:6:G:C5'	2.93	0.46
10:A:18:G:C6	10:A:57:A:N7	2.83	0.46
10:A:58:A:C1'	10:A:60:U:C5	2.99	0.46
11:AA:243:PRO:HB2	11:AA:274:ILE:HG23	1.96	0.46
11:AA:994:ARG:C	11:AA:994:ARG:CD	2.89	0.46
11:AA:1119:MET:HG3	11:AA:1204:LEU:HD13	1.97	0.46
13:AC:167:PRO:CB	21:I:103:ILE:H	2.28	0.46
14:AE:891:ASP:OD2	14:AE:1290:ARG:NH2	2.47	0.46
10:B:18:G:C8	10:B:57:A:N1	2.83	0.46
28:P:99:GLN:O	28:P:99:GLN:HG2	2.16	0.46
39:a:517:C:OP2	47:i:10:ARG:NH2	2.48	0.46
39:a:1021:A:N6	39:a:1141:U:N3	2.47	0.46
1:0:5:PHE:HB3	1:0:59:ILE:HD12	1.96	0.46
9:9:27:VAL:HG22	9:9:99:PHE:HE2	1.80	0.46
11:AA:965:GLN:HA	11:AA:968:GLU:HB3	1.97	0.46
11:AA:985:GLU:OE2	11:AA:1000:LEU:HD11	2.14	0.46
13:AC:73:GLY:HA3	13:AC:138:ALA:CB	2.46	0.46
14:AE:1036:ARG:HE	14:AE:1081:VAL:HG11	1.79	0.46
36:X:96:PRO:HG2	36:X:102:THR:HG23	1.97	0.46
39:a:2006:C:O2'	39:a:2823:A:N3	2.47	0.46
9:9:43:LYS:NZ	9:9:95:LEU:HD13	2.30	0.46
9:9:50:VAL:HG22	37:Y:119:ALA:C	2.41	0.46
10:A:41:C:C5'	25:M:143:ARG:HD2	2.46	0.46
11:AA:1032:LYS:CE	11:AA:1032:LYS:HA	2.46	0.46
14:AE:847:ASP:N	14:AE:847:ASP:OD1	2.49	0.46
10:B:58:A:C1'	10:B:60:U:C5	2.99	0.46
17:E:54:MET:O	17:E:57:ILE:HG22	2.15	0.46
20:H:135:LEU:CB	20:H:167:VAL:O	2.63	0.46
39:a:2168:G:OP1	39:a:2168:G:C8	2.68	0.46
9:9:24:SER:HB2	9:9:116:GLU:HG2	1.98	0.46
9:9:39:THR:HA	9:9:42:ARG:HH11	1.81	0.46
9:9:43:LYS:HZ1	9:9:95:LEU:HD13	1.81	0.46
11:AA:93:SER:HA	11:AA:128:PRO:HA	1.97	0.46
14:AE:123:ARG:HD3	14:AE:123:ARG:HA	1.48	0.46
14:AE:198:CYS:HA	14:AE:221:ILE:CD1	2.45	0.46
20:H:69:ASP:O	20:H:85:SER:CB	2.63	0.46
39:a:1406:U:H3	39:a:1596:A:H2	1.59	0.46
39:a:2291:U:H2'	39:a:2292:U:C6	2.51	0.46
8:7:9:U:H3'	8:7:9:U:O2	2.16	0.46
9:9:31:ARG:HE	39:a:1054:A:C5'	2.18	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:446:ASP:HA	11:AA:451:ARG:HH21	1.81	0.46
13:AD:131:CYS:SG	13:AD:132:HIS:N	2.89	0.46
13:AD:211:ILE:HD11	13:AD:215:GLU:HG3	1.98	0.46
16:D:946:A:H2'	16:D:947:G:C8	2.50	0.46
16:D:1228:C:P	36:X:107:ARG:HH12	2.38	0.46
19:G:38:VAL:HG23	20:H:75:VAL:HG21	1.92	0.46
34:V:8:LEU:HD23	34:V:25:ILE:HG21	1.97	0.46
37:Y:79:LEU:HD13	37:Y:132:ALA:HA	1.97	0.46
44:f:25:LEU:C	44:f:25:LEU:HD13	2.41	0.46
46:h:76:ALA:HB2	46:h:96:TYR:CD1	2.51	0.46
2:1:17:VAL:HG12	2:1:76:VAL:HG21	1.98	0.45
6:5:113:DC:P	11:AA:163:LYS:HD3	2.55	0.45
7:6:15:DC:N3	7:6:16:DC:C4	2.84	0.45
7:6:21:DA:C6	8:7:15:G:C2	3.03	0.45
9:9:127:ALA:O	9:9:130:PRO:HG2	2.16	0.45
14:AE:115:TRP:HB3	14:AE:1333:THR:CG2	2.46	0.45
14:AE:220:ARG:HG2	14:AE:220:ARG:NH1	2.26	0.45
21:I:75:ILE:HD13	21:I:75:ILE:C	2.40	0.45
52:n:17:MET:HE2	52:n:25:VAL:HA	1.99	0.45
8:7:14:U:H2'	8:7:15:G:C8	2.51	0.45
9:9:125:ARG:NH1	9:9:125:ARG:CA	2.73	0.45
13:AD:96:ASP:HB3	13:AD:148:ARG:HE	1.81	0.45
14:AE:201:LEU:CD1	14:AE:224:LEU:HD12	2.47	0.45
14:AE:1158:GLU:HA	14:AE:1223:LEU:HD21	1.99	0.45
10:B:14:A:H1'	10:B:22:G:N2	2.31	0.45
21:I:117:ALA:HB2	21:I:200:VAL:CG1	2.46	0.45
29:Q:34:ILE:HG12	29:Q:70:CYS:SG	2.56	0.45
38:Z:4:LYS:O	38:Z:4:LYS:HD2	2.15	0.45
38:Z:26:MET:HE2	38:Z:26:MET:HB2	1.71	0.45
39:a:68:G:N2	39:a:74:A:OP2	2.49	0.45
39:a:1394:U:H4'	39:a:1603:A:H4'	1.97	0.45
61:w:28:LEU:HD23	61:w:48:VAL:HG21	1.98	0.45
11:AA:724:VAL:HG12	11:AA:774:GLY:N	2.31	0.45
11:AA:872:TYR:O	21:I:78:GLY:O	2.34	0.45
11:AA:1029:LEU:HD11	11:AA:1033:ARG:HH21	1.82	0.45
13:AC:93:GLN:HB3	28:P:31:ARG:HD3	1.99	0.45
14:AE:87:LYS:CG	22:J:20:PHE:HE1	2.20	0.45
10:B:6:G:O2'	10:B:7:G:C5'	2.64	0.45
16:D:868:C:H2'	16:D:869:G:O4'	2.16	0.45
16:D:1240:U:OP1	25:M:116:MET:HB2	2.16	0.45
19:G:114:LEU:HD13	19:G:144:LEU:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:K:96:MET:CE	23:K:115:LEU:HD11	2.46	0.45
25:M:27:VAL:HG12	25:M:43:VAL:HG11	1.98	0.45
39:a:1695:G:N7	46:h:14:ARG:NH2	2.64	0.45
10:A:48:C:N4	10:A:59:A:C5	2.84	0.45
11:AA:957:LYS:HA	11:AA:1029:LEU:HD12	1.97	0.45
13:AC:58:GLU:HB3	13:AC:170:ARG:HG2	1.99	0.45
13:AD:199:ASP:N	13:AD:199:ASP:OD1	2.47	0.45
14:AE:385:LEU:HD23	14:AE:390:LEU:HB2	1.98	0.45
16:D:1176:A:H2'	16:D:1177:G:O4'	2.16	0.45
50:l:149:ILE:CD1	50:l:188:MET:HE3	2.46	0.45
54:p:24:ILE:CD1	54:p:72:LEU:HD21	2.44	0.45
10:A:68:C:H3'	10:A:69:C:H5"	1.96	0.45
11:AA:967:LEU:HD23	11:AA:1021:LEU:HD21	1.98	0.45
14:AE:926:PRO:HB2	14:AE:1241:TYR:HE1	1.82	0.45
10:B:37:A:N3	10:B:37:A:H5"	2.32	0.45
15:C:12:ARG:CZ	20:H:264:GLU:HA	2.46	0.45
36:X:106:ALA:HB3	36:X:110:LYS:CD	2.47	0.45
37:Y:20:SER:CB	37:Y:21:PRO:HD3	2.39	0.45
39:a:2547:A:H2'	39:a:2548:U:C6	2.52	0.45
52:n:57:LEU:HD22	52:n:89:VAL:CG2	2.46	0.45
9:9:111:ALA:HB3	9:9:114:GLU:HG3	1.98	0.45
11:AA:867:GLU:N	21:I:75:ILE:HG12	2.30	0.45
14:AE:109:SER:HB2	14:AE:296:LYS:HG2	1.98	0.45
14:AE:209:ASN:HA	14:AE:214:ARG:NH2	2.31	0.45
16:D:17:U:H2'	16:D:18:C:C6	2.52	0.45
16:D:1308:U:O5'	36:X:98:ARG:HG2	2.16	0.45
25:M:24:ALA:O	25:M:27:VAL:HG22	2.16	0.45
37:Y:124:MET:HE2	37:Y:124:MET:HB2	1.77	0.45
39:a:954:G:OP2	60:v:16:ARG:NH2	2.50	0.45
39:a:1095:A:O2'	39:a:1096:A:O4'	2.34	0.45
9:9:106:PHE:C	9:9:106:PHE:CD2	2.95	0.45
10:A:76:A:C2	53:o:31:HIS:NE2	2.85	0.45
11:AA:850:ILE:HD12	11:AA:1048:LYS:HG2	1.99	0.45
11:AA:941:LYS:HD3	11:AA:941:LYS:HA	1.78	0.45
10:B:68:C:H3'	10:B:69:C:H5"	1.96	0.45
16:D:35:G:N3	30:R:115:SER:OG	2.47	0.45
28:P:28:THR:HG21	28:P:87:LEU:CD1	2.46	0.45
39:a:784:G:H5'	39:a:785:G:OP1	2.15	0.45
39:a:1047:G:N2	39:a:1110:G:O2'	2.50	0.45
46:h:6:CYS:SG	46:h:13:ARG:NH1	2.89	0.45
56:r:15:LEU:HD13	56:r:15:LEU:C	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:x:18:LEU:HD23	62:x:25:ARG:HD2	1.99	0.45
9:9:106:PHE:CG	9:9:106:PHE:O	2.69	0.45
11:AA:914:LYS:HD3	11:AA:914:LYS:N	2.31	0.45
11:AA:976:ARG:NH2	11:AA:989:LEU:HB3	2.32	0.45
11:AA:1008:GLN:HE22	11:AA:1011:LEU:HG	1.82	0.45
11:AA:1252:SER:N	11:AA:1259:LEU:HD11	2.31	0.45
13:AC:228:LEU:HD11	13:AD:224:LEU:HD23	1.97	0.45
14:AE:1227:HIS:HA	14:AE:1230:THR:HG22	1.99	0.45
10:B:48:C:N4	10:B:59:A:C5	2.84	0.45
27:O:63:LEU:HD13	27:O:65:ILE:HD11	1.97	0.45
39:a:930:G:H1'	44:f:25:LEU:HD11	1.98	0.45
39:a:1385:A:O2'	39:a:1396:U:O2	2.35	0.45
48:j:186:LEU:HD21	63:y:4:ILE:HG21	1.98	0.45
60:v:96:ILE:HG21	60:v:126:ILE:HD12	1.97	0.45
10:A:14:A:H1'	10:A:22:G:N2	2.31	0.45
11:AA:844:LYS:HD3	11:AA:844:LYS:HA	1.47	0.45
11:AA:1034:ARG:NH1	11:AA:1034:ARG:CG	2.77	0.45
13:AD:64:VAL:HG11	13:AD:78:ILE:HG21	1.99	0.45
13:AD:86:LYS:HE3	14:AE:528:THR:HG21	1.97	0.45
14:AE:395:LYS:NZ	14:AE:399:LYS:HE2	2.32	0.45
14:AE:506:VAL:HG23	14:AE:628:GLY:HA3	1.98	0.45
14:AE:978:ARG:HD3	14:AE:999:TYR:H	1.82	0.45
10:B:49:G:C2'	10:B:50:U:H5'	2.47	0.45
16:D:1493:A:C8	16:D:1493:A:OP1	2.70	0.45
20:H:19:ARG:O	20:H:72:LEU:HD13	2.16	0.45
21:I:155:GLY:HA2	21:I:163:ALA:HB1	1.99	0.45
37:Y:19:PRO:HG2	37:Y:24:GLY:N	2.32	0.45
37:Y:23:VAL:HB	37:Y:24:GLY:H	1.65	0.45
37:Y:95:ASP:OD2	37:Y:95:ASP:N	2.50	0.45
39:a:1906:G:H4'	39:a:1906:G:OP1	2.16	0.45
6:5:114:DC:H5"	14:AE:1148:ARG:CZ	2.46	0.45
9:9:50:VAL:CG2	37:Y:120:ASP:N	2.79	0.45
11:AA:562:GLU:OE1	11:AA:662:SER:OG	2.31	0.45
11:AA:933:VAL:HG22	11:AA:935:THR:CG2	2.47	0.45
13:AC:59:VAL:O	13:AC:171:LEU:HG	2.16	0.45
14:AE:50:LYS:HD3	14:AE:50:LYS:HA	1.72	0.45
14:AE:68:TYR:HB3	14:AE:75:TYR:HE2	1.81	0.45
14:AE:76:LYS:HB3	14:AE:76:LYS:NZ	2.32	0.45
14:AE:105:ILE:HD12	14:AE:242:LEU:CD2	2.44	0.45
14:AE:213:LYS:HA	14:AE:213:LYS:HE3	1.99	0.45
10:B:18:G:O2'	10:B:60:U:N3	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:61:ARG:HG2	24:L:88:MET:HE1	1.98	0.45
19:G:76:ALA:CB	19:G:210:VAL:HG11	2.47	0.45
37:Y:42:ASN:HA	37:Y:45:THR:HB	1.98	0.45
38:Z:29:LYS:HB2	38:Z:29:LYS:HE2	1.45	0.45
39:a:645:C:H2'	39:a:647:G:C8	2.52	0.45
39:a:1007:C:OP1	57:s:37:ARG:NH2	2.50	0.45
39:a:1082:U:H3	39:a:1086:A:N6	2.15	0.45
39:a:1720:U:H2'	39:a:1721:G:O4'	2.16	0.45
52:n:29:PRO:HB2	52:n:169:LEU:HD22	1.99	0.45
3:2:1:MET:N	39:a:142:A:O2'	2.48	0.44
9:9:34:THR:HG22	9:9:38:MET:CE	2.47	0.44
11:AA:1020:GLU:HA	11:AA:1023:HIS:HD2	1.81	0.44
13:AD:16:ILE:HD13	13:AD:214:GLU:HG2	1.99	0.44
14:AE:388:ARG:HG2	14:AE:388:ARG:NH1	2.32	0.44
17:E:55:GLN:N	17:E:56:PRO:HD2	2.32	0.44
28:P:28:THR:HG21	28:P:87:LEU:HD12	1.99	0.44
37:Y:37:PHE:CD2	37:Y:37:PHE:O	2.70	0.44
37:Y:37:PHE:CE1	37:Y:56:VAL:HG11	2.51	0.44
57:s:30:THR:CG2	57:s:31:GLU:N	2.79	0.44
11:AA:596:ASP:N	11:AA:596:ASP:OD1	2.49	0.44
13:AC:49:SER:OG	13:AC:50:SER:OG	2.26	0.44
13:AD:212:ASP:O	13:AD:215:GLU:N	2.48	0.44
14:AE:75:TYR:CD2	14:AE:75:TYR:O	2.70	0.44
10:B:25:C:C2'	10:B:26:G:H5'	2.47	0.44
16:D:13:U:C2	16:D:915:A:C5	3.05	0.44
38:Z:7:ILE:HD12	38:Z:7:ILE:HA	1.77	0.44
39:a:39:G:H1'	50:l:43:THR:HG21	1.99	0.44
39:a:2070:A:H2'	39:a:2071:A:O4'	2.16	0.44
56:r:55:GLU:HA	56:r:58:LEU:HD12	1.99	0.44
57:s:114:LEU:HD12	57:s:114:LEU:HA	1.87	0.44
10:A:48:C:C5	10:A:59:A:C8	3.05	0.44
11:AA:538:LEU:HD11	11:AA:571:LEU:HD22	1.98	0.44
11:AA:960:LEU:HB3	11:AA:1025:PHE:CD1	2.53	0.44
13:AC:71:LYS:NZ	13:AC:140:ILE:HG13	2.32	0.44
14:AE:68:TYR:O	14:AE:75:TYR:CD2	2.70	0.44
14:AE:319:SER:HA	14:AE:320:ASN:HA	1.64	0.44
10:B:34:C:C5	10:B:34:C:OP1	2.70	0.44
10:B:34:C:O5'	10:B:34:C:C6	2.70	0.44
18:F:21:ARG:HH22	20:H:341:ARG:HD2	1.82	0.44
19:G:208:ARG:HH12	20:H:29:VAL:HG11	1.82	0.44
22:J:165:ARG:NH1	22:J:165:ARG:HB2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Y:125:THR:HA	37:Y:128:ILE:HG12	1.98	0.44
39:a:340:A:O2'	50:l:162:ARG:NH1	2.50	0.44
39:a:1327:A:H2'	39:a:1328:A:O4'	2.17	0.44
39:a:1589:U:C2	39:a:1590:A:C8	3.06	0.44
39:a:1925:C:C5	39:a:1925:C:OP2	2.70	0.44
7:6:15:DC:C4	7:6:16:DC:C5	3.05	0.44
9:9:72:LEU:HD22	9:9:72:LEU:C	2.42	0.44
9:9:139:LEU:CD2	38:Z:11:VAL:HG22	2.47	0.44
10:A:18:G:O2'	10:A:60:U:N3	2.48	0.44
16:D:397:A:H3'	16:D:397:A:N3	2.32	0.44
16:D:1397:C:O5'	16:D:1397:C:C6	2.70	0.44
22:J:197:GLU:HA	22:J:200:ILE:HD12	1.99	0.44
39:a:1927:A:C8	39:a:1927:A:O5'	2.70	0.44
39:a:2133:G:O2'	39:a:2157:G:N2	2.51	0.44
42:d:48:U:H2'	42:d:49:C:C6	2.52	0.44
43:e:59:GLU:O	43:e:63:ALA:HB3	2.18	0.44
11:AA:524:ILE:HB	11:AA:712:SER:HB2	1.99	0.44
13:AC:71:LYS:HZ1	13:AC:140:ILE:HD12	1.83	0.44
13:AC:92:VAL:HG12	13:AC:121:VAL:HG12	1.99	0.44
13:AC:145:LYS:HE3	13:AC:145:LYS:HB2	1.83	0.44
10:B:48:C:C5	10:B:59:A:C8	3.05	0.44
16:D:109:A:C6	16:D:326:G:C6	3.05	0.44
16:D:1340:A:H8	16:D:1340:A:O5'	1.99	0.44
20:H:33:LYS:HA	20:H:34:ASP:HA	1.61	0.44
27:O:80:ARG:O	27:O:84:THR:HG23	2.17	0.44
39:a:57:C:H2'	39:a:58:G:O4'	2.18	0.44
39:a:1363:C:O2'	39:a:1809:A:N3	2.46	0.44
9:9:106:PHE:CD2	9:9:106:PHE:O	2.70	0.44
10:A:9:G:O2'	10:A:45:G:H2'	2.18	0.44
10:A:25:C:C2'	10:A:26:G:H5'	2.48	0.44
10:A:34:C:OP1	25:M:84:THR:OG1	2.35	0.44
11:AA:95:PRO:HB3	11:AA:123:TYR:HE1	1.83	0.44
11:AA:302:ILE:O	11:AA:330:HIS:NE2	2.34	0.44
11:AA:872:TYR:CD2	21:I:74:GLY:HA2	2.53	0.44
11:AA:874:GLY:HA3	21:I:80:LYS:HG3	1.98	0.44
11:AA:939:VAL:HG12	11:AA:939:VAL:O	2.17	0.44
11:AA:1043:ALA:CB	11:AA:1044:PRO:CD	2.91	0.44
14:AE:62:PHE:CD1	14:AE:62:PHE:N	2.86	0.44
14:AE:1357:ILE:HG22	14:AE:1359:ALA:H	1.82	0.44
10:B:1:C:C5	10:B:2:G:N7	2.86	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)
16:D:684:U:H2'	16:D:685:G:O4'	2.18	0.44
16:D:915:A:H8	16:D:915:A:O5'	2.00	0.44
20:H:38:VAL:HG22	20:H:48:ILE:HD11	1.99	0.44
6:5:98:DA:C2'	6:5:99:DT:C7	2.96	0.44
6:5:116:DG:C6	6:5:117:DA:C6	3.06	0.44
10:A:49:G:C2'	10:A:50:U:H5'	2.47	0.44
11:AA:469:VAL:HA	11:AA:472:GLU:HG2	2.00	0.44
11:AA:726:TYR:O	11:AA:726:TYR:CD2	2.69	0.44
13:AD:111:THR:OG1	13:AD:126:PRO:O	2.35	0.44
10:B:49:G:O5'	10:B:49:G:C8	2.71	0.44
16:D:337:G:H2'	16:D:338:A:C8	2.52	0.44
23:K:153:VAL:HG23	23:K:164:ILE:HD13	2.00	0.44
37:Y:140:GLU:OE1	37:Y:140:GLU:N	2.50	0.44
57:s:73:VAL:HG11	57:s:75:TYR:CZ	2.53	0.44
10:A:1:C:C5	10:A:2:G:N7	2.86	0.44
10:A:56:C:OP1	39:a:2168:G:C4	2.71	0.44
11:AA:1010:GLN:C	11:AA:1010:GLN:CD	2.85	0.44
11:AA:1018:TYR:HA	11:AA:1021:LEU:HD12	2.00	0.44
14:AE:850:LYS:HB3	14:AE:855:ASP:HB2	2.00	0.44
14:AE:1026:PRO:HB2	14:AE:1028:ILE:HG23	2.00	0.44
10:B:22:G:O2'	10:B:23:C:O5'	2.36	0.44
36:X:106:ALA:HB3	36:X:110:LYS:HD2	1.98	0.44
37:Y:7:TYR:CD2	37:Y:7:TYR:O	2.71	0.44
37:Y:121:ILE:HA	37:Y:124:MET:SD	2.58	0.44
39:a:74:A:N7	39:a:88:G:C5	2.86	0.44
11:AA:857:VAL:HG11	11:AA:861:ALA:HB2	1.99	0.44
14:AE:26:SER:HB2	14:AE:236:TRP:CH2	2.51	0.44
14:AE:128:LEU:CD2	14:AE:188:LEU:HB3	2.47	0.44
14:AE:161:THR:H	14:AE:164:GLN:HB2	1.82	0.44
14:AE:1046:ILE:HG22	14:AE:1061:VAL:HA	2.00	0.44
16:D:198:G:OP2	16:D:198:G:C8	2.70	0.44
16:D:976:G:C8	16:D:1358:U:O2	2.71	0.44
19:G:16:PHE:CG	20:H:43:LYS:HA	2.53	0.44
19:G:35:ARG:CG	20:H:10:GLU:OE2	2.63	0.44
20:H:136:VAL:HA	20:H:168:VAL:O	2.18	0.44
20:H:335:ILE:HG12	20:H:342:ILE:HG23	2.00	0.44
60:v:35:ALA:HB2	60:v:102:LEU:HD11	2.00	0.44
6:5:115:DA:P	14:AE:1148:ARG:HG3	2.58	0.43
9:9:67:THR:N	9:9:68:PRO:HD3	2.33	0.43
11:AA:803:ALA:HB2	11:AA:1094:VAL:HG21	1.99	0.43
11:AA:1029:LEU:HA	11:AA:1032:LYS:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AC:65:LEU:CB	21:I:80:LYS:CB	2.88	0.43
16:D:376:G:C2	16:D:389:A:C2	3.05	0.43
16:D:1126:U:OP1	28:P:7:ARG:NH2	2.51	0.43
20:H:294:VAL:HG21	20:H:330:VAL:HG21	1.99	0.43
20:H:302:GLY:HA3	20:H:344:LEU:HD13	2.00	0.43
39:a:813:U:H2'	39:a:814:C:C6	2.53	0.43
39:a:1095:A:H2'	39:a:1096:A:C8	2.53	0.43
8:7:-14:A:H2'	8:7:-13:U:C6	2.50	0.43
10:A:18:G:N3	10:A:58:A:C5	2.87	0.43
10:A:22:G:O2'	10:A:23:C:O5'	2.36	0.43
11:AA:1032:LYS:CA	11:AA:1032:LYS:HE2	2.47	0.43
14:AE:58:CYS:SG	14:AE:60:ARG:HG2	2.59	0.43
14:AE:107:LEU:HA	14:AE:276:ASN:ND2	2.33	0.43
14:AE:213:LYS:HE3	14:AE:213:LYS:CA	2.47	0.43
14:AE:515:ARG:NH2	14:AE:718:SER:O	2.48	0.43
14:AE:1024:THR:HG23	14:AE:1123:ARG:HA	2.00	0.43
19:G:206:ALA:O	19:G:210:VAL:HG23	2.18	0.43
20:H:332:VAL:HG11	20:H:335:ILE:CG1	2.38	0.43
33:U:6:LEU:HG	33:U:17:TYR:HB3	2.00	0.43
39:a:214:G:N2	39:a:216:A:N3	2.66	0.43
39:a:705:A:O4'	46:h:9:THR:HG21	2.19	0.43
58:t:24:VAL:HG13	58:t:33:ALA:HB2	2.00	0.43
13:AD:57:THR:HG21	13:AD:147:GLN:HB2	1.99	0.43
14:AE:111:THR:HG21	14:AE:303:VAL:HB	1.99	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
16:D:324:G:N2	16:D:327:A:C8	2.86	0.43
39:a:1021:A:N3	39:a:1021:A:C3'	2.78	0.43
39:a:1386:C:H2'	39:a:1387:A:C8	2.53	0.43
64:z:76:TYR:OH	64:z:92:ARG:NH1	2.51	0.43
6:5:116:DG:OP1	14:AE:1311:LYS:NZ	2.46	0.43
9:9:71:CYS:CA	9:9:117:LEU:HD13	2.48	0.43
10:A:36:U:H2'	10:A:37:A:O4'	2.19	0.43
10:A:57:A:O5'	10:A:58:A:P	2.76	0.43
11:AA:529:ARG:HH22	11:AA:687:ARG:HH11	1.66	0.43
11:AA:998:LEU:CD2	11:AA:1011:LEU:HD13	2.49	0.43
13:AD:86:LYS:NZ	14:AE:528:THR:HB	2.33	0.43
14:AE:190:LYS:HB2	14:AE:190:LYS:HE3	1.41	0.43
14:AE:515:ARG:HH12	14:AE:724:MET:HG2	1.83	0.43
14:AE:586:GLY:HA3	14:AE:612:LEU:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:18:G:N3	10:B:58:A:C5	2.87	0.43
10:B:22:G:HO2'	10:B:23:C:P	2.40	0.43
15:C:44:ILE:HG21	20:H:339:ARG:HA	2.01	0.43
19:G:19:GLN:OE1	20:H:76:GLU:HB3	2.12	0.43
20:H:76:GLU:HA	20:H:76:GLU:OE2	2.19	0.43
37:Y:34:ILE:HG22	37:Y:34:ILE:O	2.18	0.43
37:Y:35:MET:HE3	37:Y:35:MET:HB3	1.90	0.43
50:l:170:ARG:NH2	50:l:176:ASP:OD1	2.49	0.43
9:9:16:SER:HB2	9:9:20:LYS:NZ	2.33	0.43
11:AA:1026:GLU:CG	16:D:1030:U:C1'	2.94	0.43
14:AE:111:THR:CG2	14:AE:300:GLN:HA	2.48	0.43
14:AE:894:VAL:HG22	14:AE:1258:ARG:HH11	1.83	0.43
10:B:57:A:O5'	10:B:58:A:P	2.76	0.43
19:G:114:LEU:HD13	19:G:144:LEU:HB3	1.99	0.43
20:H:109:THR:C	20:H:153:GLU:HA	2.43	0.43
21:I:50:ALA:HB2	21:I:75:ILE:HD12	2.00	0.43
36:X:23:TYR:CD2	36:X:69:LEU:HD23	2.53	0.43
51:m:12:ARG:HG3	51:m:44:VAL:HG11	2.00	0.43
58:t:76:VAL:HG12	63:y:73:VAL:HB	2.00	0.43
11:AA:300:ASP:OD1	11:AA:313:ALA:N	2.52	0.43
11:AA:796:LEU:N	11:AA:1231:TYR:OH	2.52	0.43
14:AE:1033:GLY:HA3	14:AE:1081:VAL:O	2.18	0.43
10:B:26:G:N2	10:B:45:G:N2	2.66	0.43
16:D:421:U:O2	16:D:421:U:O4'	2.37	0.43
23:K:150:PRO:O	23:K:153:VAL:HG22	2.19	0.43
23:K:156:LYS:HG2	26:N:71:VAL:HG13	2.00	0.43
36:X:75:MET:HA	36:X:75:MET:HE3	1.99	0.43
39:a:2469:A:N6	39:a:2481:G:O2'	2.52	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:971:LEU:HG	11:AA:1014:LEU:HG	2.00	0.43
11:AA:1160:ASP:OD1	11:AA:1160:ASP:N	2.52	0.43
13:AC:50:SER:HB3	13:AD:8:PHE:HZ	1.84	0.43
10:B:22:G:H2'	10:B:23:C:C5	2.52	0.43
20:H:152:LEU:CB	20:H:171:ARG:H	2.32	0.43
20:H:280:LEU:HB2	20:H:330:VAL:O	2.18	0.43
38:Z:23:ILE:HD12	38:Z:23:ILE:HA	1.77	0.43
39:a:2252:G:O2'	39:a:2253:G:H5'	2.18	0.43
39:a:2252:G:H2'	39:a:2253:G:H8	1.84	0.43
52:n:77:PHE:N	52:n:77:PHE:CD1	2.82	0.43
10:A:26:G:N2	10:A:45:G:N2	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:49:G:O5'	10:A:49:G:C8	2.71	0.43
11:AA:176:ILE:HD12	11:AA:184:LEU:HD23	1.99	0.43
11:AA:488:MET:O	11:AA:490:GLN:N	2.47	0.43
11:AA:959:ASP:HA	11:AA:962:GLU:HB2	2.01	0.43
14:AE:126:LEU:CD1	14:AE:223:LEU:HD22	2.49	0.43
14:AE:244:VAL:HA	14:AE:269:TYR:OH	2.19	0.43
14:AE:568:SER:HB3	14:AE:570:LYS:NZ	2.34	0.43
10:B:46:G:O2'	10:B:47:U:H5"	2.19	0.43
19:G:208:ARG:NH1	20:H:29:VAL:HG11	2.34	0.43
29:Q:88:GLY:H	29:Q:114:THR:HG22	1.84	0.43
39:a:1932:A:H2'	39:a:1933:G:O4'	2.19	0.43
39:a:2627:G:O2'	39:a:2781:A:N1	2.37	0.43
52:n:123:ASP:OD1	52:n:123:ASP:C	2.62	0.43
4:3:12:ILE:CG2	4:3:80:ALA:HB2	2.49	0.43
11:AA:75:LEU:HD23	11:AA:94:ALA:HB3	2.00	0.43
11:AA:565:GLU:HA	11:AA:569:ILE:HG12	2.01	0.43
14:AE:26:SER:CB	14:AE:236:TRP:CZ2	2.95	0.43
16:D:1255:G:O2'	16:D:1258:G:N3	2.47	0.43
16:D:1371:G:O3'	27:O:71:GLY:HA3	2.19	0.43
39:a:998:C:OP2	64:z:58:ARG:NH2	2.49	0.43
11:AA:805:MET:HB2	11:AA:805:MET:HE3	1.87	0.43
11:AA:1329:GLU:HA	14:AE:245:LEU:HD13	2.00	0.43
20:H:119:GLY:CA	20:H:132:PRO:C	2.92	0.43
20:H:342:ILE:HG22	20:H:344:LEU:HD12	2.01	0.43
27:O:55:VAL:O	27:O:57:MET:N	2.52	0.43
39:a:819:A:C4	39:a:1189:A:C2	3.07	0.43
7:6:12:DC:O5'	7:6:12:DC:H6	2.01	0.42
8:7:-3:U:H3'	8:7:-3:U:O2	2.18	0.42
9:9:7:ASP:OD1	9:9:7:ASP:N	2.36	0.42
11:AA:724:VAL:HG13	11:AA:774:GLY:H	1.76	0.42
11:AA:859:GLU:CG	21:I:109:PRO:HG2	2.48	0.42
14:AE:24:LEU:CD1	14:AE:232:ASN:ND2	2.82	0.42
14:AE:1106:ILE:O	14:AE:1123:ARG:N	2.45	0.42
38:Z:18:ASP:HB3	38:Z:22:LEU:HD12	2.00	0.42
39:a:2602:A:H5"	39:a:2603:G:C5'	2.49	0.42
58:t:38:ILE:HD11	58:t:112:PHE:CZ	2.54	0.42
6:5:98:DA:H2'	6:5:99:DT:H72	2.01	0.42
10:A:46:G:O2'	10:A:47:U:H5"	2.19	0.42
10:A:56:C:C2	39:a:2112:G:C5	3.07	0.42
11:AA:68:LEU:HD11	11:AA:100:LEU:HB3	2.01	0.42
11:AA:230:PHE:HB2	11:AA:333:ILE:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:47:ARG:HA	14:AE:47:ARG:NE	2.34	0.42
14:AE:839:VAL:HG12	14:AE:864:LEU:HD12	2.02	0.42
16:D:1417:G:C6	16:D:1482:G:C6	3.06	0.42
20:H:290:TYR:O	20:H:305:HIS:C	2.56	0.42
37:Y:41:PHE:HA	37:Y:68:PHE:CE2	2.55	0.42
39:a:2395:C:H2'	39:a:2396:G:O4'	2.18	0.42
55:q:3:VAL:HA	55:q:36:ARG:O	2.19	0.42
9:9:9:GLN:CD	9:9:9:GLN:C	2.85	0.42
10:A:26:G:H1	10:A:44:A:N6	2.18	0.42
11:AA:55:SER:CB	11:AA:465:ARG:HH12	2.32	0.42
14:AE:559:ALA:HB3	14:AE:562:GLU:HB3	2.01	0.42
14:AE:1064:SER:OG	14:AE:1168:GLU:OE1	2.31	0.42
15:C:12:ARG:NH2	20:H:268:VAL:CG2	2.71	0.42
16:D:537:G:OP1	30:R:110:ARG:NH2	2.48	0.42
37:Y:123:ALA:HA	37:Y:126:ARG:HG3	2.00	0.42
39:a:1250:G:OP2	59:u:21:ARG:NH2	2.52	0.42
10:A:15:G:H1	10:A:20:U:H3	1.68	0.42
11:AA:32:LEU:HD23	11:AA:32:LEU:HA	1.83	0.42
11:AA:1009:ASN:ND2	11:AA:1012:GLU:HB3	2.35	0.42
14:AE:211:GLU:CG	14:AE:215:LYS:HE3	2.44	0.42
14:AE:609:TYR:HD2	14:AE:610:ARG:NH1	2.17	0.42
14:AE:616:PRO:HA	14:AE:619:ILE:HG22	2.02	0.42
14:AE:1079:LYS:HD3	14:AE:1098:GLN:HB3	1.99	0.42
10:B:53:G:C2	10:B:54:U:C5	3.07	0.42
15:C:12:ARG:HD3	15:C:16:GLU:OE1	2.18	0.42
39:a:320:A:H2'	50:l:131:THR:HG21	2.01	0.42
39:a:973:A:O4'	39:a:1188:U:C6	2.72	0.42
10:A:53:G:C2	10:A:54:U:C5	3.07	0.42
11:AA:452:ARG:NH1	11:AA:458:GLU:OE2	2.52	0.42
11:AA:717:VAL:HG22	11:AA:782:VAL:HG12	2.00	0.42
11:AA:830:THR:HG22	11:AA:1234:LYS:NZ	2.34	0.42
11:AA:1252:SER:N	11:AA:1259:LEU:HD13	2.35	0.42
14:AE:141:PHE:CD2	14:AE:297:ARG:HB2	2.54	0.42
14:AE:201:LEU:HD11	14:AE:220:ARG:NH1	2.31	0.42
10:B:26:G:H1	10:B:44:A:N6	2.18	0.42
19:G:47:VAL:N	19:G:48:PRO:HD2	2.34	0.42
20:H:19:ARG:CD	20:H:73:ASP:OD1	2.65	0.42
20:H:61:GLU:HG2	20:H:62:ILE:HG23	2.00	0.42
39:a:1142:A:H2'	39:a:1142:A:N3	2.34	0.42
39:a:1266:G:OP1	47:i:16:ARG:NE	2.45	0.42
39:a:1394:U:C4	39:a:1395:A:C6	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:c:37:ARG:HG2	41:c:48:THR:HG23	2.00	0.42
46:h:240:PHE:CD2	46:h:240:PHE:O	2.73	0.42
50:l:134:LEU:HB2	50:l:160:ALA:HB1	2.02	0.42
10:A:58:A:HO2'	10:A:60:U:H5	1.64	0.42
13:AD:207:THR:OG1	13:AD:208:ASN:N	2.52	0.42
14:AE:144:TYR:CE1	14:AE:162:GLU:OE1	2.73	0.42
14:AE:390:LEU:N	14:AE:390:LEU:HD13	2.35	0.42
14:AE:647:PRO:HG3	14:AE:697:MET:HB3	2.02	0.42
16:D:563:A:C2	16:D:884:U:O4	2.62	0.42
16:D:826:C:O2	26:N:16:ASN:ND2	2.52	0.42
16:D:842:U:H3'	16:D:843:U:C5'	2.48	0.42
16:D:1499:A:O2'	16:D:1500:A:C5'	2.67	0.42
21:I:9:GLY:HA3	31:S:89:MET:HE3	2.01	0.42
23:K:136:VAL:O	23:K:140:THR:HG23	2.20	0.42
39:a:2615:U:C2	47:i:4:GLN:HA	2.55	0.42
8:7:-5:U:O2	8:7:-5:U:H3'	2.20	0.42
9:9:80:THR:O	39:a:1108:U:OP1	2.38	0.42
11:AA:27:LEU:O	11:AA:528:ARG:NH1	2.42	0.42
14:AE:950:ILE:HB	14:AE:1018:ALA:HB3	2.01	0.42
10:B:58:A:OP2	10:B:58:A:H8	2.02	0.42
15:C:14:THR:CG2	15:C:48:ARG:HE	2.33	0.42
16:D:502:A:H2'	16:D:503:C:O4'	2.20	0.42
18:F:32:VAL:HG11	29:Q:89:PRO:HG3	2.01	0.42
18:F:67:ARG:HD3	18:F:67:ARG:H	1.85	0.42
39:a:1020:A:C2	39:a:1141:U:C2	3.07	0.42
39:a:1925:C:OP2	39:a:1925:C:C6	2.73	0.42
47:i:43:ILE:HG22	47:i:49:TYR:HB2	2.01	0.42
58:t:107:LEU:HD21	58:t:115:ILE:HG21	2.01	0.42
4:3:39:ILE:HG22	4:3:40:ASN:N	2.34	0.42
8:7:-8:U:H6	8:7:-8:U:H3'	1.84	0.42
9:9:43:LYS:C	9:9:43:LYS:CD	2.86	0.42
11:AA:218:GLU:HG2	11:AA:299:LYS:HA	2.02	0.42
11:AA:623:LEU:HD13	11:AA:627:GLY:HA2	2.01	0.42
11:AA:1117:LEU:HD12	11:AA:1195:ILE:HG12	2.00	0.42
12:AB:7:LYS:HG2	12:AB:74:VAL:HG13	2.01	0.42
14:AE:385:LEU:CD2	14:AE:390:LEU:HB2	2.50	0.42
14:AE:388:ARG:HG2	14:AE:388:ARG:HH11	1.84	0.42
14:AE:394:ILE:O	14:AE:394:ILE:HG13	2.18	0.42
14:AE:515:ARG:HG2	14:AE:516:ASP:H	1.85	0.42
16:D:622:A:C8	16:D:623:C:C6	3.08	0.42
16:D:1515:G:H2'	16:D:1516:G:C8	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R:110:ARG:NH1	30:R:112:GLN:O	2.53	0.42
39:a:567:U:OP2	59:u:29:LYS:NZ	2.53	0.42
39:a:1082:U:N3	39:a:1086:A:C6	2.87	0.42
46:h:37:ASN:HB2	46:h:62:TYR:HB2	2.01	0.42
8:7:0:U:C5	23:K:12:GLN:CB	2.55	0.42
8:7:13:G:H5"	8:7:13:G:H8	1.84	0.42
13:AC:118:ASP:CA	28:P:89:ARG:HB3	2.35	0.42
14:AE:279:LEU:HD13	14:AE:299:LEU:HD13	2.02	0.42
14:AE:923:ILE:O	14:AE:1241:TYR:OH	2.31	0.42
16:D:1323:G:H2'	16:D:1324:A:C8	2.55	0.42
19:G:187:VAL:HG21	19:G:199:VAL:HG23	2.02	0.42
22:J:48:LEU:HD13	22:J:48:LEU:N	2.33	0.42
32:T:21:ASP:OD1	32:T:22:THR:N	2.49	0.42
39:a:126:A:O5'	51:m:19:ARG:HG3	2.19	0.42
48:j:172:VAL:HG11	48:j:175:LEU:HD21	2.01	0.42
60:v:73:ILE:HG21	60:v:91:TYR:CZ	2.55	0.42
62:x:99:TYR:OH	62:x:111:ARG:NH1	2.53	0.42
7:6:27:DG:H1'	7:6:28:DA:C5	2.55	0.42
11:AA:400:VAL:HG21	11:AA:452:ARG:HE	1.84	0.42
11:AA:914:LYS:C	11:AA:914:LYS:HE3	2.45	0.42
14:AE:848:VAL:HB	14:AE:858:VAL:HG22	2.02	0.42
15:C:12:ARG:O	15:C:16:GLU:HG3	2.19	0.42
16:D:548:G:C6	16:D:549:C:C4	3.08	0.42
20:H:119:GLY:O	20:H:120:PHE:C	2.62	0.42
20:H:332:VAL:HG12	20:H:334:ASP:N	2.33	0.42
31:S:41:ARG:O	31:S:45:VAL:HG12	2.20	0.42
36:X:4:ILE:CG1	36:X:9:ILE:HD12	2.50	0.42
39:a:2511:U:O4	39:a:2575:C:N3	2.52	0.42
39:a:2756:U:C4	39:a:2759:G:O6	2.72	0.42
39:a:2898:U:O2'	57:s:134:ALA:O	2.28	0.42
50:l:145:ASP:HA	50:l:166:LYS:HB3	2.01	0.42
2:1:92:ARG:NE	2:1:94:ASP:OD1	2.53	0.41
11:AA:257:ALA:HB2	11:AA:285:ILE:HG22	2.02	0.41
11:AA:812:PHE:HZ	14:AE:503:SER:HB2	1.85	0.41
11:AA:1251:TYR:CE2	11:AA:1301:ARG:NH1	2.88	0.41
13:AC:231:PHE:HE2	13:AD:39:LEU:HD13	1.85	0.41
14:AE:797:THR:HG22	14:AE:924:GLY:HA3	2.01	0.41
14:AE:820:ILE:HG12	14:AE:884:SER:HB2	2.02	0.41
14:AE:1350:ASN:HA	14:AE:1353:VAL:HG12	2.01	0.41
16:D:384:G:H2'	16:D:385:C:C6	2.54	0.41
16:D:429:U:O2	16:D:430:A:C8	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:D:429:U:O2	16:D:430:A:N7	2.53	0.41
16:D:972:C:O2'	28:P:57:VAL:HG21	2.18	0.41
20:H:292:CYS:SG	20:H:304:VAL:HB	2.60	0.41
39:a:1565:C:O2'	39:a:1567:G:N7	2.48	0.41
61:w:49:GLU:HB2	61:w:50:PRO:HD3	2.01	0.41
6:5:108:DT:C7	11:AA:199:ASP:HB3	2.45	0.41
9:9:25:ALA:HA	9:9:96:PHE:HE1	1.85	0.41
9:9:86:MET:HE2	9:9:86:MET:HB3	1.96	0.41
11:AA:211:ARG:HH21	11:AA:351:LEU:HD22	1.86	0.41
11:AA:593:LYS:HB3	11:AA:602:GLU:HG3	2.02	0.41
11:AA:1072:ASN:OD1	11:AA:1072:ASN:N	2.47	0.41
11:AA:1253:LEU:CD1	14:AE:253:VAL:CG1	2.95	0.41
13:AC:117:HIS:C	28:P:89:ARG:HD2	2.13	0.41
14:AE:242:LEU:C	14:AE:242:LEU:HD23	2.44	0.41
16:D:37:U:O2	16:D:548:G:N2	2.53	0.41
20:H:274:TYR:HD1	20:H:335:ILE:HD12	1.84	0.41
25:M:22:LEU:HD13	25:M:97:ASN:ND2	2.35	0.41
39:a:1028:A:N6	39:a:1125:G:H2'	2.34	0.41
39:a:1839:G:C4	39:a:1927:A:C5	3.08	0.41
39:a:2189:U:O2'	39:a:2190:G:O4'	2.36	0.41
39:a:2311:A:C2	52:n:85:ILE:HD11	2.55	0.41
46:h:76:ALA:HB2	46:h:96:TYR:CE1	2.55	0.41
9:9:118:ILE:H	9:9:119:PRO:HD2	1.86	0.41
10:A:22:G:H2'	10:A:23:C:C5	2.52	0.41
10:A:26:G:C2	10:A:45:G:N2	2.89	0.41
11:AA:395:TYR:HE2	11:AA:420:LEU:HG	1.84	0.41
11:AA:678:ARG:HD3	11:AA:678:ARG:HA	1.87	0.41
13:AD:152:TYR:HE2	14:AE:535:ARG:HH21	1.68	0.41
14:AE:137:ARG:HA	14:AE:142:GLU:HG2	2.02	0.41
16:D:791:G:N2	16:D:1497:G:O3'	2.53	0.41
16:D:860:A:H2'	16:D:861:G:O4'	2.21	0.41
16:D:1333:A:H2'	16:D:1334:G:O4'	2.19	0.41
27:O:28:ILE:HD12	27:O:28:ILE:N	2.35	0.41
39:a:1365:A:O5'	41:c:28:ARG:NH2	2.52	0.41
39:a:1921:G:O5'	39:a:1921:G:C8	2.70	0.41
39:a:2273:A:H2'	39:a:2274:A:C8	2.55	0.41
10:A:56:C:OP1	39:a:2168:G:N3	2.53	0.41
11:AA:666:SER:HB2	11:AA:1186:VAL:HG21	2.01	0.41
11:AA:839:VAL:O	11:AA:886:LYS:HD2	2.19	0.41
14:AE:930:LEU:HA	14:AE:1244:GLN:HG3	2.02	0.41
16:D:915:A:C6	16:D:916:U:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:P:57:VAL:O	28:P:58:ASN:ND2	2.52	0.41
37:Y:64:ARG:HE	37:Y:64:ARG:HB2	1.52	0.41
39:a:36:G:N3	39:a:450:G:O2'	2.53	0.41
39:a:742:A:N1	39:a:755:U:O4	2.53	0.41
39:a:879:G:H2'	39:a:880:G:O4'	2.19	0.41
39:a:948:C:H1'	39:a:984:A:C8	2.55	0.41
39:a:1169:A:H5"	39:a:1169:A:N3	2.36	0.41
39:a:1406:U:O2'	39:a:1407:G:OP2	2.39	0.41
39:a:1921:G:C2'	39:a:1922:G:H5'	2.49	0.41
42:d:8:C:O3'	62:x:25:ARG:NH1	2.51	0.41
57:s:32:LEU:HD23	57:s:54:ILE:HD13	2.01	0.41
3:2:46:ALA:O	3:2:50:LEU:HB2	2.21	0.41
8:7:20:G:H21	14:AE:427:PRO:HD3	1.86	0.41
9:9:118:ILE:CB	9:9:119:PRO:HD3	2.49	0.41
13:AC:29:GLU:HA	13:AC:30:PRO:HA	1.84	0.41
14:AE:87:LYS:HE3	14:AE:87:LYS:CA	2.41	0.41
14:AE:139:LEU:HD23	14:AE:139:LEU:HA	1.89	0.41
14:AE:513:MET:HG3	14:AE:544:LEU:HD11	2.01	0.41
16:D:1225:A:H2'	16:D:1226:C:C5	2.56	0.41
16:D:1526:G:P	18:F:42:THR:HG23	2.61	0.41
20:H:110:GLY:H	20:H:153:GLU:N	2.17	0.41
22:J:100:ASN:OD1	22:J:111:ARG:NH1	2.54	0.41
39:a:1182:G:H2'	39:a:1183:U:O4'	2.21	0.41
39:a:1406:U:C2'	39:a:1407:G:OP2	2.69	0.41
39:a:2298:A:C5	39:a:2321:U:C4	3.09	0.41
39:a:2683:C:O2	58:t:70:ARG:NH2	2.53	0.41
52:n:4:LEU:HD23	52:n:4:LEU:HA	1.96	0.41
64:z:65:ILE:CD1	64:z:92:ARG:HB2	2.49	0.41
9:9:31:ARG:NE	39:a:1054:A:O4'	2.46	0.41
11:AA:960:LEU:HD21	11:AA:1028:LYS:HB3	2.02	0.41
11:AA:1034:ARG:HG2	11:AA:1034:ARG:NH1	2.25	0.41
11:AA:1102:GLY:HA2	11:AA:1106:ARG:HH11	1.85	0.41
14:AE:136:GLU:OE1	14:AE:312:ARG:NH2	2.53	0.41
14:AE:242:LEU:HA	14:AE:243:PRO:HD3	1.95	0.41
10:B:46:G:H2'	10:B:47:U:OP2	2.21	0.41
16:D:216:U:H2'	16:D:217:C:C6	2.55	0.41
16:D:712:A:H2'	16:D:713:G:O4'	2.21	0.41
16:D:1330:U:OP2	36:X:26:GLY:HA3	2.21	0.41
16:D:1368:A:OP1	27:O:113:ARG:NH2	2.54	0.41
20:H:155:LYS:O	20:H:169:SER:CB	2.69	0.41
26:N:11:LEU:HD22	26:N:75:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Y:35:MET:O	37:Y:35:MET:SD	2.79	0.41
39:a:851:C:H2'	39:a:852:U:C6	2.55	0.41
39:a:984:A:H2'	39:a:984:A:N3	2.35	0.41
39:a:1570:A:H2'	39:a:1571:A:C8	2.55	0.41
39:a:2602:A:H5"	39:a:2603:G:H5"	2.03	0.41
39:a:2803:G:H2'	39:a:2804:U:C5	2.55	0.41
43:e:56:LEU:HD23	43:e:56:LEU:HA	1.87	0.41
61:w:67:PHE:O	61:w:71:ARG:HG2	2.21	0.41
8:7:13:G:H8	8:7:13:G:C5'	2.33	0.41
9:9:71:CYS:SG	9:9:117:LEU:HB2	2.60	0.41
11:AA:888:THR:HG22	11:AA:914:LYS:HD2	2.02	0.41
11:AA:933:VAL:O	11:AA:933:VAL:CG1	2.68	0.41
11:AA:1020:GLU:HA	11:AA:1023:HIS:CD2	2.56	0.41
11:AA:1232:MET:HE2	11:AA:1232:MET:HB3	1.94	0.41
13:AD:111:THR:OG1	13:AD:112:ALA:N	2.54	0.41
14:AE:1289:ASN:O	14:AE:1293:GLU:HB2	2.20	0.41
10:B:26:G:C2	10:B:45:G:N2	2.89	0.41
23:K:133:PRO:HA	23:K:136:VAL:HG12	2.02	0.41
39:a:126:A:OP1	51:m:45:SER:OG	2.38	0.41
39:a:493:G:H2'	39:a:494:G:O4'	2.20	0.41
39:a:1082:U:C4	39:a:1086:A:N6	2.88	0.41
39:a:1326:U:O2'	39:a:2010:G:O2'	2.35	0.41
39:a:1548:A:H2'	39:a:1549:A:C8	2.55	0.41
50:l:188:MET:HE2	50:l:193:VAL:HA	2.03	0.41
61:w:29:VAL:HG11	61:w:75:ILE:HG23	2.03	0.41
11:AA:56:VAL:HG11	11:AA:468:LEU:HD13	2.02	0.41
11:AA:1029:LEU:HD21	11:AA:1033:ARG:CZ	2.50	0.41
14:AE:390:LEU:HD13	14:AE:390:LEU:H	1.86	0.41
16:D:977:A:H1'	16:D:982:U:O4	2.20	0.41
39:a:197:A:N6	39:a:2430:A:H2'	2.36	0.41
46:h:119:GLY:O	46:h:130:LEU:HB3	2.20	0.41
59:u:109:LYS:HG2	59:u:126:ARG:HB2	2.02	0.41
9:9:61:ARG:C	9:9:65:GLU:HB2	2.45	0.41
10:A:34:C:H41	25:M:83:SER:HA	1.86	0.41
11:AA:241:LEU:N	11:AA:283:LYS:O	2.51	0.41
11:AA:868:SER:OG	11:AA:941:LYS:HB2	2.21	0.41
11:AA:873:ILE:HG22	21:I:80:LYS:H	1.86	0.41
11:AA:884:VAL:CG1	11:AA:1050:VAL:HG11	2.51	0.41
11:AA:976:ARG:HA	11:AA:979:LEU:HB2	2.02	0.41
11:AA:991:LYS:HD2	11:AA:991:LYS:H	1.80	0.41
14:AE:47:ARG:NE	14:AE:47:ARG:CA	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:68:TYR:CB	14:AE:75:TYR:HE2	2.34	0.41
14:AE:109:SER:CB	14:AE:296:LYS:HG2	2.51	0.41
14:AE:144:TYR:N	14:AE:144:TYR:CD1	2.88	0.41
14:AE:820:ILE:HD11	14:AE:822:MET:HE2	2.02	0.41
16:D:197:A:C5	16:D:221:C:H4'	2.53	0.41
23:K:150:PRO:HA	23:K:153:VAL:HG22	2.03	0.41
23:K:154:ALA:HA	23:K:164:ILE:HD11	2.03	0.41
28:P:90:LEU:HD22	28:P:90:LEU:HA	1.86	0.41
32:T:43:PHE:CE2	32:T:56:LEU:HD22	2.56	0.41
37:Y:21:PRO:HD2	37:Y:22:PRO:HD2	2.03	0.41
37:Y:78:LEU:HD22	37:Y:78:LEU:HA	1.92	0.41
38:Z:28:GLU:H	38:Z:28:GLU:HG3	1.58	0.41
39:a:207:A:H2'	39:a:208:C:O4'	2.21	0.41
39:a:476:G:H4'	39:a:502:A:N1	2.35	0.41
39:a:637:A:N1	39:a:651:G:O2'	2.51	0.41
39:a:871:U:H2'	39:a:872:U:C6	2.56	0.41
39:a:910:A:N3	39:a:2264:C:O2'	2.49	0.41
39:a:2638:G:O2'	39:a:2775:G:N2	2.41	0.41
52:n:122:PHE:CZ	52:n:167:ARG:HA	2.56	0.41
61:w:9:GLN:O	61:w:17:ARG:NH2	2.51	0.41
62:x:53:THR:HG23	62:x:74:VAL:HG21	2.03	0.41
11:AA:968:GLU:HG3	11:AA:972:PHE:CZ	2.56	0.41
11:AA:1286:THR:O	11:AA:1290:MET:HB2	2.21	0.41
13:AC:159:ILE:HD13	13:AC:159:ILE:HA	1.69	0.41
13:AD:153:VAL:HG23	13:AD:175:ALA:HB3	2.03	0.41
10:B:37:A:H5"	10:B:37:A:C4	2.56	0.41
37:Y:10:LEU:HD13	37:Y:10:LEU:HA	1.79	0.41
50:l:48:THR:HG23	50:l:86:ALA:HB3	2.02	0.41
54:p:25:THR:HG22	54:p:34:THR:HG23	2.02	0.41
9:9:31:ARG:HE	39:a:1054:A:C4'	2.26	0.40
10:A:25:C:H2'	10:A:26:G:C5'	2.52	0.40
10:A:65:C:C2'	10:A:66:C:H5'	2.49	0.40
11:AA:69:GLN:HE21	11:AA:101:ARG:HD2	1.85	0.40
11:AA:855:PRO:O	11:AA:857:VAL:N	2.54	0.40
11:AA:940:GLU:O	11:AA:940:GLU:CG	2.69	0.40
11:AA:958:LYS:NZ	11:AA:962:GLU:HG2	2.37	0.40
12:AB:8:ARG:HH11	12:AB:8:ARG:HD3	1.75	0.40
13:AD:97:GLU:HG3	13:AD:147:GLN:HG2	2.03	0.40
14:AE:102:MET:HG2	14:AE:246:PRO:CG	2.49	0.40
14:AE:161:THR:CG2	14:AE:164:GLN:HB2	2.49	0.40
14:AE:351:GLY:O	14:AE:467:ALA:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:1144:LEU:HD23	14:AE:1144:LEU:HA	1.96	0.40
16:D:915:A:C8	16:D:915:A:C3'	3.04	0.40
27:O:10:GLY:HA3	27:O:78:ALA:O	2.21	0.40
31:S:16:LEU:HD13	31:S:54:ASP:HB2	2.03	0.40
64:z:66:ASN:OD1	64:z:70:ARG:NE	2.54	0.40
10:A:7:G:O6	10:A:49:G:O6	2.39	0.40
10:A:15:G:N2	10:A:20:U:C2	2.89	0.40
11:AA:801:ARG:HH12	11:AA:1119:MET:HE1	1.86	0.40
11:AA:963:GLU:CA	11:AA:966:ILE:HD12	2.49	0.40
14:AE:201:LEU:CB	14:AE:221:ILE:HD13	2.47	0.40
10:B:7:G:O6	10:B:49:G:O6	2.39	0.40
10:B:25:C:H2'	10:B:26:G:C5'	2.51	0.40
16:D:107:G:N7	17:E:10:ARG:NH2	2.60	0.40
16:D:579:A:O2'	32:T:54:ARG:NH1	2.54	0.40
16:D:1235:U:H2'	16:D:1236:A:O4'	2.20	0.40
20:H:110:GLY:N	20:H:153:GLU:HA	2.36	0.40
37:Y:102:ARG:H	37:Y:102:ARG:HG3	1.59	0.40
37:Y:104:GLN:HB3	37:Y:105:LEU:H	1.73	0.40
39:a:5:A:H2'	39:a:6:A:C8	2.56	0.40
39:a:2294:G:OP1	62:x:10:ARG:HD3	2.21	0.40
41:c:33:LEU:O	41:c:34:HIS:CG	2.74	0.40
48:j:175:LEU:CD1	48:j:193:VAL:HG12	2.51	0.40
58:t:113:MET:HE3	58:t:116:ILE:HD11	2.01	0.40
11:AA:810:TYR:CE1	11:AA:1078:LYS:HD2	2.57	0.40
11:AA:859:GLU:HG3	21:I:109:PRO:CG	2.52	0.40
10:B:65:C:C2'	10:B:66:C:H5'	2.49	0.40
16:D:152:A:N6	16:D:170:U:C2	2.89	0.40
16:D:1061:G:H5'	28:P:61:ALA:HB2	2.02	0.40
28:P:22:THR:HA	28:P:25:ILE:HG22	2.04	0.40
36:X:16:VAL:HG13	36:X:34:LEU:CD1	2.51	0.40
39:a:67:U:C4	39:a:74:A:C6	3.04	0.40
39:a:532:A:N7	39:a:2021:C:O2'	2.47	0.40
39:a:2572:A:N7	48:j:150:GLN:NE2	2.69	0.40
39:a:2641:G:OP1	57:s:78:THR:HG22	2.21	0.40
39:a:2788:C:H2'	39:a:2789:C:C6	2.55	0.40
46:h:232:HIS:CG	46:h:240:PHE:HE1	2.40	0.40
8:7:-6:U:H4'	8:7:-5:U:H5"	2.04	0.40
9:9:8:LYS:NZ	39:a:1046:A:N6	2.69	0.40
10:A:58:A:OP2	10:A:58:A:H8	2.02	0.40
14:AE:1050:THR:HG23	14:AE:1057:SER:HB3	2.03	0.40
10:B:60:U:OP2	10:B:61:C:N4	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:D:236:A:H5"	34:V:44:LEU:HD21	2.04	0.40
16:D:1486:G:H2'	16:D:1487:G:O4'	2.22	0.40
50:l:149:ILE:HD11	50:l:188:MET:HE3	2.02	0.40
54:p:52:PHE:CZ	54:p:72:LEU:HD22	2.56	0.40
8:7:-8:U:C6	8:7:-8:U:H3'	2.57	0.40
9:9:23:LEU:HA	9:9:118:ILE:CG1	2.51	0.40
10:A:46:G:H2'	10:A:47:U:OP2	2.21	0.40
10:A:60:U:O3'	10:A:61:C:C6	2.75	0.40
11:AA:104:ILE:HD11	11:AA:116:ASP:HB2	2.02	0.40
14:AE:108:ALA:HB2	14:AE:276:ASN:OD1	2.22	0.40
10:B:71:C:H2'	10:B:72:A:C1'	2.52	0.40
16:D:218:U:H2'	16:D:219:U:O4'	2.21	0.40
16:D:580:C:H2'	16:D:581:G:O4'	2.21	0.40
16:D:1329:A:OP1	36:X:28:THR:CA	2.67	0.40
16:D:1370:G:C2	16:D:1371:G:C8	3.09	0.40
22:J:61:VAL:CG2	22:J:200:ILE:HD11	2.39	0.40
37:Y:102:ARG:HD2	37:Y:103:ALA:N	2.36	0.40
39:a:67:U:C2	39:a:74:A:N6	2.89	0.40
39:a:1421:G:C2	39:a:1422:G:C8	3.09	0.40
39:a:2315:G:C5'	52:n:157:THR:HG23	2.52	0.40
46:h:232:HIS:HA	46:h:242:LYS:HE3	2.03	0.40
61:w:10:LEU:HD11	61:w:43:GLU:HG3	2.04	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 43
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100 100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12 43
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	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	4 29
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100 100
13	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14 45
13	AD	226/329 (69%)	212 (94%)	14 (6%)	0	100 100
14	AE	1329/1407 (94%)	1200 (90%)	120 (9%)	9 (1%)	18 51
15	C	64/75 (85%)	63 (98%)	1 (2%)	0	100 100
17	E	84/87 (97%)	83 (99%)	1 (1%)	0	100 100
18	F	68/71 (96%)	68 (100%)	0	0	100 100
19	G	223/241 (92%)	210 (94%)	13 (6%)	0	100 100
20	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2 18
21	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	24 57
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100 100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21 54
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12 43
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18 51
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16 48
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16 48
28	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	12 43
29	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7 34
30	R	117/124 (94%)	116 (99%)	1 (1%)	0	100 100
31	S	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
32	T	86/89 (97%)	82 (95%)	4 (5%)	0	100 100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9 38
34	V	78/84 (93%)	74 (95%)	4 (5%)	0	100 100
35	W	81/92 (88%)	78 (96%)	3 (4%)	0	100 100
36	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6 33
37	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0 9
38	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
41	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
44	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
45	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
46	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	62
47	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/55 (91%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	57
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	41
53	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
54	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
55	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
58	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
59	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
60	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
61	w	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
62	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
63	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
64	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	45
All	All	9368/10486 (89%)	8606 (92%)	660 (7%)	102 (1%)	14	41

All (102) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU

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Mol	Chain	Res	Type
11	AA	873	ILE
11	AA	937	ASP
11	AA	993	PRO
20	H	139	ARG
20	H	153	GLU
20	H	169	SER
20	H	306	VAL
20	H	340	ARG
27	O	56	ASP
36	X	103	LYS
37	Y	48	ILE
9	9	33	VAL
9	9	119	PRO
11	AA	375	PRO
11	AA	856	ASN
11	AA	870	ILE
11	AA	940	GLU
11	AA	985	GLU
11	AA	1003	THR
11	AA	1158	LYS
14	AE	175	GLU
20	H	108	VAL
20	H	309	MET
20	H	333	LEU
37	Y	93	ASN
46	h	158	ALA
50	l	142	ALA
64	z	3	ARG
9	9	48	ALA
9	9	91	ALA
9	9	118	ILE
9	9	130	PRO
11	AA	376	PRO
11	AA	723	VAL
11	AA	728	ASP
11	AA	935	THR
11	AA	980	VAL
11	AA	1005	GLU
11	AA	1045	GLY
13	AC	164	ASP
13	AC	165	GLU
14	AE	51	PRO

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Mol	Chain	Res	Type
14	AE	805	GLN
20	H	76	GLU
20	H	142	ARG
25	M	130	ASN
28	P	58	ASN
29	Q	119	ASN
37	Y	20	SER
37	Y	64	ARG
37	Y	106	GLN
9	9	69	PHE
9	9	73	LYS
9	9	108	VAL
9	9	129	LEU
9	9	133	GLU
11	AA	850	ILE
11	AA	943	LYS
11	AA	991	LYS
11	AA	995	ASP
14	AE	174	ASP
14	AE	193	ASP
20	H	82	THR
21	I	80	LYS
36	X	105	ASN
37	Y	83	ALA
38	Z	21	GLU
52	n	40	VAL
11	AA	917	SER
11	AA	997	TRP
11	AA	1044	PRO
14	AE	91	GLU
20	H	70	VAL
37	Y	22	PRO
37	Y	71	LYS
37	Y	89	SER
38	Z	7	ILE
4	3	39	ILE
9	9	28	ALA
14	AE	49	PHE
14	AE	73	GLY
14	AE	904	ALA
37	Y	62	ALA
24	L	96	VAL

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Mol	Chain	Res	Type
37	Y	23	VAL
37	Y	100	ILE
1	0	44	GLY
11	AA	697	LYS
11	AA	1159	VAL
11	AA	1317	PRO
23	K	44	GLY
29	Q	74	VAL
33	U	64	GLY
9	9	54	VAL
52	n	62	GLY
11	AA	933	VAL
26	N	75	ILE

5.3.2 Protein sidechains (i)

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 30
2	1	93/93 (100%)	86 (92%)	7 (8%)	12 38
3	2	81/84 (96%)	77 (95%)	4 (5%)	22 47
4	3	84/85 (99%)	79 (94%)	5 (6%)	17 43
5	4	78/78 (100%)	75 (96%)	3 (4%)	29 53
9	9	112/123 (91%)	63 (56%)	49 (44%)	0 0
11	AA	1140/1157 (98%)	1027 (90%)	113 (10%)	7 28
12	AB	86/158 (54%)	85 (99%)	1 (1%)	63 72
13	AC	198/286 (69%)	183 (92%)	15 (8%)	12 37
13	AD	196/286 (68%)	193 (98%)	3 (2%)	57 69
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15 41
15	C	57/65 (88%)	55 (96%)	2 (4%)	32 54
17	E	65/66 (98%)	61 (94%)	4 (6%)	16 42
18	F	60/61 (98%)	57 (95%)	3 (5%)	22 47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
19	G	187/199 (94%)	174 (93%)	13 (7%)	14 40
20	H	137/461 (30%)	124 (90%)	13 (10%)	8 30
21	I	171/190 (90%)	163 (95%)	8 (5%)	23 48
22	J	172/173 (99%)	164 (95%)	8 (5%)	23 48
23	K	119/126 (94%)	111 (93%)	8 (7%)	15 41
24	L	91/116 (78%)	84 (92%)	7 (8%)	12 37
25	M	124/147 (84%)	113 (91%)	11 (9%)	9 32
26	N	104/105 (99%)	101 (97%)	3 (3%)	37 58
27	O	105/107 (98%)	99 (94%)	6 (6%)	18 44
28	P	86/90 (96%)	77 (90%)	9 (10%)	6 26
29	Q	90/99 (91%)	88 (98%)	2 (2%)	45 63
30	R	101/104 (97%)	95 (94%)	6 (6%)	18 43
31	S	83/84 (99%)	79 (95%)	4 (5%)	23 47
32	T	76/77 (99%)	65 (86%)	11 (14%)	3 17
33	U	65/65 (100%)	60 (92%)	5 (8%)	12 37
34	V	74/78 (95%)	71 (96%)	3 (4%)	27 51
35	W	72/79 (91%)	66 (92%)	6 (8%)	10 34
36	X	94/96 (98%)	87 (93%)	7 (7%)	13 38
37	Y	109/110 (99%)	69 (63%)	40 (37%)	0 0
38	Z	26/85 (31%)	10 (38%)	16 (62%)	0 0
40	b	58/63 (92%)	57 (98%)	1 (2%)	53 67
41	c	67/68 (98%)	64 (96%)	3 (4%)	24 48
43	e	54/55 (98%)	51 (94%)	3 (6%)	19 45
44	f	48/49 (98%)	43 (90%)	5 (10%)	7 26
45	g	59/62 (95%)	54 (92%)	5 (8%)	10 33
46	h	216/218 (99%)	199 (92%)	17 (8%)	11 36
47	i	47/48 (98%)	41 (87%)	6 (13%)	4 21
48	j	164/164 (100%)	156 (95%)	8 (5%)	22 47
49	k	47/49 (96%)	44 (94%)	3 (6%)	16 42
50	l	165/165 (100%)	151 (92%)	14 (8%)	10 33
51	m	38/38 (100%)	36 (95%)	2 (5%)	20 45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	n	148/150 (99%)	130 (88%)	18 (12%)	5 21
53	o	51/52 (98%)	47 (92%)	4 (8%)	11 36
54	p	136/138 (99%)	130 (96%)	6 (4%)	25 49
55	q	34/34 (100%)	31 (91%)	3 (9%)	9 33
56	r	114/114 (100%)	102 (90%)	12 (10%)	6 26
57	s	116/116 (100%)	106 (91%)	10 (9%)	10 33
58	t	104/104 (100%)	98 (94%)	6 (6%)	18 44
59	u	103/103 (100%)	96 (93%)	7 (7%)	14 40
60	v	109/109 (100%)	105 (96%)	4 (4%)	30 54
61	w	99/103 (96%)	91 (92%)	8 (8%)	11 35
62	x	86/87 (99%)	80 (93%)	6 (7%)	14 40
63	y	99/100 (99%)	91 (92%)	8 (8%)	11 35
64	z	89/90 (99%)	85 (96%)	4 (4%)	24 48
All	All	7791/8664 (90%)	7151 (92%)	640 (8%)	13 35

All (640) 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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
11	AA	39	ILE
11	AA	145	ILE
11	AA	376	PRO
11	AA	615	VAL
11	AA	723	VAL
11	AA	727	VAL
11	AA	728	ASP
11	AA	731	ARG
11	AA	732	ILE
11	AA	752	ASN
11	AA	753	LEU
11	AA	802	VAL
11	AA	817	LEU
11	AA	840	SER
11	AA	844	LYS
11	AA	845	LEU
11	AA	851	THR
11	AA	854	ILE
11	AA	855	PRO
11	AA	857	VAL
11	AA	862	LEU
11	AA	864	LYS
11	AA	865	LEU
11	AA	866	ASP
11	AA	867	GLU
11	AA	868	SER
11	AA	871	VAL

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Mol	Chain	Res	Type
11	AA	873	ILE
11	AA	876	GLU
11	AA	884	VAL
11	AA	886	LYS
11	AA	887	VAL
11	AA	890	LYS
11	AA	912	ASP
11	AA	913	VAL
11	AA	914	LYS
11	AA	918	LEU
11	AA	933	VAL
11	AA	936	ARG
11	AA	939	VAL
11	AA	941	LYS
11	AA	943	LYS
11	AA	944	ARG
11	AA	946	LEU
11	AA	947	GLU
11	AA	949	GLU
11	AA	950	GLU
11	AA	951	MET
11	AA	952	GLN
11	AA	953	LEU
11	AA	954	LYS
11	AA	955	GLN
11	AA	957	LYS
11	AA	958	LYS
11	AA	959	ASP
11	AA	960	LEU
11	AA	962	GLU
11	AA	963	GLU
11	AA	964	LEU
11	AA	965	GLN
11	AA	967	LEU
11	AA	968	GLU
11	AA	971	LEU
11	AA	973	SER
11	AA	974	ARG
11	AA	979	LEU
11	AA	980	VAL
11	AA	985	GLU
11	AA	988	LYS

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Mol	Chain	Res	Type
11	AA	989	LEU
11	AA	991	LYS
11	AA	992	LEU
11	AA	994	ARG
11	AA	995	ASP
11	AA	997	TRP
11	AA	998	LEU
11	AA	999	GLU
11	AA	1002	LEU
11	AA	1005	GLU
11	AA	1006	GLU
11	AA	1008	GLN
11	AA	1009	ASN
11	AA	1013	GLN
11	AA	1014	LEU
11	AA	1019	ASP
11	AA	1020	GLU
11	AA	1023	HIS
11	AA	1024	GLU
11	AA	1025	PHE
11	AA	1026	GLU
11	AA	1027	LYS
11	AA	1029	LEU
11	AA	1032	LYS
11	AA	1034	ARG
11	AA	1035	LYS
11	AA	1037	THR
11	AA	1038	GLN
11	AA	1041	ASP
11	AA	1042	LEU
11	AA	1046	VAL
11	AA	1047	LEU
11	AA	1048	LYS
11	AA	1076	ILE
11	AA	1151	LEU
11	AA	1159	VAL
11	AA	1248	THR
11	AA	1250	SER
11	AA	1252	SER
11	AA	1253	LEU
11	AA	1254	VAL
11	AA	1256	GLN

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Mol	Chain	Res	Type
11	AA	1259	LEU
11	AA	1298	VAL
12	AB	47	GLU
13	AC	62	ASP
13	AC	65	LEU
13	AC	72	GLU
13	AC	91	ARG
13	AC	134	THR
13	AC	158	ARG
13	AC	159	ILE
13	AC	160	HIS
13	AC	162	GLU
13	AC	163	GLU
13	AC	165	GLU
13	AC	166	ARG
13	AC	168	ILE
13	AC	170	ARG
13	AC	171	LEU
13	AD	110	VAL
13	AD	187	VAL
13	AD	208	ASN
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	87	LYS

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	C	33	ILE
15	C	74	HIS
17	E	6	SER
17	E	10	ARG
17	E	48	GLN
17	E	64	LYS
18	F	34	ARG
18	F	62	ARG
18	F	67	ARG
19	G	8	ASP
19	G	45	LYS
19	G	59	LYS
19	G	105	LYS
19	G	108	ARG
19	G	117	LEU
19	G	128	LYS
19	G	129	LEU
19	G	132	LYS
19	G	135	LEU
19	G	161	LEU
19	G	174	LYS
19	G	208	ARG
20	H	9	PHE
20	H	31	ILE
20	H	43	LYS
20	H	54	LYS
20	H	62	ILE
20	H	70	VAL
20	H	294	VAL
20	H	305	HIS
20	H	336	ASP

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Mol	Chain	Res	Type
20	H	337	GLU
20	H	338	GLU
20	H	339	ARG
20	H	340	ARG
21	I	14	ILE
21	I	21	THR
21	I	33	LEU
21	I	75	ILE
21	I	89	LYS
21	I	175	LEU
21	I	178	LEU
21	I	200	VAL
22	J	47	ARG
22	J	48	LEU
22	J	95	GLU
22	J	104	ARG
22	J	105	MET
22	J	116	GLN
22	J	138	SER
22	J	143	VAL
23	K	10	GLU
23	K	15	LEU
23	K	60	ILE
23	K	114	VAL
23	K	115	LEU
23	K	138	ARG
23	K	141	ILE
23	K	162	GLU
24	L	7	VAL
24	L	16	GLU
24	L	24	ARG
24	L	36	ILE
24	L	38	ARG
24	L	54	LEU
24	L	86	ARG
25	M	7	ILE
25	M	17	LYS
25	M	21	GLU
25	M	23	LEU
25	M	27	VAL
25	M	50	LEU
25	M	79	ARG

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Mol	Chain	Res	Type
25	M	91	VAL
25	M	109	ARG
25	M	130	ASN
25	M	146	GLU
26	N	96	MET
26	N	104	VAL
26	N	117	ARG
27	O	27	LYS
27	O	60	LYS
27	O	61	LEU
27	O	63	LEU
27	O	116	VAL
27	O	118	LEU
28	P	17	LEU
28	P	18	ILE
28	P	24	GLU
28	P	25	ILE
28	P	27	GLU
28	P	37	ARG
28	P	87	LEU
28	P	90	LEU
28	P	102	LEU
29	Q	15	GLN
29	Q	107	ILE
30	R	5	ASN
30	R	12	ARG
30	R	24	LEU
30	R	62	GLU
30	R	74	LEU
30	R	102	LEU
31	S	45	VAL
31	S	46	LEU
31	S	89	MET
31	S	92	GLU
32	T	10	LYS
32	T	22	THR
32	T	39	LEU
32	T	40	GLN
32	T	64	ARG
32	T	66	LEU
32	T	67	LEU
32	T	70	LEU

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Mol	Chain	Res	Type
32	T	73	LYS
32	T	84	ARG
32	T	85	LEU
33	U	1	MET
33	U	2	VAL
33	U	6	LEU
33	U	19	VAL
33	U	50	THR
34	V	46	VAL
34	V	75	LEU
34	V	81	LYS
35	W	21	LYS
35	W	33	THR
35	W	49	ILE
35	W	58	VAL
35	W	79	THR
35	W	81	ARG
36	X	16	VAL
36	X	25	VAL
36	X	29	ARG
36	X	59	GLU
36	X	93	ARG
36	X	101	ARG
36	X	117	LYS
37	Y	4	VAL
37	Y	10	LEU
37	Y	16	MET
37	Y	23	VAL
37	Y	27	LEU
37	Y	30	GLN
37	Y	36	GLU
37	Y	44	LYS
37	Y	45	THR
37	Y	48	ILE
37	Y	50	LYS
37	Y	52	LEU
37	Y	57	VAL
37	Y	58	ILE
37	Y	60	VAL
37	Y	61	TYR
37	Y	64	ARG
37	Y	65	SER

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Mol	Chain	Res	Type
37	Y	67	THR
37	Y	71	LYS
37	Y	78	LEU
37	Y	80	LYS
37	Y	81	LYS
37	Y	91	LYS
37	Y	94	LYS
37	Y	95	ASP
37	Y	99	LYS
37	Y	100	ILE
37	Y	102	ARG
37	Y	104	GLN
37	Y	108	ILE
37	Y	112	LYS
37	Y	116	MET
37	Y	124	MET
37	Y	125	THR
37	Y	126	ARG
37	Y	133	ARG
37	Y	135	MET
37	Y	137	LEU
37	Y	138	VAL
38	Z	1	SER
38	Z	2	ILE
38	Z	3	THR
38	Z	4	LYS
38	Z	6	GLN
38	Z	7	ILE
38	Z	8	ILE
38	Z	14	MET
38	Z	16	VAL
38	Z	17	MET
38	Z	19	VAL
38	Z	23	ILE
38	Z	26	MET
38	Z	28	GLU
38	Z	29	LYS
38	Z	30	PHE
40	b	70	GLU
41	c	33	LEU
41	c	48	THR
41	c	71	LEU

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Mol	Chain	Res	Type
43	e	18	LEU
43	e	58	ASN
43	e	60	LYS
44	f	3	LYS
44	f	11	ARG
44	f	25	LEU
44	f	45	ARG
44	f	55	VAL
45	g	3	LYS
45	g	16	CYS
45	g	24	ILE
45	g	36	VAL
45	g	47	LYS
46	h	51	THR
46	h	94	VAL
46	h	105	LEU
46	h	118	SER
46	h	125	LYS
46	h	130	LEU
46	h	141	VAL
46	h	156	ARG
46	h	183	LYS
46	h	187	ASP
46	h	195	VAL
46	h	202	LEU
46	h	203	ARG
46	h	204	VAL
46	h	205	LEU
46	h	242	LYS
46	h	271	ARG
47	i	9	THR
47	i	12	LYS
47	i	26	THR
47	i	27	SER
47	i	29	SER
47	i	40	ARG
48	j	13	ARG
48	j	18	ASP
48	j	91	THR
48	j	99	GLU
48	j	104	VAL
48	j	177	VAL

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Mol	Chain	Res	Type
48	j	189	VAL
48	j	193	VAL
49	k	5	ILE
49	k	17	THR
49	k	24	THR
50	l	17	THR
50	l	22	ASP
50	l	40	ARG
50	l	48	THR
50	l	57	LYS
50	l	69	ARG
50	l	77	ILE
50	l	80	SER
50	l	108	ILE
50	l	109	LEU
50	l	111	GLU
50	l	122	GLU
50	l	149	ILE
50	l	179	SER
51	m	22	MET
51	m	42	LEU
52	n	6	ASP
52	n	10	ASP
52	n	26	MET
52	n	40	VAL
52	n	47	LYS
52	n	49	LEU
52	n	57	LEU
52	n	79	ILE
52	n	80	ARG
52	n	95	ARG
52	n	105	THR
52	n	117	LEU
52	n	122	PHE
52	n	123	ASP
52	n	132	VAL
52	n	140	GLU
52	n	141	ILE
52	n	163	ASP
53	o	8	ARG
53	o	30	ARG
53	o	31	HIS

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Mol	Chain	Res	Type
53	o	55	LEU
54	p	11	VAL
54	p	85	LYS
54	p	95	ARG
54	p	125	CYS
54	p	168	VAL
54	p	171	THR
55	q	3	VAL
55	q	26	ILE
55	q	34	LYS
56	r	1	MET
56	r	9	VAL
56	r	11	ASN
56	r	12	LEU
56	r	15	LEU
56	r	41	LYS
56	r	66	ASN
56	r	72	ILE
56	r	76	GLU
56	r	94	ILE
56	r	101	ASP
56	r	127	GLU
57	s	1	MET
57	s	30	THR
57	s	31	GLU
57	s	43	GLU
57	s	57	LEU
57	s	123	LYS
57	s	124	VAL
57	s	139	VAL
57	s	140	LEU
57	s	142	ILE
58	t	35	VAL
58	t	49	ARG
58	t	67	LYS
58	t	70	ARG
58	t	80	ASP
58	t	104	THR
59	u	5	THR
59	u	27	LEU
59	u	59	ARG
59	u	73	ILE

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Mol	Chain	Res	Type
59	u	76	GLU
59	u	78	ARG
59	u	84	LYS
60	v	110	GLU
60	v	126	ILE
60	v	127	LYS
60	v	128	THR
61	w	2	ARG
61	w	20	MET
61	w	24	MET
61	w	51	LEU
61	w	65	LEU
61	w	69	ARG
61	w	95	THR
61	w	116	VAL
62	x	13	ARG
62	x	31	THR
62	x	47	VAL
62	x	48	LEU
62	x	91	SER
62	x	116	GLN
63	y	8	LEU
63	y	10	GLN
63	y	27	GLU
63	y	40	LEU
63	y	81	VAL
63	y	85	SER
63	y	102	GLU
63	y	114	LEU
64	z	18	LEU
64	z	51	ARG
64	z	109	LEU
64	z	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (70) 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

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Mol	Chain	Res	Type
5	4	12	GLN
9	9	103	ASN
9	9	122	GLN
11	AA	69	GLN
11	AA	273	HIS
11	AA	761	GLN
11	AA	808	ASN
11	AA	824	GLN
11	AA	965	GLN
11	AA	1157	GLN
11	AA	1236	ASN
13	AC	41	ASN
13	AC	132	HIS
13	AD	41	ASN
13	AD	93	GLN
13	AD	103	ASN
14	AE	196	GLN
14	AE	469	HIS
14	AE	817	HIS
14	AE	865	HIS
14	AE	1195	GLN
14	AE	1238	GLN
14	AE	1249	ASN
17	E	3	ASN
17	E	55	GLN
17	E	61	GLN
19	G	18	HIS
19	G	58	ASN
19	G	94	HIS
21	I	6	HIS
21	I	25	ASN
21	I	123	GLN
22	J	36	GLN
22	J	40	GLN
22	J	41	HIS
23	K	97	GLN
24	L	11	HIS
24	L	63	ASN
24	L	94	HIS
25	M	97	ASN
25	M	148	ASN
27	O	81	HIS

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Mol	Chain	Res	Type
27	O	126	GLN
28	P	58	ASN
29	Q	15	GLN
30	R	6	GLN
30	R	72	HIS
31	S	60	GLN
32	T	40	GLN
33	U	59	HIS
36	X	12	HIS
36	X	105	ASN
45	g	33	ASN
45	g	41	HIS
46	h	25	HIS
46	h	70	ASN
49	k	26	ASN
53	o	28	ASN
54	p	48	ASN
54	p	88	GLN
55	q	35	GLN
56	r	20	ASN
56	r	133	GLN
58	t	88	ASN
63	y	15	GLN

5.3.3 RNA (i)

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%)
16	D	1515/1542 (98%)	290 (19%)	35 (2%)
39	a	2859/2904 (98%)	540 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	34/35 (97%)	23 (67%)	5 (14%)
All	All	4677/4753 (98%)	934 (19%)	52 (1%)

All (934) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-12	G
8	7	-11	U
8	7	-10	U

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Mol	Chain	Res	Type
8	7	-8	U
8	7	-7	U
8	7	-6	U
8	7	-5	U
8	7	-4	U
8	7	-3	U
8	7	-1	U
8	7	0	U
8	7	1	U
8	7	2	U
8	7	4	U
8	7	5	U
8	7	6	U
8	7	7	G
8	7	8	A
8	7	9	U
8	7	10	U
8	7	11	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

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

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Mol	Chain	Res	Type
16	D	4	U
16	D	5	U
16	D	9	G
16	D	22	G
16	D	29	U
16	D	32	A
16	D	39	G
16	D	41	G
16	D	47	C
16	D	48	C
16	D	50	A
16	D	51	A
16	D	52	C
16	D	54	C
16	D	69	G
16	D	70	U
16	D	71	A
16	D	72	A
16	D	74	A
16	D	76	G
16	D	82	G
16	D	83	C
16	D	84	U
16	D	87	C
16	D	90	C
16	D	94	G
16	D	95	C
16	D	96	U
16	D	108	G
16	D	120	A
16	D	122	G
16	D	128	G
16	D	131	A
16	D	141	G
16	D	144	G
16	D	148	G
16	D	149	A
16	D	160	A
16	D	164	G
16	D	173	U
16	D	181	A
16	D	182	A

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Mol	Chain	Res	Type
16	D	197	A
16	D	198	G
16	D	204	G
16	D	208	U
16	D	209	U
16	D	210	C
16	D	211	G
16	D	212	G
16	D	216	U
16	D	226	G
16	D	245	U
16	D	247	G
16	D	251	G
16	D	253	A
16	D	258	G
16	D	262	A
16	D	266	G
16	D	267	C
16	D	271	C
16	D	279	A
16	D	289	G
16	D	299	G
16	D	306	A
16	D	321	A
16	D	328	C
16	D	329	A
16	D	332	G
16	D	347	G
16	D	352	C
16	D	353	A
16	D	354	G
16	D	355	C
16	D	367	U
16	D	372	C
16	D	373	A
16	D	376	G
16	D	382	A
16	D	384	G
16	D	392	C
16	D	393	A
16	D	397	A
16	D	406	G

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Mol	Chain	Res	Type
16	D	412	A
16	D	413	G
16	D	414	A
16	D	421	U
16	D	422	C
16	D	424	G
16	D	429	U
16	D	446	G
16	D	451	A
16	D	457	G
16	D	458	U
16	D	460	A
16	D	463	U
16	D	464	U
16	D	467	U
16	D	468	A
16	D	469	C
16	D	478	A
16	D	479	U
16	D	481	G
16	D	484	G
16	D	485	U
16	D	486	U
16	D	505	G
16	D	509	A
16	D	511	C
16	D	518	C
16	D	519	C
16	D	526	C
16	D	531	U
16	D	532	A
16	D	533	A
16	D	542	G
16	D	547	A
16	D	559	A
16	D	562	U
16	D	568	G
16	D	572	A
16	D	573	A
16	D	576	C
16	D	577	G
16	D	579	A

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Mol	Chain	Res	Type
16	D	596	A
16	D	628	G
16	D	633	G
16	D	641	U
16	D	642	A
16	D	649	A
16	D	650	G
16	D	653	U
16	D	665	A
16	D	666	G
16	D	687	A
16	D	700	G
16	D	723	U
16	D	724	G
16	D	731	G
16	D	734	G
16	D	747	A
16	D	748	G
16	D	755	G
16	D	760	G
16	D	777	A
16	D	793	U
16	D	794	A
16	D	815	A
16	D	817	C
16	D	828	U
16	D	829	G
16	D	832	G
16	D	841	C
16	D	844	G
16	D	845	A
16	D	849	G
16	D	874	G
16	D	887	G
16	D	902	G
16	D	914	A
16	D	916	U
16	D	926	G
16	D	934	C
16	D	935	A
16	D	954	G
16	D	960	U

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Mol	Chain	Res	Type
16	D	963	G
16	D	969	A
16	D	972	C
16	D	975	A
16	D	976	G
16	D	991	U
16	D	992	U
16	D	993	G
16	D	996	A
16	D	999	C
16	D	1004	A
16	D	1008	U
16	D	1009	U
16	D	1017	U
16	D	1018	G
16	D	1021	A
16	D	1024	G
16	D	1026	G
16	D	1028	C
16	D	1030	U
16	D	1031	C
16	D	1037	C
16	D	1043	G
16	D	1044	A
16	D	1046	A
16	D	1065	U
16	D	1085	U
16	D	1086	U
16	D	1094	G
16	D	1095	U
16	D	1099	G
16	D	1101	A
16	D	1124	G
16	D	1133	G
16	D	1135	U
16	D	1136	C
16	D	1137	C
16	D	1139	G
16	D	1140	C
16	D	1141	C
16	D	1142	G
16	D	1143	G

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Mol	Chain	Res	Type
16	D	1145	A
16	D	1146	A
16	D	1151	A
16	D	1152	A
16	D	1158	C
16	D	1159	U
16	D	1167	A
16	D	1171	A
16	D	1174	G
16	D	1175	G
16	D	1176	A
16	D	1184	G
16	D	1196	A
16	D	1197	A
16	D	1206	G
16	D	1211	U
16	D	1212	U
16	D	1213	A
16	D	1214	C
16	D	1215	G
16	D	1226	C
16	D	1227	A
16	D	1228	C
16	D	1238	A
16	D	1256	A
16	D	1257	A
16	D	1260	G
16	D	1275	A
16	D	1276	G
16	D	1278	G
16	D	1279	G
16	D	1280	A
16	D	1285	A
16	D	1286	U
16	D	1287	A
16	D	1299	A
16	D	1300	G
16	D	1302	C
16	D	1305	G
16	D	1312	G
16	D	1317	C
16	D	1320	C

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Mol	Chain	Res	Type
16	D	1323	G
16	D	1329	A
16	D	1338	G
16	D	1340	A
16	D	1346	A
16	D	1347	G
16	D	1353	G
16	D	1363	A
16	D	1370	G
16	D	1378	C
16	D	1379	G
16	D	1381	U
16	D	1391	U
16	D	1396	A
16	D	1397	C
16	D	1398	A
16	D	1404	C
16	D	1419	G
16	D	1429	A
16	D	1441	A
16	D	1446	A
16	D	1447	A
16	D	1448	C
16	D	1452	C
16	D	1453	G
16	D	1475	G
16	D	1487	G
16	D	1492	A
16	D	1493	A
16	D	1494	G
16	D	1495	U
16	D	1497	G
16	D	1503	A
16	D	1506	U
16	D	1517	G
16	D	1529	G
16	D	1530	G
16	D	1534	A
39	a	10	A
39	a	15	G
39	a	34	U
39	a	35	G

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Mol	Chain	Res	Type
39	a	46	G
39	a	58	G
39	a	60	G
39	a	63	A
39	a	71	A
39	a	74	A
39	a	75	G
39	a	83	A
39	a	84	A
39	a	85	G
39	a	96	C
39	a	102	U
39	a	103	A
39	a	110	G
39	a	114	U
39	a	118	A
39	a	119	A
39	a	120	U
39	a	122	G
39	a	131	A
39	a	136	G
39	a	139	U
39	a	140	C
39	a	141	G
39	a	145	C
39	a	163	C
39	a	165	A
39	a	181	A
39	a	196	A
39	a	199	A
39	a	200	U
39	a	215	G
39	a	216	A
39	a	222	A
39	a	225	C
39	a	248	G
39	a	249	C
39	a	261	G
39	a	264	C
39	a	265	A
39	a	266	G
39	a	267	C

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Mol	Chain	Res	Type
39	a	271	G
39	a	272	A
39	a	275	C
39	a	276	U
39	a	278	A
39	a	285	G
39	a	311	A
39	a	324	A
39	a	329	G
39	a	330	A
39	a	353	C
39	a	359	G
39	a	361	G
39	a	362	A
39	a	371	A
39	a	372	G
39	a	373	U
39	a	375	G
39	a	383	C
39	a	386	G
39	a	396	G
39	a	405	U
39	a	411	G
39	a	412	A
39	a	420	C
39	a	424	G
39	a	435	C
39	a	451	U
39	a	456	C
39	a	457	A
39	a	477	A
39	a	481	G
39	a	491	G
39	a	501	A
39	a	503	A
39	a	504	A
39	a	505	A
39	a	509	C
39	a	522	A
39	a	529	A
39	a	532	A
39	a	543	G

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Mol	Chain	Res	Type
39	a	546	U
39	a	547	A
39	a	548	G
39	a	549	G
39	a	551	G
39	a	563	A
39	a	569	U
39	a	573	U
39	a	575	A
39	a	588	U
39	a	603	A
39	a	609	A
39	a	613	A
39	a	614	A
39	a	615	U
39	a	616	A
39	a	618	G
39	a	620	G
39	a	621	A
39	a	627	A
39	a	637	A
39	a	645	C
39	a	647	G
39	a	654	A
39	a	664	G
39	a	668	A
39	a	685	A
39	a	686	U
39	a	710	U
39	a	717	C
39	a	730	A
39	a	738	G
39	a	757	G
39	a	764	A
39	a	765	C
39	a	775	G
39	a	776	G
39	a	782	A
39	a	784	G
39	a	785	G
39	a	800	A
39	a	802	A

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Mol	Chain	Res	Type
39	a	805	G
39	a	812	C
39	a	819	A
39	a	827	U
39	a	828	U
39	a	845	A
39	a	846	U
39	a	858	G
39	a	859	G
39	a	869	G
39	a	878	A
39	a	881	G
39	a	883	G
39	a	884	U
39	a	885	C
39	a	888	C
39	a	891	G
39	a	892	A
39	a	893	C
39	a	895	U
39	a	896	A
39	a	897	C
39	a	899	A
39	a	907	G
39	a	910	A
39	a	914	G
39	a	915	C
39	a	931	U
39	a	941	A
39	a	945	A
39	a	946	C
39	a	953	G
39	a	961	C
39	a	974	G
39	a	983	A
39	a	984	A
39	a	985	C
39	a	995	C
39	a	996	A
39	a	999	U
39	a	1005	C
39	a	1012	U

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Mol	Chain	Res	Type
39	a	1013	C
39	a	1022	G
39	a	1023	U
39	a	1026	G
39	a	1033	U
39	a	1041	G
39	a	1042	G
39	a	1045	C
39	a	1046	A
39	a	1047	G
39	a	1060	U
39	a	1061	U
39	a	1062	G
39	a	1063	G
39	a	1064	C
39	a	1065	U
39	a	1066	U
39	a	1067	A
39	a	1068	G
39	a	1069	A
39	a	1070	A
39	a	1071	G
39	a	1073	A
39	a	1074	G
39	a	1076	C
39	a	1079	C
39	a	1080	A
39	a	1081	U
39	a	1082	U
39	a	1083	U
39	a	1084	A
39	a	1087	G
39	a	1088	A
39	a	1090	A
39	a	1095	A
39	a	1096	A
39	a	1107	G
39	a	1110	G
39	a	1111	A
39	a	1112	G
39	a	1119	U
39	a	1122	G

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Mol	Chain	Res	Type
39	a	1132	U
39	a	1134	A
39	a	1135	C
39	a	1142	A
39	a	1143	A
39	a	1169	A
39	a	1170	C
39	a	1173	U
39	a	1174	U
39	a	1175	A
39	a	1176	U
39	a	1177	G
39	a	1178	C
39	a	1179	G
39	a	1180	U
39	a	1186	G
39	a	1238	G
39	a	1248	G
39	a	1253	A
39	a	1256	G
39	a	1266	G
39	a	1271	G
39	a	1272	A
39	a	1273	U
39	a	1301	A
39	a	1321	A
39	a	1345	C
39	a	1352	U
39	a	1365	A
39	a	1368	G
39	a	1378	A
39	a	1379	U
39	a	1380	G
39	a	1383	A
39	a	1387	A
39	a	1392	A
39	a	1395	A
39	a	1406	U
39	a	1407	G
39	a	1408	G
39	a	1411	U
39	a	1414	C

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Mol	Chain	Res	Type
39	a	1415	U
39	a	1416	G
39	a	1417	C
39	a	1419	A
39	a	1420	A
39	a	1428	C
39	a	1452	G
39	a	1453	A
39	a	1460	U
39	a	1478	G
39	a	1482	G
39	a	1490	A
39	a	1491	G
39	a	1497	U
39	a	1503	A
39	a	1508	A
39	a	1509	A
39	a	1510	G
39	a	1515	A
39	a	1529	G
39	a	1534	U
39	a	1535	A
39	a	1536	C
39	a	1537	G
39	a	1554	U
39	a	1559	U
39	a	1566	A
39	a	1569	A
39	a	1578	U
39	a	1580	A
39	a	1581	G
39	a	1582	C
39	a	1583	A
39	a	1584	U
39	a	1589	U
39	a	1590	A
39	a	1608	A
39	a	1609	A
39	a	1610	A
39	a	1647	U
39	a	1648	U
39	a	1649	G

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Mol	Chain	Res	Type
39	a	1651	G
39	a	1674	G
39	a	1677	A
39	a	1703	G
39	a	1714	U
39	a	1715	G
39	a	1718	G
39	a	1729	U
39	a	1730	C
39	a	1732	C
39	a	1738	G
39	a	1750	G
39	a	1755	A
39	a	1758	U
39	a	1764	C
39	a	1773	A
39	a	1791	A
39	a	1800	C
39	a	1801	A
39	a	1808	A
39	a	1811	G
39	a	1816	C
39	a	1829	A
39	a	1833	C
39	a	1847	A
39	a	1848	A
39	a	1858	A
39	a	1859	U
39	a	1862	G
39	a	1864	U
39	a	1869	G
39	a	1870	C
39	a	1872	A
39	a	1873	G
39	a	1905	C
39	a	1906	G
39	a	1907	G
39	a	1913	A
39	a	1914	C
39	a	1919	A
39	a	1920	C
39	a	1922	G

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Mol	Chain	Res	Type
39	a	1923	U
39	a	1924	C
39	a	1925	C
39	a	1926	U
39	a	1928	A
39	a	1929	G
39	a	1930	G
39	a	1936	A
39	a	1938	A
39	a	1955	U
39	a	1965	C
39	a	1967	C
39	a	1970	A
39	a	1971	U
39	a	1972	G
39	a	1987	A
39	a	1991	U
39	a	1992	G
39	a	1993	U
39	a	1997	C
39	a	2002	G
39	a	2022	U
39	a	2023	C
39	a	2027	G
39	a	2033	A
39	a	2043	C
39	a	2051	A
39	a	2052	A
39	a	2055	C
39	a	2056	G
39	a	2060	A
39	a	2061	G
39	a	2062	A
39	a	2063	C
39	a	2077	A
39	a	2097	A
39	a	2099	U
39	a	2100	G
39	a	2108	A
39	a	2110	G
39	a	2111	U
39	a	2113	U

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Mol	Chain	Res	Type
39	a	2115	G
39	a	2116	G
39	a	2117	A
39	a	2118	U
39	a	2121	G
39	a	2122	U
39	a	2124	G
39	a	2125	G
39	a	2126	A
39	a	2127	G
39	a	2128	G
39	a	2131	U
39	a	2132	U
39	a	2133	G
39	a	2134	A
39	a	2139	U
39	a	2141	G
39	a	2146	C
39	a	2147	A
39	a	2154	A
39	a	2157	G
39	a	2158	A
39	a	2159	G
39	a	2162	G
39	a	2163	A
39	a	2164	C
39	a	2165	C
39	a	2169	A
39	a	2171	A
39	a	2172	U
39	a	2178	C
39	a	2182	U
39	a	2183	A
39	a	2185	U
39	a	2188	U
39	a	2189	U
39	a	2190	G
39	a	2191	A
39	a	2193	G
39	a	2194	U
39	a	2198	A
39	a	2204	G

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Mol	Chain	Res	Type
39	a	2210	U
39	a	2211	A
39	a	2212	A
39	a	2213	U
39	a	2225	A
39	a	2226	C
39	a	2229	U
39	a	2238	G
39	a	2239	G
39	a	2244	U
39	a	2250	G
39	a	2268	A
39	a	2278	A
39	a	2283	C
39	a	2287	A
39	a	2297	A
39	a	2305	U
39	a	2308	G
39	a	2309	A
39	a	2315	G
39	a	2322	A
39	a	2325	G
39	a	2327	A
39	a	2333	A
39	a	2339	C
39	a	2345	G
39	a	2347	C
39	a	2350	C
39	a	2361	G
39	a	2372	U
39	a	2376	A
39	a	2383	G
39	a	2385	C
39	a	2402	U
39	a	2403	C
39	a	2406	A
39	a	2423	U
39	a	2424	C
39	a	2425	A
39	a	2426	A
39	a	2429	G
39	a	2430	A

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Mol	Chain	Res	Type
39	a	2431	U
39	a	2434	A
39	a	2435	A
39	a	2441	U
39	a	2447	G
39	a	2448	A
39	a	2470	G
39	a	2474	U
39	a	2476	A
39	a	2478	A
39	a	2484	G
39	a	2491	U
39	a	2502	G
39	a	2506	U
39	a	2507	C
39	a	2512	C
39	a	2513	A
39	a	2518	A
39	a	2520	C
39	a	2525	G
39	a	2529	G
39	a	2535	G
39	a	2547	A
39	a	2554	U
39	a	2566	A
39	a	2567	G
39	a	2572	A
39	a	2573	C
39	a	2574	G
39	a	2585	U
39	a	2586	U
39	a	2602	A
39	a	2603	G
39	a	2609	U
39	a	2610	C
39	a	2611	C
39	a	2613	U
39	a	2629	U
39	a	2663	G
39	a	2669	G
39	a	2671	G
39	a	2689	U

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Mol	Chain	Res	Type
39	a	2690	U
39	a	2714	G
39	a	2722	G
39	a	2726	A
39	a	2744	G
39	a	2748	A
39	a	2757	A
39	a	2758	A
39	a	2765	A
39	a	2777	G
39	a	2778	A
39	a	2791	G
39	a	2793	C
39	a	2796	U
39	a	2797	U
39	a	2798	U
39	a	2799	A
39	a	2801	G
39	a	2818	U
39	a	2820	A
39	a	2823	A
39	a	2825	G
39	a	2849	U
39	a	2850	A
39	a	2859	G
39	a	2861	U
39	a	2867	G
39	a	2880	C
39	a	2884	U
39	a	2885	G
39	a	2891	U
39	a	2902	C
42	d	2	G
42	d	9	G
42	d	13	G
42	d	16	G
42	d	17	C
42	d	35	C
42	d	36	C
42	d	45	A
42	d	51	G
42	d	56	G

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Mol	Chain	Res	Type
42	d	64	G
42	d	66	A
42	d	88	C
42	d	89	U
42	d	90	C
42	d	99	A
42	d	109	A

All (52) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	7	-11	U
8	7	-8	U
8	7	-6	U
8	7	-1	U
8	7	8	A
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
16	D	7	A
16	D	70	U
16	D	121	U
16	D	181	A
16	D	183	C
16	D	197	A
16	D	209	U
16	D	305	G
16	D	328	C
16	D	428	G
16	D	496	A
16	D	517	G
16	D	531	U
16	D	532	A

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Mol	Chain	Res	Type
16	D	562	U
16	D	641	U
16	D	722	G
16	D	793	U
16	D	991	U
16	D	992	U
16	D	1109	C
16	D	1145	A
16	D	1196	A
16	D	1211	U
16	D	1212	U
16	D	1213	A
16	D	1214	C
16	D	1225	A
16	D	1299	A
16	D	1396	A
16	D	1432	G
16	D	1447	A
16	D	1491	G
16	D	1492	A
16	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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

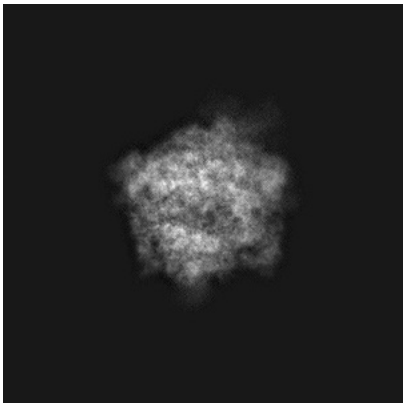
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-21469. These allow visual inspection of the internal detail of the map and identification of artifacts.

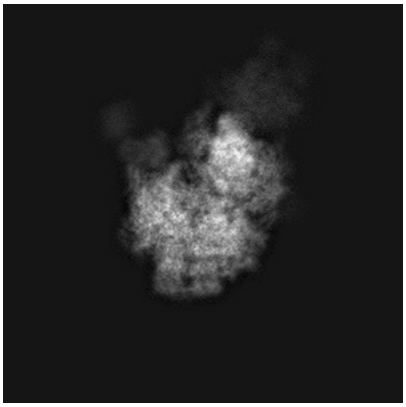
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

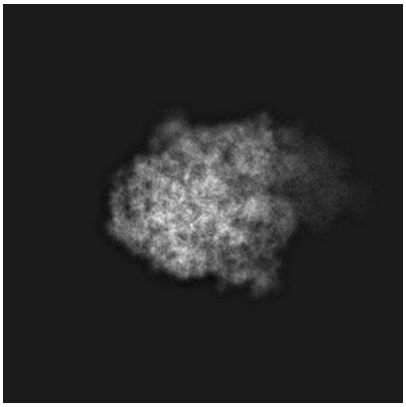
6.1.1 Primary map



X



Y

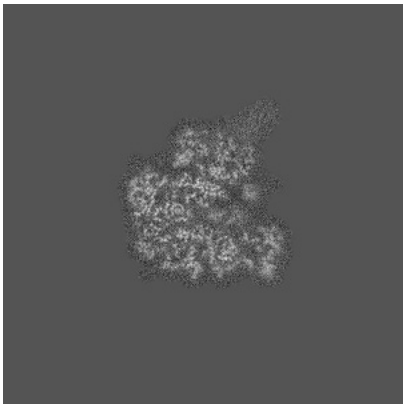


Z

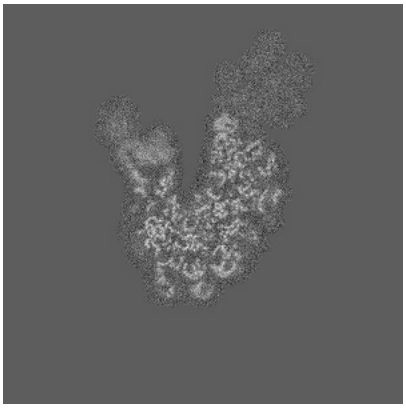
The images above show the map projected in three orthogonal directions.

6.2 Central slices

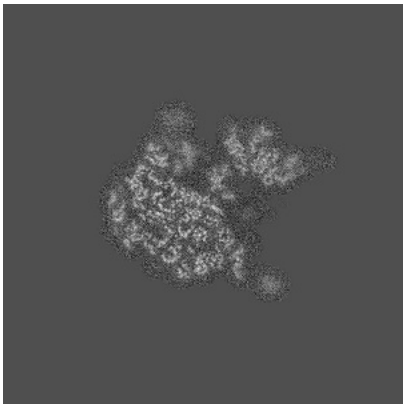
6.2.1 Primary map



X Index: 250



Y Index: 250

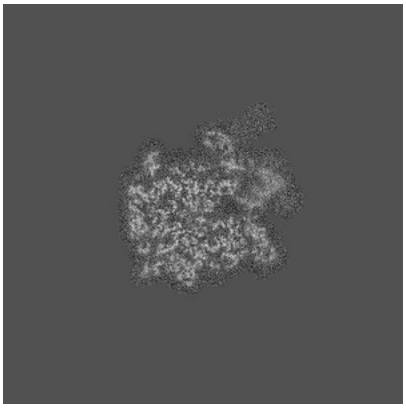


Z Index: 250

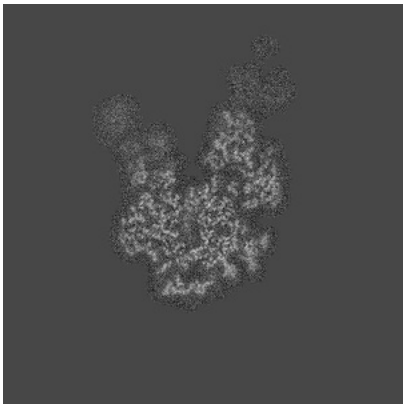
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

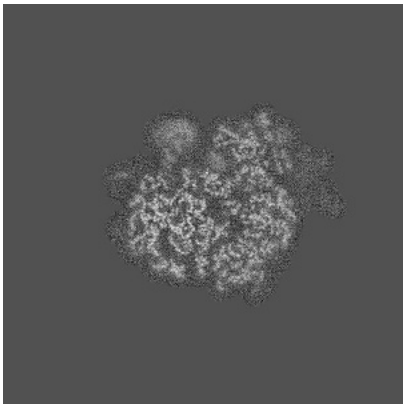
6.3.1 Primary map



X Index: 230



Y Index: 231

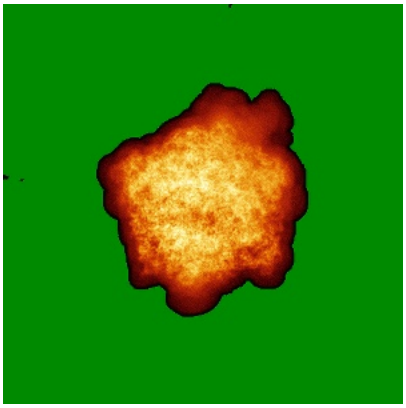


Z Index: 276

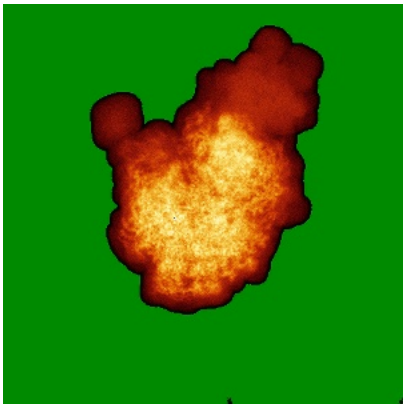
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

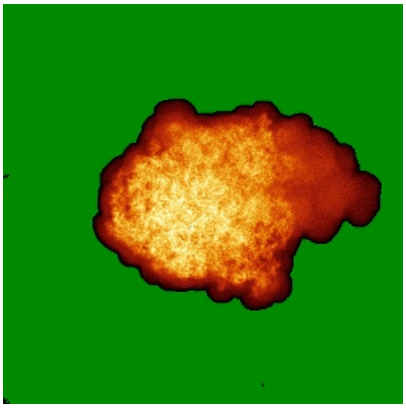
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

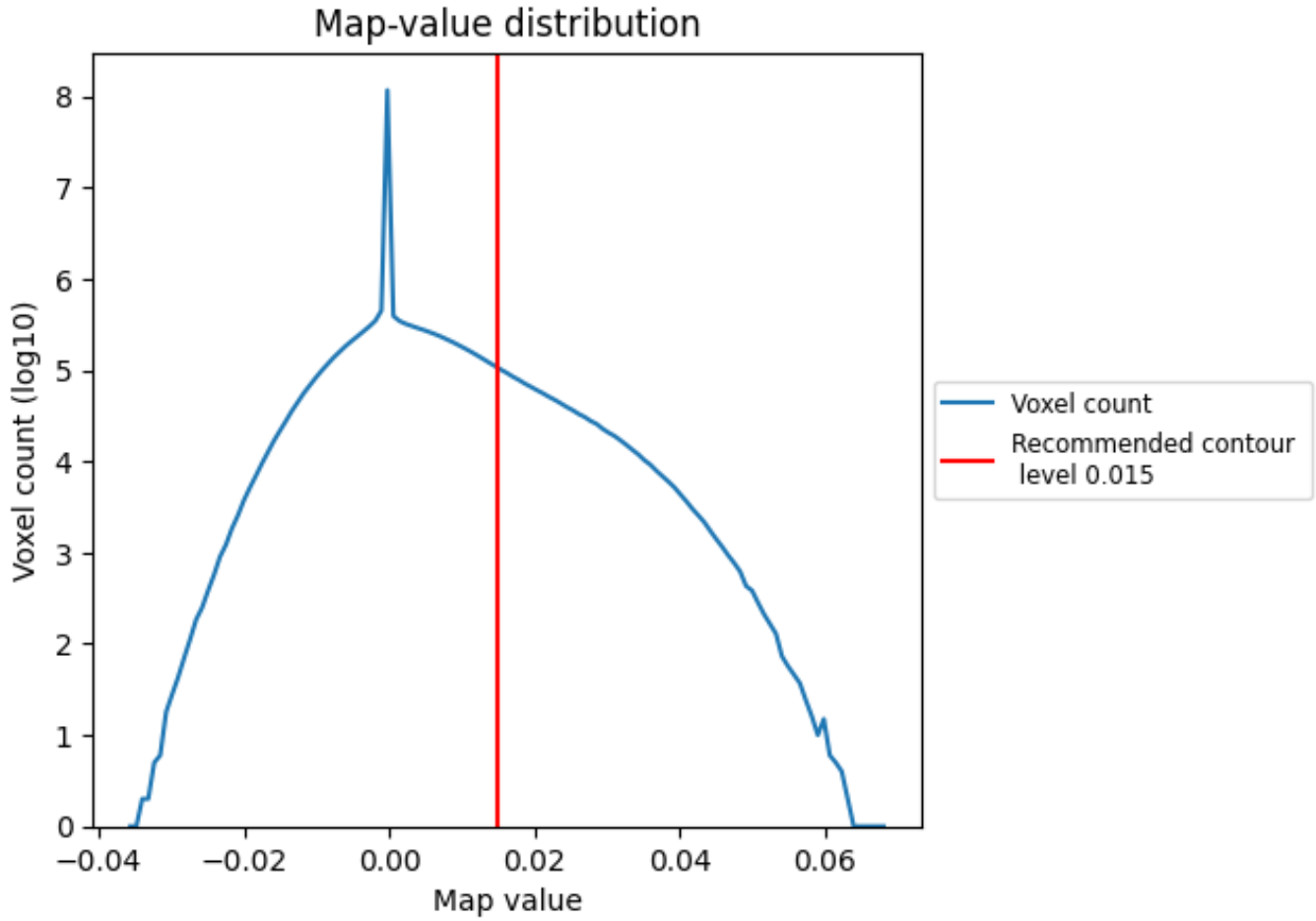
6.6 Mask visualisation (i)

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

7 Map analysis

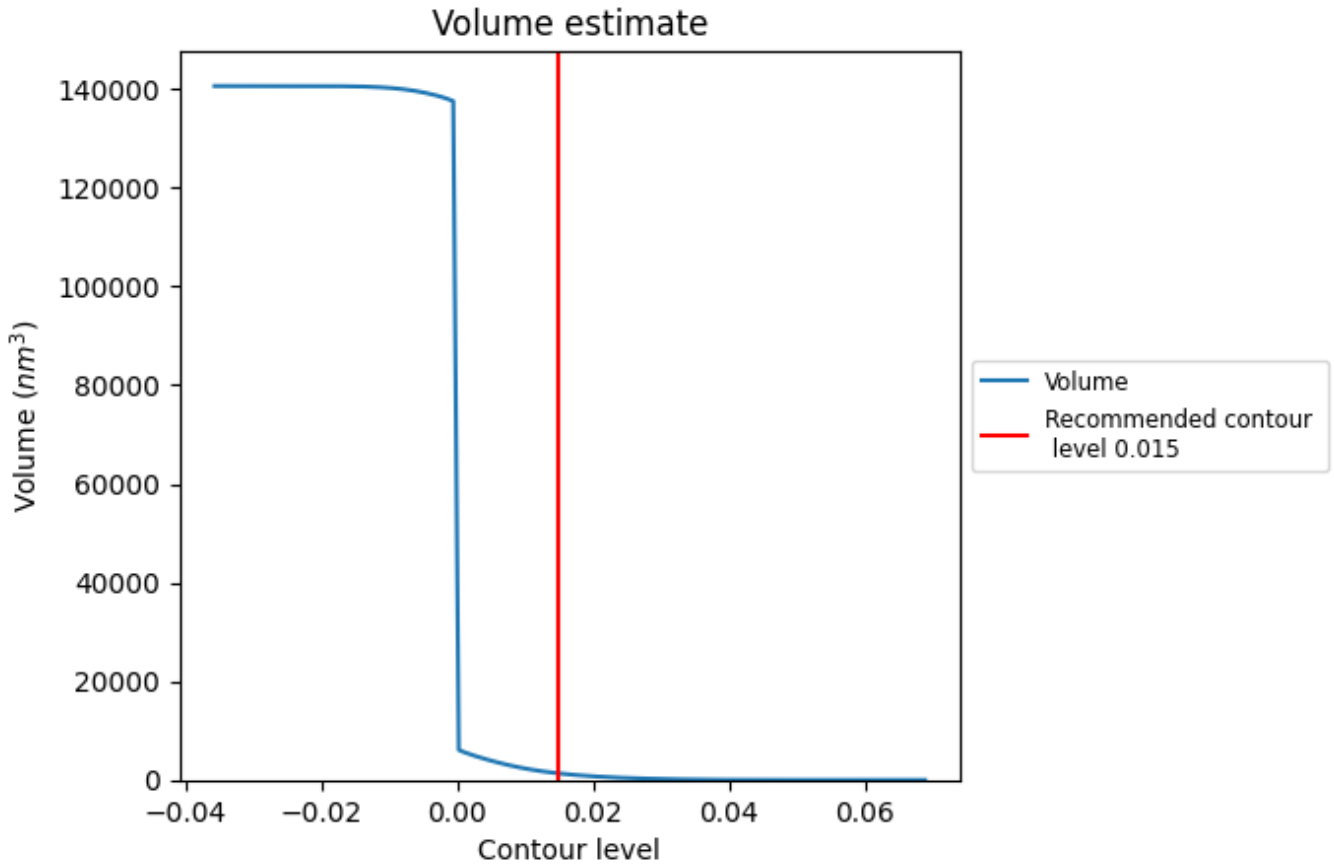
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

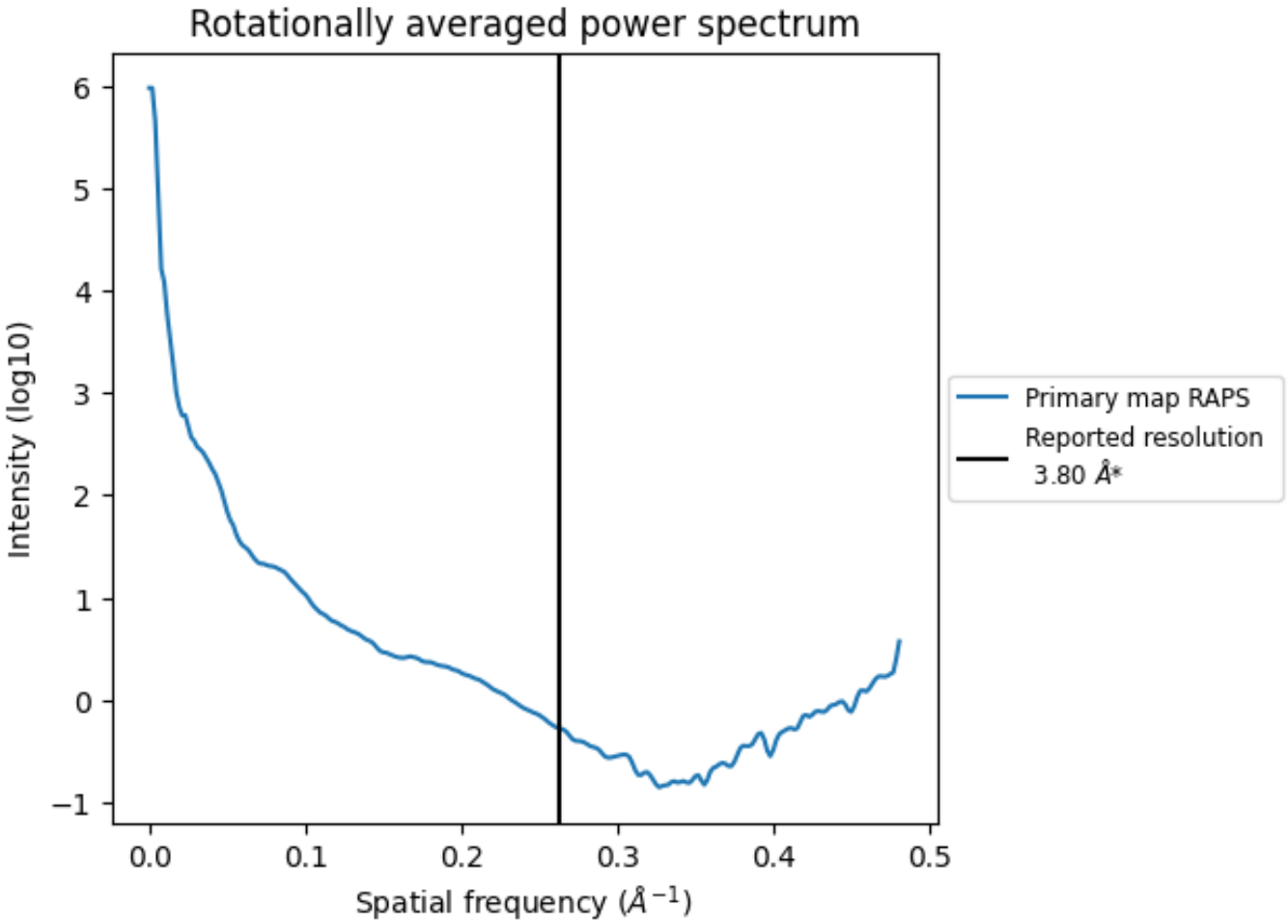
7.2 Volume estimate



The volume at the recommended contour level is 1329 nm^3; this corresponds to an approximate mass of 1201 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 (i)



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

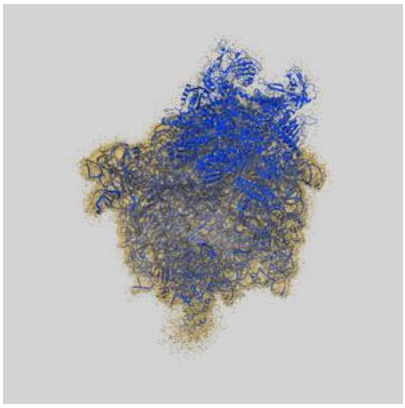
8 Fourier-Shell correlation

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

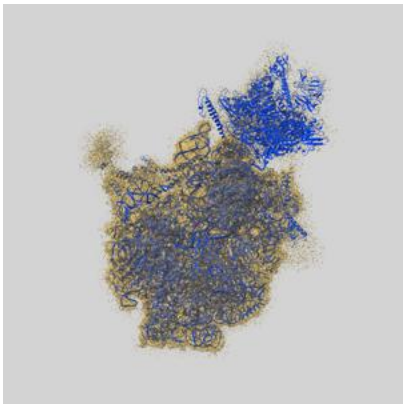
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-21469 and PDB model 6VYR. Per-residue inclusion information can be found in section 3 on page 16.

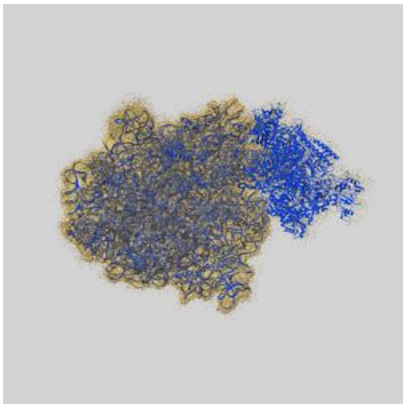
9.1 Map-model overlay



X



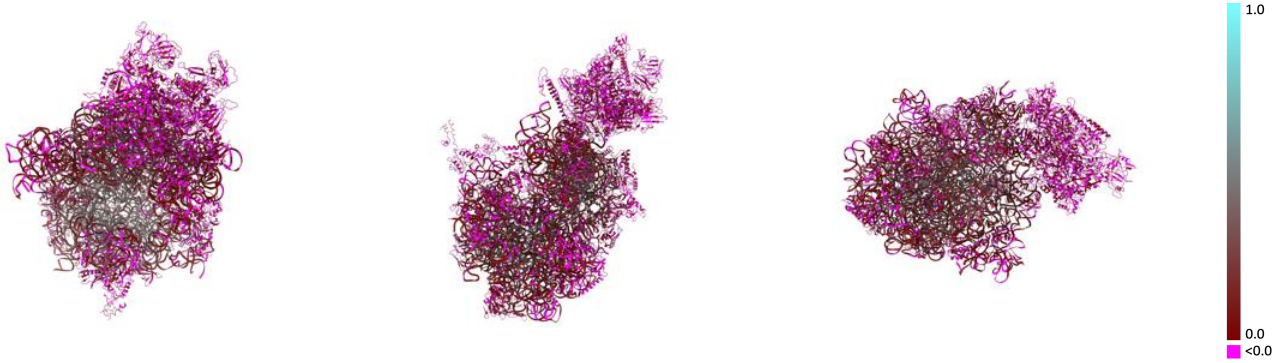
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015 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.

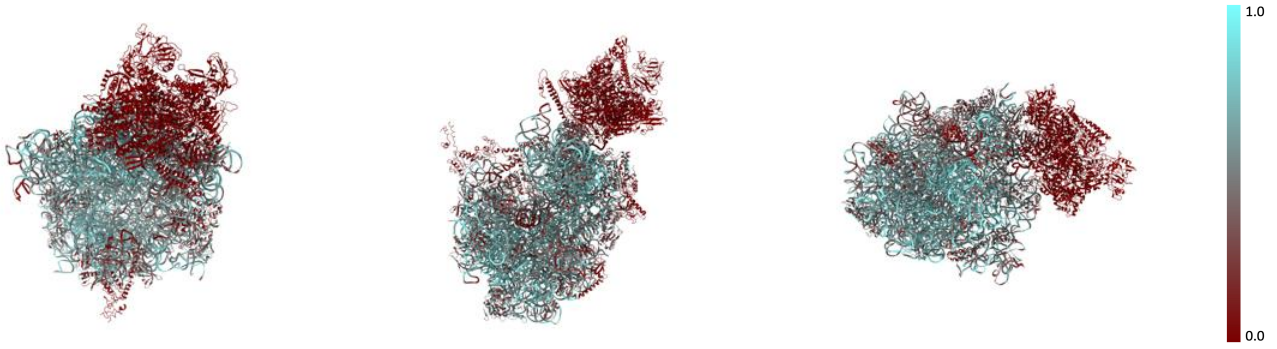
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

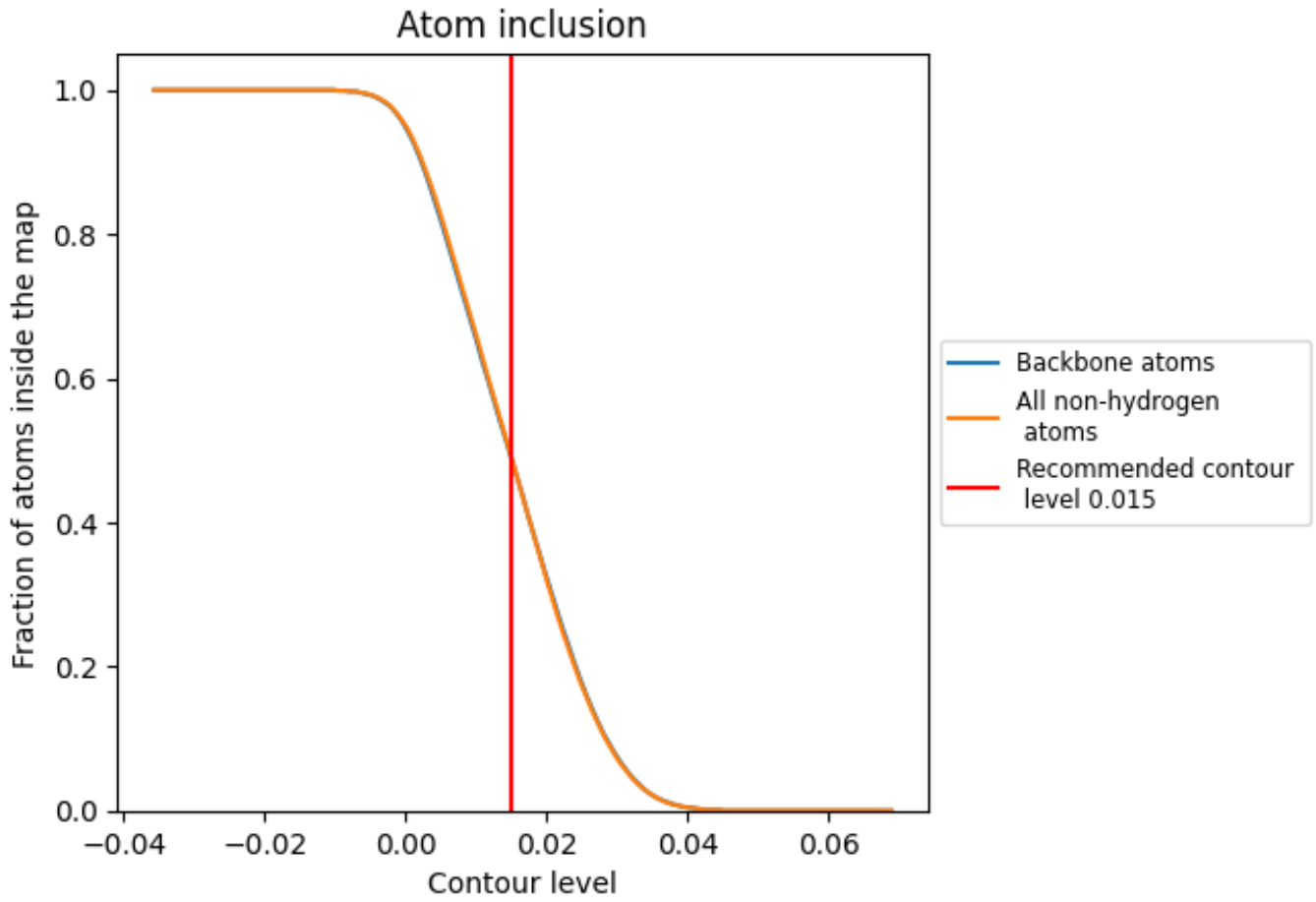
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.015).

9.4 Atom inclusion (i)



At the recommended contour level, 49% of all backbone atoms, 49% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4900	0.1410
0	0.5020	0.1730
1	0.5660	0.2430
2	0.3930	0.0870
3	0.3800	0.0780
4	0.4110	0.1050
5	0.0000	0.0260
6	0.0090	0.0170
7	0.0610	0.0740
9	0.1280	0.0060
A	0.3670	0.0850
AA	0.0070	0.0150
AB	0.0050	0.0480
AC	0.0120	0.0270
AD	0.0010	0.0030
AE	0.0050	0.0200
B	0.2700	0.0430
C	0.4300	0.1360
D	0.7020	0.1970
E	0.3500	0.0310
F	0.3850	0.1720
G	0.3910	0.1200
H	0.0280	0.0060
I	0.3870	0.1470
J	0.3990	0.1330
K	0.5800	0.2670
L	0.3550	0.0730
M	0.3640	0.1160
N	0.5370	0.2170
O	0.3820	0.0940
P	0.3430	0.1050
Q	0.4350	0.1560
R	0.5310	0.2470
S	0.3860	0.0880
T	0.4970	0.1680

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Chain	Atom inclusion	Q-score
U	0.3560	0.0690
V	0.4570	0.1840
W	0.2060	0.0050
X	0.2710	0.0200
Y	0.0800	0.0180
Z	0.0400	0.0760
a	0.6890	0.1870
b	0.4490	0.1730
c	0.4190	0.1180
d	0.6440	0.1010
e	0.3680	0.0360
f	0.5460	0.2160
g	0.2310	0.0310
h	0.4440	0.1160
i	0.5560	0.2220
j	0.4860	0.1920
k	0.3040	0.0450
l	0.4150	0.1320
m	0.5940	0.2440
n	0.3120	0.0520
o	0.4280	0.1580
p	0.3080	0.0460
q	0.4250	0.1350
r	0.1710	0.0050
s	0.5290	0.2030
t	0.4330	0.1680
u	0.4350	0.1620
v	0.4570	0.1730
w	0.5180	0.1630
x	0.3060	-0.0030
y	0.3810	0.0940
z	0.5930	0.2570