Full wwPDB EM Validation Report (i)

Mar 2, 2024 – 05:30 PM EST

PDB ID	:	5UYK
EMDB ID	:	EMD-8615
Title	:	70S ribosome bound with cognate ternary complex not base-paired to A site codon (Structure I)
Authors	:	Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on	:	2017-02-24
Resolution	:	3.90 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 (i) 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 (1)) were used in the production of this report:

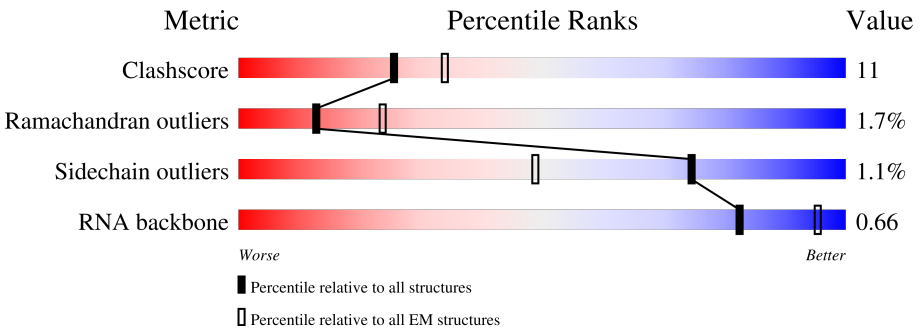
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	04	271	64% 34%
2	05	209	69% 30%
3	06	201	73% 26%
4	07	177	66% 32%
5	08	176	63% 36%
6	09	149	30% 59% 40%
7	10	131	47% 47% 47% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	11	141	35% 53% 46%
9	12	142	70% 30%
10	13	122	71% 27%
11	14	143	76% 23%
12	15	136	68% 31%
13	16	120	69% 30%
14	17	116	74% 26%
15	18	114	68% 32%
16	19	117	68% 32%
17	20	103	7% 74% 24%
18	21	110	5% 67% 32%
19	22	93	70% 30%
20	23	102	70% 29%
21	24	94	65% 35%
22	25	75	67% 33%
23	26	77	69% 31%
24	27	63	5% 57% 40%
25	28	58	76% 22%
26	29	66	11% 67% 33%
27	30	56	5% 50% 50%
28	31	50	8% 70% 30%
29	32	46	76% 24%
30	33	64	83% 16%
31	34	38	58% 39%
32	B	218	6% 57% 41%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	C	206	64% 35%
34	D	205	6% 70% 28%
35	E	157	59% 39%
36	F	100	57% 39%
37	G	151	7% 76% 24%
38	H	129	63% 37%
39	I	127	5% 59% 39%
40	J	98	14% 50% 44% 6%
41	K	116	70% 27%
42	L	123	7% 62% 35%
43	M	114	68% 29%
44	N	100	68% 32%
45	O	88	67% 32%
46	P	82	60% 39%
47	Q	80	59% 39%
48	R	65	8% 71% 26%
49	S	79	5% 58% 42%
50	T	85	68% 31%
51	U	65	26% 48% 52%
52	03	223	61% 50% 49%
53	A	1539	58% 37% 5%
54	01	2903	57% 39%
55	02	120	58% 36% 6%
56	W	77	9% 74% 22%
56	X	77	12% 53% 39% 8%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
57	V	20	55% 75% 25%
58	Y	76	18% 57% 34% 9%
59	Z	392	53% 47% 52% •

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 154412 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	04	271	2083	1288	423	365	7	0	0

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	05	209	1565	979	288	294	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	06	201	1552	974	283	290	5	0	0

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	07	177	1411	899	249	257	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	08	176	1323	832	243	246	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	09	149	1111	699	197	214	1	0	0

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	10	131	989	625	175	184	5	0	0

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	11	141	1032	651	179	196	6	0	0

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	12	142	1129	714	212	199	4	0	0

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	13	122	939	587	180	166	6	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	14	143	1045	649	206	189	1	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	15	136	1074	686	205	177	6	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	16	120	961	593	196	167	5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	17	116	892	552	178	162	0	0

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	18	114	917	574	179	163	1	0	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	19	117	947	604	192	151	0	0

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	20	103	816	516	153	145	2	0	0

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	21	110	857	532	166	156	3	0	0

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	22	93	739	466	139	132	2	0	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	23	102	780	492	146	142	0	0

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	24	94	753	479	137	134	3	0	0

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	25	75	575	356	116	102	1	0	0

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	26	77	625	388	129	106	2	0	0

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	27	63	509	313	99	95	2	0	0

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	28	58	449	281	87	79	2	0	0

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	29	66	523	323	99	95	6	0	0

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	30	56	444	269	94	80	1	0	0

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	31	50	410	263	75	72	0	0

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	32	46	377	228	90	57	2	0	0

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	33	64	504	323	105	74	2	0	0

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	34	38	302	185	65	48	4	0	0

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	B	218	1705	1081	305	312	7	0	0

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	C	206	1625	1028	305	289	3	0	0

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	E	157	1157	719	218	214	6	0	0

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	F	100	818	515	148	149	6	0	0

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	G	151	1182	735	227	216	4	0	0

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

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

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	J	98	787	493	150	143	1	0	0

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	K	116	870	535	173	159	3	0	0

- Molecule 42 is a protein called 30S ribosomal protein S12.

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

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	M	114	884	546	178	157	3	0	0

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	N	100	805	499	164	139	3	0	0

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	O	88	714	439	144	130	1	0	0

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	Q	80	649	411	121	114	3	0	0

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	R	65	536	339	100	96	1	0	0

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	S	79	638	408	120	108	2	0	0

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	U	65	545	335	117	92	1	0	0

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	03	223	1662	1039	302	315	6	0	0

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	A	1539	33012	14725	6052	10697	1538	0	0

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	01	2903	62317	27801	11468	20146	2902	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
55	02	120	2568	1145	471	833	119	0	0

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	X	77	1640	732	297	535	76	0	0
56	W	77	1640	732	297	535	76	0	0

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
57	V	20	432	195	86	132	19	0	0

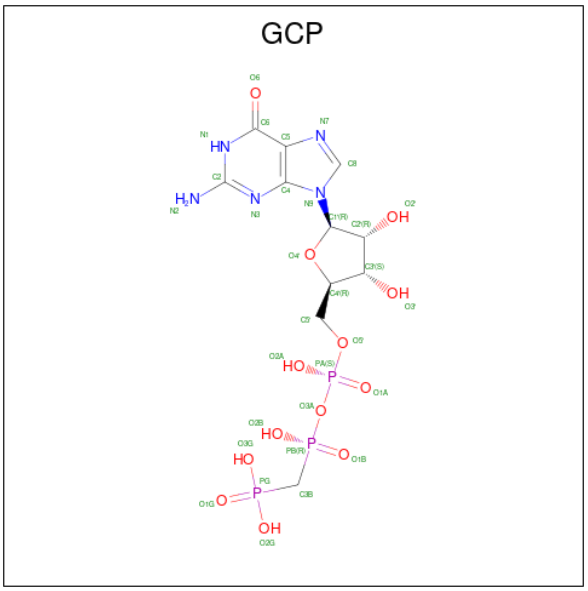
- Molecule 58 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
58	Y	76	1619	723	290	531	75	0	0

- Molecule 59 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	Z	392	3029	1915	521	580	13	0	0

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



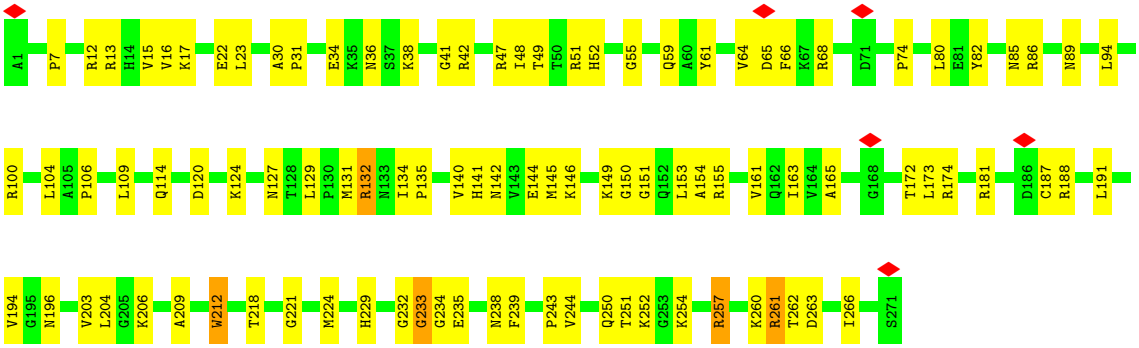
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
60	Z	1	32	11	5	13	3	0

3 Residue-property plots (i)

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

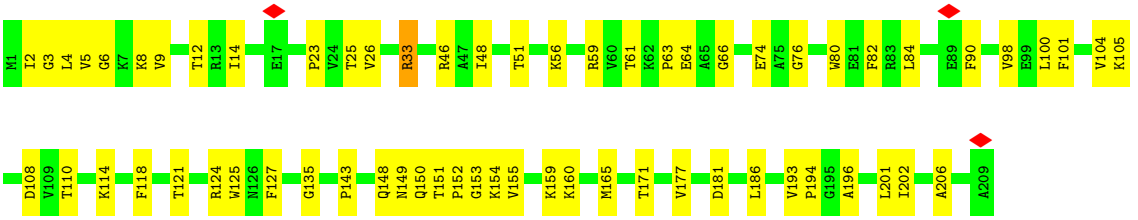
- Molecule 1: 50S ribosomal protein L2

Chain 04:



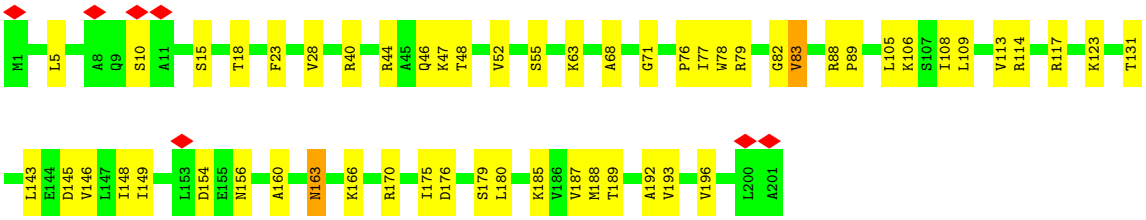
- Molecule 2: 50S ribosomal protein L3

Chain 05:



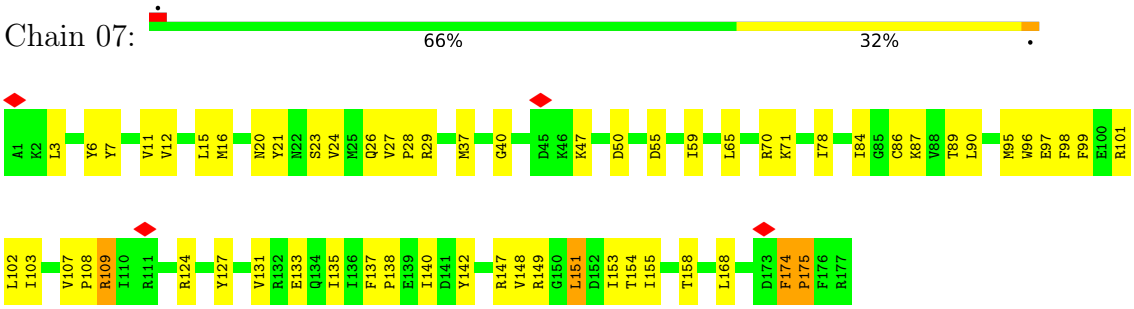
- Molecule 3: 50S ribosomal protein L4

Chain 06:



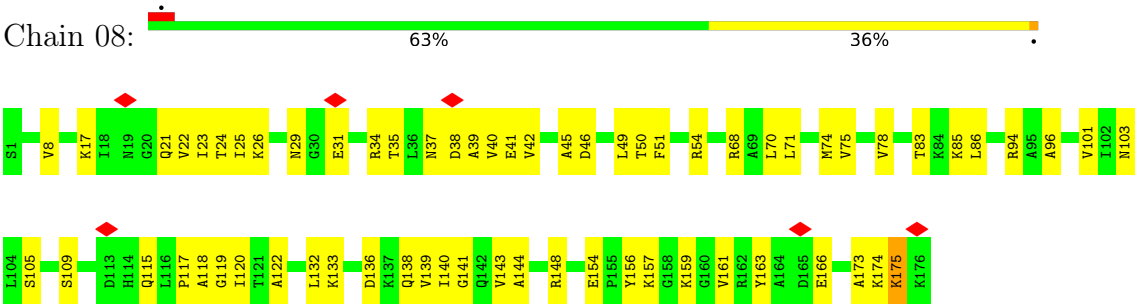
- Molecule 4: 50S ribosomal protein L5

Chain 07:



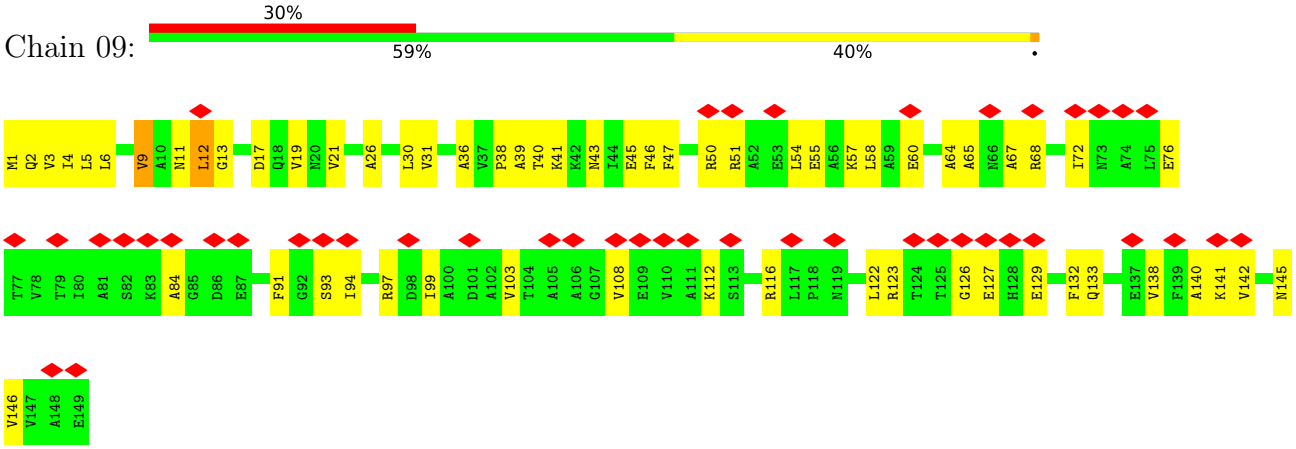
- Molecule 5: 50S ribosomal protein L6

Chain 08:



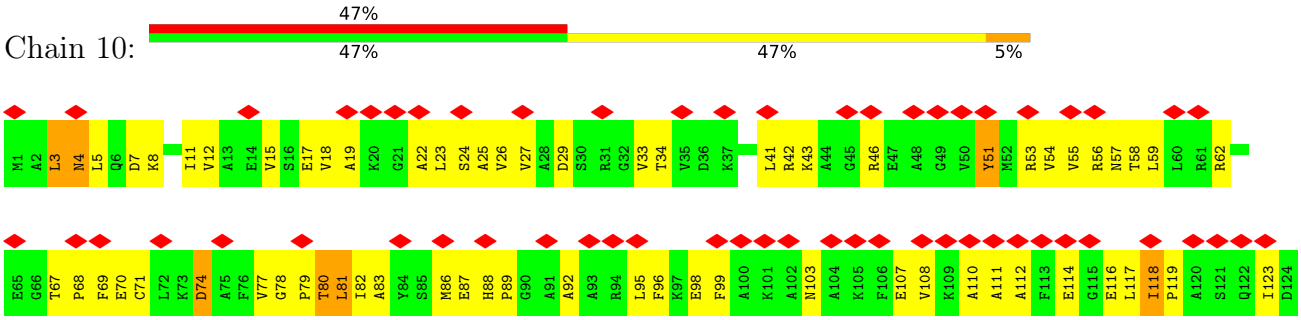
- Molecule 6: 50S ribosomal protein L9

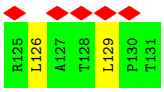
Chain 09:



- Molecule 7: 50S ribosomal protein L10

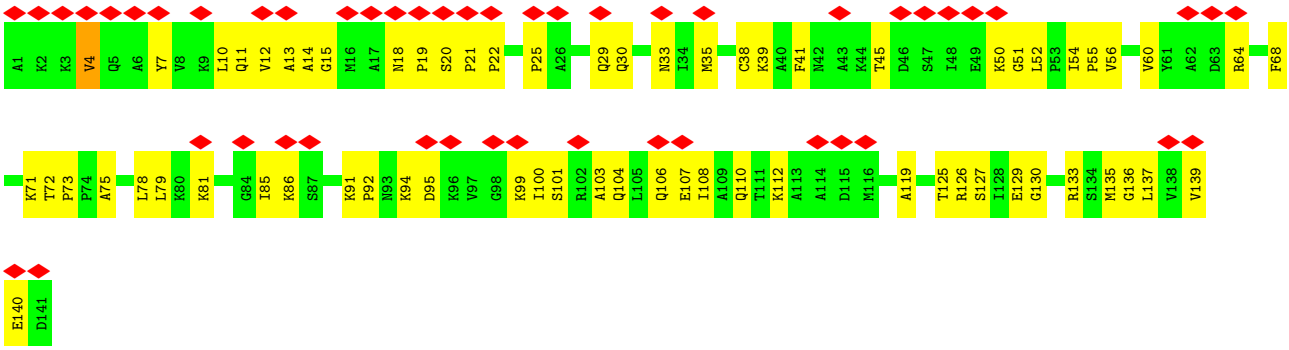
Chain 10:





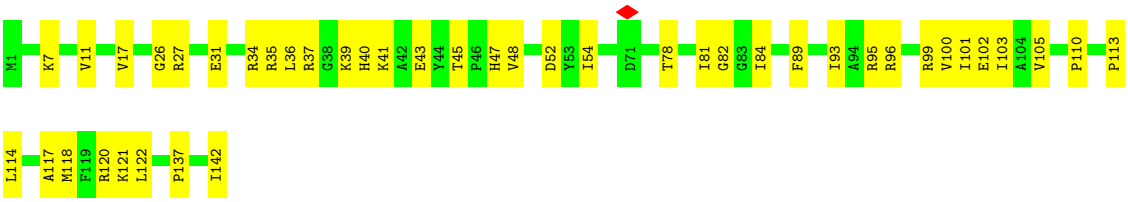
• Molecule 8: 50S ribosomal protein L11

Chain 11:



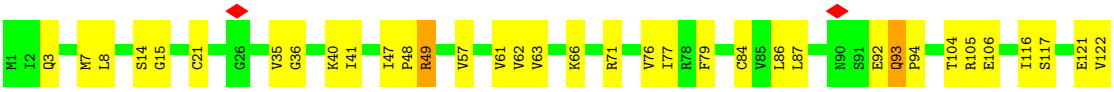
• Molecule 9: 50S ribosomal protein L13

Chain 12:



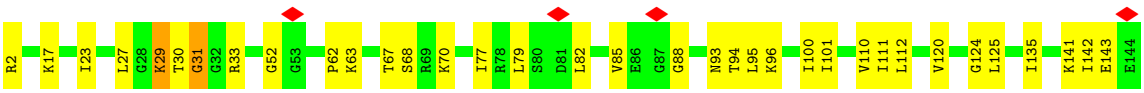
• Molecule 10: 50S ribosomal protein L14

Chain 13:



• Molecule 11: 50S ribosomal protein L15

Chain 14:

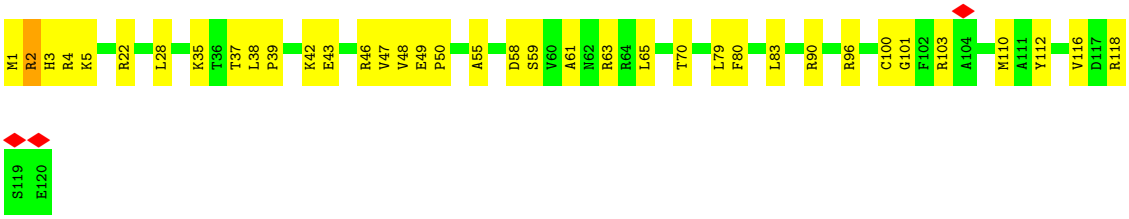


• Molecule 12: 50S ribosomal protein L16

Chain 15:

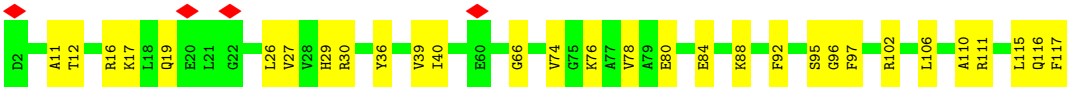
• Molecule 13: 50S ribosomal protein L17

Chain 16:



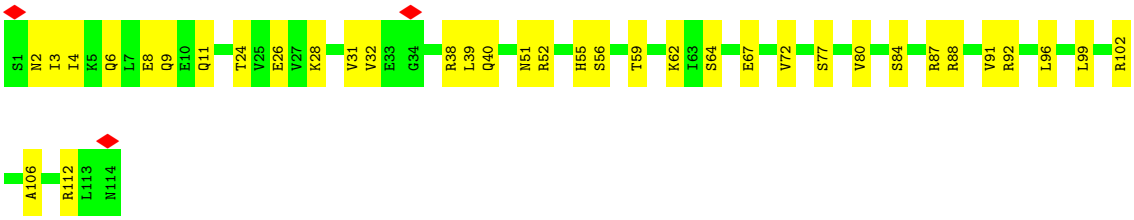
• Molecule 14: 50S ribosomal protein L18

Chain 17:



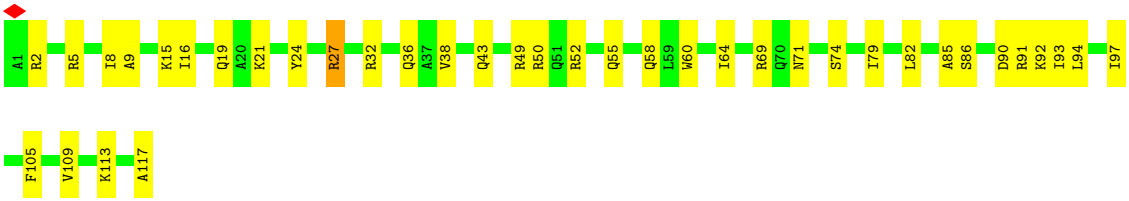
• Molecule 15: 50S ribosomal protein L19

Chain 18:



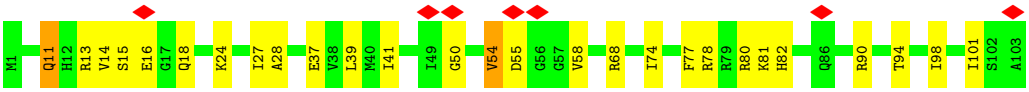
• Molecule 16: 50S ribosomal protein L20

Chain 19:



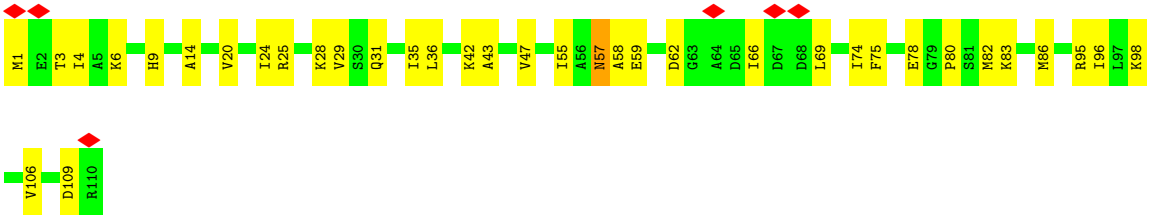
• Molecule 17: 50S ribosomal protein L21

Chain 20: 7% 74% 24%



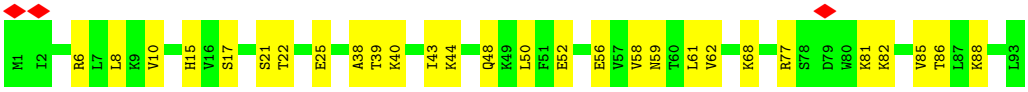
• Molecule 18: 50S ribosomal protein L22

Chain 21: 5% 67% 32%



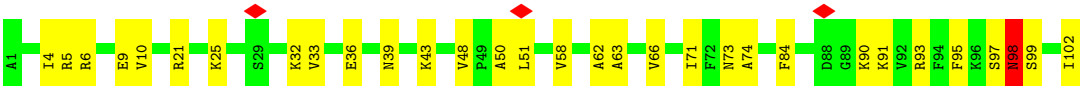
• Molecule 19: 50S ribosomal protein L23

Chain 22: 70% 30%



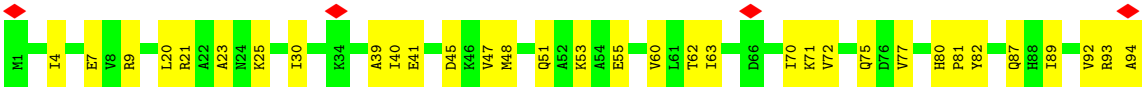
• Molecule 20: 50S ribosomal protein L24

Chain 23: 70% 29%



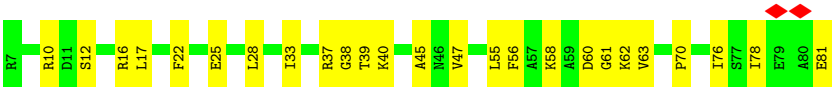
• Molecule 21: 50S ribosomal protein L25

Chain 24: 65% 35%



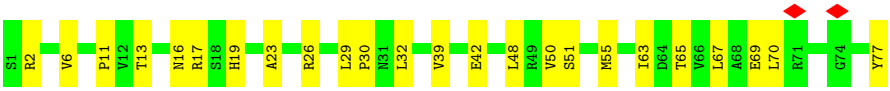
• Molecule 22: 50S ribosomal protein L27

Chain 25: 67% 33%



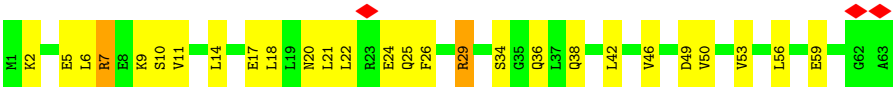
• Molecule 23: 50S ribosomal protein L28

Chain 26: 69% 31%



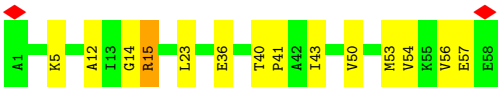
• Molecule 24: 50S ribosomal protein L29

Chain 27:



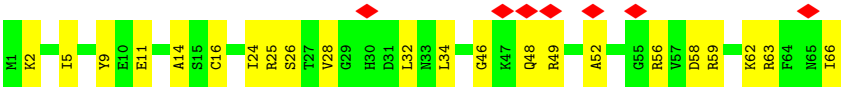
• Molecule 25: 50S ribosomal protein L30

Chain 28:



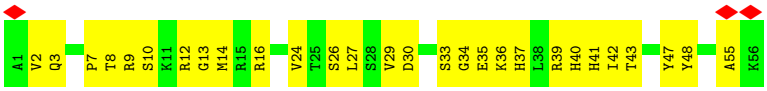
• Molecule 26: 50S ribosomal protein L31

Chain 29:



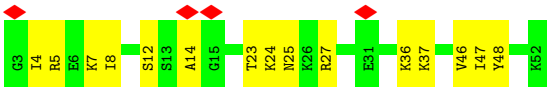
• Molecule 27: 50S ribosomal protein L32

Chain 30:



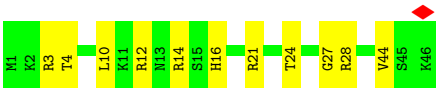
• Molecule 28: 50S ribosomal protein L33

Chain 31:



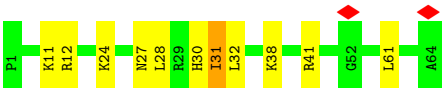
• Molecule 29: 50S ribosomal protein L34

Chain 32:



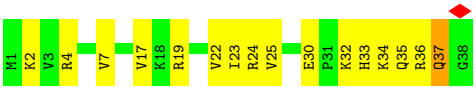
• Molecule 30: 50S ribosomal protein L35

Chain 33:



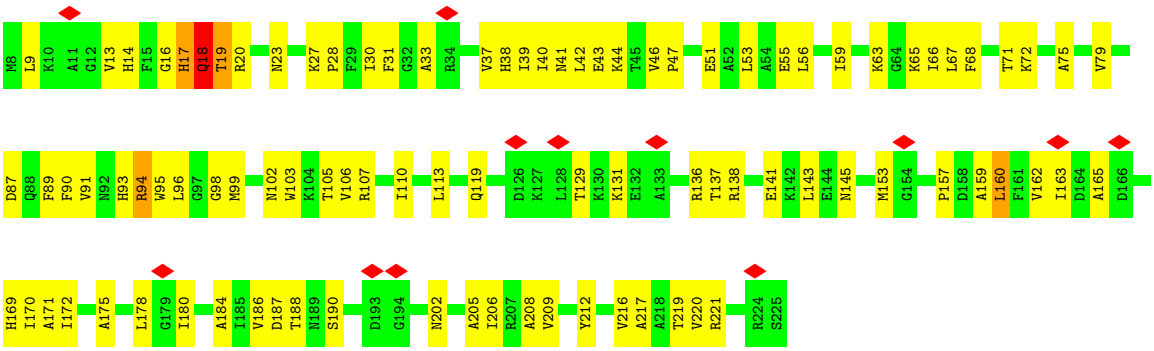
- Molecule 31: 50S ribosomal protein L36

Chain 34:



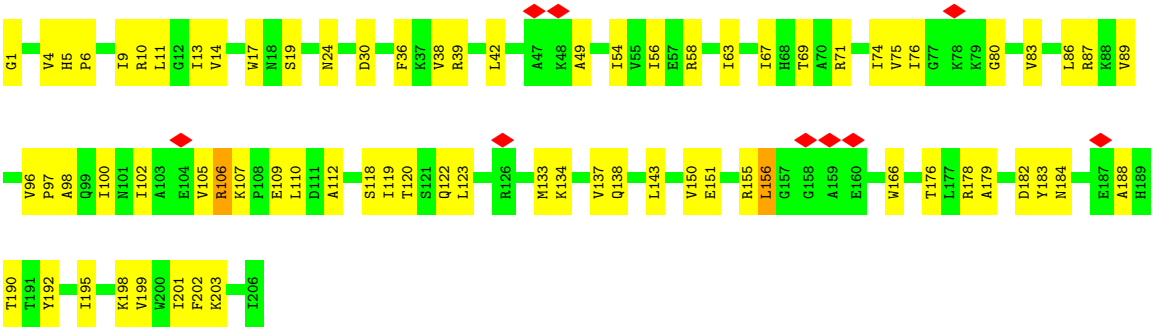
- Molecule 32: 30S ribosomal protein S2

Chain B:



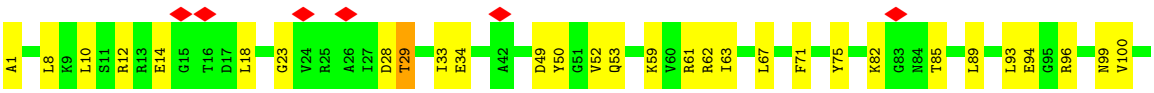
- Molecule 33: 30S ribosomal protein S3

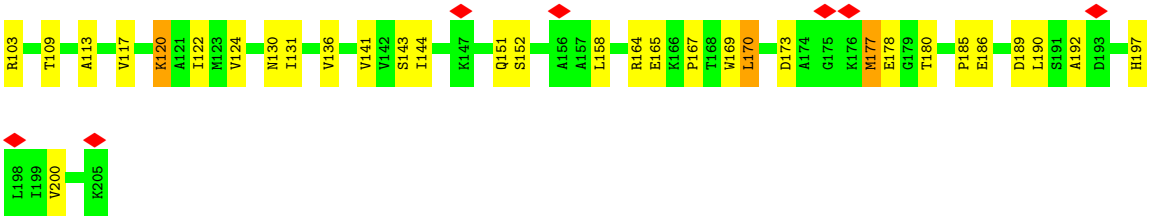
Chain C:



- Molecule 34: 30S ribosomal protein S4

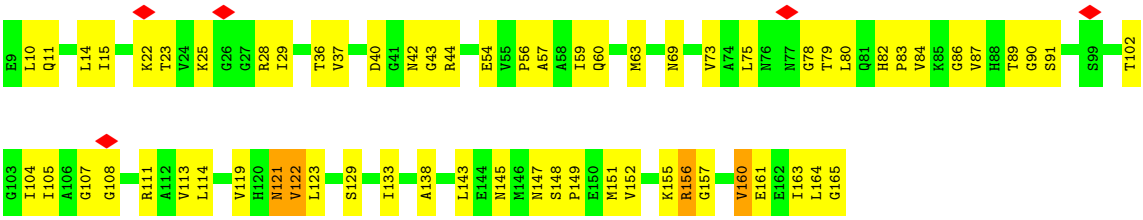
Chain D:





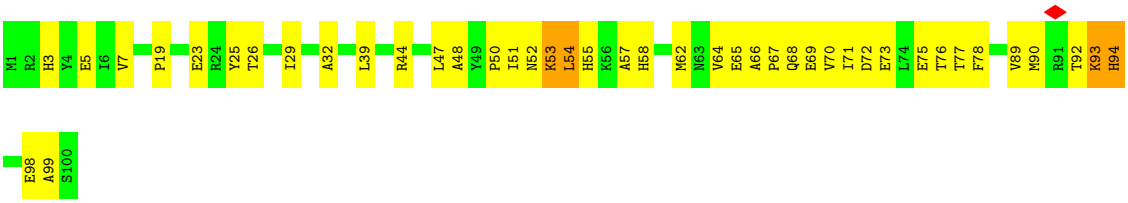
• Molecule 35: 30S ribosomal protein S5

Chain E:



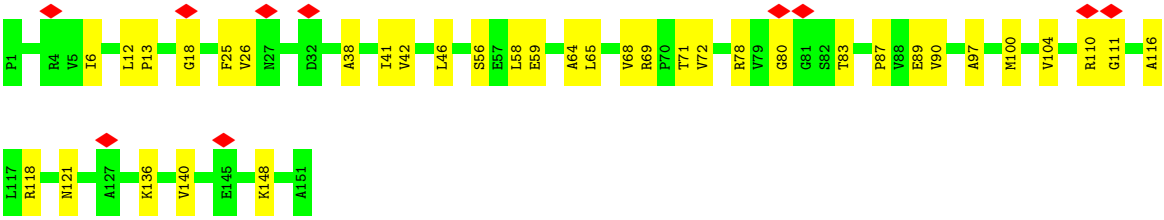
• Molecule 36: 30S ribosomal protein S6

Chain F:



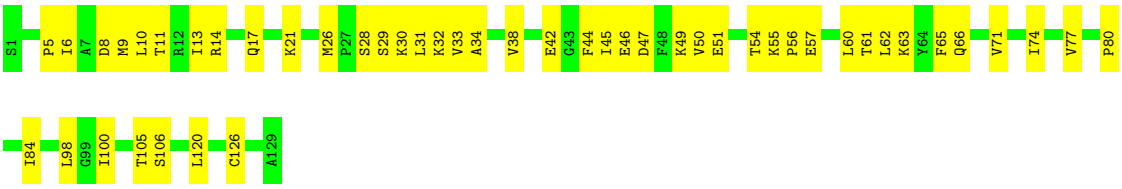
• Molecule 37: 30S ribosomal protein S7

Chain G:



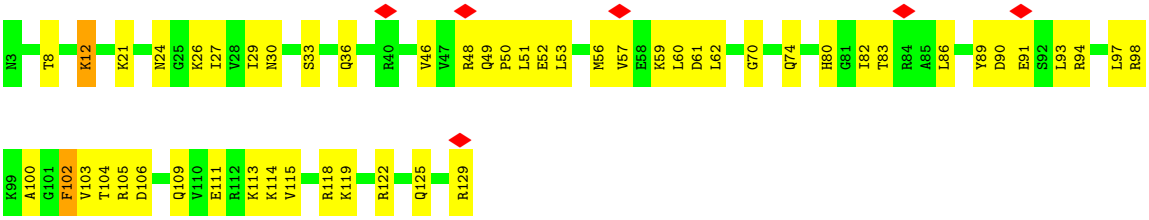
• Molecule 38: 30S ribosomal protein S8

Chain H:



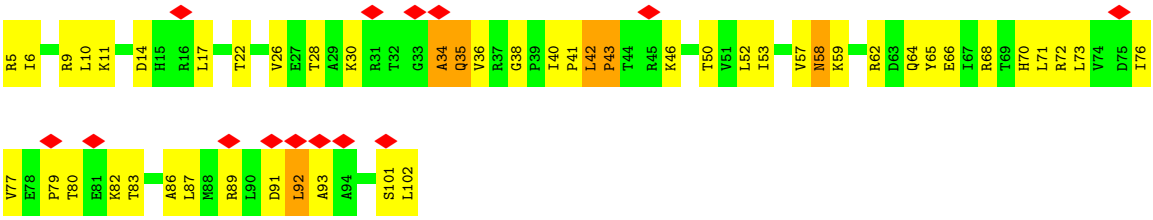
- Molecule 39: 30S ribosomal protein S9

Chain I:



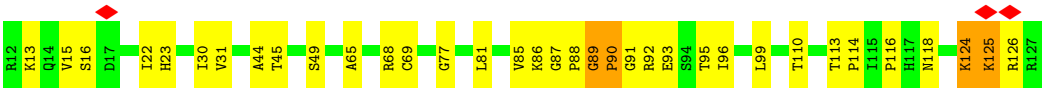
- Molecule 40: 30S ribosomal protein S10

Chain J:



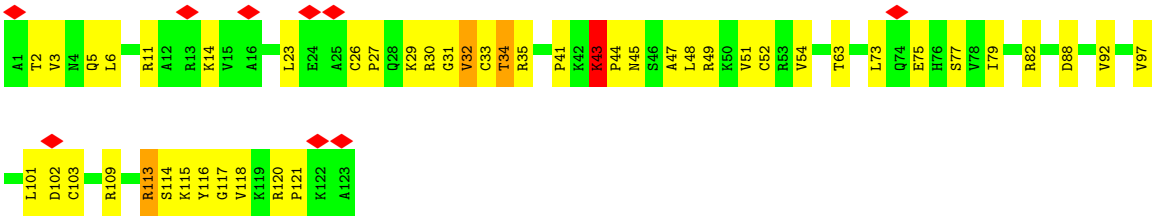
- Molecule 41: 30S ribosomal protein S11

Chain K:



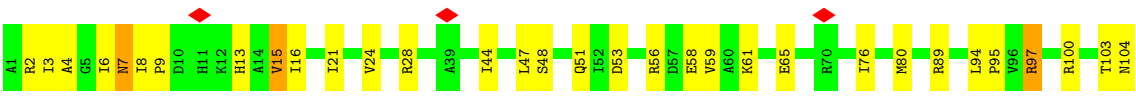
- Molecule 42: 30S ribosomal protein S12

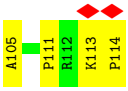
Chain L:



- Molecule 43: 30S ribosomal protein S13

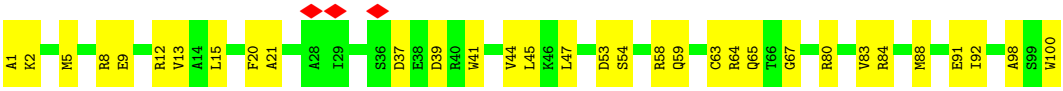
Chain M:





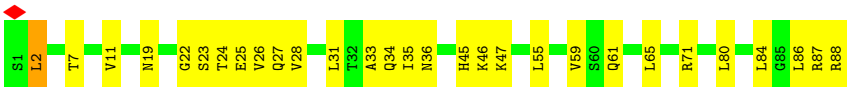
• Molecule 44: 30S ribosomal protein S14

Chain N:



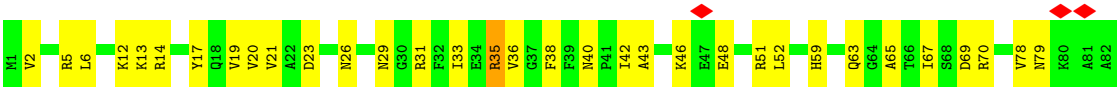
• Molecule 45: 30S ribosomal protein S15

Chain O:



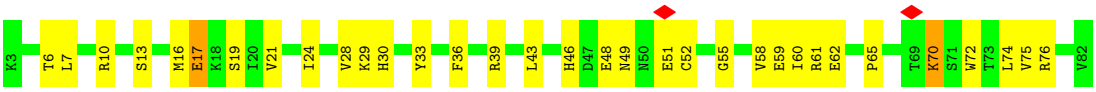
• Molecule 46: 30S ribosomal protein S16

Chain P:



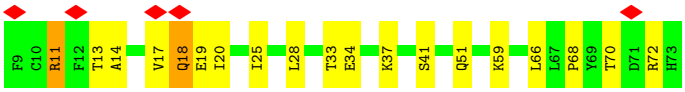
• Molecule 47: 30S ribosomal protein S17

Chain Q:



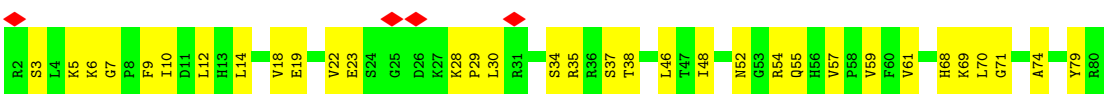
• Molecule 48: 30S ribosomal protein S18

Chain R:



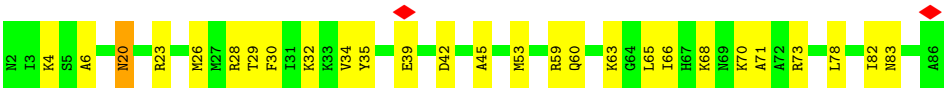
• Molecule 49: 30S ribosomal protein S19

Chain S:



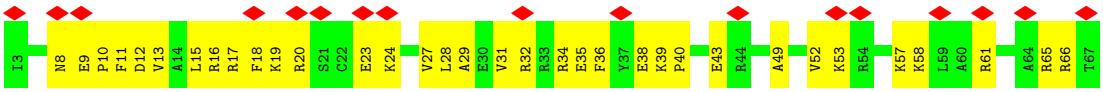
• Molecule 50: 30S ribosomal protein S20

Chain T:



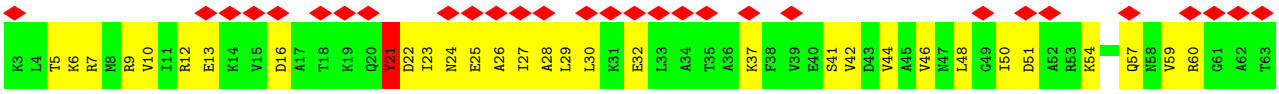
• Molecule 51: 30S ribosomal protein S21

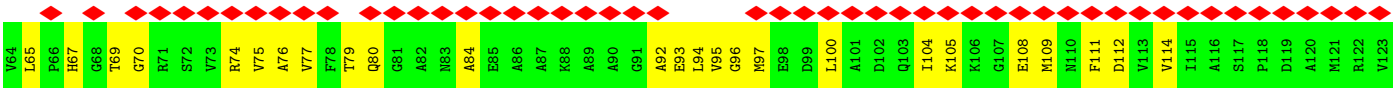
Chain U:

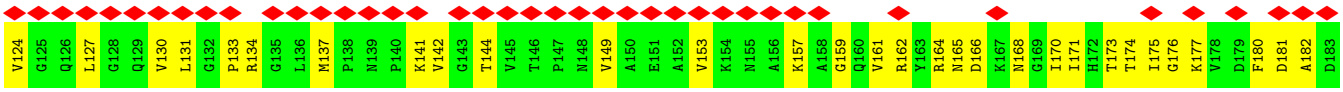


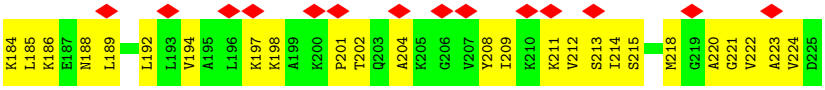
• Molecule 52: 50S ribosomal protein L1

Chain 03:



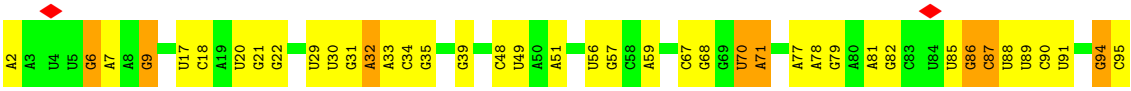


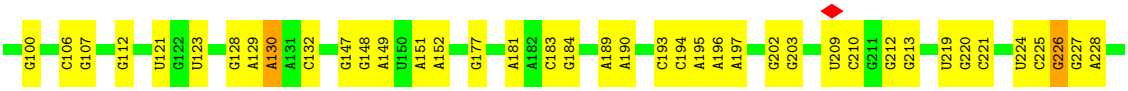


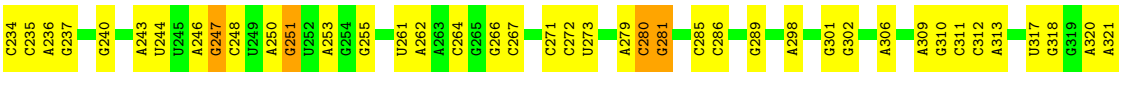


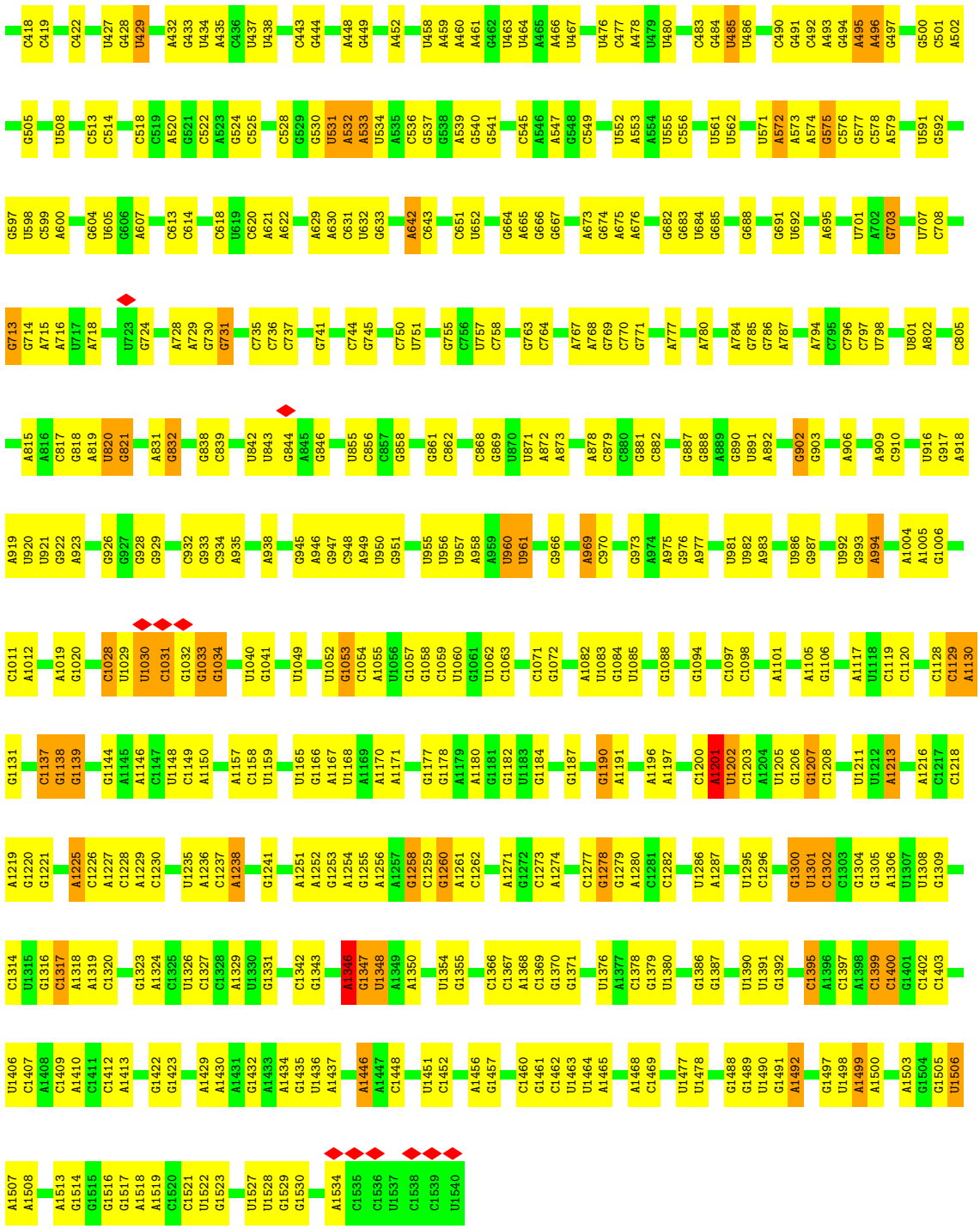
• Molecule 53: 16S ribosomal RNA

Chain A:



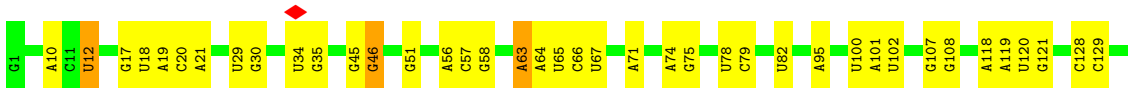


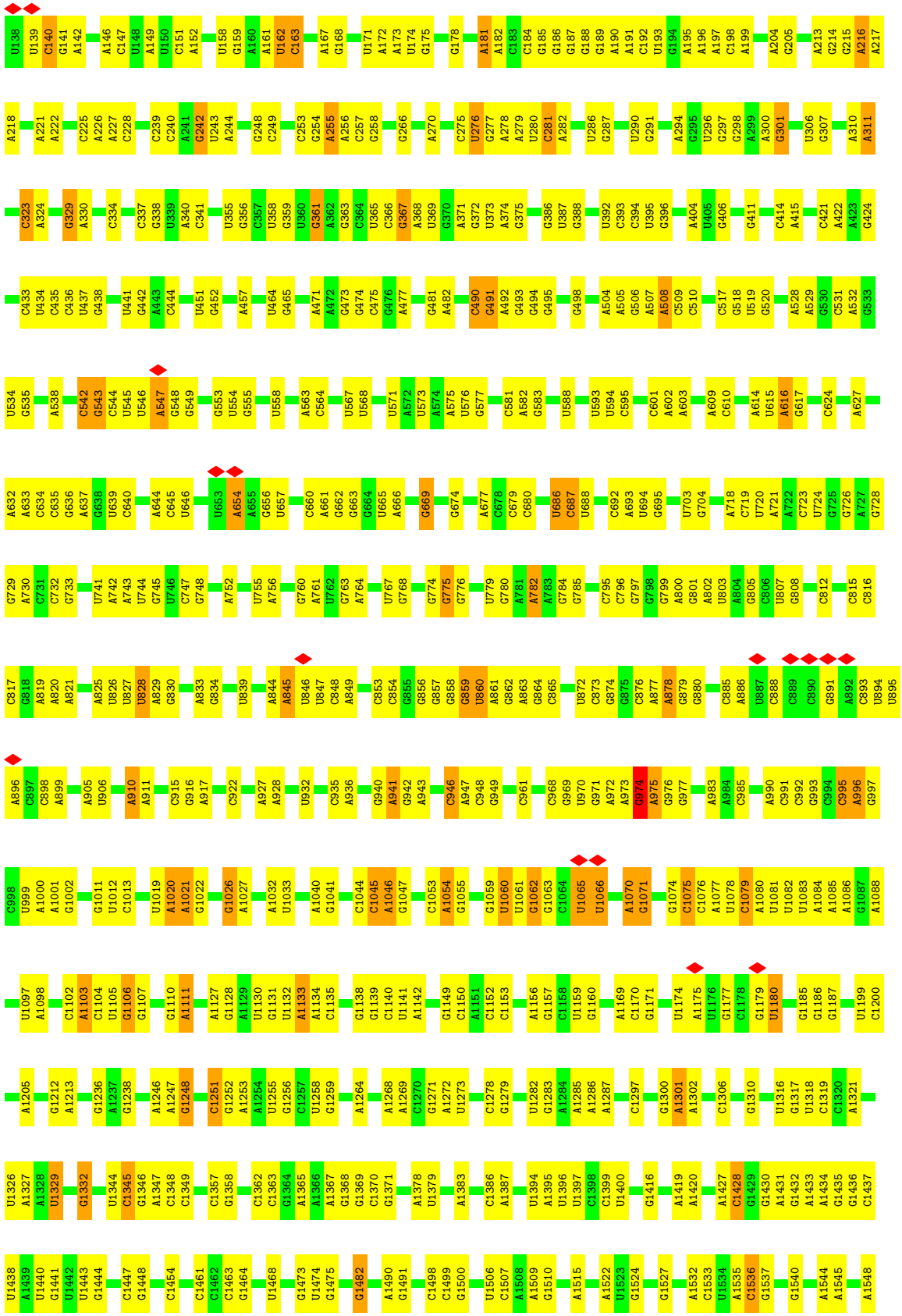


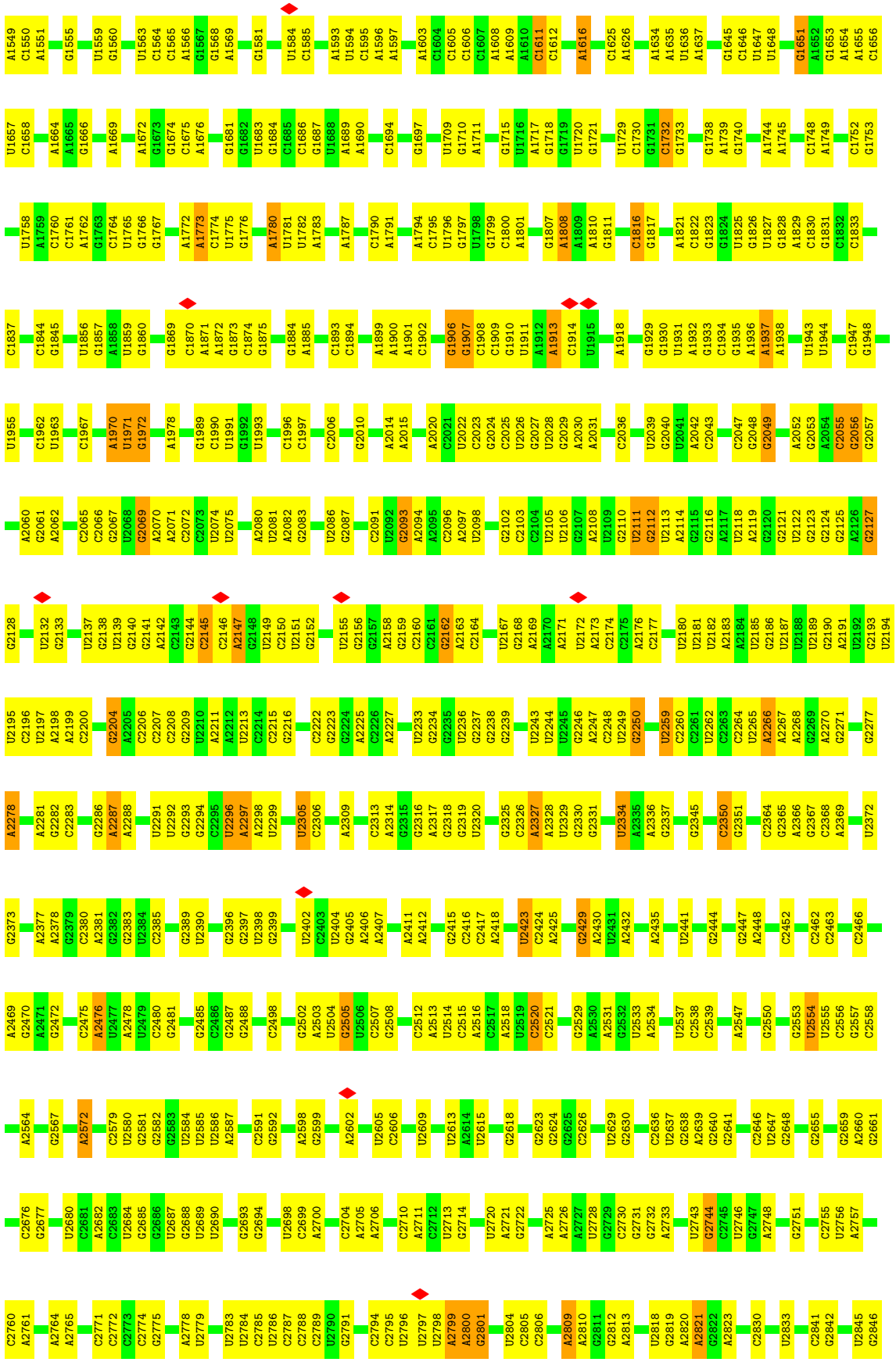


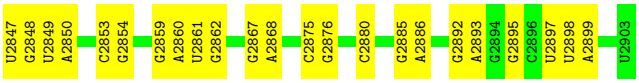
• Molecule 54: 23S ribosomal RNA

Chain 01:



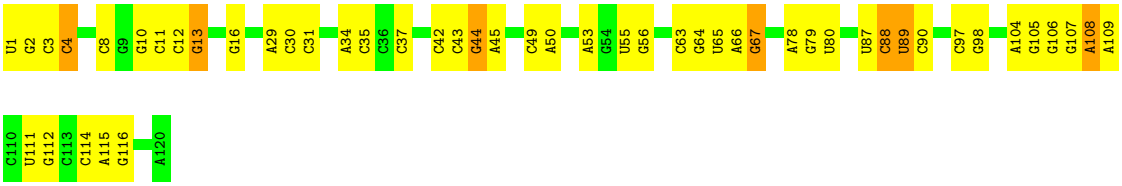

U138 U139 C140 G141 A142 A146 C147 U148 A149 U150 C151 A152 U158 G159 A160 A161 U162 C163 A167 G168 U171 A172 A173 U174 G175 G178 A181 A182 C183 C184 G185 G186 G187 G188 G189 A190 A191 C192 U193 G194 A195 A196 A197 C198 A199 A204 G205 A213 G214 G215 A216 A217
A218 A221 A222 C225 A226 A227 C228 C239 C240 A241 G242 U243 A244 G248 C249 C253 G254 A255 A256 C257 U258 G266 A270 C275 U276 G277 A278 A279 U280 C281 A282 U286 G287 U290 G291 A294 G295 U296 G297 G298 A299 A300 G301 U306 G307 A310 A311
C323 A324 G329 A330 C334 C337 G338 U339 A340 C341 U355 G356 C357 U358 G359 U360 G361 A362 G363 C364 U365 C366 G367 A368 U369 G370 A371 G372 U373 A374 G375 G386 U387 G388 U392 C393 C394 U395 G396 A404 U405 G406 G411 C414 A415 C421 A422 A423 G424
C433 U434 C435 C436 U437 G438 U441 G442 A443 C444 U451 G452 A457 U464 G465 A471 A472 G473 G474 C475 G476 A477 G481 A482 C490 G491 A492 G493 G494 G495 G498 A504 A505 G506 A507 A508 C509 C510 C517 G518 U519 G520 A528 A529 G530 C531 A532 G533
U534 G535 A538 C542 G543 C544 U545 U546 A547 G548 G549 G553 U554 G555 U558 A563 C564 U567 U568 U571 A572 U573 A574 A575 U576 G577 C581 A582 G583 U588 U593 U594 C595 C601 A602 A603 A609 C610 A614 U615 A616 G617 C624 A627
A632 A633 C634 C635 G636 A637 G638 U639 C640 A644 C645 U646 U653 A654 A655 G656 U657 C660 A661 G662 G663 G664 U665 A666 G669 G674 A677 C678 C679 C680 U686 C687 U688 C692 A693 U694 G695 U703 G704 A718 C719 U720 A721 A722 C723 U724 G725 G726 A727 G728
G729 A730 C731 C732 G733 U741 A742 A743 U744 G745 U746 C747 G748 A752 U755 A756 G760 A761 U762 G763 A764 U767 G768 G774 G775 G776 U779 G780 A781 A782 A783 G784 G785 C795 C796 G797 G798 G799 A800 G801 A802 U803 A804 G805 C806 U807 G808 C812 C815 C816
C817 G818 A819 A820 A821 A825 U826 U827 U828 A829 G830 A833 G834 U839 A844 A845 U846 U847 C848 A849 C853 C854 G855 G856 G857 G858 G859 U860 A861 G862 A863 G864 C865 U872 C873 G874 G875 C876 A877 A878 G879 G880 C885 A886 U887 C888 C889 C890 G891 A892 C893 U894 U895
A896 C897 C898 A899 A905 U906 A910 A911 C915 G916 A917 C922 A927 A928 U932 C935 A936 G940 A941 G942 A943 C946 A947 C948 G949 C961 C968 G969 U970 G971 A972 A973 G974 A975 G976 G977 A983 A984 C985 A990 C991 C992 G993 C994 C995 A996 G997
C998 U999 A1000 A1001 G1002 G1011 U1012 C1013 U1019 A1020 A1021 G1022 G1026 A1027 A1032 U1033 A1040 G1041 C1044 C1045 A1046 G1047 C1053 A1054 G1055 G1059 U1060 U1061 G1062 G1063 C1064 U1065 U1066 A1070 G1071 G1074 C1075 C1076 A1077 U1078 C1079 A1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088
U1097 A1098 C1102 A1103 C1104 U1105 G1106 G1107 G1110 A1111 A1127 G1128 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1138 G1139 C1140 U1141 A1142 G1149 C1150 A1151 C1152 C1153 A1156 G1157 C1158 U1159 G1160 A1169 C1170 G1171 U1174 A1175 U1176 G1177 C1178 G1179 U1180 G1185 G1186 G1187 U1199 C1200
A1205 G1212 A1213 G1236 A1237 G1238 A1246 A1247 G1248 C1251 G1252 A1253 A1254 U1255 G1256 C1257 U1258 G1259 A1264 A1268 A1269 C1270 G1271 A1272 U1273 C1278 G1279 U1282 G1283 A1284 A1285 A1286 A1287 C1297 G1300 A1301 A1302 C1306 G1310 U1316 U1317 U1318 C1319 C1320 A1321
U1326 A1327 A1328 U1329 G1332 U1344 C1345 G1346 A1347 C1348 C1349 C1357 G1358 C1362 C1363 G1364 A1365 A1366 A1367 G1368 G1369 C1370 G1371 A1378 U1379 A1383 C1386 A1387 U1394 A1395 U1396 U1397 C1398 C1399 U1400 G1416 A1419 A1420 A1427 C1428 G1429 G1430 A1431 G1432 A1433 A1434 G1435 G1436 C1437
U1438 A1439 U1440 G1441 U1442 U1443 G1444 C1447 G1448 C1454 C1461 C1462 C1463 G1464 U1468 G1473 U1474 G1475 G1482 A1490 G1491 C1498 C1499 G1500 U1506 C1507 A1508 A1509 G1510 A1515 A1522 U1523 G1524 G1527 A1532 C1533 U1534 A1535 C1536 G1537 G1540 A1544 A1545 A1548


A1549 C1550 A1551 G1555 U1559 G1560 U1563 C1564 C1565 A1566 G1567 G1568 A1569 G1581 U1584 C1585 A1593 U1594 C1595 A1596 A1597 A1603 C1604 C1605 C1606 C1607 A1608 A1609 A1610 C1611 C1612 A1616 C1625 A1626 A1634 A1635 U1636 A1637 G1645 C1646 U1647 U1648 G1651 A1652 G1653 A1654 A1655 C1656
U1657 C1658 A1664 A1665 G1666 A1669 A1672 G1673 G1674 C1675 A1676 G1681 G1682 U1683 G1684 C1685 C1686 G1687 U1688 A1689 A1690 C1694 G1697 U1709 G1710 A1711 G1715 U1716 A1717 G1718 G1719 U1720 G1721 U1729 C1730 G1731 C1732 G1733 G1738 A1739 G1740 A1744 A1745 C1748 A1749 C1752 G1753
U1758 A1759 C1760 C1761 A1762 G1763 C1764 U1765 G1766 G1767 A1772 A1773 C1774 U1775 G1776 A1780 U1781 U1782 A1783 A1787 C1790 A1791 A1794 C1795 U1796 G1797 U1798 G1799 C1800 A1801 G1807 A1808 A1809 A1810 G1811 C1816 G1817 A1821 C1822 G1823 G1824 U1825 G1826 U1827 G1828 A1829 C1830 G1831 C1832 C1833
C1837 C1844 G1845 U1856 G1857 A1858 U1859 G1860 G1869 C1870 A1871 A1872 G1873 C1874 G1875 G1884 A1885 C1893 C1894 A1899 A1900 A1901 C1902 G1906 G1907 C1908 C1909 G1910 U1911 A1912 A1913 C1914 U1915 A1918 G1929 G1930 U1931 A1932 G1933 C1934 G1935 A1936 A1937 A1938 U1943 U1944 C1947 G1948
U1955 C1962 U1963 C1967 A1970 U1971 G1972 A1978 G1989 C1990 U1991 G1992 U1993 C1996 C1997 C2006 G2010 A2014 A2015 A2020 C2021 U2022 C2023 G2024 C2025 U2026 G2027 U2028 G2029 A2030 A2031 C2036 U2039 G2040 U2041 A2042 C2043 C2047 G2048 G2049 A2052 G2053 A2054 C2055 G2056 G2057
A2060 G2061 A2062 C2065 C2066 G2067 U2068 G2069 A2070 A2071 C2072 C2073 U2074 U2075 A2080 U2081 A2082 G2083 U2086 G2087 C2091 U2092 G2093 A2094 A2095 C2096 A2097 U2098 G2102 C2103 C2104 U2105 U2106 G2107 A2108 U2109 G2110 U2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127
G2128 U2132 G2133 U2137 G2138 U2139 G2140 G2141 A2142 C2143 G2144 C2145 C2146 A2147 G2148 U2149 C2150 U2151 G2152 U2155 C2156 G2157 A2158 G2159 C2160 C2161 G2162 A2163 C2164 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 U2180 U2181 U2182 A2183 A2184 U2185 G2186 U2187 U2188 U2189 G2190 A2191 U2192 G2193 U2194
U2195 C2196 U2197 A2198 A2199 C2200 G2204 A2205 C2206 C2207 C2208 G2209 U2210 A2211 A2212 U2213 C2214 C2215 G2216 C2222 G2223 G2224 A2225 C2226 A2227 U2233 G2234 G2235 U2236 G2237 G2238 G2239 U2243 U2244 U2245 G2246 A2247 C2248 U2249 G2250 U2259 C2260 C2261 U2262 C2263 C2264 U2265 A2266 A2267 A2268 G2269 A2270 G2271 G2277
A2278 A2281 G2282 C2283 G2286 A2287 A2288 U2291 U2292 G2293 G2294 C2295 U2296 A2297 A2298 U2299 U2305 C2306 A2309 C2313 A2314 G2315 G2316 A2317 G2318 G2319 U2320 G2325 C2326 A2327 A2328 U2329 G2330 G2331 U2334 A2335 A2336 G2337 G2345 C2350 G2351 C2364 G2365 A2366 G2367 C2368 A2369 U2372
G2373 A2377 A2378 G2379 C2380 A2381 G2382 G2383 U2384 C2385 G2389 U2390 G2396 G2397 U2398 G2399 U2402 C2403 U2404 G2405 A2406 A2407 A2411 A2412 G2415 C2416 C2417 A2418 U2423 C2424 A2425 G2429 A2430 U2431 A2432 A2435 U2441 G2444 G2447 A2448 C2452 C2462 C2463 C2466
A2469 G2470 A2471 G2472 C2475 A2476 U2477 A2478 U2479 C2480 G2481 G2485 C2486 G2487 G2488 C2498 G2502 A2503 U2504 G2505 U2506 C2507 G2508 C2512 A2513 U2514 C2515 A2516 C2517 A2518 U2519 C2520 C2521 G2529 A2530 A2531 G2532 U2533 A2534 U2537 C2538 C2539 A2547 G2550 G2553 U2554 U2555 C2556 G2557 C2558
A2564 G2567 A2572 C2579 U2580 G2581 G2582 G2583 U2584 U2585 U2586 A2587 C2591 G2592 A2598 G2599 A2602 U2605 C2606 U2609 U2613 A2614 U2615 G2618 G2623 G2624 G2625 C2626 U2629 G2630 C2636 U2637 G2638 A2639 G2640 G2641 C2646 U2647 G2648 G2655 G2659 A2660 G2661
C2676 G2677 U2680 C2681 A2682 C2683 U2684 G2685 G2686 U2687 G2688 U2689 U2690 G2693 G2694 U2698 C2699 A2700 C2704 A2705 A2706 C2710 A2711 C2712 U2713 G2714 U2720 A2721 G2722 A2725 A2726 A2727 U2728 G2729 C2730 G2731 G2732 A2733 U2743 G2744 C2745 U2746 G2747 A2748 G2751 C2755 U2756 A2757
C2760 A2761 A2764 A2765 C2771 C2772 C2773 C2774 G2775 A2778 U2779 U2783 U2784 C2785 U2786 C2787 C2788 C2789 U2790 G2791 C2794 C2795 U2796 U2797 U2798 A2799 A2800 G2801 U2804 C2805 C2806 A2809 A2810 G2811 G2812 A2813 U2818 G2819 A2820 A2821 G2822 A2823 C2830 U2833 C2841 G2842 U2845 G2846



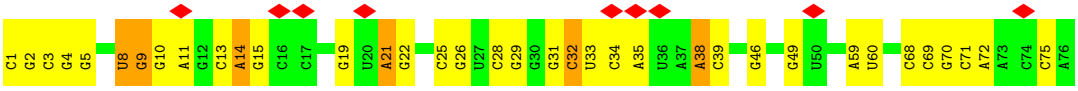
• Molecule 55: 5S ribosomal RNA

Chain 02:



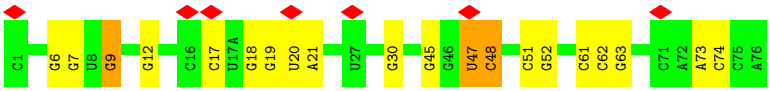
• Molecule 56: tRNAfMet

Chain X:



• Molecule 56: tRNAfMet

Chain W:

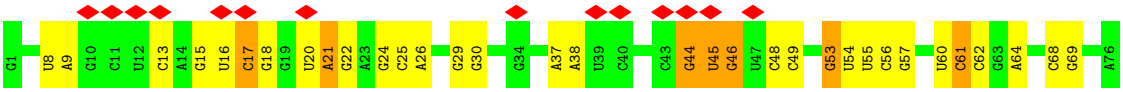


• Molecule 57: mRNA

Chain V:

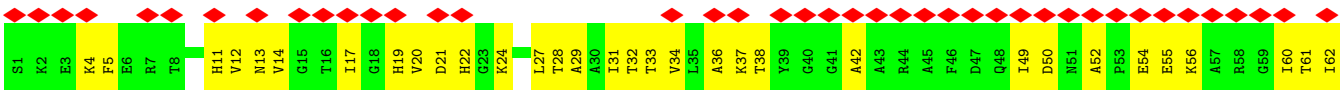
• Molecule 58: tRNAPhe

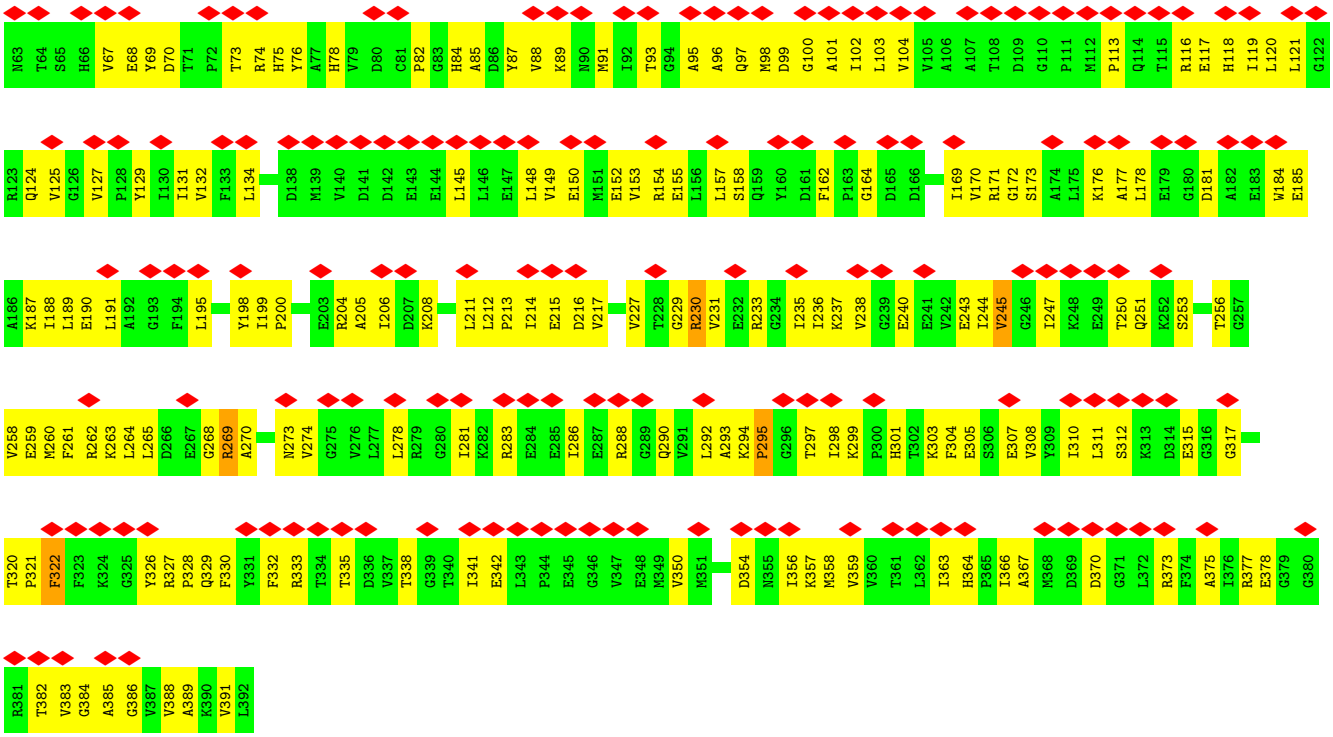
Chain Y:



• Molecule 59: Elongation factor Tu 2

Chain Z:




N63 T64 S65 H66 V67 E68 Y69 D70 T71 P72 T73 R74 H75 Y76 A77 H78 V79 D80 C81 P82 G83 H84 A85 D86 Y87 V88 K89 N90 M91 I92 T93 G94 A95 A96 Q97 M98 D99 G100 A101 I102 L103 V104 V105 A106 A107 T108 D109 G110 P111 M112 P113 Q114 T115 R116 E117 H118 I119 L120 L121 G122
R123 Q124 V125 G126 V127 P128 Y129 I130 I131 V132 F133 L134 D138 M139 V140 D141 D142 E143 E144 L145 L146 E147 L148 V149 E150 M151 E152 V153 R154 E155 L156 L157 S158 Q159 Y160 D161 F162 P163 G164 D165 D166 I169 V170 R171 G172 S173 A174 L175 K176 A177 L178 E179 G180 D181 A182 E183 W184 E185
A186 K187 I188 L189 E190 L191 A192 G193 F194 L195 Y198 I199 P200 E203 R204 A205 I206 D207 K208 L211 L212 P213 I214 E215 D216 V217 V227 T228 G229 R230 V231 E232 R233 G234 I235 I236 K237 V238 G239 E240 E241 V242 E243 I244 V245 G246 I247 K248 E249 T250 Q251 K252 S253 T256 G257
V258 E259 M260 F261 R262 K263 L264 L265 D266 E267 G268 R269 A270 N273 V274 G275 V276 L277 L278 R279 G280 I281 K282 R283 E284 E285 I286 E287 R288 G289 Q290 V291 L292 A293 K294 P295 G296 T297 I298 K299 P300 H301 T302 K303 F304 E305 S306 E307 V308 Y309 I310 L311 S312 K313 D314 E315 G316 G317
T320 P321 F322 F323 K324 G325 Y326 R327 P328 Q329 F330 Y331 F332 R333 T334 T335 D336 V337 T338 G339 T340 I341 E342 L343 P344 E345 G346 V347 E348 M349 V350 M351 D354 N355 I356 K357 M358 V359 V360 T361 L362 I363 H364 P365 I366 A367 M368 D369 D370 G371 L372 R373 F374 A375 I376 R377 E378 G379 G380
R381 T382 V383 G384 A385 G386 V387 V388 A389 K390 V391 L392

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6726	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	17.111	Depositor
Minimum map value	-6.509	Depositor
Average map value	-0.407	Depositor
Map value standard deviation	1.292	Depositor
Recommended contour level	3.47	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	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: GCP

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	04	0.32	0/2122	0.60	0/2852
2	05	0.34	0/1586	0.57	0/2134
3	06	0.33	0/1571	0.56	0/2113
4	07	0.37	0/1435	0.57	0/1926
5	08	0.31	0/1343	0.57	0/1816
6	09	0.37	0/1122	0.58	0/1515
7	10	0.41	0/1002	0.69	0/1350
8	11	0.38	0/1046	0.56	0/1410
9	12	0.33	0/1152	0.56	0/1551
10	13	0.32	0/948	0.59	0/1268
11	14	0.33	0/1054	0.61	0/1403
12	15	0.36	0/1093	0.57	0/1460
13	16	0.35	0/974	0.55	0/1301
14	17	0.32	0/902	0.52	0/1209
15	18	0.34	0/929	0.57	0/1242
16	19	0.36	0/960	0.49	0/1278
17	20	0.36	0/829	0.63	0/1107
18	21	0.30	0/864	0.60	0/1156
19	22	0.31	0/745	0.54	0/994
20	23	0.35	0/788	0.64	1/1051 (0.1%)
21	24	0.35	0/766	0.57	0/1025
22	25	0.37	0/582	0.51	0/769
23	26	0.35	0/635	0.53	0/848
24	27	0.32	0/510	0.55	0/677
25	28	0.31	0/453	0.54	0/605
26	29	0.40	0/532	0.58	0/709
27	30	0.31	0/450	0.57	0/599
28	31	0.37	0/417	0.59	0/554
29	32	0.37	0/380	0.54	0/498
30	33	0.34	0/513	0.61	0/676
31	34	0.29	0/303	0.54	0/397
32	B	0.36	0/1736	0.64	2/2338 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	C	0.33	0/1652	0.53	0/2225
34	D	0.33	0/1665	0.58	0/2227
35	E	0.34	0/1170	0.65	0/1573
36	F	0.34	0/836	0.63	0/1128
37	G	0.33	0/1196	0.57	0/1602
38	H	0.33	0/989	0.60	0/1326
39	I	0.35	0/1034	0.65	0/1375
40	J	0.33	0/797	0.64	0/1077
41	K	0.35	0/886	0.57	0/1195
42	L	0.33	0/969	0.73	2/1300 (0.2%)
43	M	0.30	0/893	0.58	0/1193
44	N	0.33	0/817	0.51	0/1088
45	O	0.33	0/722	0.54	0/964
46	P	0.36	0/659	0.60	0/884
47	Q	0.34	0/658	0.62	0/881
48	R	0.37	0/545	0.58	0/731
49	S	0.37	0/653	0.54	0/877
50	T	0.32	0/671	0.50	0/888
51	U	0.40	0/551	0.59	0/728
52	03	1.26	0/1677	0.68	0/2259
53	A	0.41	0/36963	0.68	6/57662 (0.0%)
54	01	0.41	0/69796	0.67	3/108888 (0.0%)
55	02	0.36	0/2872	0.67	0/4479
56	W	0.42	0/1832	0.66	0/2855
56	X	0.55	0/1832	0.68	0/2855
57	V	0.51	0/486	0.68	0/757
58	Y	0.51	0/1809	0.69	0/2819
59	Z	1.24	0/3085	0.69	0/4173
All	All	0.44	0/167457	0.65	14/249840 (0.0%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	B	160	LEU	O-C-N	-6.91	111.65	122.70
54	01	974	G	N9-C1'-C2'	6.48	122.42	114.00
53	A	1300	G	N9-C1'-C2'	6.31	122.21	114.00
53	A	1201	A	C2'-C3'-O3'	5.85	123.05	113.70
53	A	438	U	N1-C1'-C2'	5.84	121.59	114.00
54	01	242	G	N9-C1'-C2'	5.50	121.15	114.00
42	L	117	GLY	N-CA-C	5.41	126.62	113.10
53	A	1301	U	N1-C1'-C2'	5.40	121.02	114.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	L	43	LYS	N-CA-C	5.39	125.55	111.00
54	01	301	G	N9-C1'-C2'	5.38	121.00	114.00
32	B	17	HIS	N-CA-C	5.38	125.52	111.00
53	A	1346	A	N9-C1'-C2'	5.25	120.83	114.00
53	A	280	C	C2'-C3'-O3'	5.06	121.79	113.70
20	23	98	ASN	N-CA-C	-5.04	97.38	111.00

There are no chirality outliers.

There are no planarity outliers.

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	04	2083	0	2157	85	0
2	05	1565	0	1616	53	0
3	06	1552	0	1619	44	0
4	07	1411	0	1447	48	0
5	08	1323	0	1374	47	0
6	09	1111	0	1148	42	0
7	10	989	0	1025	67	0
8	11	1032	0	1088	52	0
9	12	1129	0	1162	41	0
10	13	939	0	1012	26	0
11	14	1045	0	1117	30	0
12	15	1074	0	1157	38	0
13	16	961	0	1000	26	0
14	17	892	0	923	22	0
15	18	917	0	965	32	0
16	19	947	0	1022	34	0
17	20	816	0	839	25	0
18	21	857	0	922	28	0
19	22	739	0	807	18	0
20	23	780	0	834	22	0
21	24	753	0	780	21	0
22	25	575	0	592	21	0
23	26	625	0	655	16	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	27	509	0	543	27	0
25	28	449	0	491	9	0
26	29	523	0	524	16	0
27	30	444	0	461	22	0
28	31	410	0	440	10	0
29	32	377	0	418	9	0
30	33	504	0	574	8	0
31	34	302	0	343	15	0
32	B	1705	0	1732	79	0
33	C	1625	0	1699	63	0
34	D	1643	0	1710	45	0
35	E	1157	0	1199	56	0
36	F	818	0	808	36	0
37	G	1182	0	1240	24	0
38	H	979	0	1034	35	0
39	I	1022	0	1070	40	0
40	J	787	0	828	39	0
41	K	870	0	878	27	0
42	L	955	0	1019	39	0
43	M	884	0	944	31	0
44	N	805	0	847	31	0
45	O	714	0	737	17	0
46	P	649	0	666	27	0
47	Q	649	0	691	31	0
48	R	536	0	552	12	0
49	S	638	0	665	26	0
50	T	665	0	714	20	0
51	U	545	0	579	29	0
52	03	1662	0	1750	101	0
53	A	33012	0	16618	425	0
54	01	62317	0	31346	822	0
55	02	2568	0	1303	43	0
56	W	1640	0	837	10	0
56	X	1640	0	837	23	0
57	V	432	0	218	3	0
58	Y	1619	0	822	23	0
59	Z	3029	0	3043	167	0
60	Z	32	0	14	4	0
All	All	154412	0	105455	2964	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 11.

All (2964) 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)
52:03:137:MET:SD	52:03:137:MET:CE	2.01	1.49
54:01:45:G:H5"	54:01:46:G:H5'	1.31	1.07
52:03:26:ALA:HB2	52:03:224:VAL:HG11	1.41	1.02
36:F:3:HIS:H	36:F:92:THR:HG22	1.30	0.97
37:G:12:LEU:HD11	39:I:49:GLN:HE22	1.30	0.95
33:C:109:GLU:HB2	33:C:143:LEU:HD13	1.49	0.94
54:01:275:C:H2'	54:01:276:U:H4'	1.50	0.93
52:03:21:TYR:HB2	52:03:224:VAL:HG12	1.51	0.92
52:03:27:ILE:HD13	52:03:186:LYS:HD3	1.50	0.91
35:E:80:LEU:HD13	35:E:122:VAL:HG11	1.53	0.91
17:20:15:SER:H	17:20:18:GLN:HE21	1.18	0.91
10:13:121:GLU:HG2	10:13:122:VAL:HG23	1.53	0.91
53:A:1206:G:H2'	53:A:1207:G:H5"	1.52	0.90
33:C:71:ARG:HD3	33:C:74:ILE:HD12	1.53	0.89
56:X:13:C:H2'	56:X:14:A:H5"	1.54	0.89
52:03:133:PRO:HG2	54:01:2169:A:H5'	1.55	0.88
15:18:38:ARG:HH22	15:18:40:GLN:HB3	1.39	0.88
53:A:112:G:H21	53:A:354:G:H5'	1.37	0.88
32:B:56:LEU:HD23	32:B:59:ILE:HD11	1.57	0.87
35:E:107:GLY:HA3	53:A:9:G:H5'	1.56	0.87
40:J:70:HIS:HB3	40:J:72:ARG:HH12	1.39	0.87
33:C:13:ILE:HG22	33:C:14:VAL:HG23	1.55	0.87
15:18:6:GLN:HA	15:18:9:GLN:HE21	1.38	0.87
3:06:146:VAL:HG12	3:06:185:LYS:HB2	1.56	0.86
52:03:37:LYS:HB2	54:01:2127:G:H5'	1.57	0.86
38:H:46:GLU:HB3	38:H:61:THR:HB	1.56	0.86
54:01:2277:G:H2'	54:01:2278:A:H5"	1.56	0.86
47:Q:46:HIS:HB2	47:Q:70:LYS:HD3	1.56	0.86
52:03:134:ARG:HG3	54:01:2169:A:H5"	1.56	0.85
11:14:67:THR:HG21	54:01:244:A:H5"	1.56	0.85
53:A:531:U:H5'	53:A:532:A:OP1	1.76	0.85
31:34:36:ARG:HG2	31:34:37:GLN:H	1.42	0.85
22:25:39:THR:H	54:01:2331:G:H4'	1.43	0.84
34:D:173:ASP:HB3	34:D:178:GLU:HB3	1.59	0.84
54:01:2800:A:H3'	54:01:2801:G:H5'	1.58	0.84
59:Z:134:LEU:HD12	59:Z:171:ARG:HG2	1.60	0.84
12:15:12:MET:HA	54:01:910:A:H62	1.43	0.83
54:01:1645:G:H5"	54:01:1646:C:H5'	1.61	0.83
12:15:45:GLN:HE21	54:01:2485:G:H5"	1.44	0.83
1:04:38:LYS:HB3	54:01:692:C:H5"	1.61	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:13:G:H21	55:02:16:G:H1'	1.43	0.82
32:B:67:LEU:HD21	32:B:91:VAL:HG23	1.60	0.82
48:R:17:VAL:HG22	48:R:18:GLN:H	1.45	0.82
18:21:66:ILE:H	18:21:66:ILE:HD12	1.44	0.82
33:C:30:ASP:HA	44:N:64:ARG:HH12	1.45	0.82
54:01:1394:U:H4'	54:01:1603:A:H4'	1.59	0.82
44:N:84:ARG:HH22	53:A:1059:C:H4'	1.45	0.81
35:E:119:VAL:HG11	35:E:122:VAL:HG22	1.63	0.81
8:11:55:PRO:HG2	8:11:71:LYS:HB2	1.62	0.81
2:05:33:ARG:H	2:05:33:ARG:HD2	1.45	0.81
59:Z:117:GLU:HA	59:Z:120:LEU:HG	1.63	0.81
7:10:24:SER:HB2	7:10:116:GLU:HG3	1.61	0.80
34:D:144:ILE:HD13	34:D:177:MET:HB3	1.62	0.80
8:11:78:LEU:HG	8:11:81:LYS:HE3	1.61	0.80
7:10:43:LYS:HA	7:10:46:ARG:HE	1.44	0.80
33:C:106:ARG:H	33:C:106:ARG:HD2	1.47	0.80
12:15:42:THR:HG22	12:15:93:VAL:HG12	1.64	0.80
43:M:6:ILE:HD11	43:M:21:ILE:HA	1.63	0.80
7:10:71:CYS:HA	7:10:117:LEU:HD12	1.62	0.79
53:A:1137:C:H5'	53:A:1138:G:H5'	1.63	0.79
56:X:25:C:H2'	56:X:26:G:H8	1.46	0.79
55:02:3:C:H2'	55:02:4:C:H5"	1.65	0.79
43:M:6:ILE:HG13	43:M:7:ASN:H	1.46	0.79
54:01:1790:C:H2'	54:01:1791:A:C5	2.18	0.78
59:Z:297:THR:HG23	59:Z:298:ILE:HD12	1.65	0.78
59:Z:206:ILE:HG22	59:Z:270:ALA:H	1.47	0.78
59:Z:332:PHE:HB2	59:Z:335:THR:HB	1.64	0.78
6:09:116:ARG:HG3	6:09:133:GLN:HG3	1.64	0.78
54:01:1053:C:H2'	54:01:1054:A:H5"	1.66	0.78
54:01:2553:G:H3'	54:01:2554:U:H5"	1.65	0.78
53:A:1259:C:H3'	53:A:1260:G:H5"	1.65	0.78
59:Z:238:VAL:HG13	59:Z:256:THR:HA	1.65	0.78
21:24:77:VAL:HG23	21:24:89:ILE:HG12	1.67	0.77
49:S:30:LEU:HB2	49:S:48:ILE:HG22	1.67	0.77
5:08:154:GLU:HG2	5:08:156:TYR:H	1.48	0.77
8:11:11:GLN:HB2	8:11:56:VAL:HG12	1.65	0.77
26:29:28:VAL:HG11	26:29:32:LEU:HD13	1.64	0.77
54:01:799:G:H5"	54:01:800:A:H2'	1.66	0.77
8:11:91:LYS:HG3	8:11:94:LYS:HE2	1.67	0.77
53:A:405:U:H3'	53:A:406:G:H5'	1.66	0.77
54:01:1105:U:H2'	54:01:1106:G:H5"	1.65	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:23:LEU:HB2	7:10:118:ILE:HG13	1.67	0.77
9:12:95:ARG:HG2	9:12:96:ARG:HG2	1.67	0.76
32:B:94:ARG:H	32:B:94:ARG:HD2	1.51	0.76
38:H:54:THR:HG23	38:H:55:LYS:HG3	1.66	0.76
8:11:100:ILE:HD11	8:11:137:LEU:HD13	1.68	0.76
53:A:769:G:H4'	53:A:1513:A:H4'	1.66	0.76
59:Z:52:ALA:HB3	59:Z:55:GLU:HG3	1.68	0.76
56:X:35:A:H61	57:V:13:A:H61	1.34	0.75
47:Q:16:MET:HG3	47:Q:19:SER:HB2	1.69	0.75
35:E:160:VAL:HG13	35:E:161:GLU:H	1.51	0.75
59:Z:227:VAL:HG11	59:Z:292:LEU:HD11	1.69	0.75
52:03:67:HIS:HB2	52:03:188:ASN:HD21	1.52	0.74
15:18:59:THR:HG22	15:18:72:VAL:HG12	1.69	0.74
43:M:15:VAL:HG23	43:M:16:ILE:HD12	1.67	0.74
53:A:1052:U:H2'	53:A:1200:C:H41	1.50	0.74
21:24:20:LEU:HD11	21:24:41:GLU:HG2	1.68	0.74
32:B:165:ALA:HB3	32:B:190:SER:HB3	1.69	0.74
58:Y:8:U:H2'	58:Y:13:C:H41	1.53	0.74
59:Z:305:GLU:HG3	59:Z:359:VAL:HG22	1.69	0.74
1:04:244:VAL:HG12	1:04:250:GLN:HA	1.70	0.73
2:05:151:THR:HB	2:05:152:PRO:HD3	1.70	0.73
6:09:65:ALA:HA	6:09:68:ARG:HD2	1.70	0.73
47:Q:59:GLU:HG3	47:Q:76:ARG:HG2	1.70	0.73
54:01:807:U:H2'	54:01:808:G:H8	1.51	0.73
54:01:1077:A:H2'	54:01:1078:U:H5'	1.70	0.73
10:13:21:CYS:HA	10:13:41:ILE:HG22	1.69	0.73
15:18:92:ARG:HD3	54:01:1753:G:H5"	1.70	0.73
34:D:164:ARG:HG2	34:D:165:GLU:H	1.54	0.73
8:11:12:VAL:HG12	8:11:13:ALA:H	1.53	0.73
52:03:27:ILE:HG21	52:03:186:LYS:HB2	1.71	0.73
33:C:39:ARG:HG3	33:C:54:ILE:HD11	1.71	0.72
49:S:5:LYS:HG3	49:S:6:LYS:HG2	1.70	0.72
4:07:133:GLU:HB3	4:07:135:ILE:HG13	1.69	0.72
42:L:3:VAL:HA	42:L:6:LEU:HD12	1.70	0.72
39:I:98:ARG:HG3	39:I:103:VAL:HG21	1.72	0.72
53:A:1033:G:H3'	53:A:1034:G:H5"	1.70	0.72
8:11:11:GLN:HB3	8:11:55:PRO:HA	1.71	0.72
40:J:53:ILE:HG12	53:A:1060:U:H5"	1.71	0.72
16:19:43:GLN:HE21	17:20:77:PHE:HB3	1.55	0.72
7:10:107:GLU:HG2	7:10:110:ALA:HB2	1.71	0.72
1:04:47:ARG:HH21	54:01:774:G:H5"	1.53	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:204:LEU:HD22	1:04:209:ALA:HB1	1.72	0.72
5:08:96:ALA:HB3	5:08:103:ASN:HB3	1.72	0.72
18:21:3:THR:HG21	18:21:58:ALA:HB2	1.72	0.71
42:L:101:LEU:O	42:L:103:CYS:N	2.22	0.71
53:A:85:U:H5"	53:A:86:G:H5'	1.70	0.71
20:23:33:VAL:HG13	20:23:66:VAL:HG22	1.71	0.71
53:A:1218:C:H2'	53:A:1219:A:C8	2.25	0.71
54:01:1807:G:H2'	54:01:1808:A:H5'	1.72	0.71
59:Z:258:VAL:HG13	59:Z:274:VAL:HG21	1.72	0.71
2:05:14:ILE:HG23	15:18:11:GLN:HE22	1.54	0.71
3:06:18:THR:HA	3:06:106:LYS:HE3	1.72	0.71
27:30:42:ILE:HG22	27:30:48:TYR:HB2	1.73	0.71
54:01:507:A:H5"	54:01:508:A:H5"	1.73	0.71
54:01:2296:U:H5"	54:01:2297:A:OP1	1.90	0.71
1:04:261:ARG:HD2	1:04:262:THR:HG23	1.72	0.71
1:04:52:HIS:HE2	1:04:218:THR:HG23	1.56	0.70
7:10:87:GLU:HG2	7:10:95:LEU:HD12	1.73	0.70
10:13:76:VAL:H	15:18:72:VAL:HG22	1.56	0.70
32:B:119:GLN:HG2	32:B:136:ARG:HH22	1.56	0.70
10:13:48:PRO:HB3	53:A:1422:G:H5'	1.73	0.70
11:14:95:LEU:HD22	11:14:100:ILE:HD11	1.72	0.70
59:Z:54:GLU:HG2	59:Z:60:ILE:HD11	1.71	0.70
1:04:257:ARG:HE	1:04:266:ILE:HD12	1.57	0.70
17:20:15:SER:H	17:20:18:GLN:NE2	1.87	0.70
42:L:45:ASN:HD22	53:A:528:C:H41	1.37	0.70
40:J:57:VAL:O	40:J:58:ASN:HB2	1.92	0.69
3:06:143:LEU:HD22	3:06:146:VAL:HG11	1.74	0.69
46:P:6:LEU:HD22	46:P:17:TYR:HB3	1.73	0.69
31:34:2:LYS:NZ	54:01:2478:A:H5"	2.07	0.69
52:03:30:LEU:HD22	52:03:42:VAL:HG21	1.74	0.69
52:03:97:MET:HB3	52:03:100:LEU:HB2	1.73	0.69
54:01:807:U:H2'	54:01:808:G:C8	2.26	0.69
54:01:2452:C:H42	54:01:2504:U:H3	1.40	0.69
12:15:55:ARG:HD3	54:01:2469:A:H4'	1.73	0.69
59:Z:21:ASP:H	60:Z:401:GCP:H3B1	1.57	0.69
36:F:54:LEU:HD23	36:F:55:HIS:O	1.93	0.69
3:06:175:ILE:HD12	3:06:180:LEU:HD11	1.74	0.69
5:08:17:LYS:HB2	5:08:24:THR:HB	1.74	0.69
11:14:111:ILE:H	11:14:111:ILE:HD12	1.58	0.69
12:15:34:LYS:HE3	12:15:131:VAL:HG11	1.74	0.69
51:U:13:VAL:HG13	51:U:15:LEU:HG	1.75	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:16:U:H2'	58:Y:17:C:H4'	1.73	0.69
59:Z:17:ILE:HG13	59:Z:103:LEU:HA	1.75	0.69
31:34:25:VAL:HB	31:34:35:GLN:HG3	1.74	0.69
35:E:133:ILE:HD12	35:E:133:ILE:H	1.58	0.69
54:01:1326:U:H2'	54:01:1327:A:H8	1.58	0.69
59:Z:103:LEU:HB3	59:Z:132:VAL:HG22	1.74	0.69
19:22:58:VAL:HG13	19:22:85:VAL:HG22	1.75	0.68
56:W:47:U:H3'	56:W:48:C:H5'	1.75	0.68
34:D:200:VAL:HG11	35:E:102:THR:HG22	1.75	0.68
38:H:5:PRO:HB2	38:H:32:LYS:HE3	1.74	0.68
40:J:9:ARG:HH12	40:J:11:LYS:NZ	1.91	0.68
40:J:10:LEU:HD23	40:J:10:LEU:H	1.58	0.68
54:01:1368:G:H2'	54:01:1369:G:H8	1.59	0.68
2:05:46:ARG:HG2	2:05:84:LEU:HD12	1.76	0.68
32:B:162:VAL:HB	32:B:184:ALA:HB2	1.75	0.68
54:01:546:U:H2'	54:01:547:A:H4'	1.75	0.68
45:O:33:ALA:HA	45:O:36:ASN:HD22	1.59	0.68
59:Z:73:THR:HG22	59:Z:74:ARG:HG3	1.75	0.68
8:11:20:SER:HB3	8:11:21:PRO:HD3	1.76	0.68
53:A:484:G:H4'	53:A:485:U:H5"	1.74	0.68
1:04:23:LEU:HD13	1:04:82:TYR:HB2	1.76	0.68
33:C:151:GLU:HG3	33:C:166:TRP:HB3	1.76	0.68
53:A:960:U:H4'	53:A:961:U:O5'	1.92	0.68
3:06:5:LEU:HD22	3:06:10:SER:HB3	1.76	0.68
32:B:16:GLY:HA2	32:B:40:ILE:HG13	1.75	0.68
8:11:119:ALA:HB2	54:01:1082:U:H5"	1.76	0.67
54:01:542:C:H2'	54:01:543:G:H5"	1.74	0.67
54:01:1026:G:H2'	54:01:1027:A:H8	1.59	0.67
1:04:154:ALA:HB2	1:04:161:VAL:HG23	1.76	0.67
6:09:126:GLY:H	6:09:146:VAL:HB	1.59	0.67
15:18:4:ILE:O	15:18:8:GLU:HG3	1.94	0.67
33:C:76:ILE:HG22	33:C:83:VAL:HG21	1.76	0.67
52:03:166:ASP:OD2	52:03:168:ASN:HB2	1.93	0.67
19:22:61:LEU:HD11	19:22:82:LYS:HD3	1.75	0.67
46:P:5:ARG:HB2	53:A:376:G:H5"	1.76	0.67
34:D:96:ARG:O	34:D:100:VAL:HG23	1.94	0.67
43:M:94:LEU:HB3	43:M:95:PRO:HD2	1.75	0.67
9:12:78:THR:HG22	54:01:2641:G:H5"	1.77	0.67
42:L:113:ARG:HB2	42:L:118:VAL:HB	1.76	0.67
1:04:74:PRO:HB3	1:04:114:GLN:HE21	1.59	0.67
18:21:83:LYS:HG2	18:21:95:ARG:HH12	1.60	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:08:41:GLU:HG3	5:08:54:ARG:HH21	1.59	0.67
15:18:88:ARG:HH11	15:18:112:ARG:NH2	1.92	0.67
26:29:58:ASP:O	26:29:62:LYS:HG3	1.96	0.66
52:03:197:LYS:HE3	52:03:209:ILE:HD13	1.77	0.66
21:24:72:VAL:HG12	21:24:93:ARG:HA	1.76	0.66
36:F:64:VAL:HG22	36:F:65:GLU:N	2.10	0.66
59:Z:294:LYS:HE2	59:Z:297:THR:HG21	1.77	0.66
7:10:7:ASP:O	7:10:11:ILE:HG12	1.95	0.66
8:11:30:GLN:HB3	8:11:60:VAL:HG11	1.76	0.66
7:10:53:ARG:HB3	7:10:55:VAL:HG22	1.76	0.66
55:02:88:C:H5"	55:02:89:U:OP1	1.96	0.66
16:19:91:ARG:HH11	54:01:997:G:H5"	1.61	0.66
55:02:3:C:C2'	55:02:4:C:H5"	2.26	0.66
1:04:153:LEU:HD11	1:04:181:ARG:NH2	2.10	0.66
41:K:23:HIS:HB3	41:K:30:ILE:HG23	1.76	0.66
40:J:52:LEU:HD12	44:N:80:ARG:NE	2.11	0.66
46:P:67:ILE:H	46:P:67:ILE:HD12	1.61	0.66
59:Z:308:VAL:HG22	59:Z:386:GLY:HA3	1.76	0.66
59:Z:326:TYR:HB3	59:Z:341:ILE:HG13	1.77	0.66
15:18:38:ARG:HH11	53:A:345:C:H5'	1.59	0.66
22:25:12:SER:HB3	54:01:2262:U:H5	1.61	0.66
58:Y:8:U:H2'	58:Y:13:C:N4	2.11	0.66
1:04:235:GLU:H	1:04:238:ASN:ND2	1.94	0.66
52:03:185:LEU:HA	52:03:188:ASN:HB2	1.78	0.66
4:07:140:ILE:HG22	4:07:142:TYR:H	1.60	0.65
32:B:71:THR:HG22	32:B:72:LYS:H	1.61	0.65
39:I:94:ARG:HA	39:I:97:LEU:HB3	1.78	0.65
41:K:116:PRO:HB3	53:A:676:A:H1'	1.78	0.65
23:26:2:ARG:HD2	23:26:29:LEU:HD22	1.77	0.65
35:E:23:THR:HA	35:E:28:ARG:HA	1.78	0.65
54:01:121:G:H4'	54:01:149:A:H5'	1.77	0.65
54:01:833:A:H2'	54:01:834:G:H8	1.60	0.65
54:01:833:A:H2'	54:01:834:G:C8	2.31	0.65
45:O:55:LEU:O	45:O:59:VAL:HG23	1.97	0.65
54:01:2277:G:C2'	54:01:2278:A:H5"	2.26	0.65
42:L:45:ASN:ND2	53:A:528:C:H41	1.94	0.65
54:01:1105:U:C2'	54:01:1106:G:H5"	2.26	0.65
54:01:2389:G:H5"	54:01:2390:U:O4'	1.95	0.65
42:L:49:ARG:HH12	53:A:522:C:H41	1.44	0.65
53:A:1205:U:H2'	53:A:1206:G:H8	1.61	0.65
10:13:40:LYS:HE3	10:13:57:VAL:HG12	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:917:A:H5”	54:01:2268:A:H61	1.61	0.65
58:Y:15:G:H2’	58:Y:16:U:H5’	1.79	0.65
39:I:125:GLN:HE22	53:A:1342:C:H1’	1.61	0.65
53:A:868:C:H2’	53:A:869:G:O4’	1.97	0.65
53:A:1088:G:H21	53:A:1167:A:H61	1.45	0.65
5:08:71:LEU:HA	5:08:74:MET:HB2	1.79	0.65
15:18:28:LYS:HB3	15:18:39:LEU:HD11	1.78	0.65
32:B:16:GLY:HA3	32:B:39:ILE:HA	1.79	0.65
52:03:76:ALA:HB3	52:03:114:VAL:HG22	1.79	0.65
20:23:48:VAL:HG22	20:23:50:ALA:H	1.61	0.64
44:N:92:ILE:H	44:N:92:ILE:HD12	1.62	0.64
53:A:212:G:H2’	53:A:213:G:H8	1.62	0.64
15:18:38:ARG:NH2	15:18:40:GLN:HB3	2.10	0.64
38:H:77:VAL:HG12	38:H:84:ILE:HD12	1.79	0.64
41:K:30:ILE:HD13	41:K:45:THR:HG22	1.80	0.64
49:S:18:VAL:O	49:S:22:VAL:HG23	1.97	0.64
2:05:101:PHE:HA	2:05:104:VAL:HG22	1.78	0.64
54:01:729:G:H4’	54:01:763:G:H5’	1.79	0.64
54:01:1509:A:H2’	54:01:1510:G:C8	2.33	0.64
2:05:148:GLN:HB2	2:05:152:PRO:HG2	1.79	0.64
9:12:7:LYS:HG2	54:01:538:A:H4’	1.77	0.64
59:Z:235:ILE:HG22	59:Z:269:ARG:HA	1.80	0.64
15:18:102:ARG:HD3	15:18:106:ALA:HB1	1.78	0.64
54:01:2267:A:H5”	54:01:2268:A:H5’	1.79	0.64
55:02:55:U:H2’	55:02:56:G:C8	2.32	0.64
7:10:57:ASN:HB2	7:10:62:ARG:HG2	1.80	0.64
11:14:79:LEU:HD23	11:14:110:VAL:HG12	1.78	0.64
52:03:57:GLN:OE1	52:03:204:ALA:HB2	1.97	0.64
53:A:1052:U:H2’	53:A:1200:C:N4	2.12	0.64
7:10:19:ALA:HA	7:10:70:GLU:HG3	1.79	0.64
32:B:47:PRO:O	32:B:51:GLU:HG3	1.98	0.64
32:B:162:VAL:HG21	32:B:172:ILE:HG12	1.79	0.64
38:H:11:THR:HA	38:H:14:ARG:NH1	2.12	0.64
52:03:65:LEU:HB2	52:03:159:GLY:HA3	1.78	0.64
32:B:31:PHE:HB2	32:B:39:ILE:HB	1.80	0.64
32:B:202:ASN:HD22	32:B:208:ALA:HB2	1.63	0.64
42:L:26:CYS:SG	42:L:29:LYS:HG2	2.38	0.64
52:03:194:VAL:HG12	52:03:198:LYS:NZ	2.12	0.64
2:05:8:LYS:HB2	2:05:201:LEU:HD11	1.80	0.64
19:22:68:LYS:HE3	19:22:77:ARG:NH2	2.13	0.64
32:B:186:VAL:HB	32:B:190:SER:HB2	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:307:GLU:HG3	59:Z:389:ALA:HB2	1.79	0.64
1:04:209:ALA:HA	1:04:212:TRP:NE1	2.13	0.63
10:13:104:THR:HG22	10:13:106:GLU:H	1.63	0.63
16:19:8:ILE:HD12	16:19:9:ALA:N	2.11	0.63
12:15:45:GLN:NE2	54:01:2485:G:H5"	2.13	0.63
18:21:1:MET:HG2	18:21:109:ASP:OD2	1.97	0.63
54:01:215:G:H4'	54:01:216:A:H4'	1.78	0.63
1:04:260:LYS:HA	1:04:263:ASP:OD2	1.97	0.63
16:19:24:TYR:HE1	54:01:17:G:H4'	1.64	0.63
25:28:12:ALA:HA	25:28:15:ARG:HD3	1.79	0.63
54:01:528:A:C2	54:01:2042:A:H2'	2.34	0.63
14:17:17:LYS:HZ1	54:01:2380:C:H5'	1.64	0.63
46:P:20:VAL:HG22	46:P:21:VAL:N	2.14	0.63
59:Z:13:ASN:HB3	59:Z:98:MET:HA	1.80	0.63
39:I:60:LEU:HD21	39:I:89:TYR:HE2	1.62	0.63
47:Q:43:LEU:HD21	53:A:236:A:H5"	1.81	0.63
10:13:116:ILE:HD12	10:13:117:SER:N	2.14	0.63
36:F:64:VAL:HG22	36:F:65:GLU:H	1.62	0.63
47:Q:7:LEU:HD22	47:Q:24:ILE:HD13	1.80	0.63
52:03:60:ARG:HB2	52:03:141:LYS:HG3	1.80	0.63
2:05:33:ARG:HD3	2:05:51:THR:HG23	1.81	0.63
24:27:9:LYS:HD3	24:27:11:VAL:H	1.64	0.63
34:D:94:GLU:HA	34:D:99:ASN:ND2	2.14	0.63
37:G:58:LEU:HD12	37:G:59:GLU:N	2.14	0.63
54:01:2167:U:H2'	54:01:2169:A:OP2	1.99	0.63
9:12:93:ILE:HD13	9:12:100:VAL:HG21	1.81	0.63
50:T:23:ARG:NH2	50:T:60:GLN:HE22	1.96	0.62
53:A:701:U:H4'	53:A:703:G:H1'	1.81	0.62
54:01:2286:G:H5"	54:01:2287:A:OP1	1.98	0.62
37:G:97:ALA:HA	37:G:100:MET:HE2	1.81	0.62
52:03:37:LYS:CB	54:01:2127:G:H5'	2.28	0.62
55:02:66:A:H5"	55:02:67:G:OP1	1.99	0.62
7:10:4:ASN:HA	7:10:7:ASP:HB2	1.79	0.62
36:F:47:LEU:HD21	36:F:57:ALA:HB3	1.82	0.62
51:U:16:ARG:HB2	51:U:19:LYS:HD3	1.82	0.62
53:A:1227:A:H2'	53:A:1228:C:H5'	1.80	0.62
59:Z:89:LYS:HG2	59:Z:288:ARG:HH22	1.64	0.62
35:E:105:ILE:HD11	35:E:123:LEU:HD22	1.81	0.62
50:T:59:ARG:NH1	53:A:177:G:H5'	2.15	0.62
52:03:60:ARG:HH11	52:03:164:ARG:HD2	1.64	0.62
6:09:127:GLU:HA	6:09:145:ASN:HA	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:D:120:LYS:HG2	34:D:130:ASN:OD1	2.00	0.62
40:J:6:ILE:HB	40:J:76:ILE:HB	1.81	0.62
47:Q:30:HIS:HD2	47:Q:33:TYR:H	1.47	0.62
53:A:1277:C:H2'	53:A:1278:G:H5"	1.81	0.62
54:01:1837:C:H2'	54:01:1899:A:H61	1.62	0.62
59:Z:338:THR:HB	59:Z:363:ILE:HD13	1.82	0.62
14:17:80:GLU:O	14:17:84:GLU:HG3	1.99	0.62
54:01:2249:U:H3'	54:01:2250:G:H5'	1.82	0.62
7:10:22:ALA:HB1	7:10:118:ILE:HD11	1.81	0.62
10:13:63:VAL:HG22	10:13:84:CYS:HA	1.80	0.62
34:D:33:ILE:HG13	34:D:34:GLU:N	2.14	0.62
44:N:1:ALA:HB2	53:A:1203:C:H5"	1.82	0.62
1:04:235:GLU:H	1:04:238:ASN:HD22	1.48	0.62
6:09:12:LEU:HD12	6:09:13:GLY:N	2.15	0.62
54:01:2800:A:C2	54:01:2895:G:H1'	2.34	0.62
59:Z:260:MET:HA	59:Z:274:VAL:HG12	1.82	0.62
5:08:26:LYS:HB2	5:08:31:GLU:HG3	1.82	0.62
6:09:17:ASP:HB3	6:09:19:VAL:HG23	1.80	0.62
32:B:66:ILE:HD12	32:B:159:ALA:HB3	1.81	0.62
32:B:75:ALA:O	32:B:79:VAL:HG23	2.00	0.62
39:I:51:LEU:HD13	39:I:56:MET:HG3	1.81	0.62
54:01:704:G:H2'	54:01:726:G:N2	2.15	0.62
55:02:3:C:C3'	55:02:4:C:H5"	2.29	0.62
49:S:69:LYS:HE3	53:A:1319:A:H5"	1.82	0.61
55:02:115:A:H2'	55:02:116:G:C8	2.35	0.61
59:Z:247:ILE:N	59:Z:290:GLN:HE21	1.98	0.61
6:09:76:GLU:HB3	6:09:142:VAL:HA	1.81	0.61
52:03:44:VAL:HG13	52:03:214:ILE:HG22	1.81	0.61
5:08:154:GLU:OE1	5:08:157:LYS:HB2	2.00	0.61
19:22:56:GLU:OE2	19:22:88:LYS:HG2	1.99	0.61
33:C:112:ALA:HB1	33:C:184:ASN:HB2	1.83	0.61
34:D:8:LEU:HD23	53:A:429:U:H5'	1.82	0.61
50:T:82:ILE:HD12	50:T:83:ASN:N	2.14	0.61
7:10:43:LYS:HE3	7:10:98:GLU:HG3	1.82	0.61
11:14:82:LEU:HG	11:14:120:VAL:HG11	1.82	0.61
12:15:11:LYS:HE3	12:15:86:LYS:HB3	1.82	0.61
34:D:61:ARG:HH21	34:D:67:LEU:HA	1.63	0.61
42:L:79:ILE:HG22	42:L:103:CYS:HB2	1.82	0.61
54:01:2636:C:H2'	54:01:2637:U:C6	2.36	0.61
3:06:154:ASP:OD2	3:06:156:ASN:HB3	2.00	0.61
9:12:37:ARG:HD3	9:12:39:LYS:HD2	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:34:33:HIS:O	31:34:35:GLN:HG2	1.99	0.61
35:E:82:HIS:HB2	35:E:83:PRO:HD2	1.82	0.61
53:A:427:U:H4'	53:A:541:G:H5"	1.82	0.61
59:Z:243:GLU:HG3	59:Z:295:PRO:HA	1.81	0.61
16:19:71:ASN:OD1	16:19:109:VAL:HG21	2.00	0.61
26:29:16:CYS:HA	26:29:34:LEU:HB2	1.81	0.61
37:G:111:GLY:HA2	37:G:118:ARG:HD3	1.82	0.61
52:03:51:ASP:HB3	52:03:54:LYS:HG3	1.82	0.61
59:Z:294:LYS:HB3	59:Z:297:THR:HG22	1.81	0.61
7:10:23:LEU:HD21	7:10:96:PHE:HB2	1.81	0.61
56:X:59:A:H2'	56:X:60:U:H5'	1.83	0.61
35:E:59:ILE:O	35:E:63:MET:HG2	2.00	0.61
44:N:100:TRP:HZ2	53:A:1368:A:H5"	1.66	0.61
52:03:75:VAL:HB	52:03:92:ALA:HA	1.83	0.61
59:Z:74:ARG:CZ	59:Z:200:PRO:HA	2.31	0.61
1:04:47:ARG:NH2	54:01:774:G:H5"	2.16	0.60
32:B:41:ASN:ND2	32:B:43:GLU:HB2	2.16	0.60
34:D:100:VAL:HG21	34:D:136:VAL:HG21	1.82	0.60
52:03:7:ARG:HE	54:01:2128:G:H4'	1.65	0.60
14:17:76:LYS:O	14:17:80:GLU:HG3	2.02	0.60
35:E:15:ILE:HD11	35:E:37:VAL:HG23	1.83	0.60
53:A:1296:C:H4'	53:A:1302:C:N4	2.16	0.60
54:01:475:C:H4'	54:01:510:C:H5'	1.81	0.60
59:Z:124:GLN:HA	59:Z:373:ARG:HG2	1.81	0.60
59:Z:312:SER:H	59:Z:315:GLU:HB2	1.66	0.60
13:16:2:ARG:HG2	54:01:1653:G:H3'	1.83	0.60
36:F:26:THR:HA	36:F:29:ILE:HD12	1.83	0.60
44:N:2:LYS:HD3	53:A:1049:U:H2'	1.84	0.60
54:01:2698:U:H2'	54:01:2699:C:C6	2.35	0.60
12:15:5:LYS:HG2	12:15:6:ARG:HG2	1.84	0.60
24:27:42:LEU:O	24:27:46:VAL:HG23	2.01	0.60
53:A:1513:A:H2'	53:A:1514:G:C8	2.37	0.60
54:01:1830:C:H2'	54:01:1831:G:H8	1.65	0.60
54:01:1936:A:H2	54:01:1943:U:H3	1.50	0.60
1:04:165:ALA:HB3	1:04:172:THR:HB	1.83	0.60
14:17:17:LYS:NZ	54:01:2380:C:H5'	2.17	0.60
34:D:12:ARG:HG2	34:D:33:ILE:HD12	1.83	0.60
53:A:1412:C:H2'	53:A:1413:A:C8	2.37	0.60
54:01:1857:G:H2'	54:01:1884:G:H22	1.66	0.60
54:01:2086:U:H2'	54:01:2087:G:C8	2.37	0.60
46:P:2:VAL:HG23	46:P:65:ALA:HA	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:P:43:ALA:HA	46:P:46:LYS:NZ	2.16	0.60
55:02:106:G:H2'	55:02:107:G:O4'	2.02	0.60
56:X:38:A:H3'	56:X:39:C:C6	2.37	0.60
56:W:17:C:H5'	56:W:61:C:OP1	2.02	0.60
59:Z:293:ALA:HB1	59:Z:298:ILE:HD13	1.82	0.60
7:10:8:LYS:O	7:10:12:VAL:HG23	2.02	0.60
9:12:27:ARG:NH2	54:01:1142:A:H4'	2.17	0.60
23:26:65:THR:O	23:26:69:GLU:HG3	2.00	0.60
31:34:2:LYS:HZ1	54:01:2478:A:H5"	1.65	0.60
45:O:86:LEU:HD12	45:O:86:LEU:O	2.02	0.60
52:03:77:VAL:HB	52:03:95:VAL:HG13	1.83	0.60
54:01:1063:G:H1	54:01:1075:C:H42	1.49	0.60
13:16:59:SER:O	13:16:63:ARG:HG2	2.02	0.60
14:17:16:ARG:HD3	14:17:19:GLN:HE21	1.66	0.60
32:B:202:ASN:HD21	32:B:205:ALA:HB3	1.67	0.60
52:03:7:ARG:NH1	52:03:218:MET:HE2	2.17	0.60
53:A:279:A:H5'	53:A:281:G:H5'	1.82	0.60
15:18:3:ILE:H	15:18:3:ILE:HD12	1.66	0.59
21:24:21:ARG:HE	21:24:87:GLN:HA	1.66	0.59
54:01:704:G:H2'	54:01:726:G:H22	1.66	0.59
7:10:17:GLU:HG2	7:10:88:HIS:NE2	2.17	0.59
8:11:92:PRO:HA	8:11:136:GLY:HA2	1.84	0.59
54:01:1060:U:H5'	54:01:1062:G:H5'	1.84	0.59
4:07:135:ILE:HG21	4:07:142:TYR:HD1	1.66	0.59
54:01:1186:G:H2'	54:01:1187:G:O4'	2.02	0.59
54:01:2070:A:H2'	54:01:2071:A:C8	2.37	0.59
54:01:2699:C:H2'	54:01:2700:A:H8	1.66	0.59
8:11:14:ALA:HB3	8:11:54:ILE:HD12	1.84	0.59
36:F:92:THR:OG1	36:F:93:LYS:N	2.34	0.59
18:21:82:MET:HB2	18:21:98:LYS:HB2	1.84	0.59
33:C:120:THR:HG23	33:C:188:ALA:HB2	1.83	0.59
53:A:236:A:H2'	53:A:237:G:C8	2.38	0.59
54:01:2215:C:H2'	54:01:2216:G:H8	1.67	0.59
59:Z:67:VAL:CG2	59:Z:78:HIS:HB3	2.32	0.59
2:05:149:ASN:HB3	54:01:2572:A:OP2	2.03	0.59
4:07:16:MET:SD	4:07:21:TYR:HB2	2.42	0.59
6:09:41:LYS:O	6:09:45:GLU:HG3	2.02	0.59
20:23:10:VAL:HG12	20:23:71:ILE:HG22	1.84	0.59
24:27:46:VAL:O	24:27:50:VAL:HG23	2.02	0.59
32:B:41:ASN:HD21	32:B:43:GLU:HB2	1.66	0.59
38:H:77:VAL:HG23	38:H:126:CYS:HA	1.82	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:17:VAL:HG23	9:12:137:PRO:HB2	1.84	0.59
22:25:38:GLY:HA2	54:01:2330:G:H21	1.67	0.59
40:J:46:LYS:HE2	40:J:68:ARG:HG2	1.83	0.59
53:A:571:U:H2'	53:A:572:A:H5"	1.84	0.59
54:01:2800:A:H3'	54:01:2801:G:C5'	2.29	0.59
10:13:79:PHE:HB3	15:18:67:GLU:OE2	2.03	0.59
34:D:10:LEU:HD13	34:D:62:ARG:HD2	1.85	0.59
45:O:23:SER:O	45:O:27:GLN:HG3	2.01	0.59
2:05:59:ARG:HH11	54:01:2830:C:H3'	1.67	0.59
7:10:74:ASP:HA	7:10:77:VAL:HG23	1.84	0.59
8:11:125:THR:O	8:11:129:GLU:HG3	2.03	0.59
46:P:20:VAL:HG23	46:P:35:ARG:HA	1.85	0.59
54:01:742:A:H2'	54:01:743:A:C8	2.38	0.59
59:Z:131:ILE:HD12	59:Z:195:LEU:HD12	1.83	0.59
38:H:45:ILE:HD13	38:H:60:LEU:HD13	1.85	0.59
53:A:1391:U:H2'	53:A:1392:G:H8	1.67	0.59
54:01:639:U:H2'	54:01:640:C:C6	2.37	0.59
54:01:968:C:H2'	54:01:969:G:H8	1.67	0.59
54:01:1159:U:H2'	54:01:1160:G:H8	1.68	0.59
11:14:17:LYS:HD3	54:01:663:G:H5"	1.84	0.58
23:26:16:ASN:ND2	54:01:2081:U:H5"	2.18	0.58
40:J:80:THR:HG22	40:J:82:LYS:H	1.68	0.58
52:03:104:ILE:O	52:03:109:MET:HG3	2.03	0.58
53:A:70:U:H5"	53:A:71:A:OP1	2.03	0.58
54:01:2190:G:H2'	54:01:2191:A:C8	2.38	0.58
59:Z:54:GLU:OE1	59:Z:62:ILE:HG21	2.03	0.58
22:25:62:LYS:O	22:25:78:ILE:HG23	2.03	0.58
27:30:30:ASP:HB3	27:30:34:GLY:H	1.68	0.58
37:G:136:LYS:O	37:G:140:VAL:HG23	2.03	0.58
47:Q:46:HIS:HB2	47:Q:70:LYS:CD	2.29	0.58
54:01:1794:A:H2'	54:01:1795:C:C6	2.38	0.58
59:Z:27:LEU:O	59:Z:31:ILE:HG13	2.03	0.58
2:05:135:GLY:O	54:01:2580:U:H5"	2.03	0.58
25:28:5:LYS:HG2	25:28:36:GLU:HG3	1.85	0.58
48:R:41:SER:HB3	48:R:51:GLN:HE21	1.68	0.58
54:01:1251:C:O2'	54:01:1252:G:H3'	2.03	0.58
1:04:16:VAL:HB	1:04:203:VAL:HG22	1.85	0.58
1:04:140:VAL:HG12	1:04:191:LEU:HD23	1.84	0.58
3:06:117:ARG:HH12	11:14:2:ARG:HG2	1.69	0.58
8:11:99:LYS:HE3	8:11:140:GLU:HG2	1.85	0.58
51:U:53:LYS:O	51:U:57:LYS:HG2	2.04	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:780:G:H2'	54:01:782:A:N7	2.17	0.58
54:01:2591:C:H2'	54:01:2592:G:C8	2.39	0.58
59:Z:68:GLU:HB2	59:Z:261:PHE:CD2	2.38	0.58
59:Z:155:GLU:HA	59:Z:158:SER:HB2	1.84	0.58
16:19:5:ARG:HB2	16:19:8:ILE:HD11	1.86	0.58
24:27:6:LEU:HD11	24:27:59:GLU:OE2	2.04	0.58
32:B:178:LEU:HG	32:B:180:ILE:HG13	1.85	0.58
33:C:151:GLU:HB3	33:C:198:LYS:HG3	1.85	0.58
35:E:10:LEU:HA	35:E:40:ASP:HA	1.86	0.58
52:03:74:ARG:H	52:03:112:ASP:HB2	1.67	0.58
53:A:902:G:H2'	53:A:903:G:H8	1.68	0.58
54:01:1053:C:C2'	54:01:1054:A:H5"	2.33	0.58
55:02:87:U:H5"	55:02:88:C:OP2	2.04	0.58
8:11:45:THR:HG22	8:11:50:LYS:HG2	1.86	0.58
32:B:67:LEU:HD23	32:B:68:PHE:N	2.19	0.58
52:03:124:VAL:HG13	52:03:127:LEU:HD12	1.86	0.58
54:01:581:C:H2'	54:01:582:A:C8	2.38	0.58
54:01:2646:C:H2'	54:01:2647:U:O4'	2.03	0.58
55:02:3:C:H3'	55:02:4:C:H5"	1.86	0.58
1:04:235:GLU:N	1:04:238:ASN:HD22	2.01	0.58
6:09:3:VAL:HG22	6:09:38:PRO:HA	1.86	0.58
40:J:91:ASP:O	40:J:92:LEU:HB2	2.04	0.58
53:A:1206:G:C2'	53:A:1207:G:H5"	2.29	0.58
54:01:2248:C:H2'	54:01:2249:U:H5'	1.85	0.58
5:08:37:ASN:ND2	5:08:39:ALA:HB3	2.19	0.58
8:11:127:SER:HA	54:01:1080:A:H1'	1.85	0.58
9:12:45:THR:HG22	9:12:47:HIS:H	1.69	0.58
9:12:114:LEU:O	9:12:118:MET:HG2	2.04	0.58
12:15:11:LYS:HD2	12:15:86:LYS:HG2	1.86	0.58
46:P:14:ARG:HH12	53:A:618:C:H1'	1.67	0.58
53:A:112:G:N2	53:A:354:G:H5'	2.13	0.58
54:01:1348:C:H2'	54:01:1349:C:H5'	1.86	0.58
59:Z:69:TYR:HE1	59:Z:78:HIS:HB2	1.68	0.58
7:10:41:LEU:HD11	7:10:54:VAL:HG11	1.85	0.58
55:02:66:A:N1	55:02:107:G:H2'	2.19	0.58
51:U:17:ARG:HA	51:U:20:ARG:HH11	1.68	0.58
53:A:770:C:H2'	53:A:771:G:H8	1.68	0.58
56:X:13:C:C2'	56:X:14:A:H5"	2.28	0.58
58:Y:61:C:H6	58:Y:61:C:H5'	1.69	0.58
59:Z:214:ILE:HD12	59:Z:290:GLN:HB2	1.86	0.58
11:14:23:ILE:HD12	11:14:23:ILE:H	1.68	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:15:52:ALA:HB2	12:15:123:LYS:HE3	1.86	0.57
18:21:55:ILE:O	18:21:59:GLU:HG2	2.04	0.57
26:29:48:GLN:NE2	26:29:52:ALA:HB2	2.19	0.57
39:I:59:LYS:HB3	39:I:60:LEU:HD12	1.86	0.57
53:A:715:A:H2'	53:A:716:A:C8	2.39	0.57
53:A:831:A:H3'	53:A:832:G:H5"	1.86	0.57
53:A:1386:G:H2'	53:A:1387:G:H8	1.69	0.57
54:01:968:C:H2'	54:01:969:G:C8	2.39	0.57
59:Z:187:LYS:HA	59:Z:190:GLU:HG3	1.86	0.57
6:09:3:VAL:HA	6:09:39:ALA:H	1.69	0.57
6:09:132:PHE:HB2	6:09:140:ALA:HB3	1.85	0.57
17:20:68:ARG:HB2	17:20:90:ARG:HH21	1.68	0.57
52:03:46:VAL:HG22	52:03:212:VAL:HG13	1.85	0.57
53:A:950:U:H2'	53:A:951:G:H8	1.69	0.57
54:01:286:U:H2'	54:01:287:G:C8	2.39	0.57
51:U:39:LYS:O	51:U:43:GLU:HG2	2.04	0.57
53:A:1391:U:H2'	53:A:1392:G:C8	2.39	0.57
24:27:49:ASP:O	24:27:53:VAL:HG23	2.04	0.57
32:B:55:GLU:O	32:B:59:ILE:HG12	2.05	0.57
54:01:917:A:H5"	54:01:2268:A:N6	2.19	0.57
54:01:1765:U:H2'	54:01:1766:G:C8	2.40	0.57
54:01:2605:U:H2'	54:01:2606:C:C6	2.39	0.57
54:01:2699:C:H2'	54:01:2700:A:C8	2.39	0.57
3:06:40:ARG:HH22	54:01:1246:A:H4'	1.68	0.57
23:26:16:ASN:HD22	54:01:2081:U:H5"	1.70	0.57
44:N:13:VAL:HA	44:N:59:GLN:HE22	1.68	0.57
53:A:501:C:H2'	53:A:502:A:H8	1.68	0.57
53:A:707:U:H2'	53:A:708:C:C6	2.39	0.57
2:05:105:LYS:HA	2:05:177:VAL:HG12	1.87	0.57
18:21:83:LYS:HG2	18:21:95:ARG:NH1	2.19	0.57
52:03:211:LYS:HE2	52:03:213:SER:HB3	1.86	0.57
59:Z:4:LYS:HA	59:Z:264:LEU:HB2	1.85	0.57
2:05:25:THR:HG21	2:05:193:VAL:HG22	1.87	0.57
4:07:90:LEU:HD12	4:07:90:LEU:O	2.05	0.57
5:08:23:ILE:HG22	5:08:25:ILE:HG13	1.86	0.57
5:08:71:LEU:O	5:08:75:VAL:HG23	2.03	0.57
34:D:49:ASP:HA	34:D:52:VAL:HG22	1.85	0.57
39:I:33:SER:H	39:I:36:GLN:HE21	1.52	0.57
44:N:20:PHE:O	44:N:21:ALA:HB3	2.04	0.57
54:01:996:A:H2'	54:01:997:G:H8	1.70	0.57
59:Z:176:LYS:HD2	59:Z:184:TRP:CD1	2.40	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:07:133:GLU:OE2	4:07:148:VAL:HG13	2.04	0.57
32:B:160:LEU:HD22	32:B:175:ALA:HB2	1.86	0.57
52:03:175:ILE:HB	52:03:188:ASN:HB3	1.86	0.57
53:A:352:C:H4'	53:A:354:G:OP1	2.04	0.57
53:A:1228:C:H2'	53:A:1229:A:H8	1.70	0.57
53:A:1369:C:H2'	53:A:1370:G:C8	2.39	0.57
59:Z:67:VAL:HG23	59:Z:78:HIS:HB3	1.86	0.57
59:Z:214:ILE:HD13	59:Z:286:ILE:HD11	1.85	0.57
6:09:94:ILE:HD11	6:09:122:LEU:HB2	1.85	0.57
33:C:9:ILE:HG23	33:C:10:ARG:HG3	1.85	0.57
53:A:312:C:H2'	53:A:313:A:C8	2.40	0.57
59:Z:328:PRO:HG2	59:Z:330:PHE:CZ	2.40	0.57
7:10:26:VAL:HB	7:10:82:ILE:HD12	1.86	0.57
9:12:45:THR:HB	9:12:48:VAL:HB	1.87	0.57
35:E:148:SER:HB2	35:E:149:PRO:HD2	1.85	0.57
51:U:58:LYS:NZ	51:U:58:LYS:HB2	2.20	0.57
3:06:192:ALA:O	3:06:196:VAL:HG23	2.05	0.56
24:27:7:ARG:HD3	24:27:7:ARG:N	2.20	0.56
35:E:54:GLU:HG2	35:E:56:PRO:HD2	1.87	0.56
39:I:49:GLN:N	39:I:50:PRO:HD2	2.20	0.56
46:P:70:ARG:NH1	53:A:452:A:H1'	2.20	0.56
52:03:12:ARG:HG2	52:03:220:ALA:HB2	1.86	0.56
52:03:48:LEU:HD12	52:03:165:ASN:ND2	2.20	0.56
53:A:358:U:H2'	53:A:359:G:H8	1.70	0.56
53:A:398:U:H2'	53:A:399:G:H8	1.69	0.56
53:A:501:C:H2'	53:A:502:A:C8	2.40	0.56
53:A:1129:C:H2'	53:A:1139:G:N7	2.19	0.56
54:01:1268:A:H2'	54:01:1269:A:O4'	2.04	0.56
59:Z:97:GLN:HE21	59:Z:229:GLY:HA2	1.70	0.56
1:04:206:LYS:HD2	54:01:729:G:C8	2.41	0.56
4:07:87:LYS:HD2	54:01:2313:C:H5"	1.87	0.56
13:16:39:PRO:HG2	54:01:1651:G:H4'	1.86	0.56
14:17:29:HIS:HB3	14:17:36:TYR:HB2	1.87	0.56
34:D:117:VAL:HG22	34:D:122:ILE:HG13	1.87	0.56
36:F:52:ASN:O	36:F:53:LYS:HG3	2.04	0.56
53:A:744:C:H2'	53:A:745:G:C8	2.40	0.56
53:A:1429:A:H2'	53:A:1430:A:H8	1.70	0.56
54:01:1717:A:H2'	54:01:1718:G:O4'	2.06	0.56
59:Z:74:ARG:HB2	59:Z:76:TYR:CZ	2.41	0.56
2:05:118:PHE:HB2	54:01:2823:A:OP1	2.04	0.56
3:06:176:ASP:OD1	3:06:179:SER:HB2	2.06	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:28:THR:HG22	40:J:86:ALA:HB1	1.86	0.56
42:L:2:THR:CG2	42:L:5:GLN:HG3	2.35	0.56
52:03:142:VAL:HG11	52:03:162:ARG:HD2	1.87	0.56
53:A:1144:G:H21	53:A:1146:A:H62	1.52	0.56
54:01:473:G:O2'	54:01:474:G:H5'	2.05	0.56
54:01:554:U:H2'	54:01:555:G:O4'	2.04	0.56
54:01:660:C:H2'	54:01:661:A:C8	2.41	0.56
54:01:679:C:H2'	54:01:680:C:C6	2.40	0.56
54:01:1149:G:H2'	54:01:1150:C:C6	2.41	0.56
54:01:2636:C:H2'	54:01:2637:U:H6	1.68	0.56
59:Z:157:LEU:HB3	59:Z:162:PHE:HB2	1.87	0.56
59:Z:366:ILE:HG13	59:Z:367:ALA:N	2.21	0.56
5:08:34:ARG:NE	5:08:70:LEU:HD13	2.19	0.56
20:23:10:VAL:HG12	20:23:71:ILE:HA	1.86	0.56
40:J:5:ARG:HG2	40:J:79:PRO:HB3	1.86	0.56
48:R:70:THR:HG23	48:R:72:ARG:H	1.71	0.56
54:01:2287:A:O2'	54:01:2288:A:H2'	2.06	0.56
54:01:2297:A:N6	54:01:2319:G:H1'	2.19	0.56
1:04:61:TYR:HE1	54:01:1816:C:H3'	1.71	0.56
15:18:52:ARG:NH2	54:01:2720:U:H5"	2.21	0.56
31:34:7:VAL:HB	31:34:35:GLN:NE2	2.20	0.56
32:B:160:LEU:HD22	32:B:175:ALA:CB	2.35	0.56
43:M:24:VAL:HA	53:A:1329:A:H5"	1.86	0.56
43:M:47:LEU:HD21	43:M:51:GLN:HB2	1.88	0.56
52:03:46:VAL:O	52:03:171:ILE:HG22	2.05	0.56
52:03:105:LYS:HA	52:03:109:MET:SD	2.46	0.56
15:18:88:ARG:HH11	15:18:112:ARG:HH21	1.52	0.56
22:25:47:VAL:HG13	22:25:56:PHE:O	2.05	0.56
54:01:1432:G:H2'	54:01:1433:A:C8	2.40	0.56
59:Z:184:TRP:O	59:Z:188:ILE:HG12	2.05	0.56
1:04:61:TYR:CE1	54:01:1816:C:H3'	2.40	0.56
8:11:78:LEU:HD13	8:11:112:LYS:NZ	2.21	0.56
38:H:6:ILE:HD11	38:H:31:LEU:HD23	1.86	0.56
52:03:27:ILE:HB	52:03:182:ALA:HB1	1.88	0.56
54:01:184:C:H2'	54:01:185:G:H8	1.70	0.56
7:10:78:GLY:N	7:10:79:PRO:HD2	2.21	0.56
33:C:118:SER:O	33:C:122:GLN:HG3	2.06	0.56
52:03:153:VAL:HG12	52:03:157:LYS:HD3	1.87	0.56
53:A:1170:A:H2'	53:A:1171:A:O4'	2.05	0.56
53:A:1399:C:H4'	53:A:1400:C:O5'	2.05	0.56
54:01:100:U:H4'	54:01:101:A:O4'	2.06	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1071:G:OP1	54:01:1071:G:H3'	2.05	0.56
54:01:1316:U:H2'	54:01:1317:G:C8	2.41	0.56
33:C:69:THR:HG21	33:C:75:VAL:HG21	1.87	0.56
35:E:152:VAL:HG11	38:H:98:LEU:HD13	1.87	0.56
44:N:80:ARG:O	44:N:83:VAL:HG12	2.06	0.56
52:03:22:ASP:H	52:03:25:GLU:HB3	1.70	0.56
53:A:1429:A:H2'	53:A:1430:A:C8	2.41	0.56
59:Z:100:GLY:HA3	59:Z:199:ILE:HD13	1.88	0.56
2:05:124:ARG:HA	2:05:165:MET:SD	2.46	0.56
7:10:59:LEU:HD22	7:10:62:ARG:NH2	2.21	0.56
17:20:78:ARG:HH12	54:01:990:A:H61	1.54	0.56
21:24:62:THR:HG22	21:24:71:LYS:HG2	1.88	0.56
46:P:20:VAL:HG22	46:P:21:VAL:H	1.71	0.56
48:R:17:VAL:HG22	48:R:18:GLN:N	2.19	0.56
53:A:89:U:H2'	53:A:90:C:O4'	2.06	0.56
53:A:797:C:H2'	53:A:798:U:C6	2.41	0.56
14:17:110:ALA:HB1	14:17:115:LEU:HD23	1.88	0.55
20:23:25:LYS:HG2	20:23:36:GLU:OE1	2.05	0.55
33:C:76:ILE:HB	33:C:80:GLY:HA2	1.88	0.55
40:J:42:LEU:HD11	40:J:73:LEU:HG	1.88	0.55
44:N:45:LEU:O	49:S:12:LEU:HD11	2.07	0.55
52:03:48:LEU:HG	52:03:171:ILE:HB	1.89	0.55
54:01:2350:C:H2'	54:01:2351:G:O4'	2.05	0.55
16:19:32:ARG:HB2	54:01:581:C:OP1	2.05	0.55
18:21:4:ILE:HG22	18:21:106:VAL:HG22	1.88	0.55
32:B:41:ASN:HD22	32:B:44:LYS:HG2	1.71	0.55
43:M:47:LEU:HD23	43:M:48:SER:O	2.06	0.55
54:01:1138:G:H2'	54:01:1139:G:O4'	2.06	0.55
54:01:2537:U:H2'	54:01:2538:C:C6	2.41	0.55
54:01:1278:C:H2'	54:01:1279:G:H8	1.71	0.55
54:01:1368:G:H2'	54:01:1369:G:C8	2.41	0.55
54:01:2329:U:H2'	54:01:2330:G:H8	1.72	0.55
13:16:47:VAL:C	13:16:50:PRO:HD2	2.26	0.55
23:26:70:LEU:HD13	23:26:77:TYR:HB3	1.88	0.55
24:27:21:LEU:HA	24:27:25:GLN:HB3	1.89	0.55
53:A:744:C:H2'	53:A:745:G:H8	1.72	0.55
54:01:161:A:H3'	54:01:162:U:H5"	1.87	0.55
54:01:703:U:H2'	54:01:704:G:O4'	2.05	0.55
39:I:104:THR:HG23	53:A:1180:A:H5'	1.89	0.55
54:01:1283:G:H1'	54:01:1329:U:O2	2.07	0.55
54:01:2799:A:H2'	54:01:2800:A:H5'	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:354:ASP:HB3	59:Z:356:ILE:HG23	1.89	0.55
5:08:8:VAL:HB	5:08:49:LEU:HB2	1.89	0.55
16:19:21:LYS:HG2	54:01:19:A:H5"	1.89	0.55
20:23:5:ARG:HG2	20:23:93:ARG:NH2	2.22	0.55
42:L:32:VAL:O	42:L:33:CYS:HB2	2.06	0.55
54:01:2111:U:H3	54:01:2147:A:H1'	1.71	0.55
59:Z:212:LEU:HD21	59:Z:229:GLY:HA3	1.89	0.55
8:11:85:ILE:HD11	8:11:137:LEU:HD21	1.88	0.55
11:14:135:ILE:HB	11:14:142:ILE:HD11	1.88	0.55
33:C:106:ARG:HG2	33:C:107:LYS:HD2	1.88	0.55
54:01:1874:C:H2'	54:01:1875:G:O4'	2.07	0.55
54:01:2155:U:H2'	54:01:2156:G:H5'	1.89	0.55
54:01:2512:C:H2'	54:01:2513:A:O4'	2.06	0.55
11:14:23:ILE:HD12	11:14:23:ILE:N	2.22	0.55
16:19:49:ARG:HG2	16:19:52:ARG:NH2	2.22	0.55
32:B:9:LEU:HD11	32:B:13:VAL:HG22	1.87	0.55
53:A:532:A:O2'	53:A:533:A:OP1	2.16	0.55
53:A:1296:C:H4'	53:A:1302:C:H42	1.72	0.55
54:01:2182:U:H2'	54:01:2183:A:C8	2.42	0.55
54:01:2423:U:O2'	54:01:2425:A:H2'	2.07	0.55
3:06:71:GLY:N	54:01:674:G:H5"	2.22	0.55
27:30:29:VAL:HB	54:01:2885:G:H1	1.71	0.55
32:B:17:HIS:HB2	32:B:188:THR:HG23	1.88	0.55
32:B:65:LYS:HB3	32:B:89:PHE:HE2	1.72	0.55
44:N:53:ASP:HA	44:N:58:ARG:HD3	1.87	0.55
53:A:220:G:O2'	53:A:221:C:H5'	2.07	0.55
53:A:236:A:H2'	53:A:237:G:H8	1.72	0.55
53:A:398:U:H2'	53:A:399:G:C8	2.42	0.55
53:A:1346:A:O2'	53:A:1347:G:H4'	2.07	0.55
54:01:365:U:H2'	54:01:366:C:C6	2.41	0.55
54:01:593:U:H2'	54:01:594:U:C6	2.42	0.55
59:Z:206:ILE:HG22	59:Z:270:ALA:N	2.19	0.55
5:08:154:GLU:HG2	5:08:157:LYS:H	1.72	0.55
8:11:33:ASN:ND2	8:11:35:MET:HB3	2.21	0.55
33:C:58:ARG:NH1	33:C:58:ARG:HB2	2.22	0.55
37:G:80:GLY:HA3	57:V:11:U:O2'	2.06	0.55
45:O:7:THR:O	45:O:11:VAL:HG23	2.06	0.55
53:A:225:C:H2'	53:A:226:G:H5"	1.89	0.55
54:01:172:A:H2'	54:01:173:A:H8	1.72	0.55
59:Z:317:GLY:HA2	59:Z:383:VAL:HA	1.87	0.55
6:09:51:ARG:HA	6:09:55:GLU:HG3	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:22:39:THR:O	19:22:43:ILE:HG13	2.07	0.54
54:01:1906:G:H2'	54:01:1907:G:H5"	1.88	0.54
54:01:2743:U:H3'	54:01:2744:G:H5"	1.88	0.54
59:Z:184:TRP:CE3	59:Z:187:LYS:HG2	2.42	0.54
7:10:51:TYR:HA	7:10:53:ARG:HH12	1.71	0.54
9:12:31:GLU:HG2	9:12:142:ILE:HG12	1.89	0.54
18:21:42:LYS:HB2	54:01:2010:G:H5"	1.88	0.54
31:34:30:GLU:HG3	31:34:32:LYS:H	1.71	0.54
48:R:59:LYS:HD3	53:A:735:C:H5'	1.89	0.54
54:01:741:U:H2'	54:01:742:A:H8	1.72	0.54
54:01:2180:U:H2'	54:01:2181:U:O4'	2.07	0.54
59:Z:13:ASN:HB2	59:Z:99:ASP:H	1.72	0.54
59:Z:21:ASP:N	60:Z:401:GCP:H3B1	2.22	0.54
59:Z:245:VAL:HA	59:Z:250:THR:HG22	1.89	0.54
4:07:55:ASP:O	4:07:59:ILE:HG13	2.07	0.54
17:20:68:ARG:HB2	17:20:90:ARG:NH2	2.22	0.54
30:33:61:LEU:HD12	30:33:61:LEU:O	2.07	0.54
32:B:18:GLN:HG2	32:B:187:ASP:OD2	2.07	0.54
33:C:133:MET:O	33:C:137:VAL:HG23	2.07	0.54
33:C:134:LYS:O	33:C:138:GLN:HG3	2.06	0.54
49:S:54:ARG:HG3	49:S:55:GLN:HG2	1.90	0.54
54:01:1609:A:H1'	54:01:1616:A:H1'	1.89	0.54
54:01:2185:U:H2'	54:01:2186:G:C8	2.43	0.54
1:04:106:PRO:HG2	1:04:109:LEU:HB2	1.87	0.54
3:06:105:LEU:HD23	3:06:108:ILE:HD11	1.88	0.54
4:07:47:LYS:HA	4:07:50:ASP:OD2	2.05	0.54
5:08:51:PHE:HZ	5:08:71:LEU:HD22	1.72	0.54
19:22:6:ARG:O	19:22:10:VAL:HG23	2.08	0.54
41:K:93:GLU:HG2	41:K:96:ILE:HD11	1.88	0.54
42:L:109:ARG:HB2	42:L:118:VAL:HG21	1.88	0.54
54:01:2368:C:H2'	54:01:2369:A:C8	2.43	0.54
54:01:2404:U:H2'	54:01:2405:G:O4'	2.07	0.54
54:01:2861:U:H2'	54:01:2862:G:H8	1.73	0.54
6:09:30:LEU:HB3	6:09:36:ALA:HB3	1.89	0.54
16:19:91:ARG:HD2	16:19:91:ARG:N	2.23	0.54
32:B:103:TRP:CH2	32:B:107:ARG:HD3	2.42	0.54
50:T:4:LYS:HG3	50:T:6:ALA:H	1.72	0.54
53:A:434:U:H2'	53:A:435:A:C8	2.42	0.54
53:A:682:G:H2'	53:A:683:G:H8	1.72	0.54
53:A:918:A:H2'	53:A:919:A:C8	2.42	0.54
53:A:1379:G:O2'	53:A:1380:U:H5'	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:57:C:H2'	54:01:58:G:O4'	2.07	0.54
54:01:969:G:H2'	54:01:970:U:C6	2.43	0.54
54:01:1447:C:H2'	54:01:1448:G:H8	1.71	0.54
54:01:2208:C:H2'	54:01:2209:G:C8	2.42	0.54
54:01:2676:C:H2'	54:01:2677:G:C8	2.43	0.54
58:Y:53:G:H4'	59:Z:320:THR:OG1	2.08	0.54
59:Z:12:VAL:HB	59:Z:76:TYR:CD1	2.43	0.54
33:C:107:LYS:HG2	33:C:110:LEU:HD12	1.90	0.54
40:J:59:LYS:HE2	40:J:62:ARG:HH21	1.73	0.54
49:S:19:GLU:O	49:S:23:GLU:HG2	2.08	0.54
53:A:70:U:H2'	53:A:94:G:N7	2.23	0.54
53:A:235:C:H2'	53:A:236:A:C8	2.43	0.54
53:A:335:C:H2'	53:A:336:A:H8	1.73	0.54
7:10:118:ILE:HB	7:10:119:PRO:HD3	1.89	0.54
10:13:66:LYS:NZ	10:13:66:LYS:HB3	2.22	0.54
24:27:26:PHE:HA	24:27:29:ARG:HE	1.73	0.54
30:33:38:LYS:HA	30:33:41:ARG:HH11	1.72	0.54
34:D:49:ASP:O	34:D:53:GLN:HG3	2.07	0.54
54:01:873:C:H2'	54:01:874:G:H8	1.72	0.54
54:01:975:A:H1'	54:01:990:A:C6	2.43	0.54
54:01:1827:U:O2'	54:01:1828:G:H5'	2.07	0.54
59:Z:304:PHE:HD2	59:Z:388:VAL:HG13	1.73	0.54
1:04:12:ARG:HH21	54:01:728:G:C5'	2.21	0.54
2:05:9:VAL:O	2:05:26:VAL:HB	2.07	0.54
4:07:23:SER:HB3	4:07:26:GLN:HG3	1.89	0.54
5:08:118:ALA:O	5:08:120:ILE:N	2.41	0.54
14:17:66:GLY:HA2	14:17:102:ARG:NH2	2.23	0.54
32:B:162:VAL:HB	32:B:184:ALA:CB	2.38	0.54
33:C:67:ILE:HD11	33:C:100:ILE:HD11	1.88	0.54
33:C:86:LEU:HA	33:C:89:VAL:HG22	1.88	0.54
35:E:79:THR:OG1	35:E:80:LEU:N	2.40	0.54
35:E:79:THR:HG23	35:E:80:LEU:O	2.08	0.54
40:J:66:GLU:HG2	44:N:98:ALA:HB2	1.88	0.54
51:U:34:ARG:HB3	51:U:36:PHE:CE2	2.43	0.54
52:03:111:PHE:CE2	52:03:114:VAL:HG23	2.43	0.54
53:A:1201:A:H1'	53:A:1202:U:OP2	2.08	0.54
54:01:290:U:H2'	54:01:291:G:H8	1.71	0.54
54:01:1909:C:H2'	54:01:1910:G:H8	1.72	0.54
54:01:2789:C:H2'	54:01:2893:A:N7	2.23	0.54
55:02:13:G:N2	55:02:16:G:H1'	2.20	0.54
59:Z:70:ASP:HA	59:Z:76:TYR:HD2	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:253:SER:HB2	59:Z:281:ILE:HD11	1.87	0.54
40:J:57:VAL:O	40:J:58:ASN:CB	2.55	0.54
47:Q:10:ARG:HH11	47:Q:55:GLY:HA2	1.72	0.54
54:01:1697:G:H4'	54:01:1978:A:H5"	1.89	0.54
59:Z:214:ILE:CD1	59:Z:286:ILE:HD11	2.37	0.54
2:05:125:TRP:CD1	2:05:160:LYS:HB3	2.42	0.54
4:07:40:GLY:HA2	4:07:84:ILE:HG13	1.89	0.54
5:08:8:VAL:HB	5:08:49:LEU:HD12	1.89	0.54
7:10:88:HIS:HB2	7:10:89:PRO:HD3	1.90	0.54
13:16:47:VAL:O	13:16:50:PRO:HD2	2.08	0.54
33:C:110:LEU:HD13	33:C:203:LYS:HE3	1.90	0.54
33:C:182:ASP:HB2	33:C:201:ILE:HB	1.90	0.54
34:D:190:LEU:HD12	34:D:190:LEU:O	2.08	0.54
36:F:50:PRO:HG3	36:F:55:HIS:CE1	2.43	0.54
49:S:54:ARG:HB3	53:A:958:A:C2	2.43	0.54
53:A:1228:C:H2'	53:A:1229:A:C8	2.43	0.54
54:01:741:U:H2'	54:01:742:A:C8	2.43	0.54
54:01:1669:A:H5"	54:01:2550:G:OP1	2.08	0.54
54:01:2144:G:H1'	54:01:2147:A:H61	1.73	0.54
59:Z:124:GLN:NE2	59:Z:385:ALA:HB1	2.22	0.54
59:Z:329:GLN:HE22	59:Z:378:GLU:HA	1.72	0.54
2:05:181:ASP:HB3	2:05:186:LEU:HB2	1.90	0.53
4:07:154:THR:HG21	54:01:2314:A:O4'	2.07	0.53
32:B:27:LYS:HB3	32:B:28:PRO:HD3	1.89	0.53
33:C:87:ARG:HG3	33:C:98:ALA:O	2.07	0.53
42:L:113:ARG:HH12	42:L:121:PRO:HD3	1.72	0.53
52:03:69:THR:HG22	52:03:174:THR:HG23	1.89	0.53
54:01:310:A:C2'	54:01:311:A:H5"	2.38	0.53
54:01:2270:A:H2'	54:01:2271:G:O4'	2.08	0.53
54:01:2398:U:H2'	54:01:2399:G:C8	2.43	0.53
18:21:86:MET:HB2	18:21:96:ILE:HD13	1.89	0.53
53:A:358:U:H2'	53:A:359:G:C8	2.42	0.53
54:01:255:A:H2'	54:01:256:A:O4'	2.08	0.53
54:01:1775:U:H2'	54:01:1776:G:O4'	2.07	0.53
54:01:2162:G:H2'	54:01:2163:A:C8	2.43	0.53
59:Z:68:GLU:HB2	59:Z:261:PHE:HD2	1.72	0.53
1:04:12:ARG:HA	1:04:15:VAL:HG23	1.90	0.53
35:E:59:ILE:HD12	35:E:60:GLN:N	2.23	0.53
41:K:124:LYS:HD3	41:K:124:LYS:H	1.74	0.53
53:A:20:U:H2'	53:A:21:G:O4'	2.08	0.53
53:A:59:A:H5"	53:A:387:U:H5"	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1306:A:N6	53:A:1331:G:H1'	2.24	0.53
53:A:1460:C:H2'	53:A:1461:G:H8	1.73	0.53
54:01:1675:C:H2'	54:01:1676:A:O4'	2.07	0.53
54:01:1689:A:H2'	54:01:1690:A:H8	1.74	0.53
59:Z:145:LEU:O	59:Z:149:VAL:HG23	2.09	0.53
1:04:261:ARG:CD	1:04:262:THR:HG23	2.39	0.53
2:05:2:ILE:HG21	2:05:90:PHE:HE2	1.73	0.53
2:05:33:ARG:H	2:05:33:ARG:CD	2.19	0.53
33:C:155:ARG:HG3	33:C:192:TYR:O	2.08	0.53
45:O:45:HIS:O	45:O:47:LYS:N	2.41	0.53
54:01:1316:U:H2'	54:01:1317:G:H8	1.73	0.53
54:01:2329:U:H2'	54:01:2330:G:C8	2.44	0.53
24:27:9:LYS:HE2	24:27:11:VAL:HG23	1.89	0.53
27:30:27:LEU:HD11	27:30:36:LYS:HB3	1.91	0.53
39:I:115:VAL:HG21	40:J:62:ARG:HB2	1.90	0.53
47:Q:48:GLU:HB2	47:Q:51:GLU:OE2	2.08	0.53
54:01:859:G:H1'	54:01:860:U:H5	1.73	0.53
54:01:1765:U:H2'	54:01:1766:G:H8	1.74	0.53
54:01:2345:G:N3	54:01:2381:A:H2'	2.24	0.53
56:W:47:U:H3'	56:W:48:C:C5'	2.39	0.53
59:Z:93:THR:HG22	59:Z:215:GLU:HG2	1.91	0.53
32:B:79:VAL:HG12	32:B:90:PHE:HB2	1.89	0.53
34:D:131:ILE:HG12	53:A:620:C:C2	2.43	0.53
38:H:65:PHE:CD2	38:H:66:GLN:HG2	2.43	0.53
53:A:891:U:O2'	53:A:892:A:H5'	2.08	0.53
54:01:435:C:H2'	54:01:436:C:H5'	1.90	0.53
54:01:742:A:H2'	54:01:743:A:H8	1.74	0.53
54:01:1310:G:H1'	54:01:1611:C:H5'	1.88	0.53
16:19:15:LYS:O	16:19:19:GLN:HG3	2.09	0.53
33:C:11:LEU:HD13	33:C:17:TRP:NE1	2.24	0.53
35:E:119:VAL:HG11	35:E:122:VAL:CG2	2.37	0.53
42:L:43:LYS:HB3	42:L:44:PRO:HD3	1.90	0.53
49:S:35:ARG:HH22	49:S:52:ASN:HA	1.74	0.53
54:01:2215:C:H2'	54:01:2216:G:C8	2.44	0.53
59:Z:212:LEU:HG	59:Z:230:ARG:O	2.08	0.53
5:08:94:ARG:HB2	5:08:105:SER:HB2	1.90	0.53
6:09:93:SER:HB3	6:09:123:ARG:HG2	1.90	0.53
8:11:21:PRO:HB2	8:11:22:PRO:HD3	1.90	0.53
8:11:94:LYS:HZ2	54:01:1076:C:H4'	1.74	0.53
12:15:42:THR:O	12:15:46:ILE:HD13	2.09	0.53
16:19:105:PHE:O	16:19:109:VAL:HG23	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:45:ILE:HG21	38:H:60:LEU:HD22	1.90	0.53
39:I:89:TYR:HB3	39:I:93:LEU:HD12	1.90	0.53
42:L:48:LEU:HB2	53:A:520:A:OP1	2.09	0.53
51:U:11:PHE:O	51:U:13:VAL:HG12	2.09	0.53
53:A:784:A:H2'	53:A:785:G:C8	2.43	0.53
53:A:1402:C:H2'	53:A:1403:C:O4'	2.09	0.53
54:01:575:A:O2'	54:01:576:U:H5'	2.09	0.53
6:09:64:ALA:O	6:09:68:ARG:HG3	2.08	0.53
46:P:70:ARG:HD3	53:A:375:U:OP1	2.09	0.53
52:03:9:ARG:O	52:03:13:GLU:HG3	2.09	0.53
53:A:335:C:H2'	53:A:336:A:C8	2.44	0.53
53:A:411:A:H1'	53:A:413:G:H1'	1.90	0.53
54:01:1141:U:H4'	54:01:1142:A:O4'	2.09	0.53
54:01:1332:G:N7	54:01:1609:A:H2'	2.24	0.53
54:01:2141:G:H2'	54:01:2142:A:C8	2.44	0.53
55:02:114:C:H2'	55:02:115:A:H8	1.72	0.53
2:05:194:PRO:HA	54:01:2680:U:H5'	1.89	0.53
16:19:50:ARG:HG2	54:01:1156:A:C8	2.44	0.53
29:32:16:HIS:HA	29:32:21:ARG:HH22	1.72	0.53
33:C:179:ALA:HB1	33:C:202:PHE:HE1	1.73	0.53
50:T:23:ARG:HH21	50:T:60:GLN:HE22	1.57	0.53
53:A:309:A:H2'	53:A:310:G:H8	1.72	0.53
54:01:2317:A:H2'	54:01:2318:G:O4'	2.09	0.53
59:Z:11:HIS:CB	59:Z:269:ARG:HH12	2.22	0.53
4:07:124:ARG:HH21	54:01:2316:G:H4'	1.74	0.52
12:15:29:GLY:HA2	12:15:106:ASP:HB2	1.91	0.52
28:31:47:ILE:HD12	28:31:47:ILE:N	2.23	0.52
33:C:54:ILE:HG22	33:C:67:ILE:HA	1.90	0.52
53:A:483:C:H2'	53:A:484:G:C8	2.43	0.52
54:01:329:G:O4'	54:01:477:A:H1'	2.09	0.52
54:01:1447:C:H2'	54:01:1448:G:C8	2.45	0.52
4:07:107:VAL:HB	4:07:108:PRO:HD3	1.91	0.52
5:08:136:ASP:OD2	5:08:139:VAL:HG23	2.09	0.52
17:20:80:ARG:NH2	54:01:571:U:H3'	2.24	0.52
51:U:17:ARG:HA	51:U:20:ARG:NH1	2.25	0.52
53:A:1409:C:H2'	53:A:1410:A:C8	2.44	0.52
53:A:1498:U:H1'	53:A:1499:A:N7	2.24	0.52
54:01:519:U:H2'	54:01:520:G:C8	2.45	0.52
54:01:1297:C:OP1	54:01:2710:C:H4'	2.08	0.52
54:01:2248:C:C2'	54:01:2249:U:H5'	2.39	0.52
59:Z:230:ARG:HA	59:Z:273:ASN:HA	1.89	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:370:ASP:OD1	59:Z:391:VAL:HG23	2.09	0.52
6:09:2:GLN:O	6:09:39:ALA:HB3	2.09	0.52
7:10:33:VAL:HG12	7:10:34:THR:N	2.25	0.52
38:H:17:GLN:NE2	38:H:71:VAL:H	2.08	0.52
42:L:115:LYS:O	42:L:116:TYR:HB2	2.09	0.52
47:Q:43:LEU:HD13	47:Q:72:TRP:NE1	2.25	0.52
53:A:1527:U:H2'	53:A:1528:U:C6	2.43	0.52
59:Z:310:ILE:HG21	59:Z:350:VAL:HG12	1.92	0.52
12:15:69:PRO:HA	12:15:94:ALA:HB2	1.89	0.52
35:E:163:ILE:HD12	35:E:164:LEU:N	2.24	0.52
38:H:29:SER:HB3	38:H:32:LYS:HD3	1.90	0.52
54:01:546:U:H2'	54:01:547:A:C4'	2.39	0.52
54:01:1047:G:H2'	54:01:1110:G:N2	2.24	0.52
59:Z:172:GLY:HA3	59:Z:187:LYS:HB3	1.91	0.52
53:A:1230:C:H5'	56:W:30:G:H5"	1.92	0.52
54:01:66:C:H2'	54:01:67:U:C6	2.44	0.52
54:01:2861:U:H2'	54:01:2862:G:C8	2.44	0.52
55:02:63:C:H2'	55:02:64:G:H8	1.75	0.52
6:09:1:MET:HB3	6:09:3:VAL:HG23	1.91	0.52
11:14:23:ILE:HG13	17:20:82:HIS:NE2	2.25	0.52
28:31:8:ILE:HG21	28:31:24:LYS:HE2	1.90	0.52
32:B:208:ALA:HB1	32:B:212:TYR:HE2	1.73	0.52
38:H:17:GLN:HE21	38:H:71:VAL:HB	1.75	0.52
53:A:418:C:H2'	53:A:419:C:C6	2.45	0.52
54:01:2629:U:O2'	54:01:2630:G:H5"	2.10	0.52
3:06:79:ARG:HH22	54:01:471:A:H5"	1.73	0.52
7:10:23:LEU:HB3	7:10:87:GLU:OE1	2.09	0.52
22:25:45:ALA:O	22:25:47:VAL:HG23	2.10	0.52
33:C:110:LEU:HG	33:C:143:LEU:HD22	1.91	0.52
55:02:37:C:H42	55:02:49:C:H1'	1.74	0.52
35:E:84:VAL:HG23	35:E:145:ASN:HD22	1.75	0.52
52:03:57:GLN:HG2	52:03:201:PRO:HB2	1.92	0.52
53:A:494:G:O2'	53:A:496:A:H1'	2.10	0.52
53:A:1406:U:H2'	53:A:1407:C:O4'	2.10	0.52
2:05:154:LYS:NZ	54:01:2024:G:H4'	2.25	0.52
5:08:23:ILE:HD13	5:08:71:LEU:HD21	1.90	0.52
10:13:15:GLY:O	10:13:47:ILE:HG12	2.10	0.52
12:15:33:LEU:HB2	12:15:117:PHE:CD1	2.45	0.52
12:15:50:ARG:HH21	12:15:50:ARG:HG2	1.74	0.52
16:19:36:GLN:NE2	54:01:564:C:H1'	2.25	0.52
24:27:2:LYS:HD2	54:01:78:U:OP2	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:26:CYS:SG	42:L:29:LYS:HE2	2.50	0.52
44:N:2:LYS:HB3	44:N:5:MET:HG2	1.92	0.52
47:Q:59:GLU:HB2	47:Q:76:ARG:H	1.74	0.52
51:U:28:LEU:HA	51:U:31:VAL:HG12	1.92	0.52
53:A:235:C:H2'	53:A:236:A:H8	1.75	0.52
53:A:410:G:H2'	53:A:429:U:C4	2.45	0.52
54:01:1437:C:H2'	54:01:1438:U:C6	2.45	0.52
7:10:103:ASN:HA	7:10:107:GLU:HB3	1.92	0.52
21:24:70:ILE:HG22	21:24:72:VAL:HG13	1.91	0.52
29:32:12:ARG:NH1	29:32:44:VAL:HG21	2.25	0.52
32:B:53:LEU:HD23	32:B:56:LEU:HD12	1.91	0.52
34:D:85:THR:HB	35:E:102:THR:HG21	1.91	0.52
34:D:141:VAL:HG12	34:D:180:THR:HG23	1.92	0.52
35:E:147:ASN:HB2	35:E:151:MET:HG3	1.91	0.52
41:K:85:VAL:HG22	41:K:110:THR:O	2.10	0.52
48:R:11:ARG:CZ	48:R:14:ALA:HB3	2.40	0.52
53:A:129:A:H1'	53:A:130:A:N7	2.25	0.52
54:01:290:U:H2'	54:01:291:G:C8	2.43	0.52
54:01:910:A:H2'	54:01:911:A:C8	2.45	0.52
54:01:927:A:H2'	54:01:928:A:C8	2.45	0.52
54:01:1625:C:H2'	54:01:1626:A:O4'	2.10	0.52
54:01:2082:A:H2'	54:01:2083:G:O4'	2.10	0.52
55:02:114:C:H2'	55:02:115:A:C8	2.44	0.52
59:Z:294:LYS:HB3	59:Z:297:THR:CG2	2.40	0.52
8:11:15:GLY:HA3	8:11:51:GLY:H	1.74	0.51
37:G:111:GLY:HA2	37:G:118:ARG:HH11	1.75	0.51
53:A:948:C:H2'	53:A:949:A:H8	1.74	0.51
54:01:942:G:H2'	54:01:943:A:O4'	2.10	0.51
54:01:2366:A:H2'	54:01:2367:G:O4'	2.10	0.51
59:Z:150:GLU:OE2	59:Z:169:ILE:HB	2.11	0.51
6:09:43:ASN:HA	6:09:46:PHE:HD2	1.75	0.51
32:B:216:VAL:O	32:B:220:VAL:HG23	2.10	0.51
33:C:11:LEU:HD13	33:C:17:TRP:HE1	1.76	0.51
35:E:122:VAL:HG23	35:E:122:VAL:O	2.11	0.51
53:A:106:C:H2'	53:A:107:G:H8	1.75	0.51
53:A:575:G:HO2'	53:A:821:G:H5'	1.74	0.51
53:A:902:G:H2'	53:A:903:G:C8	2.45	0.51
54:01:2538:C:H2'	54:01:2539:C:H6	1.75	0.51
54:01:2898:U:H2'	54:01:2899:A:H8	1.73	0.51
55:02:34:A:N6	55:02:44:G:H2'	2.25	0.51
59:Z:102:ILE:HD11	59:Z:195:LEU:HD11	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:163:ILE:HA	1:04:173:LEU:HD23	1.92	0.51
2:05:66:GLY:HA3	54:01:2787:C:H5'	1.92	0.51
14:17:26:LEU:HD23	14:17:92:PHE:HD1	1.75	0.51
14:17:74:VAL:O	14:17:78:VAL:HG23	2.11	0.51
19:22:58:VAL:HG22	19:22:85:VAL:HG13	1.92	0.51
22:25:70:PRO:HD3	55:02:12:C:H42	1.74	0.51
33:C:102:ILE:HD12	33:C:102:ILE:O	2.10	0.51
37:G:78:ARG:HB3	37:G:83:THR:HA	1.93	0.51
40:J:41:PRO:HG3	53:A:1150:A:N3	2.25	0.51
42:L:114:SER:HB3	53:A:35:G:H21	1.76	0.51
45:O:23:SER:HB3	45:O:26:VAL:HG23	1.92	0.51
52:03:215:SER:HB3	52:03:221:GLY:HA2	1.92	0.51
54:01:107:G:H2'	54:01:108:G:H8	1.75	0.51
54:01:189:G:H2'	54:01:205:G:H22	1.75	0.51
54:01:1782:U:H2'	54:01:1783:A:H5'	1.91	0.51
54:01:1971:U:H5'	54:01:1972:G:H5"	1.91	0.51
54:01:2849:U:H4'	54:01:2850:A:H5'	1.91	0.51
56:X:70:G:H2'	56:X:71:C:O4'	2.10	0.51
5:08:148:ARG:HA	5:08:161:VAL:HB	1.93	0.51
15:18:3:ILE:HD12	15:18:3:ILE:N	2.24	0.51
53:A:1062:U:H2'	53:A:1063:C:C6	2.45	0.51
54:01:582:A:H2'	54:01:583:G:C8	2.45	0.51
54:01:940:G:H3'	54:01:941:A:H5"	1.93	0.51
54:01:1761:C:H2'	54:01:1762:A:O4'	2.11	0.51
54:01:2676:C:H2'	54:01:2677:G:H8	1.74	0.51
54:01:2859:G:H2'	54:01:2860:A:C8	2.44	0.51
19:22:8:LEU:HD11	24:27:22:LEU:HD12	1.91	0.51
20:23:4:ILE:HD12	20:23:4:ILE:N	2.25	0.51
32:B:129:THR:HG22	32:B:131:LYS:H	1.75	0.51
42:L:2:THR:HG21	42:L:5:GLN:HG3	1.92	0.51
51:U:29:ALA:HA	51:U:32:ARG:HD3	1.91	0.51
52:03:149:VAL:O	52:03:153:VAL:HG23	2.10	0.51
53:A:887:G:H2'	53:A:888:G:H5'	1.93	0.51
53:A:1011:C:H2'	53:A:1012:A:C8	2.46	0.51
54:01:56:A:H2'	54:01:57:C:O4'	2.11	0.51
54:01:2185:U:H2'	54:01:2186:G:H8	1.76	0.51
56:X:38:A:H3'	56:X:39:C:H6	1.73	0.51
2:05:2:ILE:HD11	2:05:100:LEU:HD22	1.91	0.51
4:07:90:LEU:HD13	4:07:95:MET:HA	1.93	0.51
5:08:173:ALA:HB1	54:01:2531:A:C8	2.45	0.51
9:12:95:ARG:HH11	9:12:95:ARG:HG3	1.75	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:40:ILE:HD12	40:J:73:LEU:HB2	1.92	0.51
41:K:88:PRO:HG2	41:K:89:GLY:H	1.75	0.51
43:M:24:VAL:HG23	43:M:28:ARG:HB3	1.93	0.51
53:A:382:A:H2'	53:A:383:A:C8	2.44	0.51
53:A:1219:A:H2'	53:A:1220:G:C8	2.46	0.51
54:01:197:A:H4'	54:01:2069:G:OP2	2.10	0.51
54:01:1657:U:H2'	54:01:1658:C:H6	1.76	0.51
54:01:2195:U:H2'	54:01:2196:C:C6	2.46	0.51
55:02:30:C:H2'	55:02:31:C:H5'	1.91	0.51
56:X:32:C:H2'	56:X:33:U:C4	2.45	0.51
1:04:131:MET:HG3	1:04:187:CYS:O	2.11	0.51
11:14:96:LYS:HB2	11:14:96:LYS:NZ	2.26	0.51
28:31:4:ILE:HD13	28:31:27:ARG:NH2	2.26	0.51
32:B:94:ARG:HD2	32:B:94:ARG:N	2.22	0.51
34:D:151:GLN:HG3	53:A:437:U:OP1	2.11	0.51
43:M:9:PRO:HG3	43:M:44:ILE:HG13	1.93	0.51
54:01:609:A:H2'	54:01:610:C:O4'	2.11	0.51
54:01:723:C:H2'	54:01:724:U:O4'	2.11	0.51
54:01:2070:A:H2'	54:01:2071:A:H8	1.74	0.51
59:Z:34:VAL:O	59:Z:38:THR:HG23	2.11	0.51
4:07:137:PHE:HB2	4:07:140:ILE:HD13	1.93	0.51
8:11:91:LYS:HA	8:11:94:LYS:HE2	1.93	0.51
12:15:12:MET:CA	54:01:910:A:H62	2.20	0.51
12:15:66:ARG:HG3	12:15:66:ARG:HH11	1.75	0.51
27:30:43:THR:HG23	27:30:47:TYR:O	2.10	0.51
35:E:121:ASN:OD1	35:E:122:VAL:HG13	2.11	0.51
47:Q:13:SER:HB3	47:Q:21:VAL:CG1	2.40	0.51
54:01:2487:G:H2'	54:01:2488:G:C8	2.44	0.51
59:Z:33:THR:O	59:Z:37:LYS:HG3	2.09	0.51
3:06:68:ALA:HA	54:01:1255:U:C6	2.45	0.51
16:19:109:VAL:HG12	16:19:113:LYS:HE2	1.93	0.51
28:31:37:LYS:HB2	28:31:48:TYR:CE2	2.46	0.51
35:E:73:VAL:HG21	35:E:143:LEU:HD13	1.91	0.51
46:P:19:VAL:HG13	46:P:36:VAL:O	2.11	0.51
52:03:41:SER:HB2	52:03:176:GLY:O	2.10	0.51
54:01:2368:C:H2'	54:01:2369:A:H8	1.76	0.51
54:01:2812:G:H2'	54:01:2813:A:C8	2.46	0.51
59:Z:50:ASP:HB3	59:Z:56:LYS:HG3	1.92	0.51
1:04:144:GLU:HG3	1:04:188:ARG:O	2.11	0.51
4:07:102:LEU:O	4:07:107:VAL:HG23	2.11	0.51
13:16:38:LEU:HB3	13:16:39:PRO:HD3	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:16:58:ASP:OD1	13:16:63:ARG:HD3	2.11	0.51
18:21:24:ILE:HD13	18:21:36:LEU:HD11	1.93	0.51
32:B:96:LEU:H	32:B:99:MET:HE3	1.76	0.51
39:I:33:SER:HB3	39:I:36:GLN:HG2	1.93	0.51
43:M:56:ARG:HA	43:M:59:VAL:HG22	1.92	0.51
45:O:24:THR:O	45:O:28:VAL:HG23	2.11	0.51
52:03:104:ILE:HG22	52:03:109:MET:HG2	1.92	0.51
53:A:1144:G:N2	53:A:1146:A:H62	2.09	0.51
54:01:996:A:H2'	54:01:997:G:C8	2.46	0.51
54:01:1063:G:H1	54:01:1075:C:N4	2.08	0.51
54:01:1170:C:H2'	54:01:1171:G:C8	2.46	0.51
54:01:1357:C:H2'	54:01:1358:G:O4'	2.11	0.51
59:Z:120:LEU:HD12	59:Z:121:LEU:HG	1.93	0.51
59:Z:149:VAL:O	59:Z:153:VAL:HG23	2.10	0.51
11:14:95:LEU:HB3	11:14:100:ILE:HD11	1.92	0.50
14:17:88:LYS:HE2	14:17:116:GLN:HG3	1.92	0.50
33:C:56:ILE:HG22	33:C:63:ILE:HD11	1.92	0.50
33:C:71:ARG:O	33:C:75:VAL:HG23	2.11	0.50
43:M:104:ASN:O	43:M:105:ALA:HB3	2.11	0.50
47:Q:60:ILE:HG23	47:Q:72:TRP:HB3	1.91	0.50
53:A:86:G:H4'	53:A:87:C:C5	2.46	0.50
53:A:673:A:H2'	53:A:674:G:C8	2.47	0.50
53:A:1436:U:H2'	53:A:1437:A:C8	2.45	0.50
54:01:296:U:H2'	54:01:297:G:C8	2.47	0.50
54:01:2114:A:N3	54:01:2114:A:H2'	2.26	0.50
59:Z:278:LEU:HD13	59:Z:281:ILE:HG13	1.92	0.50
27:30:8:THR:HG22	54:01:2020:A:H5'	1.93	0.50
27:30:12:ARG:HH11	27:30:16:ARG:CZ	2.24	0.50
32:B:178:LEU:HD23	32:B:178:LEU:H	1.77	0.50
45:O:2:LEU:HB2	45:O:34:GLN:HE22	1.76	0.50
49:S:14:LEU:O	49:S:18:VAL:HG23	2.11	0.50
50:T:59:ARG:O	50:T:63:LYS:HG2	2.11	0.50
53:A:29:U:O2'	53:A:30:U:H5'	2.11	0.50
54:01:414:C:H2'	54:01:415:A:C8	2.45	0.50
54:01:576:U:H2'	54:01:577:G:C8	2.46	0.50
54:01:1710:G:H2'	54:01:1711:A:C8	2.46	0.50
8:11:106:GLN:O	8:11:110:GLN:HG2	2.11	0.50
18:21:20:VAL:HG21	18:21:43:ALA:HB3	1.93	0.50
32:B:30:ILE:HB	32:B:38:HIS:HB3	1.94	0.50
32:B:138:ARG:HD2	32:B:141:GLU:OE1	2.10	0.50
37:G:100:MET:O	37:G:104:VAL:HG23	2.10	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:29:SER:O	38:H:33:VAL:HG23	2.11	0.50
38:H:34:ALA:O	38:H:38:VAL:HG23	2.11	0.50
51:U:65:ARG:HA	51:U:65:ARG:HE	1.76	0.50
53:A:77:A:H2'	53:A:78:A:C8	2.46	0.50
53:A:1308:U:H2'	53:A:1309:G:C8	2.46	0.50
53:A:1521:C:H2'	53:A:1522:U:C6	2.47	0.50
54:01:876:C:H2'	54:01:877:A:O4'	2.11	0.50
54:01:2432:A:H1'	56:X:75:C:H5'	1.91	0.50
55:02:66:A:H61	55:02:107:G:H3'	1.76	0.50
4:07:127:TYR:HB3	4:07:155:ILE:HB	1.93	0.50
23:26:32:LEU:HA	23:26:51:SER:HA	1.92	0.50
36:F:51:ILE:C	36:F:53:LYS:H	2.14	0.50
36:F:68:GLN:O	36:F:71:ILE:HG22	2.10	0.50
41:K:49:SER:HB3	41:K:68:ARG:HD3	1.92	0.50
42:L:113:ARG:NH2	42:L:120:ARG:HA	2.27	0.50
53:A:1082:A:H2'	53:A:1083:U:O4'	2.12	0.50
53:A:1252:A:H2'	53:A:1253:G:O4'	2.11	0.50
54:01:732:C:H2'	54:01:733:G:O4'	2.11	0.50
54:01:992:C:H2'	54:01:993:G:C8	2.46	0.50
54:01:1159:U:H2'	54:01:1160:G:C8	2.46	0.50
54:01:2755:C:O5'	54:01:2755:C:H6	1.94	0.50
1:04:140:VAL:HG12	1:04:191:LEU:HA	1.93	0.50
25:28:23:LEU:HD11	25:28:53:MET:SD	2.51	0.50
29:32:10:LEU:O	29:32:14:ARG:HG2	2.12	0.50
32:B:93:HIS:ND1	32:B:145:ASN:HB2	2.26	0.50
54:01:879:G:H2'	54:01:880:G:H8	1.76	0.50
1:04:224:MET:HG2	54:01:782:A:C2	2.47	0.50
7:10:56:ARG:HD2	54:01:1106:G:O2'	2.12	0.50
8:11:4:VAL:HA	8:11:7:TYR:CE1	2.47	0.50
24:27:18:LEU:HG	24:27:22:LEU:HD13	1.94	0.50
52:03:221:GLY:N	54:01:2176:A:H5"	2.26	0.50
53:A:1128:C:H2'	53:A:1129:C:O4'	2.11	0.50
53:A:1205:U:H2'	53:A:1206:G:C8	2.45	0.50
54:01:355:U:H2'	54:01:356:G:H8	1.76	0.50
54:01:1822:C:H2'	54:01:1823:G:H8	1.77	0.50
54:01:1909:C:H2'	54:01:1910:G:C8	2.47	0.50
54:01:2875:C:H2'	54:01:2876:G:C8	2.47	0.50
1:04:94:LEU:HD13	1:04:100:ARG:HG2	1.92	0.50
3:06:145:ASP:HA	3:06:166:LYS:HB3	1.94	0.50
8:11:130:GLY:HA2	8:11:133:ARG:NH1	2.27	0.50
9:12:31:GLU:OE2	9:12:34:ARG:HD3	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:18:24:THR:HB	15:18:87:ARG:H	1.76	0.50
33:C:5:HIS:HB3	44:N:88:MET:CE	2.42	0.50
34:D:1:ALA:HA	34:D:67:LEU:HD11	1.94	0.50
37:G:65:LEU:HA	37:G:68:VAL:HG22	1.93	0.50
49:S:71:GLY:HA3	53:A:1320:C:O2	2.12	0.50
51:U:9:GLU:HB2	51:U:10:PRO:HD3	1.94	0.50
53:A:1207:G:H2'	53:A:1208:C:O4'	2.12	0.50
54:01:594:U:H2'	54:01:595:C:C6	2.47	0.50
54:01:940:G:C3'	54:01:941:A:H5"	2.42	0.50
54:01:971:G:H2'	54:01:972:A:O4'	2.12	0.50
54:01:1872:A:H2'	54:01:1873:G:O4'	2.11	0.50
54:01:2196:C:O2'	54:01:2197:U:H5'	2.11	0.50
54:01:2372:U:H2'	54:01:2373:G:H8	1.76	0.50
59:Z:68:GLU:HG2	59:Z:76:TYR:O	2.12	0.50
3:06:52:VAL:HG13	54:01:452:G:OP1	2.12	0.50
10:13:48:PRO:HG2	10:13:49:ARG:HD2	1.93	0.50
10:13:122:VAL:OXT	10:13:122:VAL:HG12	2.11	0.50
18:21:28:LYS:HB2	18:21:31:GLN:OE1	2.11	0.50
51:U:49:ALA:O	51:U:53:LYS:HG3	2.12	0.50
53:A:48:C:H5'	53:A:49:U:OP2	2.11	0.50
53:A:986:U:H2'	53:A:987:G:C8	2.47	0.50
53:A:1005:A:H2'	53:A:1006:G:O4'	2.12	0.50
53:A:1305:G:H22	53:A:1331:G:H2'	1.76	0.50
54:01:1300:G:H4'	54:01:1301:A:C5'	2.41	0.50
54:01:2623:G:H2'	54:01:2624:G:H8	1.76	0.50
58:Y:56:C:H2'	58:Y:57:G:H8	1.76	0.50
59:Z:5:PHE:CD1	59:Z:263:LYS:HD2	2.46	0.50
59:Z:375:ALA:HA	59:Z:385:ALA:HA	1.93	0.50
11:14:30:THR:O	11:14:33:ARG:HG2	2.11	0.50
15:18:26:GLU:HB3	15:18:84:SER:OG	2.12	0.50
20:23:39:ASN:HB3	20:23:62:ALA:HB3	1.94	0.50
21:24:53:LYS:HB3	21:24:55:GLU:OE1	2.11	0.50
27:30:40:HIS:HA	27:30:48:TYR:OH	2.12	0.50
39:I:129:ARG:HG2	39:I:129:ARG:HH11	1.77	0.50
53:A:410:G:H2'	53:A:429:U:O4	2.11	0.50
54:01:915:C:H3'	54:01:916:G:C8	2.47	0.50
54:01:1857:G:N2	54:01:1884:G:H2'	2.27	0.50
54:01:2515:C:H2'	54:01:2516:A:C8	2.47	0.50
59:Z:24:LYS:HG2	59:Z:104:VAL:HB	1.93	0.50
1:04:252:LYS:HB2	1:04:252:LYS:NZ	2.27	0.49
3:06:68:ALA:HA	54:01:1255:U:C5	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:26:GLY:HA3	54:01:1140:C:H5'	1.93	0.49
16:19:32:ARG:HG2	54:01:1252:G:N2	2.27	0.49
22:25:28:LEU:HA	22:25:60:ASP:OD1	2.12	0.49
22:25:55:LEU:HD12	22:25:76:ILE:HD12	1.93	0.49
32:B:99:MET:HA	32:B:106:VAL:HG21	1.93	0.49
35:E:119:VAL:CG1	35:E:122:VAL:HG22	2.39	0.49
38:H:100:ILE:HD12	38:H:100:ILE:O	2.12	0.49
40:J:65:TYR:OH	44:N:84:ARG:HG3	2.12	0.49
41:K:81:LEU:HD12	41:K:81:LEU:O	2.12	0.49
41:K:86:LYS:NZ	41:K:114:PRO:HD3	2.27	0.49
54:01:257:C:H2'	54:01:258:G:O4'	2.12	0.49
54:01:872:U:H2'	54:01:873:C:C6	2.47	0.49
54:01:1278:C:H2'	54:01:1279:G:C8	2.47	0.49
54:01:1434:A:H2'	54:01:1435:G:C8	2.47	0.49
54:01:1636:U:H2'	54:01:1637:A:H8	1.75	0.49
54:01:1709:U:H2'	54:01:1710:G:H8	1.77	0.49
1:04:66:PHE:HB3	1:04:150:GLY:O	2.12	0.49
3:06:46:GLN:CB	3:06:83:VAL:HG11	2.42	0.49
5:08:29:ASN:HB2	5:08:78:VAL:HA	1.94	0.49
6:09:84:ALA:HA	6:09:91:PHE:H	1.76	0.49
52:03:28:ALA:O	52:03:32:GLU:HG3	2.12	0.49
52:03:41:SER:HA	52:03:177:LYS:HA	1.94	0.49
52:03:50:ILE:HG12	52:03:165:ASN:HD21	1.77	0.49
53:A:212:G:H2'	53:A:213:G:C8	2.46	0.49
53:A:1301:U:O2	53:A:1301:U:H2'	2.11	0.49
53:A:1342:C:H2'	53:A:1343:G:C8	2.46	0.49
54:01:171:U:H2'	54:01:172:A:C8	2.47	0.49
54:01:492:A:H2'	54:01:493:G:O4'	2.12	0.49
54:01:669:G:H2'	54:01:669:G:N3	2.27	0.49
54:01:1527:G:H21	54:01:1545:A:H62	1.60	0.49
54:01:2247:A:H2'	54:01:2248:C:C6	2.47	0.49
54:01:2514:U:H2'	54:01:2515:C:C6	2.47	0.49
54:01:2771:C:H2'	54:01:2772:C:C6	2.47	0.49
54:01:2788:C:H2'	54:01:2789:C:C6	2.47	0.49
32:B:53:LEU:HA	32:B:56:LEU:HB2	1.94	0.49
42:L:31:GLY:HA3	42:L:54:VAL:CG1	2.43	0.49
42:L:51:VAL:HG22	42:L:52:CYS:N	2.27	0.49
45:O:19:ASN:OD1	53:A:750:C:H5'	2.12	0.49
46:P:51:ARG:C	46:P:52:LEU:HD12	2.32	0.49
54:01:553:G:H2'	54:01:554:U:O4'	2.11	0.49
54:01:2804:U:H2'	54:01:2805:C:C6	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:65:U:H3'	55:02:108:A:N6	2.26	0.49
2:05:61:THR:OG1	2:05:64:GLU:HG3	2.13	0.49
9:12:89:PHE:O	9:12:93:ILE:HG12	2.12	0.49
34:D:75:TYR:HA	34:D:89:LEU:HD13	1.94	0.49
41:K:85:VAL:HG21	51:U:16:ARG:HH22	1.77	0.49
54:01:1370:C:H2'	54:01:1371:G:O4'	2.13	0.49
54:01:1810:A:H2'	54:01:1811:G:O4'	2.12	0.49
54:01:2186:G:H2'	54:01:2187:U:O4'	2.12	0.49
54:01:2556:C:H2'	54:01:2557:G:O4'	2.11	0.49
54:01:2705:A:H2'	54:01:2706:A:O4'	2.12	0.49
55:02:53:A:H2'	55:02:53:A:N3	2.27	0.49
59:Z:84:HIS:HB3	59:Z:87:TYR:HD2	1.77	0.49
2:05:121:THR:HG21	2:05:143:PRO:HB3	1.93	0.49
13:16:43:GLU:OE2	13:16:46:ARG:HD3	2.13	0.49
17:20:24:LYS:HA	17:20:94:THR:OG1	2.12	0.49
50:T:20:ASN:HD21	50:T:65:LEU:HD11	1.78	0.49
53:A:476:U:H2'	53:A:477:C:C6	2.48	0.49
53:A:1254:A:H2'	53:A:1255:G:C8	2.47	0.49
53:A:1395:C:H6	53:A:1395:C:H5'	1.77	0.49
54:01:1463:C:H2'	54:01:1464:G:C8	2.48	0.49
54:01:2704:C:H2'	54:01:2705:A:O4'	2.13	0.49
59:Z:85:ALA:O	59:Z:88:VAL:HG23	2.12	0.49
3:06:189:THR:O	3:06:193:VAL:HG23	2.12	0.49
9:12:36:LEU:HD11	9:12:122:LEU:HD13	1.95	0.49
12:15:42:THR:OG1	12:15:45:GLN:HG3	2.13	0.49
23:26:19:HIS:HB3	54:01:2080:A:OP1	2.13	0.49
30:33:28:LEU:HD12	30:33:32:LEU:HD22	1.94	0.49
31:34:23:ILE:HD13	54:01:1032:A:H1'	1.93	0.49
32:B:46:VAL:HB	32:B:47:PRO:HD3	1.95	0.49
32:B:96:LEU:H	32:B:99:MET:CE	2.26	0.49
33:C:76:ILE:HA	33:C:83:VAL:HG23	1.94	0.49
42:L:49:ARG:HH22	53:A:522:C:N4	2.11	0.49
49:S:38:THR:HG22	49:S:69:LYS:HG2	1.94	0.49
53:A:181:A:N6	53:A:194:C:H2'	2.27	0.49
54:01:581:C:H2'	54:01:582:A:H8	1.77	0.49
54:01:601:C:H2'	54:01:602:A:O4'	2.13	0.49
54:01:644:A:H2'	54:01:645:C:C4'	2.43	0.49
54:01:660:C:H2'	54:01:661:A:H8	1.77	0.49
54:01:905:A:O2'	54:01:906:U:H5'	2.12	0.49
54:01:915:C:H3'	54:01:916:G:H8	1.76	0.49
54:01:1780:A:O2'	54:01:1781:U:H2'	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1857:G:H2'	54:01:1884:G:N2	2.27	0.49
54:01:1932:A:H2'	54:01:1933:G:O4'	2.12	0.49
54:01:2515:C:H2'	54:01:2516:A:H8	1.78	0.49
54:01:2637:U:H2'	54:01:2638:G:O4'	2.12	0.49
54:01:2760:C:O2'	54:01:2761:A:H5'	2.12	0.49
3:06:63:LYS:HD2	54:01:2444:G:OP2	2.13	0.49
4:07:7:TYR:O	4:07:12:VAL:HG23	2.12	0.49
24:27:9:LYS:HD3	24:27:10:SER:N	2.27	0.49
47:Q:60:ILE:CG2	47:Q:72:TRP:HB3	2.43	0.49
53:A:1202:U:H2'	53:A:1203:C:O4'	2.13	0.49
54:01:18:U:H2'	54:01:19:A:C8	2.48	0.49
54:01:873:C:H2'	54:01:874:G:C8	2.48	0.49
54:01:1474:U:H2'	54:01:1475:G:H5'	1.93	0.49
55:02:29:A:H2'	55:02:30:C:O4'	2.12	0.49
58:Y:64:A:H1'	59:Z:378:GLU:OE2	2.12	0.49
6:09:6:LEU:HD21	6:09:51:ARG:HH11	1.78	0.49
8:11:33:ASN:HB2	8:11:64:ARG:HH22	1.77	0.49
9:12:93:ILE:CD1	9:12:100:VAL:HG21	2.43	0.49
12:15:61:GLY:HA2	12:15:107:GLY:HA3	1.95	0.49
21:24:80:HIS:ND1	21:24:81:PRO:HD2	2.28	0.49
35:E:113:VAL:HG13	35:E:114:LEU:HD12	1.94	0.49
53:A:1342:C:H2'	53:A:1343:G:H8	1.77	0.49
54:01:687:C:H2'	54:01:688:U:O4'	2.13	0.49
54:01:879:G:H2'	54:01:880:G:C8	2.47	0.49
54:01:1078:U:H4'	54:01:1079:C:H5"	1.95	0.49
54:01:1082:U:H3	54:01:1086:A:H61	1.59	0.49
54:01:1683:U:H2'	54:01:1684:G:C8	2.48	0.49
54:01:2039:U:H2'	54:01:2040:G:C8	2.47	0.49
54:01:2507:C:H2'	54:01:2508:G:H8	1.78	0.49
59:Z:11:HIS:HA	59:Z:75:HIS:HB3	1.95	0.49
5:08:118:ALA:O	5:08:120:ILE:HG12	2.12	0.49
15:18:99:LEU:O	15:18:99:LEU:HD23	2.12	0.49
17:20:37:GLU:O	17:20:39:LEU:HD12	2.13	0.49
23:26:6:VAL:HG23	23:26:50:VAL:HG12	1.95	0.49
44:N:37:ASP:OD1	44:N:39:ASP:HB3	2.13	0.49
53:A:831:A:H2'	53:A:832:G:O4'	2.13	0.49
54:01:1077:A:C2'	54:01:1078:U:H5'	2.40	0.49
54:01:2364:C:H2'	54:01:2365:G:O4'	2.13	0.49
59:Z:366:ILE:HG13	59:Z:367:ALA:H	1.77	0.49
7:10:26:VAL:HB	7:10:82:ILE:HG23	1.94	0.49
14:17:106:LEU:O	14:17:106:LEU:HD23	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:I:46:VAL:HA	39:I:49:GLN:HG3	1.95	0.49
39:I:111:GLU:HB3	39:I:114:LYS:NZ	2.27	0.49
40:J:91:ASP:O	40:J:92:LEU:CB	2.60	0.49
41:K:125:LYS:HD2	53:A:797:C:OP1	2.13	0.49
52:03:7:ARG:NE	54:01:2128:G:H4'	2.28	0.49
52:03:23:ILE:HG23	52:03:189:LEU:HD23	1.95	0.49
53:A:350:G:H2'	53:A:351:G:C8	2.48	0.49
53:A:1308:U:H2'	53:A:1309:G:H8	1.77	0.49
54:01:1367:A:H2'	54:01:1368:G:H5'	1.94	0.49
54:01:2074:U:H2'	54:01:2075:U:C6	2.48	0.49
54:01:2158:A:H4'	54:01:2159:G:O4'	2.13	0.49
54:01:2898:U:H2'	54:01:2899:A:C8	2.48	0.49
59:Z:97:GLN:NE2	59:Z:229:GLY:HA2	2.27	0.49
59:Z:326:TYR:O	59:Z:341:ILE:HG12	2.13	0.49
3:06:88:ARG:HB3	3:06:89:PRO:HD2	1.95	0.48
3:06:149:ILE:CG2	3:06:188:MET:HG2	2.43	0.48
16:19:74:SER:HB2	54:01:1011:G:OP1	2.13	0.48
21:24:30:ILE:HG13	21:24:40:ILE:HG13	1.95	0.48
33:C:5:HIS:HB3	44:N:88:MET:HE3	1.95	0.48
35:E:119:VAL:HG12	35:E:121:ASN:H	1.78	0.48
42:L:63:THR:HG23	42:L:92:VAL:HA	1.95	0.48
46:P:12:LYS:HD2	53:A:393:A:OP2	2.13	0.48
46:P:70:ARG:HH11	53:A:452:A:H1'	1.77	0.48
52:03:161:VAL:HB	52:03:173:THR:OG1	2.13	0.48
53:A:149:A:H1'	53:A:1446:A:H2	1.78	0.48
53:A:524:G:H2'	53:A:525:C:C6	2.48	0.48
53:A:932:C:H2'	53:A:933:G:C8	2.48	0.48
54:01:1709:U:H2'	54:01:1710:G:C8	2.47	0.48
54:01:1869:G:H3'	54:01:1870:C:C5'	2.43	0.48
1:04:120:ASP:HB2	6:09:91:PHE:HZ	1.78	0.48
16:19:90:ASP:OD2	16:19:92:LYS:HB3	2.13	0.48
18:21:14:ALA:HB2	18:21:78:GLU:HB3	1.96	0.48
24:27:26:PHE:O	24:27:29:ARG:HD3	2.13	0.48
25:28:40:THR:OG1	25:28:41:PRO:HD2	2.13	0.48
38:H:106:SER:HA	53:A:642:A:C8	2.48	0.48
40:J:22:THR:O	40:J:26:VAL:HG23	2.13	0.48
47:Q:17:GLU:OE2	53:A:255:G:H1'	2.13	0.48
54:01:296:U:H2'	54:01:297:G:H8	1.78	0.48
54:01:767:U:H2'	54:01:768:G:H8	1.78	0.48
54:01:2141:G:H2'	54:01:2142:A:H8	1.77	0.48
54:01:2195:U:H2'	54:01:2196:C:H6	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:91:MET:HE3	59:Z:118:HIS:HA	1.95	0.48
1:04:149:LYS:HD3	54:01:2204:G:H4'	1.95	0.48
4:07:131:VAL:HG22	4:07:151:LEU:O	2.14	0.48
9:12:52:ASP:O	9:12:54:ILE:HG13	2.13	0.48
9:12:113:PRO:HD2	54:01:558:U:P	2.53	0.48
16:19:79:ILE:HG21	16:19:91:ARG:NH2	2.28	0.48
49:S:35:ARG:NH2	49:S:52:ASN:HA	2.28	0.48
53:A:757:U:H2'	53:A:758:C:O4'	2.13	0.48
53:A:1432:G:H1'	53:A:1468:A:N6	2.28	0.48
54:01:1947:C:H2'	54:01:1948:G:H8	1.78	0.48
5:08:37:ASN:HB3	5:08:40:VAL:HG23	1.94	0.48
5:08:140:ILE:HD12	5:08:141:GLY:N	2.28	0.48
29:32:24:THR:HG23	29:32:27:GLY:H	1.76	0.48
32:B:153:MET:CE	32:B:157:PRO:HG3	2.43	0.48
33:C:1:GLY:HA3	53:A:1060:U:H5	1.78	0.48
39:I:114:LYS:HE3	53:A:1187:G:H5'	1.94	0.48
41:K:87:GLY:H	41:K:113:THR:HG22	1.77	0.48
49:S:38:THR:HA	49:S:69:LYS:HA	1.95	0.48
53:A:195:A:H2'	53:A:196:A:C8	2.48	0.48
53:A:1097:C:H2'	53:A:1098:C:C6	2.48	0.48
8:11:126:ARG:HE	54:01:1081:U:P	2.37	0.48
13:16:28:LEU:HD23	13:16:48:VAL:HG11	1.96	0.48
18:21:66:ILE:H	18:21:66:ILE:CD1	2.20	0.48
39:I:119:LYS:HE3	53:A:1350:A:OP2	2.13	0.48
54:01:253:C:H2'	54:01:254:G:O4'	2.14	0.48
54:01:441:U:O2'	54:01:442:G:H5'	2.12	0.48
54:01:2199:A:H2'	54:01:2200:C:O4'	2.12	0.48
2:05:186:LEU:HD21	15:18:3:ILE:HG21	1.96	0.48
4:07:65:LEU:HD22	55:02:42:C:C5	2.48	0.48
4:07:140:ILE:HD12	4:07:140:ILE:N	2.29	0.48
6:09:50:ARG:O	6:09:55:GLU:HG3	2.13	0.48
6:09:76:GLU:HA	6:09:142:VAL:HG13	1.95	0.48
13:16:90:ARG:HB2	13:16:90:ARG:NH1	2.28	0.48
24:27:9:LYS:HD3	24:27:11:VAL:N	2.27	0.48
29:32:3:ARG:HB3	54:01:1612:C:O2'	2.13	0.48
47:Q:29:LYS:HB2	47:Q:36:PHE:CE1	2.48	0.48
52:03:75:VAL:HG21	52:03:153:VAL:HG13	1.95	0.48
53:A:151:A:H2'	53:A:152:A:O4'	2.14	0.48
53:A:545:C:O2'	53:A:549:C:H5"	2.13	0.48
53:A:909:A:H2'	53:A:910:C:O4'	2.14	0.48
54:01:799:G:H3'	54:01:800:A:C8	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1906:G:C3'	54:01:1907:G:H5"	2.44	0.48
54:01:2024:G:H2'	54:01:2025:C:O4'	2.14	0.48
2:05:121:THR:HB	2:05:127:PHE:CD2	2.48	0.48
9:12:27:ARG:HH21	54:01:1142:A:H4'	1.79	0.48
40:J:50:THR:HG23	40:J:64:GLN:HG2	1.95	0.48
42:L:30:ARG:HB3	53:A:363:A:OP2	2.14	0.48
45:O:22:GLY:HA3	53:A:750:C:O2	2.13	0.48
52:03:180:PHE:HD2	52:03:185:LEU:HD21	1.76	0.48
53:A:312:C:H2'	53:A:313:A:H8	1.77	0.48
53:A:691:G:H2'	53:A:692:U:C6	2.49	0.48
54:01:225:C:H2'	54:01:226:A:O4'	2.14	0.48
54:01:1825:U:H2'	54:01:1826:G:H8	1.79	0.48
54:01:2710:C:H2'	54:01:2711:A:C8	2.48	0.48
59:Z:181:ASP:O	59:Z:185:GLU:HB3	2.13	0.48
59:Z:243:GLU:CG	59:Z:295:PRO:HA	2.43	0.48
59:Z:327:ARG:NH2	59:Z:363:ILE:HG21	2.29	0.48
1:04:48:ILE:O	1:04:48:ILE:HG23	2.13	0.48
11:14:68:SER:HB2	54:01:632:A:H5"	1.95	0.48
12:15:76:LYS:HD3	12:15:77:PRO:HD2	1.96	0.48
14:17:26:LEU:HD13	14:17:39:VAL:HG22	1.95	0.48
15:18:31:VAL:HG22	15:18:32:VAL:N	2.29	0.48
32:B:98:GLY:O	32:B:102:ASN:HB3	2.12	0.48
40:J:59:LYS:HE2	40:J:62:ARG:NH2	2.29	0.48
40:J:91:ASP:CG	40:J:92:LEU:H	2.17	0.48
42:L:11:ARG:HD2	53:A:562:U:H1'	1.96	0.48
46:P:36:VAL:O	46:P:36:VAL:HG13	2.14	0.48
48:R:33:THR:HG22	48:R:37:LYS:H	1.79	0.48
53:A:359:G:H2'	53:A:360:G:O4'	2.13	0.48
53:A:948:C:H2'	53:A:949:A:C8	2.49	0.48
53:A:1033:G:C3'	53:A:1034:G:H5"	2.40	0.48
54:01:1506:U:H2'	54:01:1507:C:C6	2.49	0.48
54:01:2047:C:H2'	54:01:2048:G:C8	2.48	0.48
54:01:2243:U:H2'	54:01:2244:U:C6	2.49	0.48
54:01:2264:C:H2'	54:01:2265:U:O4'	2.14	0.48
55:02:63:C:H2'	55:02:64:G:C8	2.49	0.48
59:Z:102:ILE:HG23	59:Z:131:ILE:O	2.13	0.48
59:Z:299:LYS:NZ	59:Z:301:HIS:HA	2.28	0.48
59:Z:326:TYR:HB3	59:Z:341:ILE:CG1	2.44	0.48
1:04:144:GLU:HA	1:04:151:GLY:HA2	1.95	0.48
3:06:48:THR:O	3:06:52:VAL:HG23	2.14	0.48
13:16:101:GLY:H	27:30:41:HIS:HD2	1.62	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:24:75:GLN:HB2	21:24:92:VAL:HG23	1.96	0.48
32:B:102:ASN:O	32:B:105:THR:HG22	2.13	0.48
34:D:124:VAL:HG23	34:D:141:VAL:O	2.14	0.48
42:L:113:ARG:HH22	42:L:120:ARG:HA	1.78	0.48
53:A:492:C:H2'	53:A:493:A:C8	2.48	0.48
53:A:1368:A:O2'	53:A:1369:C:H5'	2.13	0.48
54:01:158:U:H2'	54:01:159:G:O4'	2.13	0.48
54:01:181:A:H2'	54:01:182:A:C8	2.49	0.48
54:01:2848:G:O2'	54:01:2849:U:H5'	2.13	0.48
59:Z:19:HIS:HB3	59:Z:22:HIS:CE1	2.49	0.48
59:Z:173:SER:HB3	59:Z:184:TRP:CD2	2.49	0.48
3:06:47:LYS:O	3:06:83:VAL:HB	2.14	0.48
9:12:35:ARG:HA	9:12:40:HIS:HD2	1.78	0.48
13:16:118:ARG:NH1	27:30:55:ALA:HB3	2.28	0.48
15:18:52:ARG:H	15:18:56:SER:HB3	1.79	0.48
22:25:40:LYS:HE3	54:01:2330:G:O2'	2.13	0.48
36:F:71:ILE:HD11	36:F:89:VAL:HG21	1.95	0.48
52:03:29:LEU:HD23	52:03:222:VAL:HG13	1.96	0.48
54:01:226:A:H2'	54:01:227:A:O4'	2.13	0.48
54:01:323:C:H2'	54:01:1205:A:N1	2.29	0.48
54:01:1900:A:H1'	54:01:1970:A:H2'	1.94	0.48
54:01:2281:A:O2'	54:01:2282:G:H5'	2.14	0.48
59:Z:55:GLU:HA	59:Z:60:ILE:HG13	1.96	0.48
13:16:96:ARG:NH1	13:16:116:VAL:HG13	2.29	0.47
18:21:24:ILE:HD11	18:21:74:ILE:HD13	1.94	0.47
20:23:32:LYS:HB3	20:23:63:ALA:HB1	1.96	0.47
31:34:25:VAL:HG21	31:34:35:GLN:HE21	1.79	0.47
35:E:54:GLU:HB3	35:E:57:ALA:HB3	1.96	0.47
36:F:93:LYS:O	36:F:94:HIS:HB2	2.14	0.47
41:K:92:ARG:HE	51:U:24:LYS:NZ	2.12	0.47
42:L:114:SER:CB	53:A:35:G:H21	2.27	0.47
52:03:24:ASN:OD1	52:03:27:ILE:HD11	2.14	0.47
53:A:78:A:H2'	53:A:79:G:O4'	2.13	0.47
53:A:202:G:H21	53:A:466:A:H61	1.62	0.47
53:A:494:G:H2'	53:A:496:A:H8	1.79	0.47
53:A:539:A:H2'	53:A:540:G:C8	2.48	0.47
53:A:831:A:C3'	53:A:832:G:H5"	2.43	0.47
54:01:286:U:H2'	54:01:287:G:H8	1.76	0.47
54:01:1020:A:H1'	54:01:1021:A:OP2	2.14	0.47
54:01:2507:C:H2'	54:01:2508:G:C8	2.49	0.47
59:Z:217:VAL:HB	59:Z:283:ARG:NH1	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:297:THR:HG23	59:Z:298:ILE:CD1	2.41	0.47
5:08:41:GLU:HA	5:08:54:ARG:HH21	1.79	0.47
18:21:29:VAL:HG23	18:21:69:LEU:O	2.14	0.47
24:27:7:ARG:HD3	24:27:7:ARG:H	1.79	0.47
32:B:53:LEU:HD22	32:B:219:THR:HG21	1.97	0.47
46:P:46:LYS:HE2	46:P:48:GLU:O	2.14	0.47
51:U:35:GLU:O	51:U:36:PHE:HB2	2.14	0.47
53:A:770:C:H2'	53:A:771:G:C8	2.49	0.47
54:01:1681:G:N3	54:01:1762:A:H2'	2.29	0.47
54:01:1893:C:H2'	54:01:1894:C:H5'	1.96	0.47
56:X:4:G:H2'	56:X:5:G:C8	2.49	0.47
56:X:71:C:H2'	56:X:72:A:C8	2.48	0.47
3:06:77:ILE:HG13	3:06:78:TRP:HD1	1.78	0.47
19:22:40:LYS:HA	19:22:43:ILE:HD12	1.95	0.47
20:23:93:ARG:CB	20:23:102:ILE:HD12	2.45	0.47
34:D:62:ARG:HG3	34:D:62:ARG:HH11	1.79	0.47
34:D:131:ILE:HD12	34:D:131:ILE:N	2.29	0.47
34:D:186:GLU:HB3	34:D:189:ASP:OD2	2.14	0.47
38:H:105:THR:HB	38:H:120:LEU:HD11	1.96	0.47
45:O:71:ARG:HG2	45:O:71:ARG:HH11	1.79	0.47
53:A:81:A:H2	53:A:88:U:H3	1.63	0.47
53:A:271:C:H2'	53:A:272:C:C6	2.49	0.47
53:A:621:A:H2'	53:A:622:A:C8	2.50	0.47
54:01:45:G:H5"	54:01:46:G:C5'	2.23	0.47
54:01:392:U:H2'	54:01:393:C:C6	2.48	0.47
54:01:1053:C:C3'	54:01:1054:A:H5"	2.44	0.47
54:01:2151:U:H2'	54:01:2152:G:C8	2.50	0.47
58:Y:25:C:H2'	58:Y:26:A:O4'	2.14	0.47
59:Z:5:PHE:HD1	59:Z:263:LYS:HD2	1.78	0.47
59:Z:34:VAL:HG21	59:Z:188:ILE:HB	1.96	0.47
2:05:12:THR:HG21	15:18:4:ILE:HG23	1.97	0.47
2:05:159:LYS:HE2	54:01:2512:C:O2'	2.13	0.47
5:08:138:GLN:HE22	54:01:2746:U:H1'	1.80	0.47
7:10:112:ALA:HB1	7:10:123:ILE:HD12	1.95	0.47
12:15:71:LYS:HE3	12:15:73:ILE:HD11	1.96	0.47
37:G:71:THR:O	37:G:90:VAL:HG12	2.15	0.47
38:H:11:THR:HA	38:H:14:ARG:HH12	1.79	0.47
45:O:31:LEU:O	45:O:35:ILE:HG13	2.14	0.47
52:03:218:MET:HG2	54:01:2174:C:O2	2.14	0.47
53:A:106:C:H2'	53:A:107:G:C8	2.49	0.47
53:A:838:G:H2'	53:A:839:C:O4'	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:215:G:C4'	54:01:216:A:H4'	2.43	0.47
54:01:2411:A:H2'	54:01:2412:A:C8	2.49	0.47
54:01:2557:G:H2'	54:01:2558:C:C6	2.49	0.47
3:06:23:PHE:HB2	3:06:114:ARG:HH22	1.80	0.47
3:06:79:ARG:NH2	54:01:471:A:H5"	2.29	0.47
7:10:3:LEU:HB3	54:01:1044:C:OP2	2.14	0.47
8:11:56:VAL:HG21	8:11:68:PHE:HB2	1.96	0.47
33:C:67:ILE:CD1	33:C:100:ILE:HD11	2.45	0.47
36:F:32:ALA:HB1	36:F:70:VAL:HG21	1.95	0.47
36:F:64:VAL:CG2	36:F:65:GLU:N	2.78	0.47
39:I:104:THR:HG22	39:I:106:ASP:H	1.79	0.47
52:03:70:GLY:HA3	52:03:177:LYS:HG2	1.96	0.47
54:01:394:C:H2'	54:01:395:U:O4'	2.14	0.47
54:01:1859:U:H2'	54:01:1860:G:H8	1.79	0.47
54:01:2472:G:H2'	54:01:2475:C:H42	1.80	0.47
54:01:2743:U:C3'	54:01:2744:G:H5"	2.45	0.47
59:Z:299:LYS:HZ2	59:Z:301:HIS:HA	1.79	0.47
5:08:163:TYR:HB2	5:08:166:GLU:HB2	1.95	0.47
7:10:25:ALA:HB3	7:10:99:PHE:CD2	2.50	0.47
8:11:72:THR:HG23	8:11:73:PRO:HD2	1.96	0.47
9:12:41:LYS:HG2	9:12:43:GLU:OE1	2.14	0.47
39:I:83:THR:HG21	39:I:102:PHE:HB3	1.96	0.47
40:J:36:VAL:HG22	40:J:38:GLY:H	1.78	0.47
40:J:52:LEU:HB2	44:N:80:ARG:HD2	1.96	0.47
49:S:35:ARG:HD2	53:A:1221:G:OP1	2.15	0.47
53:A:950:U:H2'	53:A:951:G:C8	2.50	0.47
53:A:1500:A:H5"	53:A:1508:A:H5"	1.96	0.47
54:01:2105:U:H2'	54:01:2106:U:O4'	2.14	0.47
54:01:2533:U:H2'	54:01:2534:A:O4'	2.14	0.47
55:02:1:U:H2'	55:02:2:G:C8	2.50	0.47
2:05:33:ARG:HD2	2:05:33:ARG:N	2.23	0.47
2:05:108:ASP:OD2	2:05:206:ALA:HA	2.13	0.47
4:07:29:ARG:CZ	4:07:158:THR:HG21	2.44	0.47
4:07:70:ARG:NH2	4:07:71:LYS:HG2	2.30	0.47
4:07:174:PHE:HA	4:07:175:PRO:HD2	1.70	0.47
5:08:86:LEU:HG	5:08:163:TYR:HA	1.97	0.47
6:09:47:PHE:HD1	6:09:51:ARG:HD2	1.80	0.47
20:23:95:PHE:O	20:23:99:SER:HA	2.14	0.47
21:24:21:ARG:HA	21:24:25:LYS:O	2.14	0.47
27:30:3:GLN:HA	54:01:2615:U:C2	2.49	0.47
32:B:91:VAL:HG11	32:B:95:TRP:HD1	1.80	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:137:THR:O	32:B:141:GLU:HG3	2.14	0.47
33:C:13:ILE:N	33:C:13:ILE:HD12	2.30	0.47
34:D:96:ARG:HG2	34:D:96:ARG:HH11	1.78	0.47
36:F:3:HIS:H	36:F:92:THR:CG2	2.14	0.47
39:I:29:ILE:HG12	39:I:30:ASN:OD1	2.15	0.47
42:L:113:ARG:HH22	42:L:120:ARG:HG3	1.79	0.47
43:M:13:HIS:NE2	53:A:1296:C:H5'	2.28	0.47
45:O:87:ARG:HG3	45:O:88:ARG:H	1.80	0.47
50:T:28:ARG:HH12	53:A:1437:A:H5"	1.80	0.47
52:03:131:LEU:HA	52:03:134:ARG:HB2	1.97	0.47
53:A:189:A:H2'	53:A:190:A:O4'	2.14	0.47
53:A:371:A:H2'	53:A:372:C:O4'	2.14	0.47
54:01:20:C:H2'	54:01:21:A:C8	2.50	0.47
54:01:65:U:H2'	54:01:66:C:C6	2.49	0.47
54:01:437:U:H2'	54:01:438:G:C8	2.50	0.47
54:01:729:G:H4'	54:01:763:G:C5'	2.44	0.47
54:01:755:U:H2'	54:01:756:A:C8	2.49	0.47
54:01:1657:U:H2'	54:01:1658:C:C6	2.50	0.47
54:01:1748:C:H2'	54:01:1749:A:C8	2.50	0.47
54:01:2137:U:H2'	54:01:2138:G:H8	1.78	0.47
54:01:2291:U:H2'	54:01:2292:U:C6	2.49	0.47
54:01:2853:C:H2'	54:01:2854:G:C8	2.49	0.47
59:Z:148:LEU:O	59:Z:152:GLU:HG3	2.15	0.47
59:Z:231:VAL:CG1	59:Z:270:ALA:HA	2.45	0.47
59:Z:261:PHE:O	59:Z:262:ARG:HB2	2.15	0.47
1:04:59:GLN:HA	54:01:1568:G:H5'	1.97	0.47
2:05:110:THR:HG23	2:05:171:THR:OG1	2.15	0.47
3:06:44:ARG:HD2	54:01:444:C:OP2	2.15	0.47
8:11:119:ALA:HB2	54:01:1082:U:C5'	2.43	0.47
24:27:2:LYS:HE2	54:01:102:U:H1'	1.96	0.47
30:33:11:LYS:HB2	30:33:11:LYS:NZ	2.30	0.47
34:D:169:TRP:CG	34:D:185:PRO:HG3	2.50	0.47
35:E:14:LEU:HA	35:E:36:THR:HG22	1.96	0.47
35:E:22:LYS:HB3	35:E:29:ILE:CG2	2.44	0.47
35:E:56:PRO:O	35:E:59:ILE:HG13	2.15	0.47
37:G:65:LEU:HD23	37:G:69:ARG:HH21	1.80	0.47
44:N:41:TRP:HA	44:N:44:VAL:HG22	1.95	0.47
54:01:1468:U:H2'	54:01:1522:A:H61	1.78	0.47
54:01:1856:U:H2'	54:01:1857:G:O4'	2.14	0.47
54:01:2065:C:H2'	54:01:2066:C:C6	2.50	0.47
7:10:3:LEU:HD12	7:10:5:LEU:HG	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:117:ALA:HA	9:12:120:ARG:NH2	2.29	0.47
13:16:103:ARG:NH1	54:01:1287:A:H5'	2.29	0.47
21:24:4:ILE:HB	21:24:63:ILE:HG12	1.97	0.47
22:25:12:SER:HB3	54:01:2262:U:C5	2.45	0.47
36:F:93:LYS:O	36:F:94:HIS:CB	2.63	0.47
49:S:46:LEU:O	49:S:61:VAL:HG23	2.15	0.47
53:A:575:G:O2'	53:A:821:G:H5'	2.14	0.47
53:A:1354:U:H2'	53:A:1355:G:H8	1.80	0.47
54:01:337:C:H2'	54:01:338:G:O4'	2.15	0.47
54:01:1065:U:H5'	54:01:1066:U:OP2	2.14	0.47
54:01:2785:C:H2'	54:01:2786:U:C6	2.49	0.47
55:02:10:G:H2'	55:02:11:C:O4'	2.14	0.47
56:X:31:G:H2'	56:X:32:C:H5'	1.97	0.47
59:Z:11:HIS:HB3	59:Z:204:ARG:HH12	1.78	0.47
59:Z:189:LEU:O	59:Z:189:LEU:HD23	2.15	0.47
2:05:14:ILE:HG23	15:18:11:GLN:NE2	2.28	0.47
7:10:27:VAL:O	7:10:82:ILE:HA	2.15	0.47
8:11:78:LEU:HD21	8:11:108:ILE:HD13	1.97	0.47
8:11:130:GLY:HA2	8:11:133:ARG:HH12	1.80	0.47
21:24:47:VAL:O	21:24:51:GLN:HG2	2.15	0.47
26:29:56:ARG:HH12	49:S:68:HIS:CE1	2.33	0.47
32:B:33:ALA:HB3	32:B:37:VAL:HG13	1.97	0.47
44:N:47:LEU:HD21	53:A:1317:C:H4'	1.96	0.47
47:Q:46:HIS:CB	47:Q:70:LYS:HD3	2.36	0.47
54:01:12:U:O2	54:01:2626:C:H4'	2.15	0.47
54:01:760:G:H2'	54:01:761:A:O4'	2.14	0.47
54:01:1040:A:H2'	54:01:1041:G:H8	1.79	0.47
54:01:1139:G:O2'	54:01:1140:C:H5'	2.15	0.47
54:01:1857:G:H1'	54:01:1885:A:N6	2.29	0.47
59:Z:33:THR:HG21	59:Z:178:LEU:HA	1.97	0.47
2:05:56:LYS:HB2	2:05:56:LYS:NZ	2.31	0.46
7:10:54:VAL:HG22	7:10:83:ALA:HB1	1.96	0.46
19:22:21:SER:O	19:22:25:GLU:HG2	2.14	0.46
23:26:16:ASN:HB2	23:26:26:ARG:HB3	1.96	0.46
39:I:12:LYS:HG3	39:I:109:GLN:OE1	2.15	0.46
52:03:27:ILE:HG21	52:03:186:LYS:CB	2.43	0.46
53:A:123:U:H5"	53:A:311:C:O2'	2.15	0.46
53:A:477:C:H2'	53:A:478:A:C8	2.49	0.46
53:A:1462:C:H2'	53:A:1463:U:C6	2.50	0.46
53:A:1513:A:H2'	53:A:1514:G:H8	1.80	0.46
54:01:1103:A:H2'	54:01:1103:A:N3	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1169:A:H2'	54:01:1170:C:O4'	2.16	0.46
54:01:1752:C:H5"	54:01:2862:G:H5'	1.96	0.46
54:01:2487:G:H2'	54:01:2488:G:H8	1.79	0.46
2:05:125:TRP:CG	2:05:160:LYS:HB3	2.50	0.46
5:08:139:VAL:O	5:08:143:VAL:HG23	2.15	0.46
7:10:18:VAL:HA	7:10:86:MET:HE1	1.98	0.46
7:10:92:ALA:HB1	7:10:129:LEU:HB3	1.96	0.46
8:11:101:SER:HB3	8:11:104:GLN:OE1	2.14	0.46
28:31:47:ILE:HD12	28:31:47:ILE:H	1.80	0.46
32:B:208:ALA:HB1	32:B:212:TYR:CE2	2.51	0.46
34:D:143:SER:C	34:D:144:ILE:HD12	2.36	0.46
50:T:23:ARG:HH11	50:T:23:ARG:HG3	1.81	0.46
54:01:306:U:H2'	54:01:307:G:O4'	2.15	0.46
54:01:1468:U:H2'	54:01:1522:A:N6	2.31	0.46
54:01:2006:C:H5'	54:01:2049:G:OP1	2.15	0.46
54:01:2478:A:C2	54:01:2529:G:H2'	2.50	0.46
1:04:17:LYS:HD2	54:01:1565:C:H5"	1.98	0.46
4:07:99:PHE:O	4:07:103:ILE:HG12	2.15	0.46
7:10:33:VAL:HA	54:01:1055:G:H4'	1.97	0.46
26:29:66:ILE:O	26:29:66:ILE:HG12	2.15	0.46
28:31:5:ARG:NH1	28:31:25:ASN:HB2	2.31	0.46
36:F:64:VAL:CG2	36:F:65:GLU:H	2.28	0.46
44:N:15:LEU:CD2	44:N:54:SER:HB3	2.46	0.46
53:A:1273:C:H2'	53:A:1274:A:O4'	2.15	0.46
54:01:542:C:C2'	54:01:543:G:H5"	2.43	0.46
54:01:991:C:H5'	54:01:1185:G:H2'	1.97	0.46
59:Z:173:SER:HB3	59:Z:184:TRP:CG	2.51	0.46
2:05:48:ILE:HG23	2:05:84:LEU:HD21	1.97	0.46
7:10:29:ASP:N	7:10:81:LEU:HD22	2.30	0.46
10:13:105:ARG:HG2	10:13:122:VAL:HG13	1.98	0.46
12:15:75:GLU:HB3	12:15:90:GLU:HG3	1.98	0.46
13:16:79:LEU:HD23	13:16:83:LEU:HD12	1.98	0.46
19:22:50:LEU:HD23	24:27:26:PHE:CE2	2.51	0.46
25:28:40:THR:HG23	25:28:43:ILE:H	1.81	0.46
28:31:12:SER:HA	28:31:48:TYR:CD1	2.51	0.46
32:B:9:LEU:HD11	32:B:13:VAL:HG13	1.98	0.46
33:C:5:HIS:CG	44:N:88:MET:HB3	2.50	0.46
35:E:87:VAL:HA	35:E:91:SER:O	2.15	0.46
39:I:21:LYS:O	39:I:60:LEU:HB3	2.15	0.46
53:A:458:U:H2'	53:A:459:A:C8	2.51	0.46
53:A:490:C:H2'	53:A:491:G:C8	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1456:A:H2'	53:A:1457:G:O4'	2.15	0.46
54:01:300:A:H2'	54:01:334:C:H1'	1.97	0.46
54:01:853:C:H2'	54:01:854:C:C6	2.50	0.46
54:01:2841:C:H2'	54:01:2842:G:C8	2.51	0.46
1:04:146:LYS:HB2	1:04:149:LYS:HB2	1.97	0.46
7:10:23:LEU:HD13	7:10:118:ILE:HB	1.98	0.46
8:11:25:PRO:O	8:11:29:GLN:HB2	2.16	0.46
11:14:124:GLY:C	11:14:125:LEU:HD12	2.35	0.46
15:18:91:VAL:HG21	15:18:96:LEU:HD21	1.97	0.46
32:B:95:TRP:CZ2	32:B:171:ALA:HA	2.50	0.46
33:C:19:SER:HB2	44:N:91:GLU:O	2.14	0.46
34:D:103:ARG:HB3	34:D:170:LEU:HD21	1.98	0.46
37:G:42:VAL:O	37:G:46:LEU:HD13	2.16	0.46
40:J:70:HIS:C	40:J:71:LEU:HD12	2.36	0.46
43:M:3:ILE:H	43:M:7:ASN:HB3	1.80	0.46
54:01:745:G:O2'	54:01:748:G:H1'	2.16	0.46
54:01:1127:A:H2'	54:01:1128:G:H5"	1.97	0.46
54:01:1386:C:H2'	54:01:1387:A:H8	1.80	0.46
54:01:1869:G:H3'	54:01:1870:C:H5"	1.98	0.46
54:01:2102:G:H2'	54:01:2103:C:O4'	2.16	0.46
54:01:2121:G:H2'	54:01:2122:U:O4'	2.16	0.46
54:01:2504:U:C2'	54:01:2505:G:H5'	2.46	0.46
54:01:2508:G:H1	54:01:2580:U:H3	1.64	0.46
56:W:73:A:H5"	56:W:74:C:O4'	2.15	0.46
1:04:131:MET:HA	1:04:134:ILE:HD12	1.98	0.46
8:11:72:THR:HG21	8:11:112:LYS:HG2	1.98	0.46
9:12:99:ARG:O	9:12:103:ILE:HG13	2.15	0.46
13:16:22:ARG:HG3	13:16:70:THR:HA	1.97	0.46
20:23:91:LYS:NZ	54:01:82:U:H5'	2.31	0.46
23:26:55:MET:SD	54:01:2091:C:H4'	2.56	0.46
33:C:143:LEU:HD23	33:C:143:LEU:O	2.15	0.46
44:N:8:ARG:HB3	44:N:12:ARG:HH12	1.81	0.46
48:R:25:ILE:HG21	48:R:66:LEU:HB3	1.98	0.46
51:U:40:PRO:HA	51:U:43:GLU:HG2	1.98	0.46
53:A:1489:G:H2'	53:A:1490:U:C6	2.50	0.46
54:01:162:U:O2'	54:01:163:C:H5'	2.14	0.46
54:01:898:C:H2'	54:01:899:A:O4'	2.15	0.46
59:Z:11:HIS:HB2	59:Z:269:ARG:HH12	1.81	0.46
1:04:48:ILE:HD11	1:04:51:ARG:HA	1.97	0.46
2:05:56:LYS:HB2	2:05:56:LYS:HZ2	1.80	0.46
9:12:36:LEU:HG	9:12:54:ILE:HD12	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:15:45:GLN:HE21	54:01:2485:G:C5'	2.21	0.46
16:19:27:ARG:HB3	16:19:27:ARG:HH11	1.80	0.46
18:21:9:HIS:HE1	18:21:80:PRO:HG2	1.80	0.46
32:B:113:LEU:HD13	32:B:143:LEU:HG	1.98	0.46
34:D:10:LEU:HD22	34:D:62:ARG:CZ	2.46	0.46
35:E:156:ARG:NE	35:E:163:ILE:HG21	2.30	0.46
37:G:110:ARG:HH12	37:G:121:ASN:CB	2.28	0.46
52:03:50:ILE:CD1	52:03:165:ASN:HD21	2.29	0.46
53:A:381:C:H2'	53:A:382:A:O4'	2.15	0.46
53:A:513:C:H2'	53:A:514:C:C6	2.50	0.46
53:A:1119:C:H2'	53:A:1120:C:C6	2.50	0.46
54:01:198:C:O2'	54:01:199:A:H5'	2.16	0.46
54:01:576:U:H2'	54:01:577:G:H8	1.79	0.46
54:01:656:G:O2'	54:01:657:U:H5'	2.16	0.46
54:01:1105:U:C3'	54:01:1106:G:H5"	2.45	0.46
54:01:2123:G:H2'	54:01:2124:G:H8	1.81	0.46
3:06:76:PRO:HA	3:06:82:GLY:HA2	1.97	0.46
7:10:42:ARG:O	7:10:46:ARG:HG3	2.16	0.46
16:19:2:ARG:HD2	54:01:1248:G:C2	2.50	0.46
33:C:106:ARG:H	33:C:106:ARG:CD	2.23	0.46
34:D:197:HIS:HE1	35:E:104:ILE:H	1.64	0.46
38:H:9:MET:O	38:H:13:ILE:HG13	2.14	0.46
41:K:124:LYS:NZ	53:A:780:A:H5"	2.31	0.46
42:L:73:LEU:N	42:L:73:LEU:HD12	2.31	0.46
52:03:48:LEU:HD22	52:03:208:TYR:CE1	2.50	0.46
53:A:234:C:H2'	53:A:235:C:C6	2.50	0.46
53:A:434:U:H2'	53:A:435:A:H8	1.80	0.46
53:A:664:G:H22	53:A:741:G:H1	1.64	0.46
54:01:815:C:H2'	54:01:816:C:C6	2.50	0.46
54:01:1133:A:H4'	54:01:1134:A:H5"	1.98	0.46
54:01:1179:G:C5	54:01:1180:U:H1'	2.51	0.46
54:01:1430:G:H2'	54:01:1431:A:O4'	2.16	0.46
54:01:1443:U:H2'	54:01:1444:G:C8	2.50	0.46
54:01:1790:C:H2'	54:01:1791:A:N7	2.30	0.46
56:W:6:G:O2'	56:W:7:G:H5'	2.16	0.46
1:04:221:GLY:H	54:01:1826:G:P	2.39	0.46
19:22:44:LYS:O	19:22:48:GLN:HG2	2.15	0.46
20:23:90:LYS:NZ	54:01:100:U:H2'	2.31	0.46
21:24:9:ARG:HD3	21:24:39:ALA:HB1	1.97	0.46
31:34:19:ARG:HD2	31:34:24:ARG:HD2	1.98	0.46
39:I:70:GLY:O	39:I:74:GLN:HG3	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:34:ALA:O	40:J:35:GLN:HB3	2.16	0.46
47:Q:58:VAL:HG22	47:Q:59:GLU:N	2.30	0.46
50:T:70:LYS:HA	50:T:73:ARG:NH1	2.31	0.46
52:03:133:PRO:O	54:01:2169:A:H4'	2.15	0.46
53:A:56:U:H2'	53:A:57:G:C8	2.50	0.46
53:A:373:A:H61	53:A:391:G:H1'	1.81	0.46
53:A:1499:A:H2'	53:A:1500:A:H8	1.80	0.46
54:01:29:U:H2'	54:01:30:G:C8	2.50	0.46
54:01:2818:U:H2'	54:01:2819:G:H8	1.80	0.46
59:Z:212:LEU:HA	59:Z:213:PRO:HD3	1.74	0.46
59:Z:377:ARG:HD2	59:Z:378:GLU:N	2.31	0.46
3:06:149:ILE:HG21	3:06:188:MET:HG2	1.98	0.46
6:09:116:ARG:CG	6:09:133:GLN:HG3	2.40	0.46
12:15:41:LEU:HA	12:15:45:GLN:OE1	2.16	0.46
33:C:10:ARG:HA	33:C:13:ILE:HD13	1.98	0.46
53:A:861:G:H2'	53:A:862:C:C6	2.51	0.46
53:A:1460:C:H2'	53:A:1461:G:C8	2.50	0.46
54:01:118:A:N3	54:01:178:G:H1'	2.30	0.46
54:01:197:A:H2'	54:01:198:C:O4'	2.16	0.46
54:01:1127:A:C2'	54:01:1128:G:H5"	2.46	0.46
54:01:2066:C:O2'	54:01:2067:G:H5'	2.16	0.46
54:01:2259:U:H2'	54:01:2260:C:C6	2.51	0.46
59:Z:97:GLN:HB3	59:Z:273:ASN:ND2	2.31	0.46
59:Z:303:LYS:HE3	59:Z:342:GLU:OE1	2.16	0.46
3:06:77:ILE:HG13	3:06:78:TRP:CD1	2.52	0.45
5:08:154:GLU:HB3	5:08:159:LYS:H	1.80	0.45
5:08:174:LYS:HG3	54:01:2529:G:H4'	1.98	0.45
9:12:84:ILE:HG23	9:12:84:ILE:O	2.16	0.45
16:19:86:SER:HB3	17:20:50:GLY:O	2.16	0.45
18:21:57:ASN:HD21	54:01:495:G:H1'	1.81	0.45
28:31:36:LYS:HG3	28:31:47:ILE:HG13	1.99	0.45
32:B:42:LEU:O	32:B:46:VAL:HG23	2.17	0.45
34:D:82:LYS:HE2	53:A:2:A:H4'	1.98	0.45
35:E:84:VAL:CG2	35:E:145:ASN:HD22	2.28	0.45
35:E:161:GLU:HA	35:E:164:LEU:HD11	1.98	0.45
44:N:63:CYS:HB3	44:N:67:GLY:H	1.80	0.45
45:O:61:GLN:O	45:O:65:LEU:HG	2.16	0.45
53:A:1071:C:H2'	53:A:1072:G:H8	1.81	0.45
53:A:1130:A:H2'	53:A:1131:G:O4'	2.16	0.45
53:A:1219:A:H2'	53:A:1220:G:H8	1.80	0.45
53:A:1271:A:H5'	53:A:1314:C:H5"	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:693:A:H2'	54:01:694:U:O4'	2.17	0.45
54:01:1386:C:H2'	54:01:1387:A:C8	2.51	0.45
54:01:1434:A:H2'	54:01:1435:G:H8	1.81	0.45
54:01:1482:G:H1'	54:01:1509:A:C2	2.51	0.45
54:01:2853:C:H2'	54:01:2854:G:H8	1.80	0.45
59:Z:304:PHE:CE2	59:Z:388:VAL:HG22	2.51	0.45
2:05:114:LYS:HG2	2:05:196:ALA:HB2	1.98	0.45
18:21:31:GLN:O	18:21:35:ILE:HG13	2.15	0.45
20:23:73:ASN:O	20:23:74:ALA:HB3	2.16	0.45
42:L:47:ALA:HB3	42:L:49:ARG:HE	1.80	0.45
53:A:90:C:H2'	53:A:91:U:C5	2.50	0.45
54:01:20:C:H2'	54:01:21:A:H8	1.81	0.45
54:01:616:A:H2'	54:01:617:G:O4'	2.16	0.45
54:01:861:A:H2'	54:01:862:G:O4'	2.15	0.45
54:01:1111:A:H2'	54:01:1111:A:N3	2.31	0.45
54:01:1773:A:C2'	54:01:1774:C:H5'	2.46	0.45
54:01:2475:C:C2'	54:01:2476:A:H5'	2.46	0.45
54:01:2579:C:O2'	54:01:2580:U:H5'	2.16	0.45
54:01:2584:U:H2'	54:01:2585:U:H2'	1.98	0.45
1:04:51:ARG:HB2	1:04:52:HIS:ND1	2.31	0.45
6:09:67:ALA:HA	6:09:138:VAL:HG11	1.98	0.45
7:10:11:ILE:O	7:10:15:VAL:HG23	2.16	0.45
27:30:39:ARG:HD3	54:01:2886:A:N1	2.31	0.45
33:C:36:PHE:CE2	44:N:65:GLN:HG2	2.51	0.45
35:E:40:ASP:OD1	35:E:44:ARG:HB2	2.16	0.45
38:H:80:PRO:HG2	53:A:878:A:H5"	1.98	0.45
53:A:70:U:H4'	53:A:71:A:H8	1.80	0.45
53:A:552:U:H2'	53:A:553:A:C8	2.50	0.45
53:A:695:A:H2	53:A:787:A:HO2'	1.63	0.45
53:A:1235:U:O2'	53:A:1305:G:H5'	2.15	0.45
53:A:1434:A:H2'	53:A:1435:G:O4'	2.15	0.45
54:01:718:A:H2'	54:01:719:C:O4'	2.16	0.45
54:01:2193:G:H2'	54:01:2194:U:C6	2.52	0.45
54:01:2469:A:H2'	54:01:2470:G:O4'	2.17	0.45
58:Y:56:C:H2'	58:Y:57:G:C8	2.51	0.45
7:10:67:THR:HG23	7:10:74:ASP:HB2	1.98	0.45
19:22:62:VAL:HG22	19:22:81:LYS:HE2	1.98	0.45
35:E:156:ARG:HG2	38:H:42:GLU:O	2.17	0.45
37:G:12:LEU:HD12	37:G:13:PRO:HD2	1.98	0.45
38:H:49:LYS:NZ	38:H:49:LYS:HB2	2.31	0.45
38:H:63:LYS:NZ	38:H:63:LYS:HB3	2.32	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:51:VAL:HG22	42:L:52:CYS:H	1.82	0.45
47:Q:6:THR:C	47:Q:7:LEU:HD12	2.36	0.45
52:03:181:ASP:HB2	52:03:184:LYS:HG2	1.98	0.45
53:A:224:U:H2'	53:A:225:C:C6	2.52	0.45
53:A:250:A:H4'	53:A:251:G:O5'	2.17	0.45
53:A:629:A:H2'	53:A:630:A:O4'	2.17	0.45
53:A:1397:C:H2'	57:V:22:A:N6	2.31	0.45
54:01:189:G:H2'	54:01:205:G:N2	2.31	0.45
54:01:828:U:H2'	54:01:829:A:C8	2.52	0.45
54:01:1326:U:H2'	54:01:1327:A:C8	2.45	0.45
54:01:1937:A:O2'	54:01:1938:A:H3'	2.16	0.45
54:01:2480:C:H2'	54:01:2481:G:O4'	2.16	0.45
54:01:2538:C:H2'	54:01:2539:C:C6	2.51	0.45
59:Z:154:ARG:HG2	59:Z:164:GLY:O	2.17	0.45
1:04:12:ARG:HA	1:04:15:VAL:CG2	2.47	0.45
1:04:42:ARG:HE	1:04:48:ILE:HB	1.82	0.45
4:07:78:ILE:O	4:07:78:ILE:HG13	2.17	0.45
10:13:14:SER:OG	10:13:86:LEU:HD12	2.17	0.45
11:14:79:LEU:CD1	11:14:112:LEU:HA	2.47	0.45
18:21:6:LYS:HG3	54:01:494:G:H4'	1.99	0.45
19:22:56:GLU:HB2	19:22:86:THR:OG1	2.16	0.45
46:P:33:ILE:N	46:P:33:ILE:HD12	2.32	0.45
53:A:597:G:H2'	53:A:598:U:H5'	1.98	0.45
54:01:893:C:H2'	54:01:894:U:O4'	2.16	0.45
54:01:1246:A:H2'	54:01:1247:A:O4'	2.16	0.45
54:01:2298:A:H2'	54:01:2299:U:O4'	2.17	0.45
1:04:22:GLU:HB3	1:04:80:LEU:HD12	1.99	0.45
1:04:41:GLY:O	1:04:49:THR:N	2.49	0.45
1:04:174:ARG:HG2	1:04:174:ARG:HH11	1.81	0.45
4:07:3:LEU:HA	4:07:6:TYR:HB3	1.98	0.45
7:10:43:LYS:NZ	7:10:43:LYS:HB3	2.31	0.45
8:11:14:ALA:HB1	8:11:45:THR:OG1	2.16	0.45
12:15:34:LYS:HD3	21:24:82:TYR:HA	1.99	0.45
12:15:62:LYS:HD3	12:15:64:TRP:CZ2	2.52	0.45
18:21:9:HIS:CE1	18:21:80:PRO:HG2	2.52	0.45
24:27:20:ASN:O	24:27:24:GLU:HB2	2.16	0.45
24:27:26:PHE:HA	24:27:29:ARG:NE	2.32	0.45
27:30:8:THR:CG2	54:01:2020:A:H5'	2.47	0.45
36:F:73:GLU:O	36:F:77:THR:HG23	2.15	0.45
42:L:41:PRO:HD2	42:L:47:ALA:H	1.82	0.45
48:R:25:ILE:HA	48:R:28:LEU:HB3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S:9:PHE:CD2	53:A:1318:A:H4'	2.52	0.45
50:T:66:ILE:HG21	50:T:71:ALA:HB2	1.99	0.45
53:A:1492:A:H2'	54:01:1913:A:H2	1.82	0.45
54:01:128:C:H2'	54:01:129:C:C6	2.51	0.45
55:02:30:C:C2'	55:02:31:C:H5'	2.46	0.45
56:X:59:A:C2'	56:X:60:U:H5'	2.46	0.45
59:Z:236:ILE:HA	59:Z:240:GLU:OE1	2.16	0.45
2:05:98:VAL:O	2:05:98:VAL:HG22	2.17	0.45
3:06:15:SER:HB2	3:06:18:THR:HB	1.99	0.45
4:07:98:PHE:HD1	4:07:101:ARG:HH11	1.63	0.45
7:10:96:PHE:HE2	7:10:126:LEU:HB2	1.82	0.45
9:12:47:HIS:ND1	9:12:48:VAL:HG23	2.31	0.45
19:22:15:HIS:HE1	19:22:17:SER:HB3	1.82	0.45
26:29:2:LYS:HB2	26:29:5:ILE:HD11	1.98	0.45
26:29:11:GLU:HA	26:29:25:ARG:HA	1.98	0.45
29:32:12:ARG:HH11	29:32:44:VAL:HG21	1.80	0.45
33:C:39:ARG:HH21	33:C:56:ILE:HG12	1.81	0.45
34:D:71:PHE:HE1	34:D:93:LEU:HD11	1.82	0.45
52:03:84:ALA:HA	52:03:95:VAL:HG11	1.97	0.45
53:A:337:G:H2'	53:A:338:A:C8	2.51	0.45
53:A:1251:A:H2'	53:A:1252:A:C8	2.51	0.45
54:01:146:A:H2'	54:01:147:C:C6	2.52	0.45
54:01:582:A:H2'	54:01:583:G:H8	1.80	0.45
54:01:1796:U:H2'	54:01:1797:G:C8	2.51	0.45
54:01:2097:A:H2'	54:01:2098:U:O4'	2.16	0.45
59:Z:95:ALA:HB1	59:Z:125:VAL:HG11	1.99	0.45
5:08:83:THR:HG23	5:08:133:LYS:HG2	1.98	0.45
34:D:29:THR:O	34:D:29:THR:HG22	2.17	0.45
34:D:50:TYR:CD2	53:A:508:U:H4'	2.51	0.45
35:E:43:GLY:O	35:E:73:VAL:N	2.47	0.45
36:F:72:ASP:O	36:F:76:THR:HG23	2.17	0.45
38:H:10:LEU:HD22	38:H:74:ILE:CD1	2.46	0.45
42:L:41:PRO:HG3	42:L:49:ARG:HG2	1.99	0.45
47:Q:59:GLU:HB3	47:Q:75:VAL:HB	1.99	0.45
53:A:460:A:H2'	53:A:461:A:C8	2.52	0.45
53:A:684:U:H2'	53:A:685:G:O4'	2.17	0.45
53:A:871:U:H5"	53:A:872:A:OP2	2.16	0.45
54:01:367:G:H2'	54:01:368:A:O4'	2.16	0.45
54:01:2377:A:H2'	54:01:2378:A:C8	2.52	0.45
59:Z:176:LYS:HB3	59:Z:181:ASP:HB2	1.99	0.45
59:Z:247:ILE:HG12	59:Z:364:HIS:HB3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:310:ILE:HG21	59:Z:350:VAL:CG1	2.47	0.45
7:10:67:THR:CG2	7:10:74:ASP:HB2	2.46	0.45
15:18:52:ARG:HB3	15:18:55:HIS:HB2	1.99	0.45
20:23:93:ARG:HB2	20:23:102:ILE:HD12	1.99	0.45
21:24:60:VAL:HG11	21:24:71:LYS:HE3	1.99	0.45
31:34:22:VAL:O	31:34:24:ARG:HG3	2.16	0.45
34:D:158:LEU:HD23	34:D:158:LEU:O	2.17	0.45
43:M:3:ILE:HG12	43:M:7:ASN:OD1	2.16	0.45
43:M:76:ILE:O	43:M:80:MET:HE2	2.17	0.45
46:P:23:ASP:HB3	46:P:26:ASN:OD1	2.17	0.45
51:U:11:PHE:CG	51:U:12:ASP:N	2.85	0.45
51:U:65:ARG:HA	51:U:65:ARG:NE	2.32	0.45
52:03:175:ILE:HD12	52:03:185:LEU:HB3	1.99	0.45
53:A:285:C:H2'	53:A:286:C:C6	2.51	0.45
53:A:881:G:H2'	53:A:882:C:O4'	2.16	0.45
53:A:1148:U:H2'	53:A:1149:C:O4'	2.17	0.45
53:A:1258:G:H2'	53:A:1259:C:C6	2.51	0.45
53:A:1436:U:H2'	53:A:1437:A:H8	1.82	0.45
54:01:63:A:H2'	54:01:64:A:H8	1.81	0.45
54:01:195:A:H2'	54:01:198:C:N4	2.31	0.45
54:01:2806:C:H42	54:01:2892:G:H1	1.64	0.45
2:05:202:ILE:N	2:05:202:ILE:HD12	2.32	0.45
4:07:7:TYR:HA	4:07:11:VAL:CG2	2.46	0.45
4:07:15:LEU:HD11	4:07:168:LEU:HA	1.98	0.45
4:07:24:VAL:O	4:07:27:VAL:HG12	2.17	0.45
4:07:138:PRO:HB3	26:29:32:LEU:HD11	1.99	0.45
9:12:35:ARG:HA	9:12:40:HIS:CD2	2.51	0.45
11:14:70:LYS:HD3	54:01:633:A:H5"	1.99	0.45
12:15:58:LYS:HA	12:15:58:LYS:HD3	1.79	0.45
16:19:82:LEU:HA	16:19:85:ALA:HB3	1.98	0.45
20:23:9:GLU:OE2	20:23:21:ARG:HG2	2.17	0.45
35:E:160:VAL:HG13	35:E:161:GLU:N	2.27	0.45
37:G:56:SER:HB3	37:G:59:GLU:HG2	1.99	0.45
39:I:24:ASN:ND2	39:I:26:LYS:HE3	2.32	0.45
40:J:35:GLN:HG2	40:J:77:VAL:HB	1.99	0.45
41:K:118:ASN:OD1	53:A:718:A:H5'	2.16	0.45
44:N:20:PHE:O	44:N:21:ALA:CB	2.65	0.45
51:U:39:LYS:N	51:U:40:PRO:CD	2.80	0.45
53:A:1522:U:H2'	53:A:1523:G:H8	1.81	0.45
54:01:184:C:H2'	54:01:185:G:C8	2.51	0.45
54:01:213:A:H2'	54:01:214:G:C8	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1900:A:O4'	54:01:1970:A:H5"	2.17	0.45
54:01:2145:C:H3'	54:01:2146:C:H5'	1.99	0.45
1:04:129:LEU:N	1:04:129:LEU:HD23	2.33	0.44
4:07:147:ARG:HG3	4:07:148:VAL:N	2.32	0.44
34:D:59:LYS:O	34:D:63:ILE:HG13	2.17	0.44
52:03:181:ASP:HB2	52:03:184:LYS:CG	2.47	0.44
54:01:172:A:H2'	54:01:173:A:C8	2.51	0.44
54:01:720:U:H2'	54:01:721:A:C8	2.52	0.44
54:01:1346:G:H2'	54:01:1347:A:H8	1.82	0.44
54:01:2137:U:H2'	54:01:2138:G:C8	2.51	0.44
54:01:2553:G:H1'	54:01:2582:G:H21	1.82	0.44
54:01:2799:A:C2'	54:01:2800:A:H5'	2.47	0.44
54:01:2875:C:H2'	54:01:2876:G:H8	1.82	0.44
59:Z:14:VAL:HG21	59:Z:69:TYR:OH	2.16	0.44
1:04:257:ARG:HE	1:04:266:ILE:CD1	2.28	0.44
9:12:37:ARG:HH22	9:12:110:PRO:HG3	1.83	0.44
10:13:48:PRO:HB3	53:A:1422:G:C5'	2.44	0.44
15:18:62:LYS:HE2	15:18:64:SER:HB3	1.99	0.44
37:G:25:PHE:HD1	37:G:100:MET:HB3	1.82	0.44
52:03:144:THR:HG23	52:03:162:ARG:HD3	2.00	0.44
53:A:1492:A:H2'	54:01:1913:A:C2	2.53	0.44
54:01:281:C:H2'	54:01:282:A:H8	1.82	0.44
54:01:1083:U:H2'	54:01:1085:A:OP2	2.17	0.44
54:01:1440:U:H2'	54:01:1441:G:C8	2.52	0.44
1:04:89:ASN:OD1	1:04:196:ASN:HB2	2.16	0.44
7:10:51:TYR:HA	7:10:53:ARG:NH1	2.32	0.44
8:11:10:LEU:HD21	54:01:1061:U:H5"	1.99	0.44
12:15:78:LEU:HD23	12:15:79:ALA:N	2.32	0.44
13:16:61:ALA:O	13:16:65:LEU:HD13	2.18	0.44
21:24:45:ASP:O	21:24:48:MET:HB3	2.16	0.44
38:H:28:SER:HB3	38:H:56:PRO:HB2	1.99	0.44
39:I:26:LYS:C	39:I:27:ILE:HD12	2.38	0.44
51:U:34:ARG:HD2	51:U:36:PHE:CZ	2.53	0.44
52:03:96:GLY:HA3	52:03:104:ILE:HD11	1.99	0.44
53:A:128:G:H2'	53:A:129:A:C8	2.53	0.44
54:01:297:G:H2'	54:01:298:G:O4'	2.18	0.44
54:01:974:G:H1'	54:01:975:A:C8	2.53	0.44
54:01:1908:C:O2	56:W:12:G:H4'	2.17	0.44
59:Z:377:ARG:HA	59:Z:382:THR:HA	1.99	0.44
17:20:16:GLU:HB2	17:20:101:ILE:HG12	1.99	0.44
31:34:36:ARG:CG	31:34:37:GLN:H	2.13	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:F:3:HIS:HB2	36:F:92:THR:HA	1.98	0.44
39:I:82:ILE:O	39:I:86:LEU:HG	2.16	0.44
51:U:36:PHE:C	51:U:38:GLU:H	2.19	0.44
52:03:5:THR:O	52:03:9:ARG:N	2.48	0.44
53:A:994:A:C8	53:A:1216:A:H4'	2.53	0.44
53:A:1254:A:H2'	53:A:1255:G:H8	1.80	0.44
54:01:279:A:H2'	54:01:280:U:H5'	1.98	0.44
54:01:677:A:O2'	54:01:2071:A:H5'	2.17	0.44
54:01:878:A:H3'	54:01:879:G:H8	1.83	0.44
54:01:2847:U:H2'	54:01:2848:G:O4'	2.17	0.44
55:02:65:U:H3'	55:02:108:A:H61	1.83	0.44
59:Z:117:GLU:HA	59:Z:120:LEU:CG	2.40	0.44
26:29:46:GLY:HA2	26:29:49:ARG:HG2	2.00	0.44
40:J:59:LYS:HD3	53:A:973:G:OP1	2.17	0.44
43:M:6:ILE:O	43:M:8:ILE:HG13	2.16	0.44
50:T:23:ARG:O	50:T:26:MET:HG2	2.17	0.44
53:A:674:G:H2'	53:A:675:A:C8	2.52	0.44
53:A:916:U:H2'	53:A:917:G:H8	1.82	0.44
53:A:946:A:H2'	53:A:947:G:C8	2.52	0.44
53:A:1040:U:H2'	53:A:1041:G:C8	2.52	0.44
53:A:1088:G:N2	53:A:1167:A:H61	2.12	0.44
53:A:1261:A:H3'	53:A:1262:C:H6	1.83	0.44
53:A:1354:U:H2'	53:A:1355:G:C8	2.52	0.44
53:A:1464:U:H2'	53:A:1465:A:C8	2.52	0.44
54:01:1689:A:H2'	54:01:1690:A:C8	2.52	0.44
54:01:1744:A:H3'	54:01:1745:A:H8	1.83	0.44
54:01:1947:C:H2'	54:01:1948:G:C8	2.52	0.44
54:01:2028:U:H2'	54:01:2029:G:C8	2.53	0.44
54:01:2730:C:H2'	54:01:2731:G:H8	1.82	0.44
59:Z:131:ILE:HD11	59:Z:198:TYR:HB3	2.00	0.44
59:Z:170:VAL:HG13	59:Z:190:GLU:HB2	2.00	0.44
59:Z:211:LEU:HB3	59:Z:233:ARG:HG2	1.99	0.44
7:10:3:LEU:CD1	7:10:5:LEU:HG	2.47	0.44
9:12:113:PRO:O	9:12:117:ALA:N	2.50	0.44
10:13:49:ARG:NH2	53:A:1423:G:H5'	2.33	0.44
14:17:110:ALA:O	14:17:115:LEU:HB3	2.17	0.44
20:23:84:PHE:HB2	54:01:297:G:H5"	1.99	0.44
29:32:44:VAL:HG13	29:32:44:VAL:O	2.17	0.44
33:C:156:LEU:HD12	33:C:156:LEU:O	2.18	0.44
36:F:92:THR:C	36:F:94:HIS:H	2.21	0.44
41:K:126:ARG:HA	41:K:126:ARG:NE	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:41:PRO:HB3	42:L:88:ASP:OD1	2.17	0.44
43:M:76:ILE:O	43:M:80:MET:HG3	2.17	0.44
46:P:38:PHE:CE1	46:P:51:ARG:HB2	2.52	0.44
49:S:79:TYR:CZ	53:A:1226:C:H4'	2.52	0.44
53:A:736:C:H2'	53:A:737:C:C6	2.52	0.44
53:A:1236:A:H4'	53:A:1304:G:H4'	2.00	0.44
54:01:186:G:H2'	54:01:187:G:H8	1.83	0.44
54:01:217:A:H2'	54:01:218:A:O4'	2.18	0.44
54:01:1300:G:H4'	54:01:1301:A:H5"	1.99	0.44
54:01:2259:U:H2'	54:01:2260:C:H6	1.83	0.44
56:X:8:U:H5'	56:X:49:G:OP2	2.18	0.44
59:Z:259:GLU:OE1	59:Z:262:ARG:HA	2.17	0.44
2:05:3:GLY:C	2:05:4:LEU:HD12	2.36	0.44
4:07:3:LEU:HD12	4:07:96:TRP:HE3	1.83	0.44
8:11:39:LYS:HE2	8:11:39:LYS:HA	1.99	0.44
8:11:79:LEU:HD12	8:11:135:MET:HG3	1.99	0.44
8:11:139:VAL:HG13	8:11:139:VAL:O	2.18	0.44
22:25:17:LEU:HD21	22:25:37:ARG:NH2	2.33	0.44
22:25:22:PHE:HD2	54:01:922:C:H1'	1.82	0.44
34:D:113:ALA:O	34:D:117:VAL:HG23	2.18	0.44
36:F:39:LEU:HD23	36:F:62:MET:HA	1.99	0.44
53:A:32:A:H2'	53:A:33:A:C8	2.53	0.44
53:A:219:U:H2'	53:A:220:G:H8	1.83	0.44
53:A:1057:G:H2'	53:A:1058:G:O4'	2.17	0.44
54:01:66:C:H2'	54:01:67:U:H6	1.81	0.44
54:01:310:A:H2'	54:01:311:A:H5"	1.98	0.44
54:01:310:A:O2'	54:01:311:A:H5"	2.18	0.44
54:01:395:U:H2'	54:01:396:G:C8	2.53	0.44
54:01:665:U:H2'	54:01:666:A:C8	2.52	0.44
54:01:665:U:H2'	54:01:666:A:H8	1.83	0.44
54:01:1536:C:H4'	54:01:1537:G:C2	2.52	0.44
54:01:1593:A:H2'	54:01:1594:U:C6	2.53	0.44
54:01:2111:U:N3	54:01:2147:A:H1'	2.32	0.44
54:01:2462:C:H2'	54:01:2463:C:C6	2.52	0.44
54:01:2581:G:H2'	54:01:2581:G:N3	2.33	0.44
55:02:49:C:H2'	55:02:50:A:H8	1.83	0.44
3:06:109:LEU:O	3:06:113:VAL:HG23	2.18	0.44
7:10:78:GLY:N	7:10:79:PRO:CD	2.81	0.44
17:20:54:VAL:HG12	17:20:55:ASP:N	2.33	0.44
22:25:16:ARG:HG3	54:01:2270:A:O2'	2.18	0.44
33:C:96:VAL:HB	33:C:97:PRO:HD2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:37:VAL:HG11	35:E:113:VAL:HG23	2.00	0.44
39:I:115:VAL:HG23	53:A:1367:C:H5"	1.99	0.44
40:J:9:ARG:HH12	40:J:11:LYS:HZ3	1.65	0.44
53:A:448:A:H3'	53:A:449:G:C8	2.53	0.44
53:A:714:G:H2'	53:A:715:A:C8	2.53	0.44
53:A:820:U:H3'	53:A:821:G:C5'	2.48	0.44
54:01:1019:U:H3	54:01:1142:A:H62	1.65	0.44
54:01:1344:U:H3'	54:01:1345:C:H5'	1.98	0.44
54:01:1664:A:H61	54:01:1996:C:H42	1.66	0.44
54:01:2159:G:H2'	54:01:2160:C:O4'	2.17	0.44
54:01:2756:U:H4'	54:01:2757:A:OP1	2.17	0.44
59:Z:212:LEU:HD12	59:Z:231:VAL:HG22	2.00	0.44
3:06:55:SER:HB2	54:01:797:G:OP1	2.17	0.44
16:19:93:ILE:HG13	17:20:11:GLN:HB3	1.99	0.44
23:26:13:THR:CG2	54:01:188:G:H5'	2.46	0.44
26:29:2:LYS:HB2	26:29:5:ILE:CD1	2.48	0.44
27:30:2:VAL:HG21	54:01:2057:G:H1'	1.99	0.44
32:B:96:LEU:N	32:B:99:MET:HE3	2.33	0.44
32:B:163:ILE:HD11	32:B:209:VAL:HG12	1.99	0.44
33:C:6:PRO:HD2	33:C:183:TYR:CD2	2.53	0.44
35:E:15:ILE:HD12	35:E:15:ILE:N	2.33	0.44
42:L:82:ARG:HD3	42:L:97:VAL:HG22	1.99	0.44
44:N:84:ARG:NH2	53:A:1059:C:H4'	2.23	0.44
49:S:48:ILE:HG13	49:S:59:VAL:HG23	2.00	0.44
51:U:49:ALA:O	51:U:52:VAL:HG12	2.18	0.44
52:03:194:VAL:HG12	52:03:198:LYS:HZ3	1.79	0.44
53:A:413:G:H2'	53:A:428:G:N2	2.32	0.44
53:A:1165:U:H2'	53:A:1166:G:O4'	2.18	0.44
54:01:239:C:H2'	54:01:240:C:O4'	2.17	0.44
54:01:856:G:H2'	54:01:857:G:C8	2.53	0.44
54:01:863:A:H2'	54:01:864:G:C8	2.53	0.44
54:01:2014:A:H2'	54:01:2015:A:C8	2.52	0.44
54:01:2055:C:H2'	54:01:2504:U:H5'	2.00	0.44
54:01:2586:U:H2'	54:01:2587:A:C8	2.52	0.44
54:01:2730:C:H2'	54:01:2731:G:C8	2.52	0.44
59:Z:129:TYR:CE2	59:Z:200:PRO:HD2	2.53	0.44
1:04:233:GLY:HA3	54:01:2598:A:H5"	1.99	0.43
5:08:26:LYS:CB	5:08:31:GLU:HG3	2.46	0.43
5:08:42:VAL:HG23	5:08:50:THR:O	2.17	0.43
6:09:47:PHE:HA	6:09:51:ARG:HB2	2.00	0.43
16:19:93:ILE:O	16:19:97:ILE:HG13	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:20:14:VAL:HG21	17:20:98:ILE:HG13	1.99	0.43
17:20:74:ILE:N	17:20:74:ILE:HD12	2.33	0.43
32:B:94:ARG:HH21	51:U:66:ARG:HH11	1.66	0.43
39:I:118:ARG:NH2	39:I:122:ARG:HG2	2.33	0.43
46:P:78:VAL:O	46:P:78:VAL:HG22	2.18	0.43
52:03:21:TYR:CD2	52:03:25:GLU:HG2	2.53	0.43
53:A:147:G:H2'	53:A:148:G:C8	2.53	0.43
53:A:618:C:H3'	53:A:620:C:OP2	2.18	0.43
53:A:1032:G:H21	53:A:1033:G:H4'	1.83	0.43
53:A:1177:G:H2'	53:A:1178:G:O4'	2.18	0.43
53:A:1488:G:O2'	53:A:1489:G:H5'	2.17	0.43
54:01:654:A:H3'	54:01:654:A:N3	2.33	0.43
59:Z:101:ALA:H	59:Z:127:VAL:HG11	1.81	0.43
59:Z:244:ILE:HD13	59:Z:251:GLN:HG3	1.99	0.43
1:04:23:LEU:HD21	1:04:89:ASN:ND2	2.33	0.43
1:04:153:LEU:HD11	1:04:181:ARG:HH22	1.83	0.43
7:10:8:LYS:HD3	54:01:1046:A:N1	2.34	0.43
9:12:41:LYS:HG2	9:12:43:GLU:CD	2.38	0.43
14:17:92:PHE:HB2	14:17:117:PHE:CD2	2.53	0.43
20:23:90:LYS:HZ1	54:01:100:U:H2'	1.81	0.43
36:F:5:GLU:O	36:F:7:VAL:HG23	2.18	0.43
38:H:50:VAL:HG22	38:H:50:VAL:O	2.17	0.43
46:P:26:ASN:ND2	46:P:31:ARG:HB3	2.33	0.43
47:Q:10:ARG:NH1	47:Q:55:GLY:HA2	2.32	0.43
52:03:57:GLN:HB3	52:03:201:PRO:HG2	1.99	0.43
53:A:1225:A:H2'	53:A:1225:A:N3	2.34	0.43
54:01:490:C:HO2'	54:01:491:G:P	2.41	0.43
54:01:848:C:H2'	54:01:849:A:C8	2.53	0.43
54:01:1097:U:H2'	54:01:1098:A:O4'	2.17	0.43
54:01:1199:U:H2'	54:01:1200:C:C6	2.52	0.43
54:01:2093:G:H2'	54:01:2094:A:H8	1.83	0.43
54:01:2236:U:H2'	54:01:2237:G:O4'	2.17	0.43
1:04:234:GLY:HA3	1:04:238:ASN:HB2	2.00	0.43
1:04:254:LYS:O	54:01:1797:G:H4'	2.18	0.43
4:07:28:PRO:HB2	4:07:168:LEU:HD22	2.00	0.43
10:13:36:GLY:HA2	10:13:62:VAL:O	2.18	0.43
10:13:93:GLN:HA	10:13:94:PRO:HD2	1.83	0.43
19:22:22:THR:HA	19:22:25:GLU:HG2	2.00	0.43
22:25:10:ARG:HH11	22:25:10:ARG:HG3	1.83	0.43
35:E:40:ASP:OD2	35:E:42:ASN:HB3	2.18	0.43
39:I:49:GLN:N	39:I:50:PRO:CD	2.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:I:113:LYS:HE2	39:I:118:ARG:O	2.17	0.43
50:T:34:VAL:HG11	50:T:78:LEU:HD21	1.99	0.43
52:03:180:PHE:HB2	52:03:185:LEU:HD11	2.00	0.43
53:A:452:A:H61	53:A:480:U:H3	1.66	0.43
53:A:631:C:H3'	53:A:632:U:H5'	1.99	0.43
53:A:767:A:H2'	53:A:768:A:O4'	2.19	0.43
53:A:955:U:H3	53:A:1225:A:H61	1.65	0.43
54:01:437:U:H2'	54:01:438:G:H8	1.82	0.43
54:01:635:C:H2'	54:01:636:G:C8	2.52	0.43
54:01:1772:A:H2'	54:01:1773:A:H4'	2.00	0.43
54:01:2207:C:H2'	54:01:2208:C:C6	2.54	0.43
54:01:2277:G:C3'	54:01:2278:A:H5"	2.48	0.43
54:01:2293:G:H2'	54:01:2294:G:C8	2.53	0.43
59:Z:321:PRO:HA	59:Z:350:VAL:O	2.17	0.43
1:04:131:MET:HE2	1:04:187:CYS:HB2	2.00	0.43
1:04:145:MET:SD	1:04:181:ARG:NH2	2.91	0.43
3:06:123:LYS:HA	3:06:189:THR:HG23	2.00	0.43
4:07:135:ILE:HG21	4:07:142:TYR:CD1	2.49	0.43
6:09:1:MET:N	6:09:21:VAL:O	2.43	0.43
6:09:72:ILE:HB	6:09:108:VAL:HG22	2.00	0.43
11:14:93:ASN:O	11:14:94:THR:HB	2.18	0.43
25:28:40:THR:CG2	25:28:43:ILE:HG12	2.48	0.43
25:28:56:VAL:HG22	25:28:57:GLU:N	2.33	0.43
26:29:59:ARG:O	26:29:63:ARG:HG3	2.18	0.43
28:31:14:ALA:HB2	28:31:46:VAL:HG13	2.00	0.43
36:F:66:ALA:HB1	36:F:67:PRO:HD2	2.00	0.43
43:M:7:ASN:ND2	43:M:9:PRO:HD3	2.34	0.43
46:P:13:LYS:HE3	53:A:392:C:H4'	2.00	0.43
46:P:20:VAL:CG2	46:P:21:VAL:N	2.81	0.43
48:R:34:GLU:HB3	51:U:18:PHE:HZ	1.84	0.43
50:T:28:ARG:O	50:T:32:LYS:HG2	2.18	0.43
52:03:60:ARG:HB2	52:03:141:LYS:CG	2.47	0.43
53:A:599:C:H2'	53:A:600:A:C8	2.52	0.43
53:A:1316:G:H2'	53:A:1317:C:H5"	1.99	0.43
54:01:1934:C:H2'	54:01:1935:G:O4'	2.18	0.43
54:01:2452:C:N4	54:01:2504:U:H3	2.12	0.43
54:01:2795:C:H2'	54:01:2796:U:O4'	2.18	0.43
59:Z:119:ILE:HG21	59:Z:157:LEU:HD23	2.01	0.43
3:06:149:ILE:HD12	3:06:170:ARG:O	2.18	0.43
4:07:109:ARG:HH11	43:M:2:ARG:NE	2.16	0.43
7:10:118:ILE:HD13	7:10:118:ILE:HA	1.90	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:13:61:VAL:HB	10:13:87:LEU:HD11	2.00	0.43
11:14:85:VAL:HG11	11:14:95:LEU:HD23	2.00	0.43
32:B:102:ASN:O	32:B:106:VAL:HG23	2.18	0.43
32:B:119:GLN:HG2	32:B:136:ARG:NH2	2.30	0.43
33:C:105:VAL:O	33:C:105:VAL:HG13	2.17	0.43
33:C:190:THR:HG21	33:C:195:ILE:HD12	2.01	0.43
39:I:70:GLY:HA3	53:A:1371:G:O3'	2.18	0.43
53:A:193:C:O2'	53:A:194:C:H5'	2.18	0.43
53:A:1490:U:H2'	53:A:1491:G:O4'	2.18	0.43
53:A:1516:G:H2'	53:A:1518:A:OP2	2.18	0.43
54:01:435:C:C2'	54:01:436:C:H5'	2.48	0.43
54:01:755:U:H2'	54:01:756:A:H8	1.83	0.43
54:01:1499:C:H2'	54:01:1500:G:H8	1.84	0.43
54:01:1654:A:H2'	54:01:1655:A:H8	1.83	0.43
54:01:2327:A:H2'	54:01:2328:A:C8	2.54	0.43
54:01:2417:C:H2'	54:01:2418:A:H8	1.84	0.43
54:01:2743:U:H2'	54:01:2744:G:C4'	2.49	0.43
59:Z:17:ILE:HG13	59:Z:103:LEU:HD12	2.00	0.43
1:04:85:ASN:HD21	54:01:1817:G:H5'	1.84	0.43
1:04:235:GLU:HG2	54:01:2599:G:C8	2.54	0.43
5:08:51:PHE:CE2	5:08:68:ARG:HA	2.54	0.43
5:08:85:LYS:C	5:08:86:LEU:HD12	2.39	0.43
12:15:125:PRO:HB3	54:01:2485:G:O3'	2.19	0.43
14:17:40:ILE:HD13	55:02:8:C:O2'	2.19	0.43
32:B:19:THR:OG1	32:B:20:ARG:N	2.51	0.43
33:C:38:VAL:HG23	33:C:39:ARG:N	2.34	0.43
41:K:22:ILE:HG12	41:K:31:VAL:HG13	2.01	0.43
51:U:11:PHE:C	51:U:13:VAL:H	2.21	0.43
52:03:93:GLU:C	52:03:94:LEU:HD12	2.39	0.43
52:03:133:PRO:HG3	54:01:2168:G:O3'	2.18	0.43
52:03:175:ILE:HG23	52:03:192:LEU:HD22	1.99	0.43
53:A:86:G:H4'	53:A:87:C:C6	2.53	0.43
53:A:132:C:H5'	53:A:262:A:O2'	2.19	0.43
53:A:243:A:H4'	53:A:244:U:H3'	2.01	0.43
54:01:184:C:H4'	54:01:217:A:H2	1.83	0.43
54:01:825:A:H2'	54:01:826:U:O4'	2.19	0.43
54:01:1783:A:N1	54:01:2587:A:H2'	2.33	0.43
54:01:2139:U:H2'	54:01:2140:G:C8	2.53	0.43
54:01:2190:G:H2'	54:01:2191:A:H8	1.84	0.43
54:01:2660:A:H2'	54:01:2661:G:O4'	2.18	0.43
55:02:79:G:H2'	55:02:80:U:O4'	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:X:31:G:C2'	56:X:32:C:H5'	2.48	0.43
56:W:51:C:H2'	56:W:52:G:O4'	2.18	0.43
1:04:132:ARG:HD3	1:04:132:ARG:H	1.84	0.43
5:08:22:VAL:HG22	5:08:35:THR:OG1	2.18	0.43
5:08:144:ALA:HB1	5:08:163:TYR:HE1	1.83	0.43
6:09:5:LEU:HD23	6:09:9:VAL:HG21	2.00	0.43
9:12:99:ARG:HA	9:12:102:GLU:HB3	2.00	0.43
15:18:51:ASN:O	54:01:2845:U:H5"	2.18	0.43
19:22:8:LEU:HD13	24:27:21:LEU:HB3	2.01	0.43
22:25:33:ILE:HD11	22:25:78:ILE:HD11	1.99	0.43
41:K:44:ALA:HB3	41:K:69:CYS:HB2	2.00	0.43
51:U:23:GLU:HB3	51:U:27:VAL:HG22	1.99	0.43
53:A:321:A:O2'	53:A:322:C:H5'	2.18	0.43
53:A:730:G:C5	53:A:731:G:H1'	2.53	0.43
54:01:1906:G:C2'	54:01:1907:G:H5"	2.49	0.43
58:Y:29:G:H2'	58:Y:30:G:C8	2.53	0.43
58:Y:60:U:O2'	58:Y:61:C:H5'	2.18	0.43
7:10:118:ILE:CB	7:10:119:PRO:HD3	2.48	0.43
10:13:7:MET:C	10:13:8:LEU:HD12	2.38	0.43
14:17:111:ARG:HB2	14:17:117:PHE:CE1	2.54	0.43
24:27:38:GLN:O	54:01:95:A:H4'	2.18	0.43
34:D:14:GLU:OE1	34:D:59:LYS:HB2	2.19	0.43
35:E:129:SER:HB2	53:A:20:U:OP2	2.18	0.43
35:E:152:VAL:O	35:E:156:ARG:HB3	2.19	0.43
35:E:156:ARG:HG3	38:H:44:PHE:CZ	2.54	0.43
36:F:19:PRO:O	36:F:23:GLU:HG3	2.19	0.43
37:G:87:PRO:HG3	37:G:148:LYS:HA	1.99	0.43
53:A:728:A:H2'	53:A:729:A:C8	2.53	0.43
53:A:801:U:H2'	53:A:802:A:H8	1.84	0.43
53:A:922:G:H2'	53:A:923:A:C8	2.54	0.43
54:01:796:C:H2'	54:01:797:G:H8	1.84	0.43
54:01:1362:C:H2'	54:01:1363:C:O4'	2.19	0.43
54:01:1710:G:H1'	54:01:2859:G:H21	1.83	0.43
54:01:2026:U:H2'	54:01:2027:G:O4'	2.19	0.43
54:01:2725:A:H2'	54:01:2726:A:H2'	2.00	0.43
58:Y:68:C:H2'	58:Y:69:G:C8	2.53	0.43
1:04:64:VAL:HB	1:04:66:PHE:CZ	2.54	0.43
4:07:147:ARG:HG3	4:07:148:VAL:H	1.84	0.43
11:14:141:LYS:HE2	11:14:143:GLU:HB3	2.00	0.43
17:20:27:ILE:HG22	17:20:28:ALA:N	2.34	0.43
17:20:58:VAL:O	17:20:58:VAL:HG13	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:21:86:MET:HB2	18:21:96:ILE:CD1	2.48	0.43
24:27:5:GLU:O	24:27:56:LEU:HD13	2.19	0.43
36:F:5:GLU:HB2	36:F:90:MET:HB2	2.00	0.43
36:F:67:PRO:HG2	36:F:70:VAL:HG23	1.99	0.43
38:H:51:GLU:O	38:H:57:GLU:N	2.51	0.43
49:S:10:ILE:HG22	49:S:37:SER:HB2	2.01	0.43
49:S:34:SER:O	49:S:70:LEU:HD12	2.19	0.43
52:03:7:ARG:HH11	54:01:2128:G:H4'	1.84	0.43
52:03:105:LYS:HE3	52:03:130:VAL:HG21	2.01	0.43
53:A:604:G:H2'	53:A:605:U:O4'	2.18	0.43
53:A:763:G:H2'	53:A:764:C:C6	2.54	0.43
53:A:1237:C:OP1	53:A:1238:A:H1'	2.19	0.43
54:01:191:A:H2'	54:01:192:C:C6	2.53	0.43
54:01:374:A:H2'	54:01:375:G:O4'	2.19	0.43
54:01:826:U:H5"	54:01:2429:G:P	2.59	0.43
58:Y:55:U:H2'	58:Y:57:G:OP2	2.18	0.43
59:Z:206:ILE:HB	59:Z:235:ILE:HG23	2.01	0.43
13:16:2:ARG:HA	13:16:5:LYS:HG3	2.00	0.43
20:23:4:ILE:HD12	20:23:4:ILE:H	1.83	0.43
32:B:67:LEU:HD21	32:B:91:VAL:CG2	2.40	0.43
41:K:95:THR:O	41:K:99:LEU:HD13	2.19	0.43
43:M:9:PRO:CG	43:M:44:ILE:HG13	2.49	0.43
53:A:408:A:H2'	53:A:409:U:O4'	2.18	0.43
53:A:591:U:H2'	53:A:592:G:H8	1.84	0.43
53:A:682:G:H2'	53:A:683:G:C8	2.53	0.43
53:A:1157:A:H4'	53:A:1158:C:O5'	2.19	0.43
54:01:193:U:H4'	54:01:803:U:H4'	2.01	0.43
54:01:817:C:O2'	54:01:839:U:H5"	2.18	0.43
54:01:1152:C:H2'	54:01:1153:C:C6	2.54	0.43
54:01:1683:U:H2'	54:01:1684:G:H8	1.84	0.43
54:01:1697:G:C4'	54:01:1978:A:H5"	2.49	0.43
56:X:68:C:H2'	56:X:69:C:O4'	2.19	0.43
1:04:235:GLU:N	1:04:238:ASN:ND2	2.60	0.42
2:05:154:LYS:HZ2	54:01:2024:G:H4'	1.82	0.42
4:07:97:GLU:CG	26:29:25:ARG:HB2	2.48	0.42
6:09:26:ALA:O	6:09:31:VAL:HG23	2.19	0.42
7:10:58:THR:HG21	7:10:82:ILE:H	1.85	0.42
8:11:12:VAL:HG12	8:11:13:ALA:N	2.28	0.42
13:16:37:THR:HG22	13:16:110:MET:HE1	2.00	0.42
36:F:44:ARG:HA	36:F:58:HIS:HA	2.00	0.42
37:G:38:ALA:O	37:G:42:VAL:HG23	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:I:62:LEU:HD12	39:I:62:LEU:N	2.34	0.42
51:U:17:ARG:HA	51:U:20:ARG:HG2	2.00	0.42
53:A:227:G:H2'	53:A:228:A:O4'	2.19	0.42
53:A:443:C:H2'	53:A:444:G:H8	1.83	0.42
54:01:1844:C:H2'	54:01:1845:G:H8	1.82	0.42
56:X:21:A:N6	56:X:46:G:H2'	2.34	0.42
1:04:7:PRO:HB3	1:04:13:ARG:HA	2.01	0.42
1:04:257:ARG:HG3	54:01:1799:G:OP1	2.19	0.42
5:08:157:LYS:HD2	54:01:2659:G:OP1	2.19	0.42
20:23:43:LYS:O	20:23:58:VAL:N	2.52	0.42
22:25:22:PHE:CD2	54:01:922:C:H1'	2.54	0.42
22:25:25:GLU:O	22:25:63:VAL:HG23	2.19	0.42
30:33:38:LYS:CA	30:33:41:ARG:HH11	2.32	0.42
42:L:47:ALA:C	42:L:48:LEU:HD12	2.39	0.42
47:Q:46:HIS:HB2	47:Q:70:LYS:CG	2.48	0.42
50:T:70:LYS:HA	50:T:73:ARG:HH12	1.83	0.42
53:A:225:C:C3'	53:A:226:G:H5"	2.49	0.42
53:A:666:G:H2'	53:A:667:G:C8	2.54	0.42
53:A:969:A:H2'	53:A:970:C:O4'	2.18	0.42
54:01:548:G:H2'	54:01:549:G:O4'	2.19	0.42
54:01:795:C:H2'	54:01:796:C:C6	2.54	0.42
54:01:992:C:H2'	54:01:993:G:H8	1.84	0.42
54:01:1655:A:H2'	54:01:1656:C:O4'	2.19	0.42
54:01:2123:G:H2'	54:01:2124:G:C8	2.55	0.42
59:Z:29:ALA:HB2	59:Z:49:ILE:HD12	2.00	0.42
59:Z:60:ILE:HA	60:Z:401:GCP:O2G	2.19	0.42
3:06:188:MET:CE	3:06:196:VAL:HG21	2.49	0.42
5:08:132:LEU:HD12	5:08:132:LEU:O	2.19	0.42
15:18:77:SER:O	15:18:80:VAL:HG22	2.19	0.42
17:20:15:SER:N	17:20:18:GLN:HE21	2.01	0.42
25:28:50:VAL:O	25:28:54:VAL:HG22	2.19	0.42
35:E:75:LEU:O	35:E:75:LEU:HD12	2.19	0.42
38:H:30:LYS:HD2	53:A:643:C:OP1	2.19	0.42
47:Q:13:SER:HB3	47:Q:21:VAL:HG11	2.00	0.42
50:T:30:PHE:O	50:T:34:VAL:HG23	2.20	0.42
53:A:244:U:O4	53:A:906:A:H1'	2.18	0.42
53:A:555:U:H2'	53:A:556:C:C6	2.54	0.42
54:01:190:A:H5"	54:01:204:A:H61	1.84	0.42
54:01:310:A:O2'	54:01:311:A:H2'	2.20	0.42
54:01:433:C:O2'	54:01:434:U:H5'	2.19	0.42
54:01:935:C:H2'	54:01:936:A:C8	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1258:U:H2'	54:01:1259:G:C8	2.54	0.42
54:01:1282:U:H2'	54:01:1283:G:O4'	2.20	0.42
54:01:1532:A:H1'	54:01:1540:G:N2	2.34	0.42
54:01:1773:A:H2'	54:01:1774:C:H5'	2.00	0.42
58:Y:15:G:C2'	58:Y:16:U:H5'	2.46	0.42
1:04:48:ILE:HG22	54:01:779:U:OP1	2.20	0.42
5:08:21:GLN:NE2	5:08:38:ASP:HA	2.33	0.42
7:10:43:LYS:CB	7:10:46:ARG:HH21	2.32	0.42
7:10:69:PHE:CD2	7:10:70:GLU:HG2	2.55	0.42
7:10:81:LEU:HA	54:01:1107:G:H4'	2.00	0.42
12:15:53:MET:HB2	12:15:120:ALA:HB2	2.02	0.42
12:15:78:LEU:HD23	12:15:79:ALA:HB2	2.01	0.42
13:16:49:GLU:HB2	13:16:50:PRO:HD3	2.02	0.42
14:17:27:VAL:HG13	14:17:95:SER:OG	2.20	0.42
30:33:30:HIS:ND1	30:33:31:ILE:HG13	2.35	0.42
43:M:16:ILE:HD12	43:M:16:ILE:H	1.84	0.42
44:N:45:LEU:HG	49:S:12:LEU:HD22	2.02	0.42
47:Q:74:LEU:HD12	47:Q:75:VAL:N	2.34	0.42
49:S:28:LYS:HE3	49:S:29:PRO:HD2	2.02	0.42
52:03:6:LYS:O	52:03:10:VAL:HG23	2.19	0.42
52:03:46:VAL:HG13	52:03:212:VAL:HG22	2.02	0.42
53:A:578:C:H2'	53:A:579:A:C8	2.54	0.42
53:A:797:C:H2'	53:A:798:U:H6	1.83	0.42
53:A:945:G:H2'	53:A:945:G:N3	2.34	0.42
53:A:1030:U:H3'	53:A:1031:C:H5'	2.01	0.42
53:A:1030:U:H5	53:A:1033:G:H21	1.67	0.42
54:01:799:G:H3'	54:01:800:A:H8	1.84	0.42
54:01:844:A:H5'	54:01:845:A:OP1	2.20	0.42
54:01:917:A:H2	55:02:79:G:H21	1.68	0.42
54:01:1565:C:O2'	54:01:1566:A:H2'	2.19	0.42
54:01:2149:U:H2'	54:01:2150:C:O4'	2.18	0.42
58:Y:37:A:H2'	58:Y:38:A:O4'	2.20	0.42
3:06:105:LEU:O	3:06:109:LEU:HD13	2.18	0.42
9:12:113:PRO:HD2	54:01:558:U:OP1	2.20	0.42
11:14:63:LYS:HA	30:33:12:ARG:HG2	2.00	0.42
15:18:2:ASN:ND2	54:01:2876:G:H5"	2.34	0.42
22:25:58:LYS:HE3	54:01:2366:A:H4'	2.02	0.42
27:30:10:SER:O	27:30:14:MET:HG3	2.20	0.42
32:B:102:ASN:ND2	32:B:105:THR:HG21	2.34	0.42
36:F:75:GLU:HA	36:F:78:PHE:HD2	1.83	0.42
50:T:35:TYR:O	50:T:39:GLU:HG2	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:482:A:H1'	54:01:498:G:N2	2.34	0.42
54:01:1285:A:H2'	54:01:1286:A:H5'	2.01	0.42
54:01:2783:U:H2'	54:01:2784:U:C6	2.54	0.42
54:01:2897:U:H2'	54:01:2898:U:C6	2.54	0.42
59:Z:177:ALA:CB	59:Z:188:ILE:HG13	2.49	0.42
1:04:134:ILE:HA	1:04:135:PRO:HD3	1.94	0.42
1:04:260:LYS:HB3	54:01:2227:A:H5"	2.00	0.42
6:09:99:ILE:O	6:09:103:VAL:HG23	2.19	0.42
7:10:27:VAL:HG23	7:10:110:ALA:HA	2.02	0.42
7:10:116:GLU:HB3	7:10:117:LEU:H	1.72	0.42
8:11:127:SER:HB2	54:01:1080:A:N3	2.35	0.42
9:12:7:LYS:O	9:12:11:VAL:HG23	2.20	0.42
13:16:55:ALA:HA	13:16:80:PHE:CE1	2.55	0.42
14:17:29:HIS:HA	14:17:97:PHE:CE2	2.55	0.42
20:23:10:VAL:HA	20:23:71:ILE:HA	2.02	0.42
32:B:96:LEU:O	32:B:99:MET:HG2	2.19	0.42
32:B:206:ILE:O	32:B:209:VAL:HG22	2.20	0.42
32:B:217:ALA:O	32:B:221:ARG:HB2	2.19	0.42
35:E:164:LEU:HD12	35:E:165:GLY:N	2.34	0.42
36:F:25:TYR:O	36:F:29:ILE:HG13	2.19	0.42
37:G:72:VAL:HG12	37:G:89:GLU:HA	2.02	0.42
37:G:110:ARG:HH22	37:G:121:ASN:HB3	1.84	0.42
40:J:42:LEU:HA	40:J:43:PRO:HD2	1.73	0.42
43:M:53:ASP:HA	43:M:56:ARG:HH11	1.85	0.42
52:03:57:GLN:HG2	52:03:201:PRO:CB	2.50	0.42
53:A:390:U:H2'	53:A:391:G:C8	2.55	0.42
53:A:878:A:H2'	53:A:879:C:C6	2.55	0.42
53:A:1477:U:H2'	53:A:1478:U:C6	2.54	0.42
54:01:140:C:H3'	54:01:140:C:OP2	2.19	0.42
54:01:1748:C:H2'	54:01:1749:A:H8	1.84	0.42
54:01:2246:G:H2'	54:01:2247:A:C8	2.55	0.42
58:Y:9:A:C2	58:Y:44:G:H2'	2.54	0.42
59:Z:243:GLU:CD	59:Z:295:PRO:HA	2.39	0.42
12:15:38:ARG:CD	55:02:90:C:H4'	2.50	0.42
14:17:12:THR:HB	54:01:2334:U:H4'	2.01	0.42
18:21:25:ARG:NH2	54:01:519:U:H5"	2.34	0.42
24:27:14:LEU:O	24:27:14:LEU:HD23	2.20	0.42
40:J:14:ASP:OD2	40:J:17:LEU:HB2	2.19	0.42
42:L:120:ARG:NH1	53:A:500:G:H5'	2.34	0.42
52:03:104:ILE:HG23	52:03:108:GLU:O	2.20	0.42
52:03:170:ILE:HG21	54:01:2177:C:H1'	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:17:U:H2'	53:A:18:C:C6	2.54	0.42
53:A:67:C:H2'	53:A:68:G:C8	2.55	0.42
53:A:539:A:H2'	53:A:540:G:H8	1.84	0.42
53:A:651:C:H2'	53:A:652:U:C6	2.55	0.42
53:A:855:U:H2'	53:A:856:C:C6	2.54	0.42
53:A:1053:G:H4'	53:A:1055:A:OP1	2.19	0.42
54:01:151:C:H2'	54:01:152:A:C8	2.54	0.42
54:01:464:U:H1'	54:01:686:U:H5	1.84	0.42
54:01:935:C:H2'	54:01:936:A:H8	1.85	0.42
54:01:995:C:H6	54:01:995:C:H5'	1.85	0.42
54:01:1318:U:H2'	54:01:1319:C:C6	2.54	0.42
54:01:1989:G:H2'	54:01:1990:C:O4'	2.19	0.42
54:01:2415:G:H2'	54:01:2416:C:C6	2.54	0.42
54:01:2818:U:H2'	54:01:2819:G:C8	2.54	0.42
55:02:30:C:H2'	55:02:31:C:C5'	2.49	0.42
56:X:14:A:H2'	56:X:15:G:O4'	2.20	0.42
59:Z:20:VAL:HA	60:Z:401:GCP:O1G	2.19	0.42
59:Z:67:VAL:HG22	59:Z:78:HIS:HB3	1.99	0.42
59:Z:191:LEU:O	59:Z:195:LEU:HB2	2.19	0.42
59:Z:311:LEU:HG	59:Z:384:GLY:HA2	2.01	0.42
59:Z:322:PHE:N	59:Z:322:PHE:CD1	2.87	0.42
3:06:163:ASN:ND2	54:01:323:C:H5"	2.35	0.42
4:07:148:VAL:HG12	4:07:148:VAL:O	2.20	0.42
10:13:41:ILE:C	10:13:41:ILE:HD12	2.40	0.42
12:15:36:VAL:HG13	21:24:82:TYR:CD2	2.55	0.42
14:17:30:ARG:HG2	14:17:30:ARG:HH11	1.84	0.42
16:19:8:ILE:H	16:19:8:ILE:HG13	1.70	0.42
23:26:17:ARG:HE	23:26:23:ALA:HB2	1.85	0.42
25:28:14:GLY:C	25:28:15:ARG:HD2	2.39	0.42
41:K:126:ARG:HH21	53:A:796:C:H4'	1.84	0.42
43:M:97:ARG:HG2	43:M:97:ARG:HH11	1.84	0.42
46:P:40:ASN:OD1	46:P:42:ILE:HG12	2.20	0.42
53:A:301:G:H2'	53:A:302:G:H8	1.84	0.42
53:A:713:G:H2'	53:A:714:G:C8	2.55	0.42
53:A:1071:C:H2'	53:A:1072:G:C8	2.54	0.42
54:01:355:U:H2'	54:01:356:G:C8	2.54	0.42
54:01:624:C:O2'	54:01:657:U:H5"	2.20	0.42
54:01:633:A:H2'	54:01:634:C:H5'	2.00	0.42
54:01:1474:U:C2'	54:01:1475:G:H5'	2.49	0.42
54:01:2721:A:H2'	54:01:2722:G:O4'	2.20	0.42
55:02:78:A:H2'	55:02:79:G:O4'	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:30:ALA:HB3	1:04:31:PRO:HD3	2.02	0.42
2:05:135:GLY:HA2	54:01:743:A:OP1	2.20	0.42
2:05:149:ASN:CG	2:05:150:GLN:H	2.23	0.42
4:07:89:THR:O	55:02:43:C:H1'	2.20	0.42
7:10:111:ALA:O	7:10:114:GLU:HG2	2.20	0.42
8:11:99:LYS:O	8:11:100:ILE:HD13	2.20	0.42
11:14:23:ILE:HG13	17:20:82:HIS:CE1	2.55	0.42
11:14:27:LEU:O	11:14:31:GLY:HA2	2.19	0.42
11:14:79:LEU:HD11	11:14:112:LEU:HA	2.02	0.42
20:23:97:SER:O	20:23:98:ASN:CB	2.67	0.42
27:30:33:SER:CB	27:30:35:GLU:HG3	2.50	0.42
33:C:38:VAL:O	33:C:42:LEU:HD13	2.19	0.42
36:F:98:GLU:HB3	36:F:99:ALA:H	1.67	0.42
41:K:44:ALA:HB3	41:K:65:ALA:O	2.20	0.42
53:A:928:G:H2'	53:A:929:G:H8	1.85	0.42
54:01:280:U:H2'	54:01:281:C:C2	2.55	0.42
54:01:767:U:H2'	54:01:768:G:C8	2.55	0.42
54:01:859:G:O2'	54:01:860:U:P	2.77	0.42
54:01:1844:C:H2'	54:01:1845:G:C8	2.55	0.42
54:01:2233:U:H2'	54:01:2234:G:H8	1.84	0.42
54:01:2774:C:H2'	54:01:2775:G:O4'	2.20	0.42
56:X:1:C:H2'	56:X:2:G:C8	2.55	0.42
59:Z:113:PRO:O	59:Z:116:ARG:HB3	2.20	0.42
1:04:65:ASP:OD2	1:04:68:ARG:HD2	2.20	0.42
1:04:104:LEU:HD12	1:04:142:ASN:ND2	2.35	0.42
1:04:243:PRO:O	1:04:251:THR:HG22	2.20	0.42
1:04:252:LYS:HB2	1:04:252:LYS:HZ3	1.84	0.42
5:08:34:ARG:HE	5:08:70:LEU:HD13	1.81	0.42
7:10:29:ASP:H	7:10:81:LEU:HD22	1.83	0.42
8:11:75:ALA:O	8:11:79:LEU:N	2.50	0.42
9:12:117:ALA:HA	9:12:120:ARG:HH21	1.83	0.42
11:14:62:PRO:HG2	30:33:24:LYS:HB3	2.02	0.42
13:16:1:MET:O	13:16:2:ARG:HG3	2.20	0.42
17:20:78:ARG:NH1	54:01:990:A:H61	2.17	0.42
33:C:13:ILE:HD12	33:C:13:ILE:H	1.85	0.42
39:I:80:HIS:CD2	39:I:105:ARG:HA	2.55	0.42
43:M:100:ARG:HH12	43:M:103:THR:CB	2.33	0.42
53:A:1295:U:H2'	53:A:1296:C:C6	2.54	0.42
54:01:358:U:H2'	54:01:359:G:O4'	2.20	0.42
54:01:2292:U:H2'	54:01:2293:G:C8	2.55	0.42
54:01:2520:C:O2'	54:01:2521:C:H5'	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:55:GLY:H	54:01:692:C:P	2.43	0.41
1:04:86:ARG:HG2	1:04:86:ARG:HH11	1.86	0.41
2:05:6:GLY:O	2:05:201:LEU:N	2.47	0.41
7:10:67:THR:HB	7:10:68:PRO:HD3	2.02	0.41
12:15:33:LEU:HD11	12:15:128:THR:OG1	2.20	0.41
16:19:60:TRP:O	16:19:64:ILE:HG13	2.20	0.41
22:25:61:GLY:HA2	22:25:81:GLU:OXT	2.20	0.41
24:27:9:LYS:HE2	24:27:11:VAL:CG2	2.50	0.41
32:B:63:LYS:HD2	32:B:63:LYS:HA	1.86	0.41
32:B:202:ASN:ND2	32:B:208:ALA:HB2	2.31	0.41
35:E:108:GLY:H	53:A:9:G:H4'	1.85	0.41
47:Q:39:ARG:HG3	47:Q:39:ARG:HH11	1.85	0.41
53:A:6:G:O2'	53:A:298:A:H1'	2.20	0.41
54:01:78:U:H2'	54:01:79:C:C6	2.55	0.41
54:01:195:A:H2'	54:01:198:C:H41	1.84	0.41
54:01:1550:C:H2'	54:01:1551:A:C8	2.55	0.41
54:01:1686:C:H2'	54:01:1687:G:O4'	2.20	0.41
54:01:2114:A:O2'	54:01:2167:U:H5'	2.19	0.41
54:01:2819:G:H2'	54:01:2821:A:N7	2.35	0.41
56:X:1:C:H2'	56:X:2:G:H8	1.84	0.41
2:05:33:ARG:HH22	2:05:74:GLU:HB3	1.85	0.41
2:05:155:VAL:HG21	54:01:2618:G:H21	1.85	0.41
4:07:153:ILE:HD12	4:07:153:ILE:N	2.35	0.41
8:11:30:GLN:CB	8:11:60:VAL:HG21	2.50	0.41
10:13:71:ARG:HH11	10:13:77:ILE:HD11	1.85	0.41
27:30:27:LEU:HD12	27:30:37:HIS:O	2.21	0.41
33:C:112:ALA:HA	33:C:201:ILE:HD12	2.02	0.41
36:F:47:LEU:HD13	36:F:51:ILE:HG13	2.01	0.41
52:03:16:ASP:HB2	52:03:21:TYR:HE1	1.85	0.41
53:A:396:C:H2'	53:A:397:A:H5"	2.01	0.41
53:A:613:C:H2'	53:A:614:C:C6	2.55	0.41
54:01:107:G:H2'	54:01:108:G:C8	2.55	0.41
54:01:392:U:H2'	54:01:393:C:H6	1.85	0.41
54:01:946:C:H2'	54:01:947:A:H8	1.85	0.41
54:01:1074:G:H2'	54:01:1075:C:O4'	2.20	0.41
54:01:1548:A:H2'	54:01:1549:A:C8	2.55	0.41
54:01:1595:C:H2'	54:01:1596:A:H8	1.86	0.41
54:01:1720:U:H2'	54:01:1721:G:O4'	2.20	0.41
54:01:1796:U:H2'	54:01:1797:G:H8	1.85	0.41
54:01:2266:A:H4'	54:01:2267:A:N3	2.35	0.41
54:01:2305:U:H2'	54:01:2306:C:C6	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2328:A:H2'	54:01:2329:U:C6	2.55	0.41
54:01:2684:U:H2'	54:01:2685:G:O4'	2.20	0.41
55:02:49:C:H2'	55:02:50:A:C8	2.55	0.41
55:02:88:C:C5'	55:02:89:U:OP1	2.67	0.41
3:06:148:ILE:HD13	3:06:187:VAL:HG11	2.02	0.41
4:07:40:GLY:HA2	4:07:84:ILE:CG1	2.50	0.41
4:07:97:GLU:HG2	26:29:25:ARG:HB2	2.02	0.41
5:08:29:ASN:HD22	5:08:78:VAL:C	2.23	0.41
9:12:35:ARG:HB2	9:12:54:ILE:HD11	2.02	0.41
10:13:3:GLN:HE21	54:01:1666:G:H1'	1.85	0.41
21:24:7:GLU:HB2	21:24:41:GLU:HB3	2.02	0.41
23:26:63:ILE:O	23:26:67:LEU:HD13	2.20	0.41
32:B:14:HIS:HB2	32:B:202:ASN:HB2	2.01	0.41
32:B:16:GLY:HA2	32:B:40:ILE:H	1.85	0.41
32:B:107:ARG:HA	32:B:110:ILE:HD12	2.02	0.41
33:C:150:VAL:HG12	33:C:199:VAL:HG23	2.01	0.41
33:C:176:THR:HG22	33:C:178:ARG:HG2	2.03	0.41
37:G:41:ILE:HG23	37:G:116:ALA:HA	2.02	0.41
41:K:118:ASN:O	53:A:716:A:H1'	2.20	0.41
49:S:35:ARG:NH1	49:S:74:ALA:HB3	2.35	0.41
53:A:225:C:H2'	53:A:226:G:O4'	2.20	0.41
53:A:459:A:H2'	53:A:460:A:C8	2.55	0.41
54:01:340:A:H2'	54:01:341:C:O4'	2.20	0.41
54:01:2055:C:H5'	54:01:2056:G:O5'	2.19	0.41
54:01:2564:A:OP1	54:01:2648:G:H4'	2.21	0.41
59:Z:32:THR:O	59:Z:36:ALA:N	2.53	0.41
59:Z:205:ALA:HB1	59:Z:208:LYS:HE3	2.02	0.41
1:04:124:LYS:HB3	1:04:127:ASN:OD1	2.21	0.41
1:04:154:ALA:CB	1:04:161:VAL:HG23	2.48	0.41
8:11:103:ALA:O	8:11:107:GLU:HG3	2.20	0.41
10:13:76:VAL:H	15:18:72:VAL:CG2	2.28	0.41
11:14:29:LYS:HG2	11:14:30:THR:HG23	2.03	0.41
21:24:72:VAL:HA	21:24:94:ALA:H	1.84	0.41
31:34:4:ARG:HB3	54:01:2466:C:OP1	2.20	0.41
32:B:169:HIS:CE1	32:B:170:ILE:HG23	2.55	0.41
33:C:1:GLY:HA3	53:A:1060:U:C5	2.55	0.41
44:N:9:GLU:O	44:N:13:VAL:HG23	2.21	0.41
47:Q:59:GLU:O	47:Q:74:LEU:HA	2.20	0.41
47:Q:61:ARG:HD2	47:Q:62:GLU:O	2.20	0.41
52:03:21:TYR:N	52:03:223:ALA:O	2.43	0.41
53:A:323:U:H2'	53:A:324:G:O4'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1084:G:H2'	53:A:1085:U:C5	2.56	0.41
53:A:1323:G:H2'	53:A:1324:A:C8	2.55	0.41
54:01:167:A:H2'	54:01:168:G:O4'	2.20	0.41
54:01:801:G:H3'	54:01:802:A:H5'	2.02	0.41
54:01:2206:C:H2'	54:01:2207:C:C6	2.55	0.41
54:01:2639:A:H2'	54:01:2640:G:O4'	2.20	0.41
54:01:2845:U:H2'	54:01:2846:G:C8	2.55	0.41
55:02:111:U:H2'	55:02:112:G:H8	1.85	0.41
56:X:9:G:H5"	56:X:11:A:N7	2.36	0.41
58:Y:45:U:H3'	58:Y:46:G:H5"	2.03	0.41
59:Z:215:GLU:OE2	59:Z:216:ASP:HB2	2.19	0.41
59:Z:328:PRO:HG2	59:Z:330:PHE:CE1	2.55	0.41
1:04:141:HIS:CD2	1:04:194:VAL:HG22	2.56	0.41
6:09:50:ARG:O	6:09:54:LEU:HB3	2.19	0.41
7:10:80:THR:O	7:10:82:ILE:HG12	2.20	0.41
9:12:118:MET:HA	9:12:121:LYS:HG2	2.01	0.41
11:14:95:LEU:HB3	11:14:100:ILE:CG1	2.50	0.41
13:16:100:CYS:HB3	27:30:42:ILE:HD11	2.02	0.41
17:20:14:VAL:HG23	17:20:18:GLN:NE2	2.36	0.41
23:26:48:LEU:HD21	23:26:77:TYR:HB2	2.03	0.41
27:30:24:VAL:HG22	27:30:26:SER:HB2	2.02	0.41
35:E:84:VAL:HG23	35:E:145:ASN:ND2	2.34	0.41
39:I:61:ASP:C	39:I:62:LEU:HD12	2.41	0.41
47:Q:28:VAL:HG22	47:Q:29:LYS:N	2.35	0.41
52:03:7:ARG:HE	54:01:2128:G:C4'	2.29	0.41
52:03:212:VAL:HG12	52:03:214:ILE:HG23	2.02	0.41
53:A:149:A:H1'	53:A:1446:A:C2	2.54	0.41
53:A:219:U:H2'	53:A:220:G:C8	2.56	0.41
53:A:1040:U:H2'	53:A:1041:G:H8	1.85	0.41
53:A:1326:U:O2'	53:A:1327:C:H5'	2.20	0.41
54:01:774:G:O2'	54:01:775:G:H5"	2.21	0.41
54:01:894:U:O2'	54:01:895:U:H5'	2.20	0.41
54:01:947:A:H2'	54:01:948:C:C6	2.56	0.41
54:01:1213:A:N6	54:01:1236:G:H1'	2.35	0.41
54:01:1399:C:H2'	54:01:1400:U:C6	2.55	0.41
54:01:1433:A:H2'	54:01:1434:A:O4'	2.21	0.41
55:02:104:A:H2'	55:02:105:G:O4'	2.21	0.41
58:Y:44:G:H1'	58:Y:45:U:C6	2.55	0.41
59:Z:96:ALA:HB2	59:Z:333:ARG:O	2.20	0.41
1:04:224:MET:SD	1:04:229:HIS:HB2	2.60	0.41
2:05:5:VAL:HG11	2:05:80:TRP:CZ3	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:33:VAL:HG12	7:10:34:THR:H	1.86	0.41
8:11:19:PRO:C	8:11:22:PRO:HD2	2.41	0.41
12:15:34:LYS:HA	12:15:101:VAL:HA	2.02	0.41
16:19:55:GLN:HA	16:19:58:GLN:HG2	2.02	0.41
18:21:43:ALA:O	18:21:47:VAL:HG12	2.20	0.41
23:26:11:PRO:HG3	23:26:30:PRO:HD2	2.03	0.41
27:30:9:ARG:O	27:30:13:GLY:N	2.54	0.41
32:B:202:ASN:ND2	32:B:205:ALA:HB3	2.34	0.41
34:D:94:GLU:HA	34:D:99:ASN:HD22	1.83	0.41
35:E:86:GLY:O	35:E:138:ALA:HB1	2.21	0.41
39:I:89:TYR:HB3	39:I:93:LEU:CD1	2.51	0.41
41:K:15:VAL:HG22	41:K:16:SER:N	2.35	0.41
41:K:126:ARG:NH2	53:A:796:C:H4'	2.35	0.41
46:P:59:HIS:O	46:P:63:GLN:HG2	2.19	0.41
47:Q:52:CYS:SG	47:Q:74:LEU:HD22	2.61	0.41
48:R:13:THR:HG21	48:R:20:ILE:HD11	2.02	0.41
52:03:16:ASP:HB2	52:03:21:TYR:CE1	2.55	0.41
53:A:443:C:H2'	53:A:444:G:C8	2.56	0.41
53:A:785:G:H2'	53:A:786:G:H8	1.86	0.41
53:A:785:G:O2'	53:A:786:G:H5'	2.20	0.41
53:A:994:A:C5	53:A:1216:A:H4'	2.56	0.41
53:A:1468:A:O2'	53:A:1469:C:H5'	2.20	0.41
53:A:1497:G:O2'	53:A:1498:U:H5'	2.21	0.41
54:01:999:U:O2'	54:01:1000:A:H5'	2.21	0.41
54:01:1435:G:O2'	54:01:1436:G:H5'	2.20	0.41
54:01:1672:A:C2	54:01:2582:G:H5'	2.55	0.41
54:01:1837:C:H2'	54:01:1899:A:N6	2.34	0.41
54:01:2555:U:H2'	54:01:2556:C:H5'	2.02	0.41
58:Y:24:G:H2'	58:Y:25:C:O4'	2.21	0.41
5:08:101:VAL:HG22	5:08:115:GLN:HG3	2.02	0.41
8:11:10:LEU:HD11	54:01:1070:A:C2	2.56	0.41
13:16:38:LEU:HD11	13:16:42:LYS:HE2	2.03	0.41
16:19:113:LYS:O	16:19:117:ALA:N	2.54	0.41
21:24:23:ALA:O	21:24:25:LYS:HG3	2.20	0.41
36:F:48:ALA:HB1	48:R:68:PRO:HG3	2.02	0.41
36:F:69:GLU:HA	36:F:72:ASP:OD2	2.21	0.41
37:G:6:ILE:HD12	37:G:6:ILE:O	2.20	0.41
39:I:105:ARG:CZ	53:A:1117:A:H5"	2.51	0.41
41:K:90:PRO:HG2	41:K:91:GLY:H	1.84	0.41
42:L:14:LYS:HE3	53:A:562:U:H5	1.85	0.41
53:A:552:U:H2'	53:A:553:A:H8	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1028:C:H2'	53:A:1029:U:O4'	2.20	0.41
53:A:1506:U:O2'	53:A:1507:A:H5'	2.20	0.41
54:01:464:U:H2'	54:01:465:G:O4'	2.21	0.41
54:01:948:C:H2'	54:01:949:G:C8	2.56	0.41
54:01:1739:A:H2'	54:01:1740:G:O4'	2.20	0.41
54:01:2093:G:H2'	54:01:2094:A:C8	2.55	0.41
54:01:2623:G:H2'	54:01:2624:G:C8	2.54	0.41
58:Y:61:C:H2'	58:Y:62:C:O4'	2.21	0.41
59:Z:28:THR:HG23	59:Z:78:HIS:CD2	2.56	0.41
3:06:23:PHE:CE1	3:06:28:VAL:HG21	2.56	0.41
8:11:38:CYS:O	8:11:41:PHE:HB3	2.20	0.41
9:12:81:ILE:HG23	9:12:82:GLY:N	2.36	0.41
9:12:101:ILE:O	9:12:105:VAL:HG23	2.20	0.41
11:14:77:ILE:N	11:14:77:ILE:HD12	2.35	0.41
13:16:3:HIS:O	13:16:4:ARG:HB2	2.21	0.41
16:19:91:ARG:NH1	54:01:997:G:H5"	2.31	0.41
27:30:39:ARG:HB3	27:30:40:HIS:ND1	2.36	0.41
28:31:7:LYS:HA	28:31:23:THR:HA	2.03	0.41
29:32:21:ARG:HH21	29:32:21:ARG:HG2	1.86	0.41
32:B:106:VAL:O	32:B:110:ILE:HG13	2.21	0.41
33:C:39:ARG:HH21	33:C:56:ILE:CG1	2.33	0.41
34:D:109:THR:HG21	53:A:408:A:OP1	2.21	0.41
43:M:89:ARG:HH21	43:M:95:PRO:HG2	1.85	0.41
45:O:80:LEU:O	45:O:84:LEU:HD13	2.20	0.41
49:S:57:VAL:HG13	49:S:57:VAL:O	2.21	0.41
52:03:185:LEU:HD23	52:03:188:ASN:HD22	1.86	0.41
53:A:34:C:H2'	53:A:35:G:C8	2.56	0.41
53:A:536:C:H2'	53:A:537:G:C8	2.56	0.41
53:A:1211:U:H4'	53:A:1213:A:N3	2.36	0.41
53:A:1498:U:H6	53:A:1499:A:H62	1.69	0.41
54:01:193:U:H4'	54:01:803:U:C4'	2.51	0.41
54:01:270:A:N1	54:01:369:U:H4'	2.36	0.41
54:01:615:U:H5"	54:01:616:A:OP2	2.21	0.41
54:01:976:G:H2'	54:01:977:G:C8	2.55	0.41
54:01:1794:A:H2'	54:01:1795:C:H6	1.85	0.41
54:01:2417:C:H2'	54:01:2418:A:C8	2.56	0.41
54:01:2809:A:H2'	54:01:2810:A:C8	2.55	0.41
59:Z:305:GLU:HA	59:Z:359:VAL:HA	2.02	0.41
59:Z:312:SER:O	59:Z:317:GLY:N	2.51	0.41
4:07:109:ARG:HE	43:M:2:ARG:NH1	2.19	0.41
6:09:129:GLU:OE2	6:09:141:LYS:HB3	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:95:ARG:HG3	9:12:95:ARG:NH1	2.34	0.41
12:15:41:LEU:HG	12:15:96:ILE:HG13	2.02	0.41
12:15:66:ARG:HG3	12:15:66:ARG:NH1	2.35	0.41
16:19:93:ILE:HG23	17:20:13:ARG:HB2	2.03	0.41
17:20:81:LYS:HD2	54:01:973:A:H5"	2.03	0.41
18:21:24:ILE:HD11	18:21:74:ILE:CD1	2.51	0.41
22:25:39:THR:HG21	54:01:2336:A:H61	1.86	0.41
23:26:39:VAL:HG12	23:26:42:GLU:H	1.86	0.41
27:30:7:PRO:HG2	54:01:1264:A:H5'	2.02	0.41
29:32:3:ARG:HD3	29:32:4:THR:H	1.86	0.41
32:B:65:LYS:HB3	32:B:89:PHE:CE2	2.53	0.41
34:D:18:LEU:HD22	34:D:63:ILE:HG12	2.03	0.41
34:D:141:VAL:HA	34:D:180:THR:HA	2.03	0.41
35:E:160:VAL:HG22	35:E:161:GLU:N	2.36	0.41
38:H:5:PRO:O	38:H:8:ASP:HB3	2.21	0.41
38:H:9:MET:HG3	38:H:26:MET:SD	2.61	0.41
39:I:48:ARG:O	39:I:52:GLU:HG2	2.21	0.41
43:M:58:GLU:OE2	43:M:61:LYS:HD2	2.20	0.41
45:O:25:GLU:H	45:O:25:GLU:CD	2.24	0.41
47:Q:65:PRO:O	53:A:264:C:O2'	2.37	0.41
52:03:176:GLY:HA3	52:03:180:PHE:CD2	2.56	0.41
53:A:320:A:H2'	53:A:321:A:C8	2.56	0.41
53:A:750:C:H2'	53:A:751:U:C6	2.55	0.41
53:A:981:U:H2'	53:A:982:U:C5	2.56	0.41
53:A:1390:U:H2'	53:A:1391:U:C6	2.55	0.41
54:01:534:U:H2'	54:01:535:G:C8	2.56	0.41
54:01:534:U:H2'	54:01:535:G:H8	1.85	0.41
54:01:662:G:O2'	54:01:663:G:H5'	2.21	0.41
54:01:744:U:H2'	54:01:745:G:O4'	2.21	0.41
54:01:1544:A:H2'	54:01:1545:A:C8	2.56	0.41
54:01:1596:A:H2'	54:01:1597:A:O4'	2.21	0.41
54:01:1605:C:H2'	54:01:1606:C:O4'	2.20	0.41
54:01:1911:U:H2'	54:01:1918:A:N1	2.36	0.41
54:01:2318:G:H2'	54:01:2319:G:O4'	2.20	0.41
54:01:2396:G:H2'	54:01:2397:G:H8	1.86	0.41
54:01:2687:U:H2'	54:01:2688:G:O4'	2.21	0.41
59:Z:102:ILE:CG2	59:Z:191:LEU:HD11	2.51	0.41
6:09:4:ILE:HB	6:09:39:ALA:HB2	2.03	0.41
6:09:57:LYS:HA	6:09:60:GLU:HB2	2.03	0.41
7:10:96:PHE:CE2	7:10:126:LEU:HB2	2.56	0.41
7:10:118:ILE:H	7:10:119:PRO:HD2	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:16:35:LYS:HD2	13:16:112:TYR:CE1	2.56	0.41
19:22:15:HIS:CE1	19:22:17:SER:HB3	2.56	0.41
35:E:151:MET:O	35:E:155:LYS:HG3	2.21	0.41
38:H:21:LYS:O	38:H:62:LEU:HD12	2.21	0.41
40:J:26:VAL:O	40:J:30:LYS:N	2.45	0.41
50:T:70:LYS:HE2	53:A:261:U:OP2	2.20	0.41
52:03:59:VAL:O	52:03:164:ARG:HA	2.21	0.41
53:A:463:U:H2'	53:A:464:U:O4'	2.21	0.41
53:A:858:G:O6	53:A:869:G:H3'	2.21	0.41
53:A:956:U:H2'	53:A:957:U:O4'	2.21	0.41
54:01:1001:A:H2'	54:01:1002:G:O4'	2.21	0.41
54:01:1732:C:O2'	54:01:1733:G:H5'	2.21	0.41
54:01:2047:C:H2'	54:01:2048:G:H8	1.85	0.41
59:Z:61:THR:HB	59:Z:82:PRO:HB3	2.02	0.41
1:04:86:ARG:HH12	1:04:155:ARG:HH21	1.69	0.40
3:06:131:THR:HG22	3:06:160:ALA:O	2.21	0.40
4:07:109:ARG:HE	43:M:2:ARG:CZ	2.34	0.40
5:08:122:ALA:HA	5:08:132:LEU:HA	2.03	0.40
6:09:54:LEU:O	6:09:58:LEU:HG	2.21	0.40
6:09:97:ARG:HG2	6:09:112:LYS:HD3	2.03	0.40
18:21:75:PHE:CD1	18:21:75:PHE:N	2.89	0.40
24:27:34:SER:OG	24:27:36:GLN:HG3	2.21	0.40
26:29:9:TYR:CE1	26:29:26:SER:HA	2.55	0.40
26:29:14:ALA:HB2	26:29:24:ILE:HG12	2.03	0.40
33:C:49:ALA:HB1	33:C:75:VAL:HG22	2.03	0.40
35:E:156:ARG:HH12	38:H:100:ILE:HG23	1.87	0.40
40:J:28:THR:CG2	40:J:86:ALA:HB1	2.51	0.40
46:P:67:ILE:HD12	46:P:67:ILE:N	2.33	0.40
53:A:938:A:C2	53:A:1376:U:H1'	2.56	0.40
53:A:982:U:H4'	53:A:983:A:O5'	2.21	0.40
53:A:1347:G:C2'	53:A:1348:U:OP2	2.69	0.40
53:A:1366:C:H2'	53:A:1367:C:C6	2.56	0.40
54:01:1086:A:N3	54:01:1086:A:H3'	2.36	0.40
54:01:1102:C:H2'	54:01:1103:A:O4'	2.21	0.40
54:01:2144:G:H1'	54:01:2147:A:N6	2.37	0.40
54:01:2238:G:N3	54:01:2238:G:H2'	2.36	0.40
54:01:2640:G:H2'	54:01:2641:G:H8	1.86	0.40
59:Z:212:LEU:HD21	59:Z:229:GLY:CA	2.50	0.40
5:08:173:ALA:C	5:08:175:LYS:H	2.25	0.40
16:19:64:ILE:HD13	16:19:94:LEU:HD22	2.01	0.40
31:34:17:VAL:HG12	31:34:19:ARG:HG3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:83:THR:O	40:J:87:LEU:HG	2.20	0.40
41:K:86:LYS:HZ2	41:K:114:PRO:HD3	1.85	0.40
53:A:317:U:H2'	53:A:318:G:C8	2.56	0.40
53:A:372:C:N4	53:A:387:U:H2'	2.35	0.40
53:A:495:A:H4'	53:A:496:A:OP1	2.20	0.40
53:A:505:G:H4'	53:A:534:U:C4	2.57	0.40
53:A:620:C:H2'	53:A:621:A:O4'	2.21	0.40
53:A:715:A:H2'	53:A:716:A:H8	1.82	0.40
53:A:920:U:H2'	53:A:921:U:C6	2.56	0.40
54:01:174:U:H2'	54:01:175:G:C8	2.56	0.40
54:01:1318:U:H2'	54:01:1319:C:H6	1.86	0.40
54:01:1636:U:H2'	54:01:1637:A:C8	2.54	0.40
54:01:1637:A:H5'	54:01:1760:C:O2'	2.21	0.40
54:01:2693:G:O2'	54:01:2694:G:H5'	2.21	0.40
55:02:97:C:H2'	55:02:98:G:O4'	2.20	0.40
56:X:28:C:H2'	56:X:29:G:H8	1.86	0.40
56:W:9:G:N3	56:W:45:G:H2'	2.36	0.40
58:Y:21:A:H3'	58:Y:46:G:O6	2.21	0.40
59:Z:265:LEU:HD21	59:Z:268:GLY:HA2	2.03	0.40
1:04:153:LEU:HD11	1:04:181:ARG:HH21	1.83	0.40
2:05:23:PRO:HG2	54:01:2728:U:O2'	2.21	0.40
6:09:9:VAL:HG12	6:09:11:ASN:H	1.86	0.40
8:11:86:LYS:HD3	8:11:86:LYS:N	2.37	0.40
10:13:87:LEU:HB3	10:13:92:GLU:O	2.21	0.40
12:15:50:ARG:HG2	12:15:50:ARG:NH2	2.35	0.40
18:21:74:ILE:HG23	18:21:74:ILE:O	2.21	0.40
24:27:17:GLU:HB2	24:27:53:VAL:HG11	2.03	0.40
31:34:2:LYS:HZ3	54:01:2478:A:H5"	1.82	0.40
33:C:4:VAL:HB	53:A:1190:G:OP2	2.21	0.40
37:G:26:VAL:HG13	37:G:42:VAL:HG21	2.03	0.40
40:J:101:SER:C	40:J:102:LEU:HD12	2.41	0.40
43:M:89:ARG:NH2	43:M:94:LEU:HB3	2.37	0.40
47:Q:17:GLU:OE1	53:A:273:U:H1'	2.22	0.40
52:03:48:LEU:HD11	52:03:59:VAL:HG11	2.04	0.40
53:A:202:G:H2'	53:A:203:G:C8	2.57	0.40
53:A:666:G:H2'	53:A:667:G:H8	1.85	0.40
53:A:1019:A:H2'	53:A:1020:G:O4'	2.22	0.40
53:A:1105:A:H2'	53:A:1106:G:H8	1.86	0.40
53:A:1386:G:H2'	53:A:1387:G:C8	2.54	0.40
54:01:493:G:O2'	54:01:494:G:H5'	2.21	0.40
54:01:543:G:H2'	54:01:544:C:O4'	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:567:U:H2'	54:01:568:U:O4'	2.21	0.40
54:01:820:A:H2'	54:01:821:A:C8	2.56	0.40
54:01:864:G:H2'	54:01:865:C:C6	2.56	0.40
54:01:1443:U:H2'	54:01:1444:G:H8	1.83	0.40
54:01:1563:U:H2'	54:01:1564:C:C6	2.57	0.40
1:04:239:PHE:HE2	54:01:1902:C:H5"	1.87	0.40
6:09:40:THR:HG22	6:09:41:LYS:H	1.86	0.40
7:10:25:ALA:HB3	7:10:99:PHE:CE2	2.57	0.40
9:12:34:ARG:NH2	16:19:69:ARG:HD2	2.37	0.40
11:14:100:ILE:HG13	11:14:101:ILE:HG23	2.02	0.40
16:19:16:ILE:HG23	16:19:38:VAL:HG21	2.03	0.40
17:20:41:ILE:HD12	17:20:54:VAL:HG11	2.04	0.40
36:F:47:LEU:HD21	36:F:57:ALA:CB	2.51	0.40
39:I:53:LEU:HD21	39:I:100:ALA:HB2	2.03	0.40
39:I:105:ARG:HD3	39:I:105:ARG:O	2.21	0.40
40:J:53:ILE:HG12	53:A:1060:U:C5'	2.47	0.40
42:L:113:ARG:NH2	42:L:120:ARG:HG3	2.36	0.40
50:T:42:ASP:CB	50:T:45:ALA:HB3	2.51	0.40
52:03:60:ARG:CB	52:03:141:LYS:HG3	2.48	0.40
54:01:1045:C:H5'	54:01:1046:A:C5'	2.51	0.40
54:01:1396:U:H5"	54:01:1397:U:OP2	2.21	0.40
54:01:1427:A:H4'	54:01:1428:C:O4'	2.21	0.40
54:01:1473:G:H2'	54:01:1474:U:O4'	2.22	0.40
54:01:1635:A:H2'	54:01:1636:U:O4'	2.21	0.40
54:01:2052:A:H2'	54:01:2053:G:H8	1.87	0.40
54:01:2113:U:O5'	54:01:2113:U:H6	2.04	0.40
58:Y:8:U:H5'	58:Y:49:C:OP2	2.21	0.40
2:05:51:THR:OG1	2:05:76:GLY:HA3	2.22	0.40
2:05:61:THR:HB	2:05:63:PRO:HD2	2.03	0.40
2:05:82:PHE:HE1	2:05:202:ILE:HG23	1.86	0.40
3:06:40:ARG:NH2	54:01:1246:A:H4'	2.33	0.40
3:06:46:GLN:HB3	3:06:83:VAL:HG11	2.03	0.40
4:07:37:MET:HB3	4:07:86:CYS:SG	2.61	0.40
6:09:40:THR:H	6:09:43:ASN:HB2	1.87	0.40
7:10:118:ILE:H	7:10:119:PRO:CD	2.34	0.40
8:11:52:LEU:O	8:11:54:ILE:HG13	2.22	0.40
14:17:11:ALA:HB2	14:17:96:GLY:N	2.36	0.40
33:C:119:ILE:O	33:C:123:LEU:HG	2.21	0.40
43:M:97:ARG:HG2	43:M:97:ARG:NH1	2.37	0.40
43:M:113:LYS:H	43:M:114:PRO:HD2	1.85	0.40
50:T:20:ASN:HD21	50:T:65:LEU:CD1	2.34	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:79:THR:HB	52:03:80:GLN:H	1.76	0.40
53:A:243:A:H62	53:A:281:G:H1'	1.86	0.40
53:A:247:G:O2'	53:A:248:C:H5'	2.21	0.40
53:A:432:A:H2'	53:A:433:G:O4'	2.21	0.40
53:A:1278:G:OP1	53:A:1279:G:H5'	2.21	0.40
54:01:277:G:H1'	54:01:361:G:O6	2.21	0.40
54:01:517:C:H2'	54:01:518:G:O4'	2.21	0.40
54:01:1766:G:H2'	54:01:1767:G:H8	1.86	0.40
54:01:2086:U:H2'	54:01:2087:G:H8	1.84	0.40
54:01:2112:G:H2'	54:01:2113:U:H5'	2.03	0.40
54:01:2222:C:H2'	54:01:2223:G:O4'	2.22	0.40
54:01:2732:G:O2'	54:01:2733:A:H5'	2.22	0.40
56:W:62:C:H2'	56:W:63:G:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	04	269/271 (99%)	241 (90%)	26 (10%)	2 (1%)	22	60
2	05	207/209 (99%)	185 (89%)	21 (10%)	1 (0%)	29	67
3	06	199/201 (99%)	174 (87%)	24 (12%)	1 (0%)	29	67
4	07	175/177 (99%)	155 (89%)	16 (9%)	4 (2%)	6	38
5	08	174/176 (99%)	157 (90%)	12 (7%)	5 (3%)	4	33
6	09	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	11	46
7	10	129/131 (98%)	95 (74%)	27 (21%)	7 (5%)	2	22
8	11	139/141 (99%)	111 (80%)	27 (19%)	1 (1%)	22	60
9	12	140/142 (99%)	130 (93%)	10 (7%)	0	100	100
10	13	120/122 (98%)	100 (83%)	18 (15%)	2 (2%)	9	43

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	14	141/143 (99%)	116 (82%)	21 (15%)	4 (3%)	5	34
12	15	134/136 (98%)	122 (91%)	10 (8%)	2 (2%)	10	45
13	16	118/120 (98%)	103 (87%)	15 (13%)	0	100	100
14	17	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
15	18	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
16	19	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
17	20	101/103 (98%)	82 (81%)	18 (18%)	1 (1%)	15	52
18	21	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
19	22	91/93 (98%)	80 (88%)	10 (11%)	1 (1%)	14	51
20	23	100/102 (98%)	84 (84%)	13 (13%)	3 (3%)	4	33
21	24	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
22	25	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	26	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	27	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	28	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
26	29	64/66 (97%)	50 (78%)	14 (22%)	0	100	100
27	30	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	31	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
29	32	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
30	33	62/64 (97%)	56 (90%)	4 (6%)	2 (3%)	4	32
31	34	36/38 (95%)	28 (78%)	6 (17%)	2 (6%)	2	21
32	B	216/218 (99%)	173 (80%)	40 (18%)	3 (1%)	11	46
33	C	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
34	D	203/205 (99%)	174 (86%)	23 (11%)	6 (3%)	4	33
35	E	155/157 (99%)	119 (77%)	27 (17%)	9 (6%)	1	21
36	F	98/100 (98%)	73 (74%)	21 (21%)	4 (4%)	3	27
37	G	149/151 (99%)	127 (85%)	20 (13%)	2 (1%)	12	48
38	H	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	19	57
39	I	125/127 (98%)	103 (82%)	16 (13%)	6 (5%)	2	24
40	J	96/98 (98%)	78 (81%)	10 (10%)	8 (8%)	1	14
41	K	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	L	121/123 (98%)	93 (77%)	19 (16%)	9 (7%)	1	16
43	M	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	5	35
44	N	98/100 (98%)	83 (85%)	15 (15%)	0	100	100
45	O	86/88 (98%)	80 (93%)	4 (5%)	2 (2%)	6	38
46	P	80/82 (98%)	68 (85%)	11 (14%)	1 (1%)	12	48
47	Q	78/80 (98%)	66 (85%)	9 (12%)	3 (4%)	3	28
48	R	63/65 (97%)	56 (89%)	5 (8%)	2 (3%)	4	32
49	S	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	5	35
50	T	83/85 (98%)	79 (95%)	3 (4%)	1 (1%)	13	49
51	U	63/65 (97%)	43 (68%)	19 (30%)	1 (2%)	9	44
52	03	221/223 (99%)	193 (87%)	27 (12%)	1 (0%)	29	67
59	Z	390/392 (100%)	349 (90%)	39 (10%)	2 (0%)	29	67
All	All	6457/6563 (98%)	5581 (86%)	765 (12%)	111 (2%)	13	43

All (111) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	04	232	GLY
3	06	83	VAL
4	07	175	PRO
5	08	46	ASP
5	08	119	GLY
6	09	9	VAL
7	10	80	THR
10	13	35	VAL
12	15	58	LYS
17	20	54	VAL
20	23	6	ARG
20	23	98	ASN
31	34	37	GLN
35	E	25	LYS
35	E	122	VAL
35	E	160	VAL
36	F	53	LYS
36	F	54	LEU
36	F	94	HIS
38	H	47	ASP
39	I	57	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
39	I	90	ASP
39	I	91	GLU
40	J	34	ALA
40	J	58	ASN
40	J	89	ARG
40	J	92	LEU
42	L	102	ASP
43	M	65	GLU
45	O	46	LYS
47	Q	49	ASN
48	R	19	GLU
51	U	8	ASN
4	07	149	ARG
5	08	45	ALA
5	08	175	LYS
6	09	12	LEU
7	10	81	LEU
11	14	31	GLY
30	33	27	ASN
32	B	87	ASP
35	E	11	GLN
35	E	89	THR
35	E	157	GLY
39	I	102	PHE
41	K	89	GLY
42	L	23	LEU
42	L	35	ARG
42	L	77	SER
46	P	79	ASN
47	Q	70	LYS
48	R	18	GLN
50	T	68	LYS
52	03	21	TYR
59	Z	295	PRO
7	10	4	ASN
10	13	93	GLN
11	14	29	LYS
19	22	38	ALA
34	D	23	GLY
34	D	29	THR
34	D	167	PRO
34	D	192	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	G	64	ALA
39	I	12	LYS
40	J	35	GLN
40	J	93	ALA
41	K	125	LYS
42	L	32	VAL
42	L	75	GLU
43	M	4	ALA
47	Q	17	GLU
59	Z	42	ALA
1	04	233	GLY
4	07	20	ASN
4	07	174	PHE
30	33	31	ILE
31	34	34	LYS
34	D	152	SER
35	E	78	GLY
35	E	90	GLY
35	E	121	ASN
39	I	8	THR
41	K	13	LYS
42	L	34	THR
45	O	2	LEU
7	10	51	TYR
7	10	108	VAL
7	10	118	ILE
11	14	52	GLY
11	14	88	GLY
20	23	51	LEU
32	B	18	GLN
32	B	19	THR
34	D	120	LYS
36	F	93	LYS
37	G	18	GLY
42	L	43	LYS
49	S	3	SER
7	10	74	ASP
40	J	42	LEU
40	J	43	PRO
5	08	117	PRO
8	11	4	VAL
41	K	90	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
41	K	77	GLY
42	L	27	PRO
43	M	111	PRO
49	S	7	GLY
2	05	153	GLY
12	15	69	PRO

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	04	216/216 (100%)	210 (97%)	6 (3%)	43	66
2	05	164/164 (100%)	163 (99%)	1 (1%)	86	91
3	06	165/165 (100%)	164 (99%)	1 (1%)	86	91
4	07	148/148 (100%)	146 (99%)	2 (1%)	67	81
5	08	137/137 (100%)	136 (99%)	1 (1%)	84	90
6	09	114/114 (100%)	114 (100%)	0	100	100
7	10	100/100 (100%)	99 (99%)	1 (1%)	76	86
8	11	109/109 (100%)	107 (98%)	2 (2%)	59	77
9	12	116/116 (100%)	116 (100%)	0	100	100
10	13	103/103 (100%)	102 (99%)	1 (1%)	76	86
11	14	102/102 (100%)	102 (100%)	0	100	100
12	15	109/109 (100%)	109 (100%)	0	100	100
13	16	100/100 (100%)	99 (99%)	1 (1%)	76	86
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	88 (99%)	1 (1%)	73	84
17	20	84/84 (100%)	83 (99%)	1 (1%)	71	83
18	21	93/93 (100%)	91 (98%)	2 (2%)	52	71
19	22	80/80 (100%)	78 (98%)	2 (2%)	47	69

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	23	83/83 (100%)	83 (100%)	0	100	100
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	53 (96%)	2 (4%)	35	61
25	28	48/48 (100%)	47 (98%)	1 (2%)	53	73
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	45 (100%)	0	100	100
29	32	38/38 (100%)	37 (97%)	1 (3%)	46	68
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	34 (100%)	0	100	100
32	B	180/180 (100%)	177 (98%)	3 (2%)	60	78
33	C	170/170 (100%)	167 (98%)	3 (2%)	59	77
34	D	172/172 (100%)	169 (98%)	3 (2%)	60	78
35	E	119/119 (100%)	116 (98%)	3 (2%)	47	69
36	F	87/87 (100%)	87 (100%)	0	100	100
37	G	124/124 (100%)	124 (100%)	0	100	100
38	H	104/104 (100%)	104 (100%)	0	100	100
39	I	105/105 (100%)	105 (100%)	0	100	100
40	J	86/86 (100%)	86 (100%)	0	100	100
41	K	89/89 (100%)	88 (99%)	1 (1%)	73	84
42	L	103/103 (100%)	101 (98%)	2 (2%)	57	75
43	M	92/92 (100%)	89 (97%)	3 (3%)	38	63
44	N	83/83 (100%)	83 (100%)	0	100	100
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	62 (95%)	3 (5%)	27	55
47	Q	74/74 (100%)	74 (100%)	0	100	100
48	R	56/56 (100%)	55 (98%)	1 (2%)	59	77
49	S	70/70 (100%)	70 (100%)	0	100	100
50	T	65/65 (100%)	62 (95%)	3 (5%)	27	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	U	55/55 (100%)	54 (98%)	1 (2%)	59	77
52	03	174/174 (100%)	172 (99%)	2 (1%)	73	84
59	Z	324/325 (100%)	317 (98%)	7 (2%)	52	71
All	All	5349/5350 (100%)	5288 (99%)	61 (1%)	74	84

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	04	34	GLU
1	04	36	ASN
1	04	132	ARG
1	04	212	TRP
1	04	257	ARG
1	04	261	ARG
2	05	33	ARG
3	06	163	ASN
4	07	109	ARG
4	07	151	LEU
5	08	109	SER
7	10	3	LEU
8	11	18	ASN
8	11	95	ASP
10	13	49	ARG
13	16	2	ARG
16	19	27	ARG
17	20	11	GLN
18	21	57	ASN
18	21	62	ASP
19	22	52	GLU
19	22	59	ASN
24	27	7	ARG
24	27	29	ARG
25	28	15	ARG
29	32	28	ARG
32	B	18	GLN
32	B	23	ASN
32	B	94	ARG
33	C	24	ASN
33	C	106	ARG
33	C	156	LEU
34	D	28	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	D	170	LEU
34	D	177	MET
35	E	69	ASN
35	E	111	ARG
35	E	156	ARG
41	K	124	LYS
42	L	34	THR
42	L	113	ARG
43	M	7	ASN
43	M	15	VAL
43	M	97	ARG
46	P	29	ASN
46	P	35	ARG
46	P	69	ASP
48	R	11	ARG
50	T	20	ASN
50	T	29	THR
50	T	53	MET
51	U	61	ARG
52	03	21	TYR
52	03	202	THR
59	Z	230	ARG
59	Z	237	LYS
59	Z	245	VAL
59	Z	269	ARG
59	Z	322	PHE
59	Z	357	LYS
59	Z	358	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
1	04	36	ASN
1	04	85	ASN
1	04	114	GLN
1	04	196	ASN
1	04	238	ASN
2	05	150	GLN
3	06	41	GLN
3	06	92	HIS
3	06	94	GLN
3	06	163	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	07	51	ASN
5	08	21	GLN
5	08	29	ASN
5	08	37	ASN
5	08	72	ASN
5	08	138	GLN
6	09	66	ASN
8	11	18	ASN
8	11	30	GLN
8	11	33	ASN
10	13	3	GLN
12	15	13	HIS
13	16	9	GLN
13	16	62	ASN
13	16	81	ASN
14	17	19	GLN
15	18	9	GLN
16	19	36	GLN
16	19	43	GLN
17	20	18	GLN
18	21	9	HIS
18	21	57	ASN
20	23	68	ASN
23	26	16	ASN
24	27	20	ASN
24	27	39	GLN
24	27	41	HIS
24	27	58	ASN
25	28	19	HIS
26	29	20	ASN
26	29	48	GLN
26	29	61	ASN
27	30	41	HIS
31	34	35	GLN
32	B	23	ASN
32	B	41	ASN
32	B	108	GLN
32	B	169	HIS
32	B	177	ASN
33	C	24	ASN
33	C	139	ASN
34	D	88	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	D	197	HIS
35	E	69	ASN
35	E	145	ASN
36	F	11	HIS
36	F	55	HIS
37	G	27	ASN
38	H	15	ASN
38	H	17	GLN
38	H	75	GLN
39	I	36	GLN
39	I	49	GLN
39	I	125	GLN
40	J	20	GLN
42	L	45	ASN
44	N	42	ASN
45	O	36	ASN
46	P	79	ASN
47	Q	8	GLN
47	Q	30	HIS
48	R	51	GLN
49	S	68	HIS
50	T	20	ASN
50	T	51	ASN
50	T	60	GLN
52	03	67	HIS
52	03	148	ASN
52	03	165	ASN
52	03	188	ASN
59	Z	48	GLN
59	Z	97	GLN
59	Z	124	GLN
59	Z	273	ASN
59	Z	290	GLN
59	Z	329	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	161 (10%)	10 (0%)
54	01	2902/2903 (99%)	355 (12%)	12 (0%)
55	02	119/120 (99%)	9 (7%)	1 (0%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
56	W	76/77 (98%)	7 (9%)	0
56	X	76/77 (98%)	11 (14%)	0
57	V	19/20 (95%)	2 (10%)	0
58	Y	75/76 (98%)	12 (16%)	0
All	All	4805/4812 (99%)	557 (11%)	23 (0%)

All (557) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	7	A
53	A	9	G
53	A	22	G
53	A	31	G
53	A	32	A
53	A	39	G
53	A	51	A
53	A	71	A
53	A	82	G
53	A	86	G
53	A	87	C
53	A	94	G
53	A	95	C
53	A	100	G
53	A	121	U
53	A	130	A
53	A	183	C
53	A	184	G
53	A	197	A
53	A	209	U
53	A	210	C
53	A	226	G
53	A	240	G
53	A	247	G
53	A	251	G
53	A	253	A
53	A	266	G
53	A	267	C
53	A	281	G
53	A	289	G
53	A	306	A
53	A	328	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	345	C
53	A	346	G
53	A	352	C
53	A	367	U
53	A	372	C
53	A	398	U
53	A	411	A
53	A	413	G
53	A	422	C
53	A	429	U
53	A	467	U
53	A	485	U
53	A	486	U
53	A	496	A
53	A	497	G
53	A	518	C
53	A	530	G
53	A	531	U
53	A	532	A
53	A	533	A
53	A	547	A
53	A	561	U
53	A	572	A
53	A	573	A
53	A	574	A
53	A	575	G
53	A	576	C
53	A	577	G
53	A	607	A
53	A	633	G
53	A	642	A
53	A	665	A
53	A	688	G
53	A	703	G
53	A	713	G
53	A	724	G
53	A	731	G
53	A	755	G
53	A	777	A
53	A	794	A
53	A	805	C
53	A	815	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	817	C
53	A	818	G
53	A	819	A
53	A	820	U
53	A	821	G
53	A	832	G
53	A	842	U
53	A	843	U
53	A	844	G
53	A	846	G
53	A	873	A
53	A	890	G
53	A	902	G
53	A	926	G
53	A	934	C
53	A	935	A
53	A	960	U
53	A	961	U
53	A	966	G
53	A	969	A
53	A	975	A
53	A	976	G
53	A	977	A
53	A	992	U
53	A	993	G
53	A	994	A
53	A	1004	A
53	A	1028	C
53	A	1030	U
53	A	1031	C
53	A	1033	G
53	A	1034	G
53	A	1053	G
53	A	1054	C
53	A	1094	G
53	A	1101	A
53	A	1129	C
53	A	1130	A
53	A	1137	C
53	A	1138	G
53	A	1139	G
53	A	1159	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	1168	U
53	A	1182	G
53	A	1184	G
53	A	1191	A
53	A	1196	A
53	A	1197	A
53	A	1201	A
53	A	1202	U
53	A	1207	G
53	A	1213	A
53	A	1225	A
53	A	1238	A
53	A	1241	G
53	A	1256	A
53	A	1258	G
53	A	1260	G
53	A	1278	G
53	A	1280	A
53	A	1282	C
53	A	1286	U
53	A	1287	A
53	A	1300	G
53	A	1302	C
53	A	1317	C
53	A	1346	A
53	A	1347	G
53	A	1348	U
53	A	1378	C
53	A	1395	C
53	A	1400	C
53	A	1446	A
53	A	1448	C
53	A	1451	U
53	A	1452	C
53	A	1492	A
53	A	1499	A
53	A	1503	A
53	A	1505	G
53	A	1506	U
53	A	1517	G
53	A	1519	A
53	A	1529	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	1530	G
53	A	1534	A
54	01	10	A
54	01	12	U
54	01	34	U
54	01	35	G
54	01	46	G
54	01	51	G
54	01	63	A
54	01	71	A
54	01	74	A
54	01	75	G
54	01	119	A
54	01	120	U
54	01	139	U
54	01	140	C
54	01	141	G
54	01	142	A
54	01	162	U
54	01	163	C
54	01	181	A
54	01	196	A
54	01	216	A
54	01	221	A
54	01	222	A
54	01	228	C
54	01	242	G
54	01	243	U
54	01	248	G
54	01	249	C
54	01	255	A
54	01	266	G
54	01	276	U
54	01	278	A
54	01	281	C
54	01	294	A
54	01	301	G
54	01	311	A
54	01	323	C
54	01	324	A
54	01	329	G
54	01	330	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	361	G
54	01	363	G
54	01	367	G
54	01	371	A
54	01	372	G
54	01	373	U
54	01	386	G
54	01	387	U
54	01	388	G
54	01	404	A
54	01	406	G
54	01	411	G
54	01	422	A
54	01	424	G
54	01	451	U
54	01	457	A
54	01	481	G
54	01	491	G
54	01	504	A
54	01	505	A
54	01	506	G
54	01	508	A
54	01	509	C
54	01	529	A
54	01	531	C
54	01	532	A
54	01	542	C
54	01	543	G
54	01	545	U
54	01	547	A
54	01	563	A
54	01	573	U
54	01	588	U
54	01	603	A
54	01	614	A
54	01	616	A
54	01	627	A
54	01	637	A
54	01	646	U
54	01	654	A
54	01	669	G
54	01	686	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	687	C
54	01	695	G
54	01	730	A
54	01	747	C
54	01	752	A
54	01	764	A
54	01	775	G
54	01	776	G
54	01	782	A
54	01	784	G
54	01	785	G
54	01	805	G
54	01	812	C
54	01	819	A
54	01	827	U
54	01	828	U
54	01	830	G
54	01	845	A
54	01	846	U
54	01	847	U
54	01	858	G
54	01	859	G
54	01	860	U
54	01	878	A
54	01	885	C
54	01	886	A
54	01	888	C
54	01	891	G
54	01	896	A
54	01	910	A
54	01	932	U
54	01	941	A
54	01	946	C
54	01	961	C
54	01	974	G
54	01	975	A
54	01	983	A
54	01	985	C
54	01	995	C
54	01	996	A
54	01	1012	U
54	01	1013	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1021	A
54	01	1022	G
54	01	1026	G
54	01	1033	U
54	01	1045	C
54	01	1046	A
54	01	1054	A
54	01	1059	G
54	01	1060	U
54	01	1062	G
54	01	1065	U
54	01	1066	U
54	01	1070	A
54	01	1071	G
54	01	1075	C
54	01	1079	C
54	01	1084	A
54	01	1088	A
54	01	1103	A
54	01	1104	C
54	01	1106	G
54	01	1111	A
54	01	1131	G
54	01	1132	U
54	01	1133	A
54	01	1135	C
54	01	1157	G
54	01	1174	U
54	01	1175	A
54	01	1177	G
54	01	1180	U
54	01	1212	G
54	01	1238	G
54	01	1248	G
54	01	1251	C
54	01	1253	A
54	01	1256	G
54	01	1271	G
54	01	1272	A
54	01	1273	U
54	01	1301	A
54	01	1302	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1306	C
54	01	1321	A
54	01	1329	U
54	01	1332	G
54	01	1345	C
54	01	1365	A
54	01	1378	A
54	01	1379	U
54	01	1383	A
54	01	1395	A
54	01	1416	G
54	01	1419	A
54	01	1420	A
54	01	1428	C
54	01	1454	C
54	01	1461	C
54	01	1482	G
54	01	1490	A
54	01	1491	G
54	01	1498	C
54	01	1515	A
54	01	1524	G
54	01	1533	C
54	01	1535	A
54	01	1536	C
54	01	1555	G
54	01	1559	U
54	01	1560	G
54	01	1569	A
54	01	1581	G
54	01	1584	U
54	01	1585	C
54	01	1608	A
54	01	1611	C
54	01	1616	A
54	01	1634	A
54	01	1647	U
54	01	1648	U
54	01	1651	G
54	01	1674	G
54	01	1694	C
54	01	1715	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1729	U
54	01	1730	C
54	01	1732	C
54	01	1738	G
54	01	1758	U
54	01	1764	C
54	01	1773	A
54	01	1780	A
54	01	1787	A
54	01	1800	C
54	01	1801	A
54	01	1808	A
54	01	1816	C
54	01	1821	A
54	01	1829	A
54	01	1833	C
54	01	1871	A
54	01	1901	A
54	01	1906	G
54	01	1907	G
54	01	1913	A
54	01	1914	C
54	01	1929	G
54	01	1930	G
54	01	1931	U
54	01	1937	A
54	01	1944	U
54	01	1955	U
54	01	1962	C
54	01	1963	U
54	01	1967	C
54	01	1970	A
54	01	1971	U
54	01	1972	G
54	01	1991	U
54	01	1993	U
54	01	1997	C
54	01	2022	U
54	01	2023	C
54	01	2030	A
54	01	2031	A
54	01	2036	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	2043	C
54	01	2049	G
54	01	2055	C
54	01	2056	G
54	01	2060	A
54	01	2061	G
54	01	2062	A
54	01	2069	G
54	01	2072	C
54	01	2093	G
54	01	2096	C
54	01	2108	A
54	01	2110	G
54	01	2111	U
54	01	2112	G
54	01	2116	G
54	01	2118	U
54	01	2119	A
54	01	2125	G
54	01	2127	G
54	01	2132	U
54	01	2133	G
54	01	2145	C
54	01	2147	A
54	01	2162	G
54	01	2164	C
54	01	2171	A
54	01	2172	U
54	01	2173	A
54	01	2189	U
54	01	2198	A
54	01	2204	G
54	01	2211	A
54	01	2213	U
54	01	2225	A
54	01	2239	G
54	01	2250	G
54	01	2259	U
54	01	2266	A
54	01	2278	A
54	01	2283	C
54	01	2287	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	2297	A
54	01	2305	U
54	01	2309	A
54	01	2320	U
54	01	2325	G
54	01	2327	A
54	01	2334	U
54	01	2337	G
54	01	2350	C
54	01	2383	G
54	01	2385	C
54	01	2402	U
54	01	2406	A
54	01	2407	A
54	01	2423	U
54	01	2424	C
54	01	2429	G
54	01	2430	A
54	01	2435	A
54	01	2441	U
54	01	2447	G
54	01	2448	A
54	01	2476	A
54	01	2498	C
54	01	2502	G
54	01	2503	A
54	01	2505	G
54	01	2518	A
54	01	2520	C
54	01	2547	A
54	01	2554	U
54	01	2567	G
54	01	2572	A
54	01	2602	A
54	01	2609	U
54	01	2613	U
54	01	2655	G
54	01	2682	A
54	01	2689	U
54	01	2690	U
54	01	2713	U
54	01	2714	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	2744	G
54	01	2748	A
54	01	2751	G
54	01	2764	A
54	01	2765	A
54	01	2778	A
54	01	2779	U
54	01	2791	G
54	01	2794	C
54	01	2797	U
54	01	2798	U
54	01	2799	A
54	01	2800	A
54	01	2801	G
54	01	2809	A
54	01	2820	A
54	01	2821	A
54	01	2833	U
54	01	2867	G
54	01	2868	A
54	01	2880	C
55	02	4	C
55	02	13	G
55	02	35	C
55	02	44	G
55	02	45	A
55	02	67	G
55	02	89	U
55	02	108	A
55	02	109	A
56	X	3	C
56	X	8	U
56	X	9	G
56	X	10	G
56	X	14	A
56	X	19	G
56	X	21	A
56	X	22	G
56	X	32	C
56	X	34	C
56	X	38	A
57	V	12	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
57	V	19	U
56	W	9	G
56	W	18	G
56	W	19	G
56	W	20	U
56	W	21	A
56	W	47	U
56	W	48	C
58	Y	17	C
58	Y	18	G
58	Y	20	U
58	Y	21	A
58	Y	22	G
58	Y	44	G
58	Y	45	U
58	Y	46	G
58	Y	48	C
58	Y	53	G
58	Y	54	U
58	Y	61	C

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	70	U
53	A	246	A
53	A	280	C
53	A	495	A
53	A	531	U
53	A	960	U
53	A	1190	G
53	A	1201	A
53	A	1347	G
53	A	1399	C
54	01	242	G
54	01	372	G
54	01	421	C
54	01	490	C
54	01	858	G
54	01	859	G
54	01	1020	A
54	01	1130	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1378	A
54	01	1930	G
54	01	2296	U
54	01	2326	C
55	02	88	C

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
60	GCP	Z	401	-	27,34,34	2.03	8 (29%)	34,54,54	4.00	18 (52%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GCP	Z	401	-	-	9/15/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	Z	401	GCP	O4'-C1'	4.68	1.47	1.41
60	Z	401	GCP	PB-O3A	-3.92	1.54	1.58
60	Z	401	GCP	C6-N1	3.84	1.39	1.33
60	Z	401	GCP	C5-C6	3.54	1.47	1.41
60	Z	401	GCP	C2'-C1'	2.97	1.58	1.53
60	Z	401	GCP	C2-N1	2.30	1.39	1.35
60	Z	401	GCP	C2'-C3'	2.22	1.59	1.53
60	Z	401	GCP	PB-O2B	-2.12	1.51	1.56

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	Z	401	GCP	C1'-N9-C4	13.35	150.09	126.64
60	Z	401	GCP	C5-C6-N1	-9.07	111.03	123.43
60	Z	401	GCP	O1G-PG-C3B	-7.45	95.19	111.24
60	Z	401	GCP	C2-N1-C6	6.79	126.72	115.93
60	Z	401	GCP	O4'-C1'-C2'	-6.74	97.07	106.93
60	Z	401	GCP	O5'-PA-O1A	-4.03	93.32	109.07
60	Z	401	GCP	C4-C5-C6	-3.99	116.99	120.80
60	Z	401	GCP	O2B-PB-O1B	3.65	122.25	110.07
60	Z	401	GCP	C2-N3-C4	-3.56	111.30	115.36
60	Z	401	GCP	O3'-C3'-C4'	-3.27	101.59	111.05
60	Z	401	GCP	PB-O3A-PA	3.25	142.87	132.56
60	Z	401	GCP	O3G-PG-O1G	2.96	120.21	112.39
60	Z	401	GCP	O2G-PG-C3B	2.95	113.55	106.40
60	Z	401	GCP	O4'-C4'-C5'	2.75	118.43	109.37
60	Z	401	GCP	N3-C2-N1	-2.55	123.83	127.22
60	Z	401	GCP	C4-C5-N7	2.52	112.03	109.40
60	Z	401	GCP	C3'-C2'-C1'	-2.23	97.63	100.98
60	Z	401	GCP	O2A-PA-O1A	2.14	122.81	112.24

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	Z	401	GCP	PB-C3B-PG-O1G
60	Z	401	GCP	PB-C3B-PG-O2G
60	Z	401	GCP	PG-C3B-PB-O1B
60	Z	401	GCP	C5'-O5'-PA-O3A
60	Z	401	GCP	O4'-C4'-C5'-O5'
60	Z	401	GCP	C3'-C4'-C5'-O5'
60	Z	401	GCP	C5'-O5'-PA-O2A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
60	Z	401	GCP	PB-C3B-PG-O3G
60	Z	401	GCP	C5'-O5'-PA-O1A

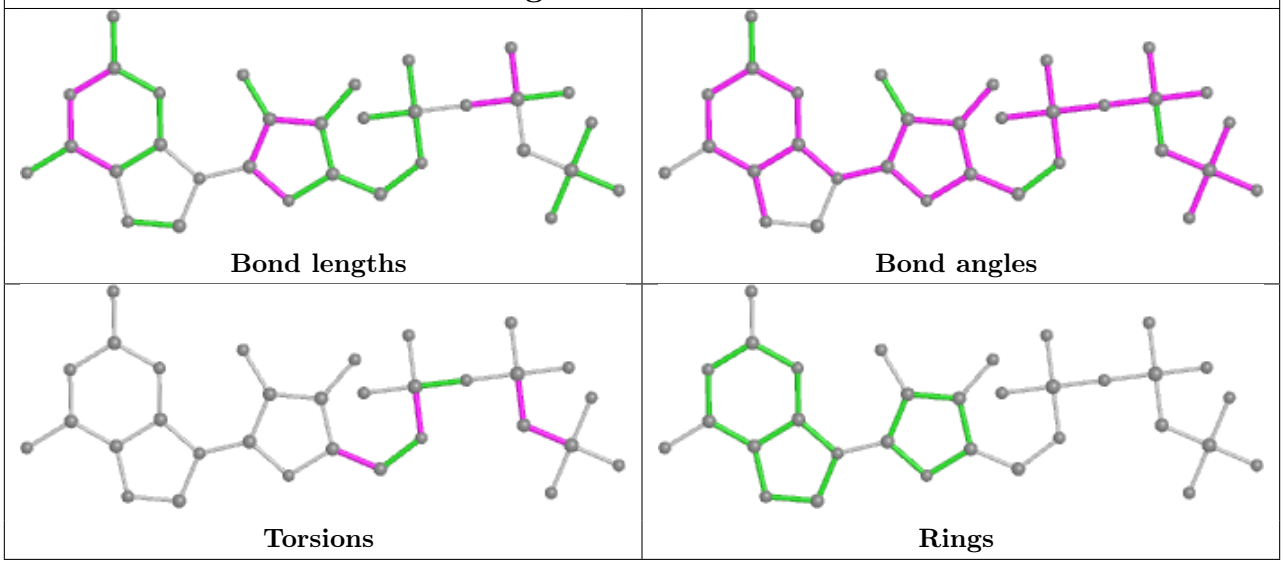
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	Z	401	GCP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GCP Z 401



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.

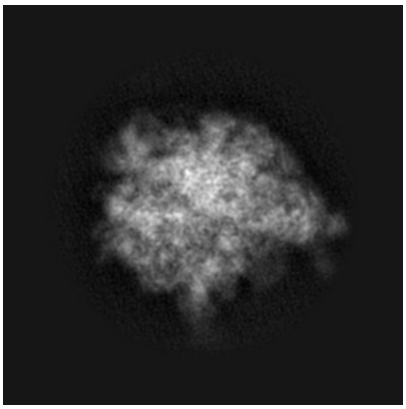
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8615. These allow visual inspection of the internal detail of the map and identification of artifacts.

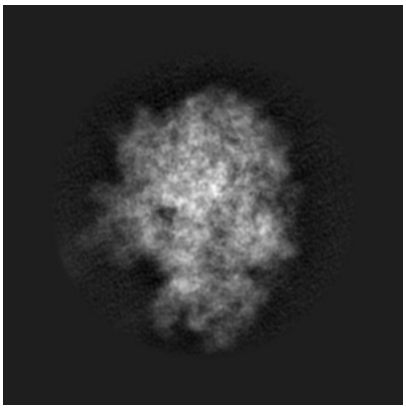
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

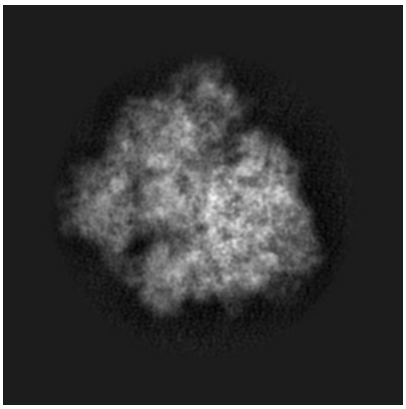
6.1.1 Primary map



X

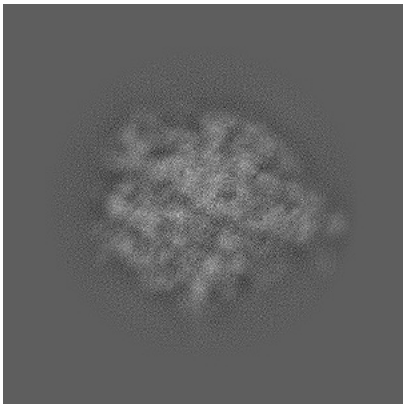


Y

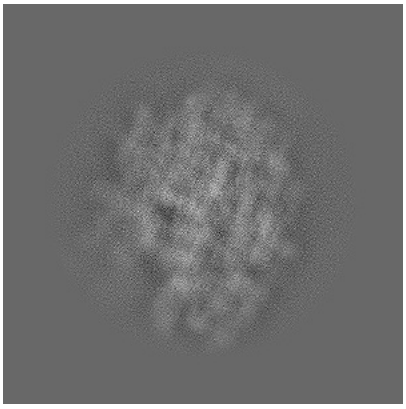


Z

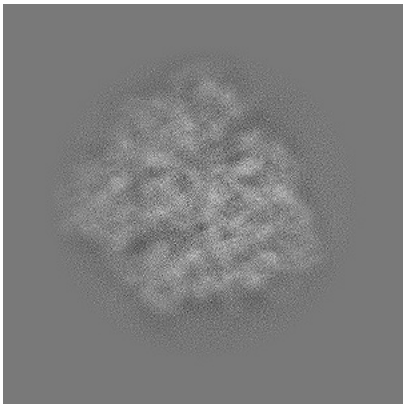
6.1.2 Raw map



X



Y

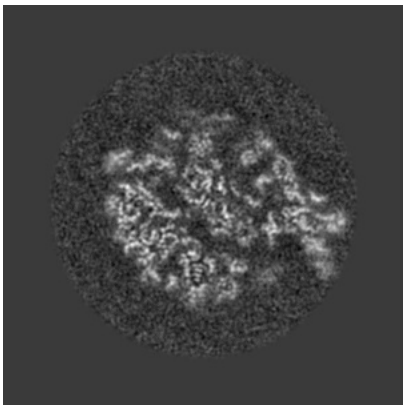


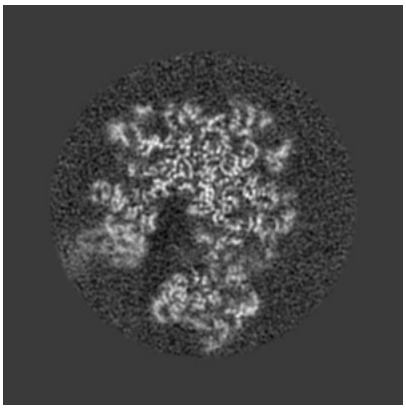
Z

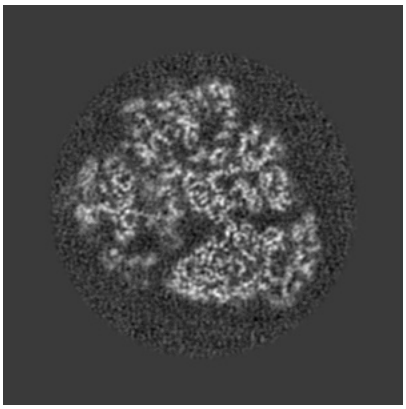
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

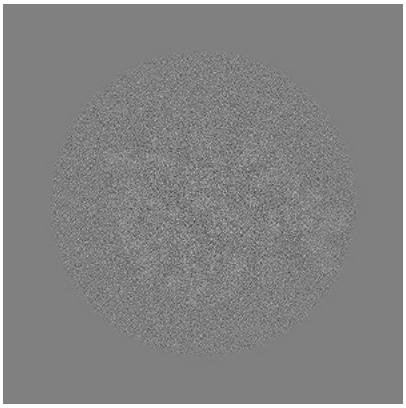
6.2.1 Primary map

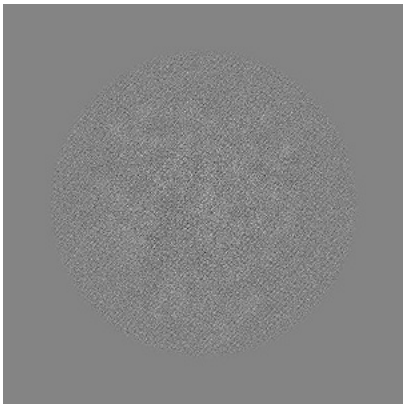

X Index: 240

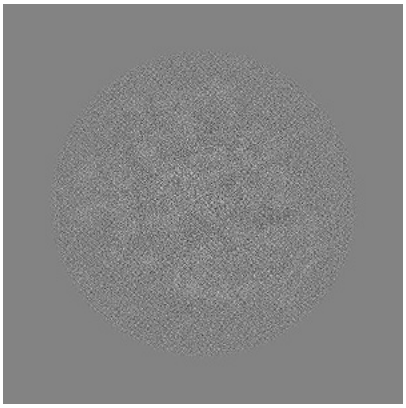

Y Index: 240


Z Index: 240

6.2.2 Raw map


X Index: 240

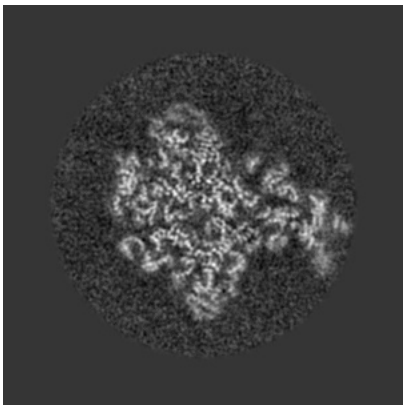

Y Index: 240

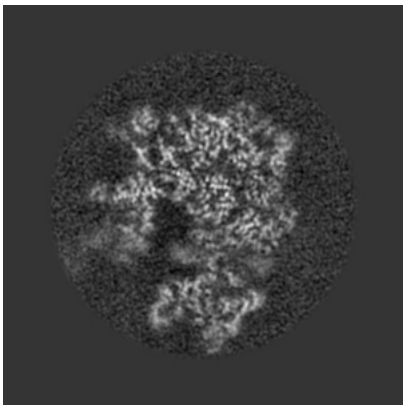

Z Index: 240

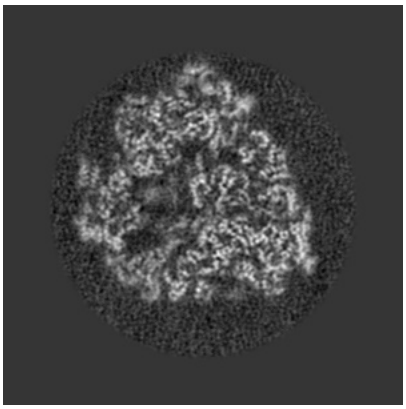
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

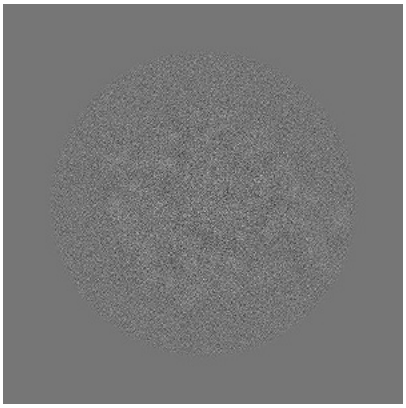
6.3.1 Primary map

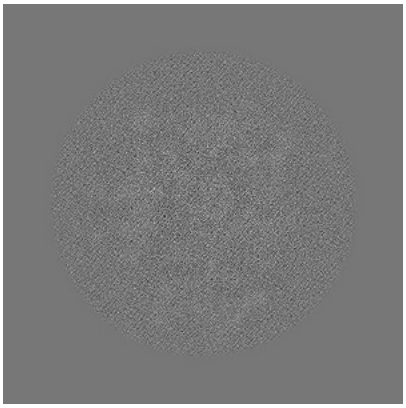

X Index: 251

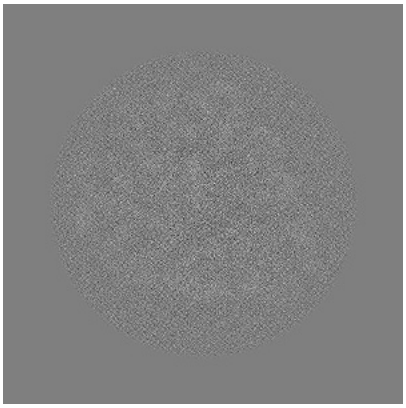

Y Index: 247


Z Index: 227

6.3.2 Raw map


X Index: 237

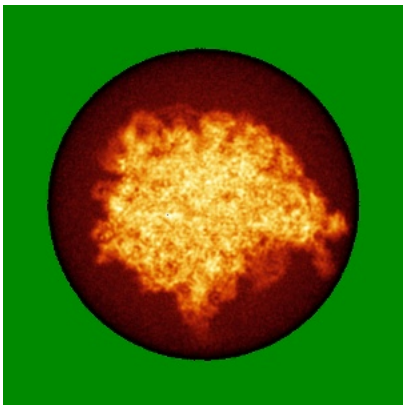

Y Index: 248

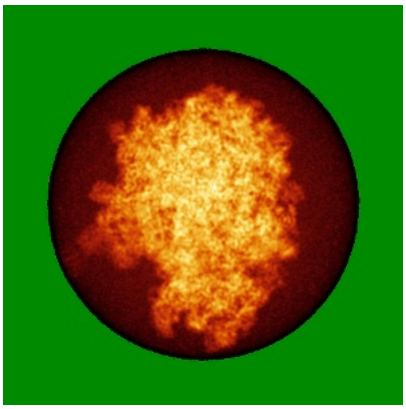

Z Index: 234

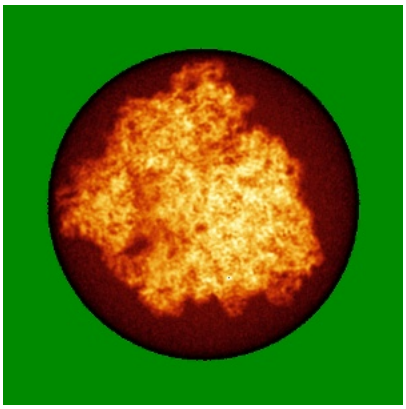
The images above show the largest variance slices of the map in three orthogonal directions.

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

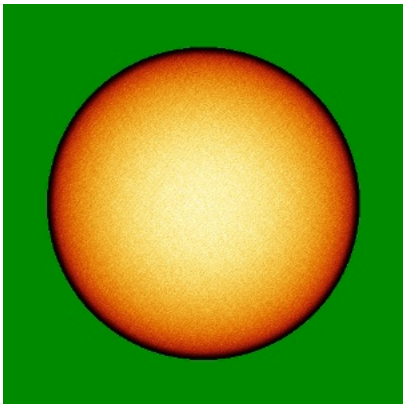
6.4.1 Primary map

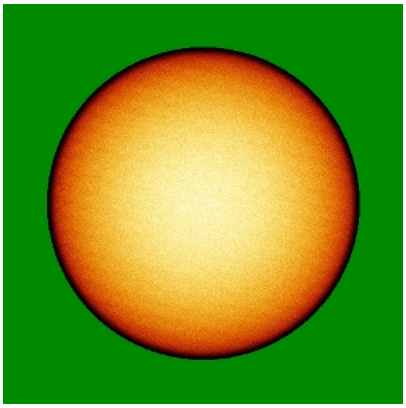

X

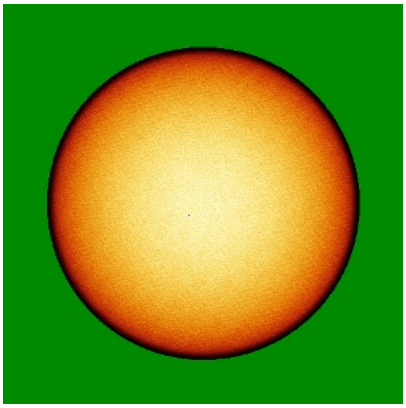

Y


Z

6.4.2 Raw 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

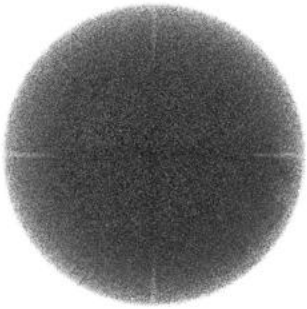
X

Y

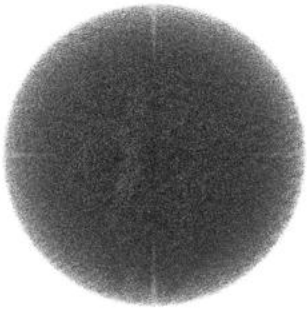
Z

The images above show the 3D surface view of the map at the recommended contour level 3.47. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

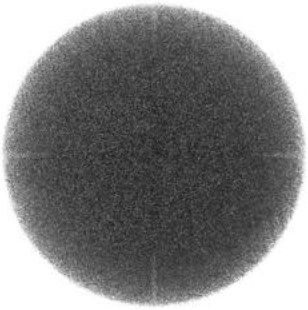
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

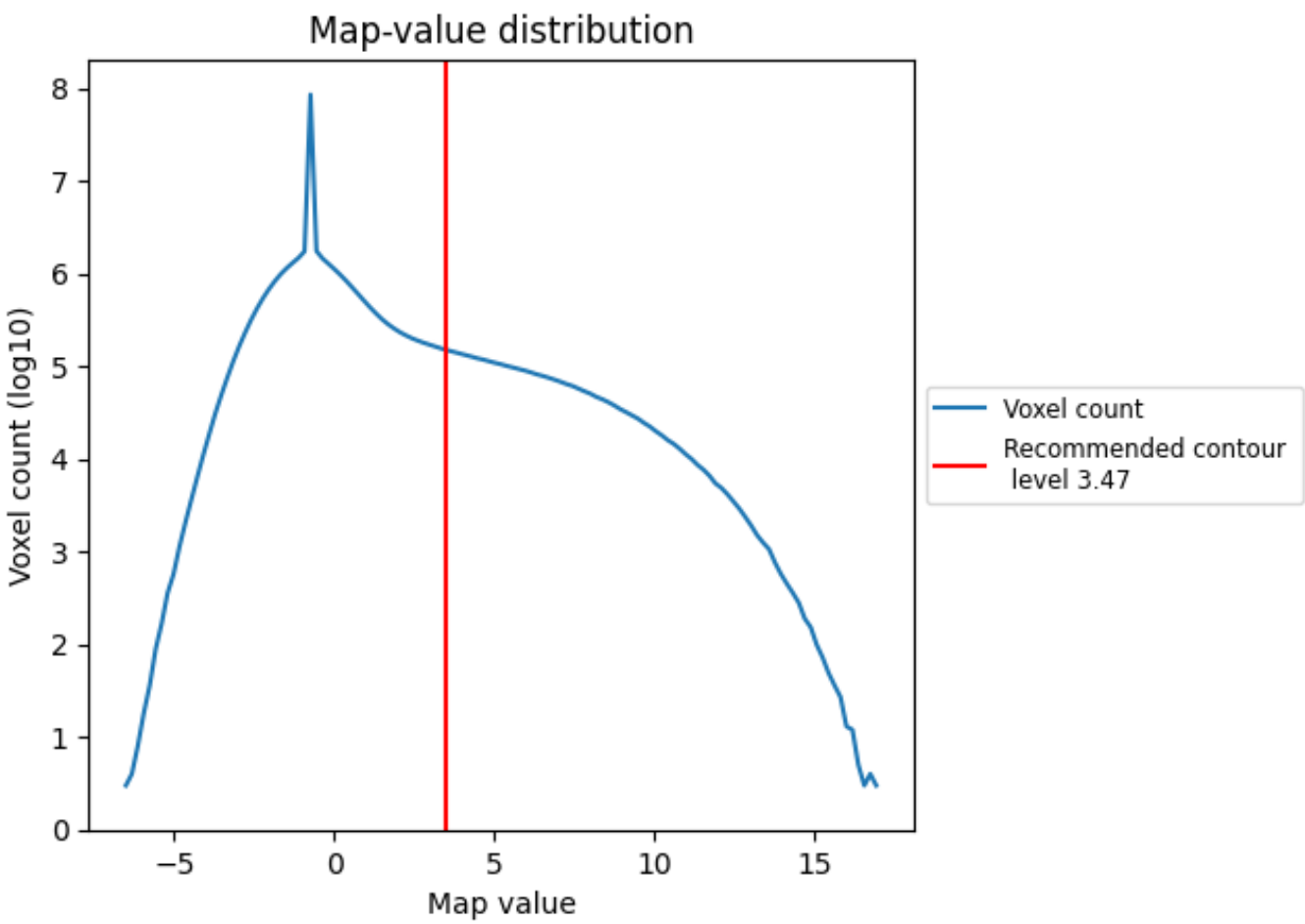
6.6 Mask visualisation (i)

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

7 Map analysis (i)

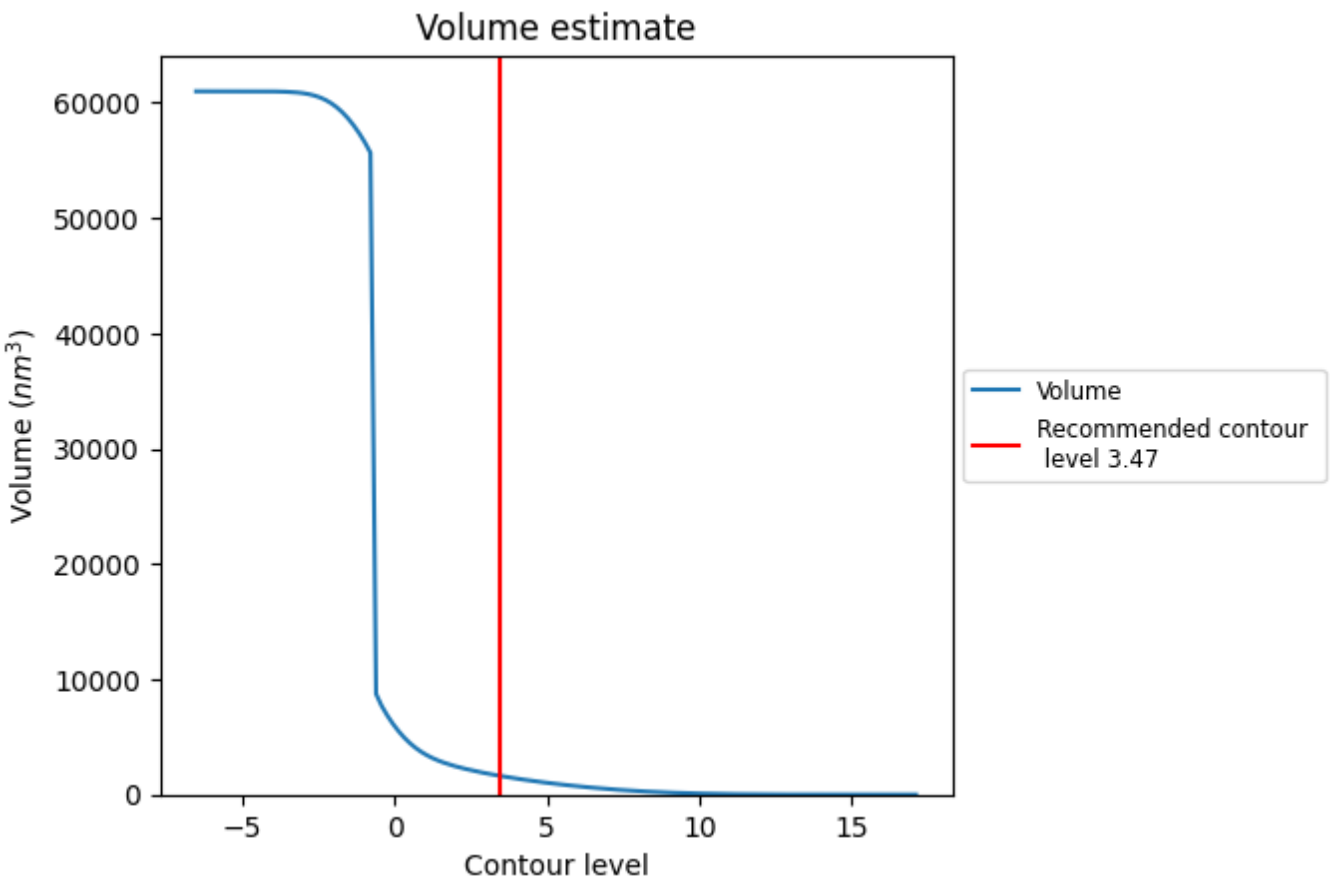
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

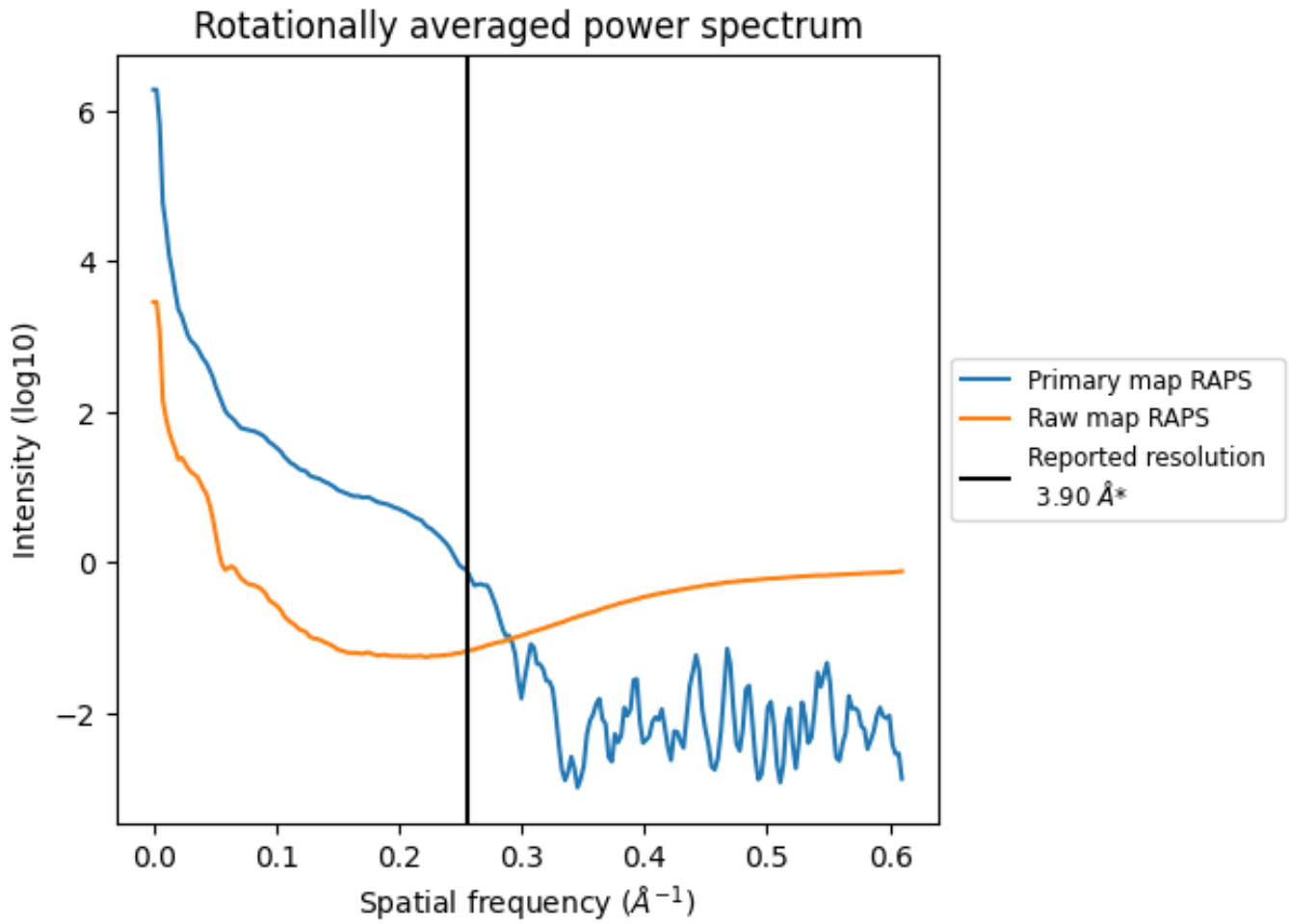
7.2 Volume estimate (i)



The volume at the recommended contour level is 1616 nm^3; this corresponds to an approximate mass of 1460 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)

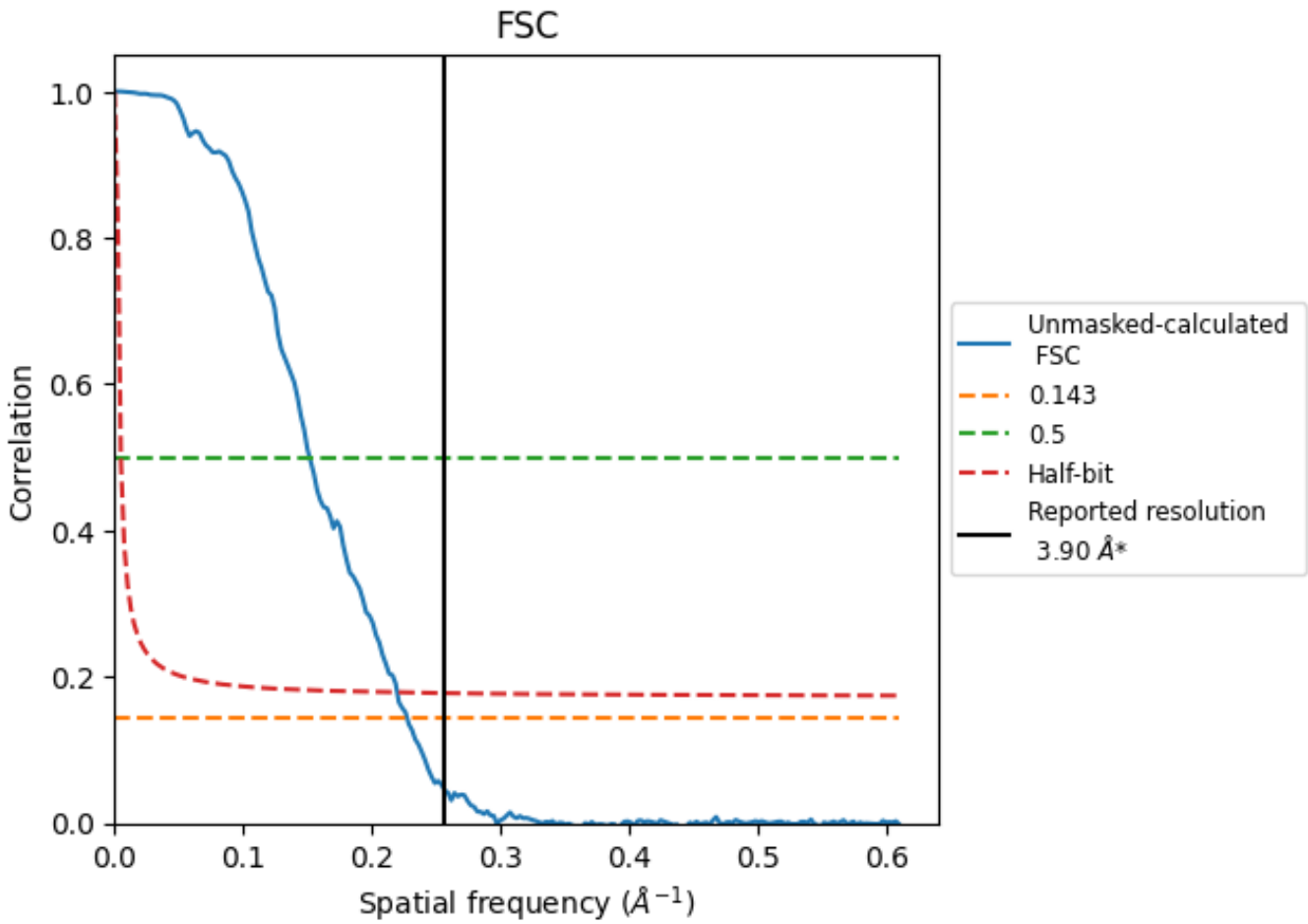


*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8.2 Resolution estimates (i)

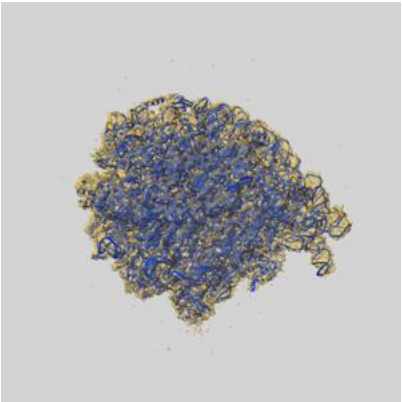
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.40	6.60	4.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.40 differs from the reported value 3.9 by more than 10 %

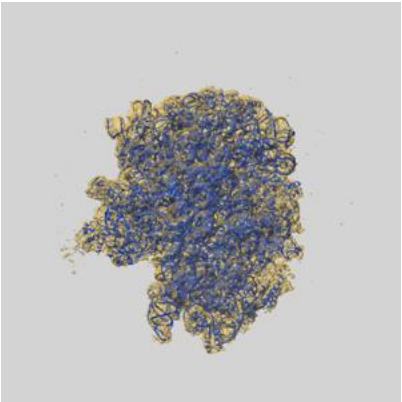
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8615 and PDB model 5UYK. Per-residue inclusion information can be found in section 3 on page 16.

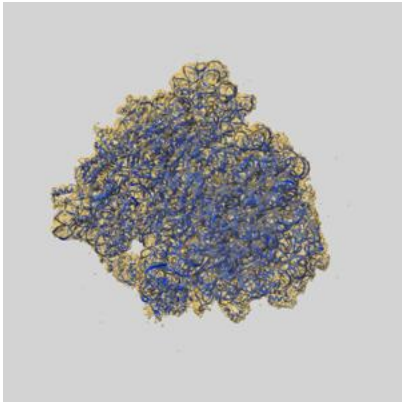
9.1 Map-model overlay (i)



X



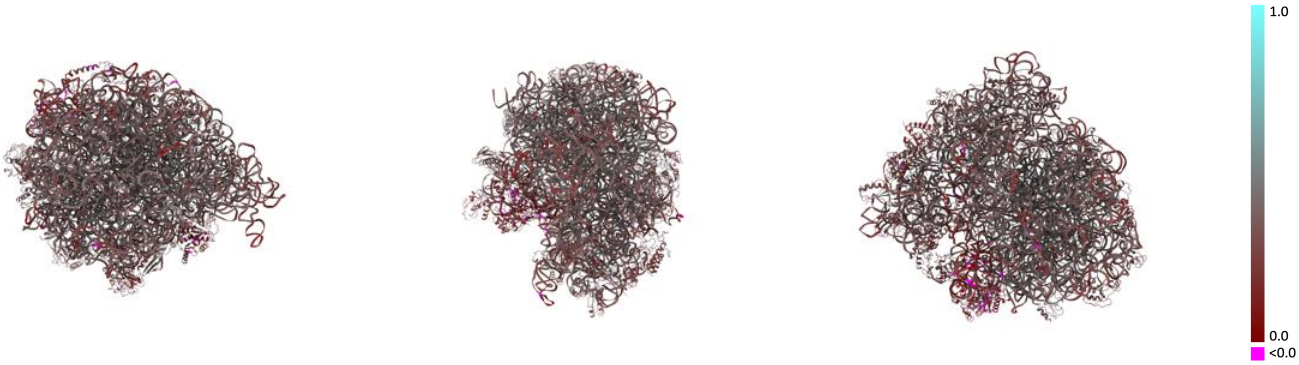
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

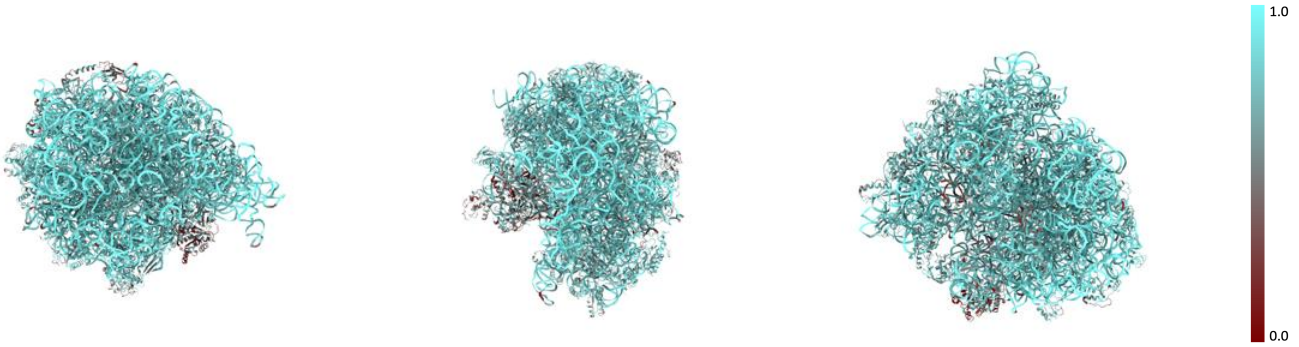
9.2 Q-score mapped to coordinate model (i)



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.

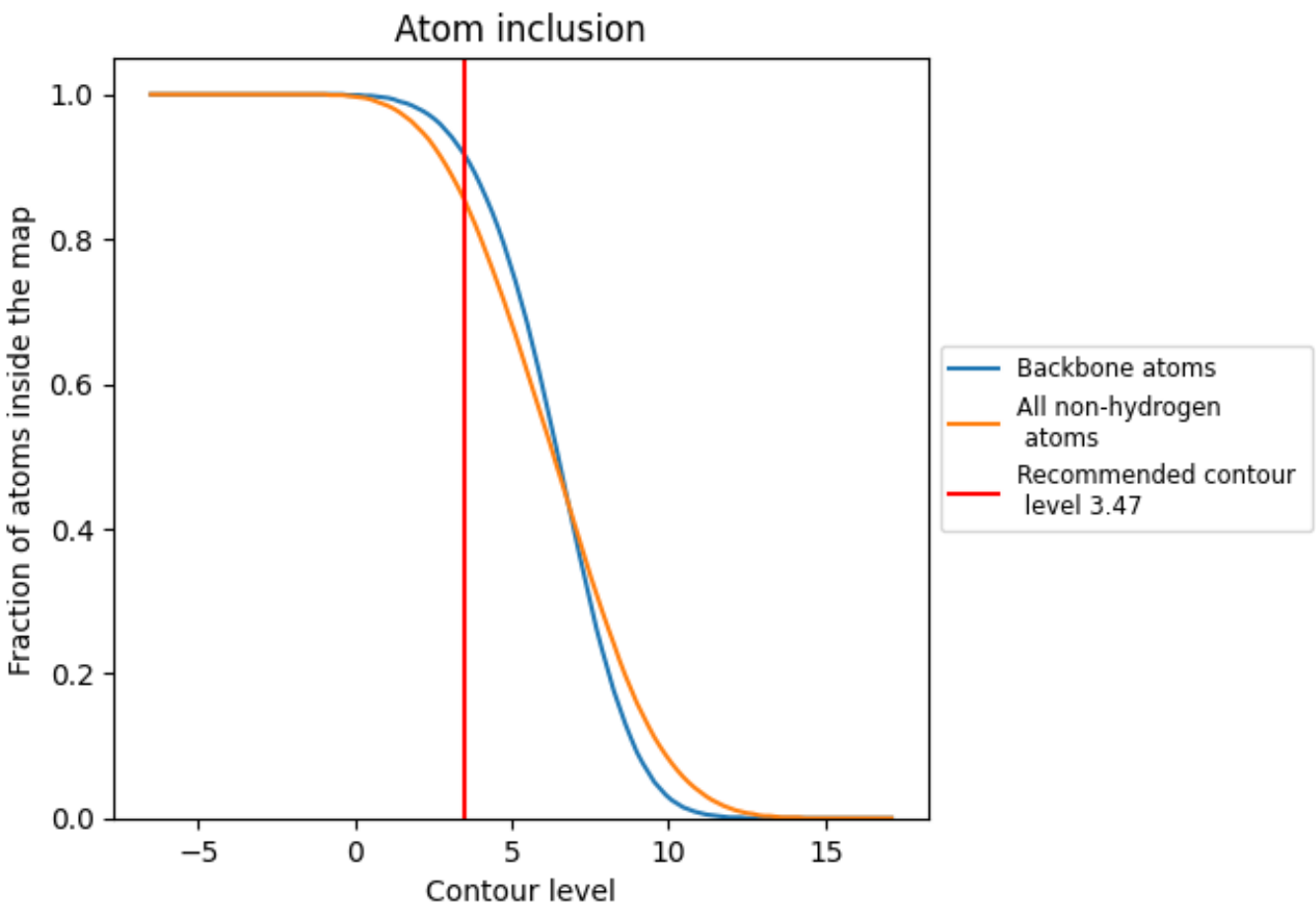
9.3 Atom inclusion mapped to coordinate model (i)



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 (3.47).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (3.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8560	0.3540
01	0.9450	0.3760
02	0.9540	0.3590
03	0.3760	0.1730
04	0.7860	0.4080
05	0.7830	0.3950
06	0.7510	0.3530
07	0.7870	0.3250
08	0.7820	0.3550
09	0.5250	0.2890
10	0.4380	0.1870
11	0.5110	0.1820
12	0.7790	0.3820
13	0.7120	0.4000
14	0.7740	0.3740
15	0.7090	0.3840
16	0.8000	0.3750
17	0.7970	0.3330
18	0.7250	0.3680
19	0.7870	0.3780
20	0.7500	0.3730
21	0.7440	0.3770
22	0.7750	0.3660
23	0.7680	0.3370
24	0.7790	0.3520
25	0.7640	0.3850
26	0.7700	0.3750
27	0.7520	0.3000
28	0.7460	0.3690
29	0.7130	0.2840
30	0.7640	0.3680
31	0.7020	0.3670
32	0.8080	0.3950
33	0.7700	0.3980
34	0.7770	0.4180

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
A	0.9410	0.3650
B	0.7210	0.3030
C	0.7280	0.3550
D	0.7330	0.3220
E	0.7620	0.3680
F	0.8030	0.3520
G	0.7290	0.3230
H	0.7960	0.3680
I	0.7610	0.3090
J	0.6680	0.3140
K	0.7770	0.3550
L	0.7430	0.3830
M	0.7610	0.3260
N	0.7640	0.3370
O	0.7990	0.3440
P	0.8040	0.3630
Q	0.7520	0.3550
R	0.7650	0.3570
S	0.7620	0.3210
T	0.7570	0.3270
U	0.5830	0.2790
V	0.3840	0.2420
W	0.6670	0.3220
X	0.6880	0.1750
Y	0.5960	0.1750
Z	0.3930	0.2260