



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:27 AM UTC

PDB ID : 5UYM / pdb_00005uym
EMDB ID : EMD-8617
Title : 70S ribosome bound with cognate ternary complex base-paired to A site codon, closed 30S (Structure III)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

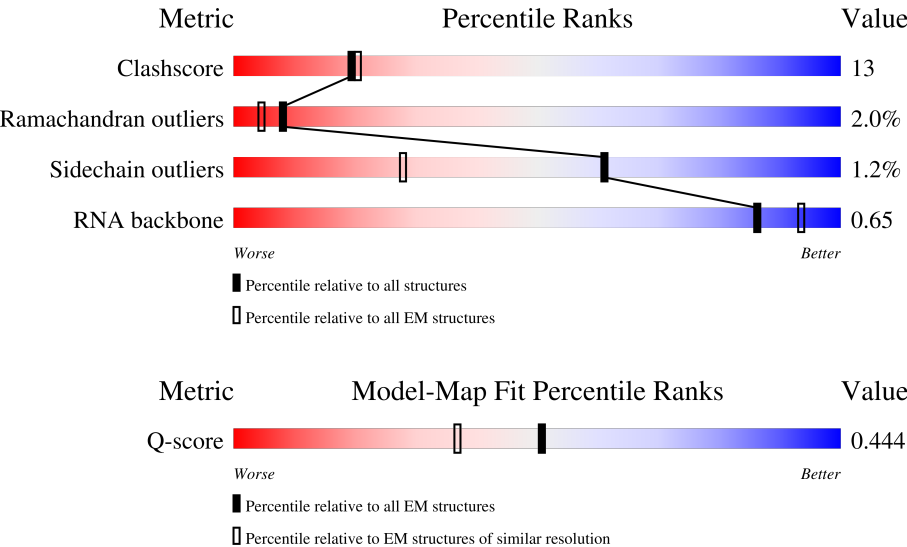
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	04	271	
2	05	209	
3	06	201	

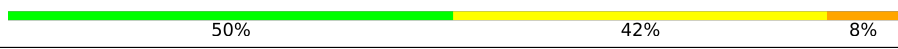
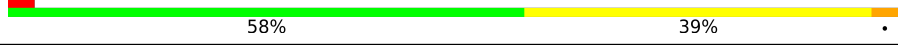
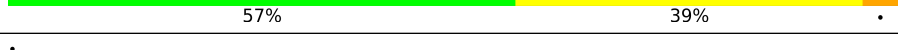
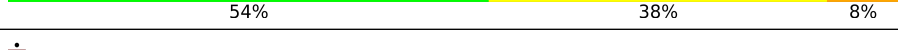
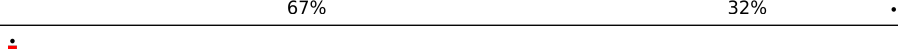
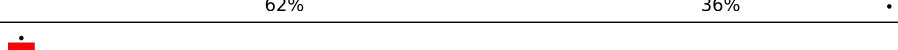
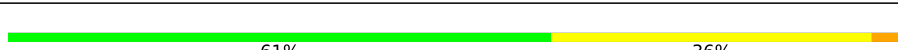
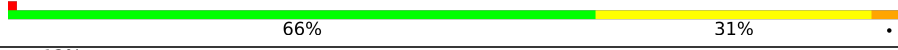
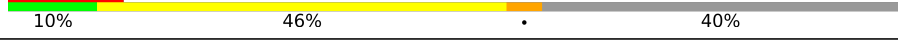
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Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	

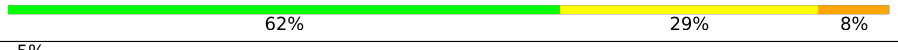
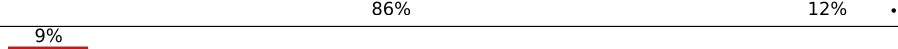
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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	223	
53	A	1539	

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Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	18	
58	Y	76	
59	Z	392	

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 154139 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
1	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

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

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

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

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

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
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

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

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 58 is a RNA chain called Phe-tRNA^{Phe}.

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

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

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

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	12	1	Total	Mg	0
			1	1	
60	25	1	Total	Mg	0
			1	1	
60	N	1	Total	Mg	0
			1	1	
60	A	107	Total	Mg	0
			107	107	
60	01	263	Total	Mg	0
			263	263	

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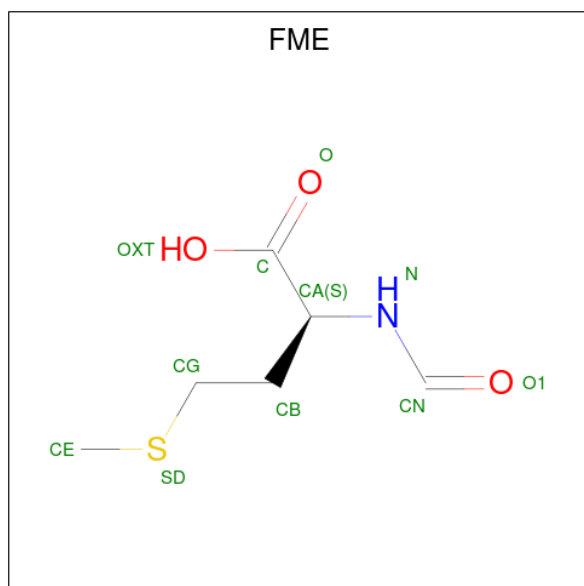
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Mol	Chain	Residues	Atoms		AltConf
60	02	6	Total	Mg	0
			6	6	
60	V	2	Total	Mg	0
			2	2	
60	W	1	Total	Mg	0
			1	1	
60	Z	1	Total	Mg	0
			1	1	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

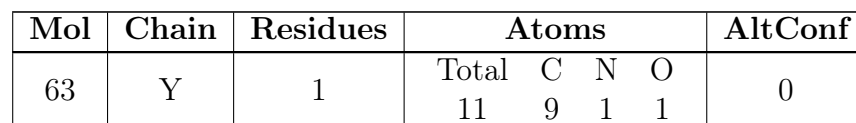
Mol	Chain	Residues	Atoms		AltConf
61	29	1	Total	Zn	0
			1	1	
61	34	1	Total	Zn	0
			1	1	

- Molecule 62 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
62	W	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 63 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



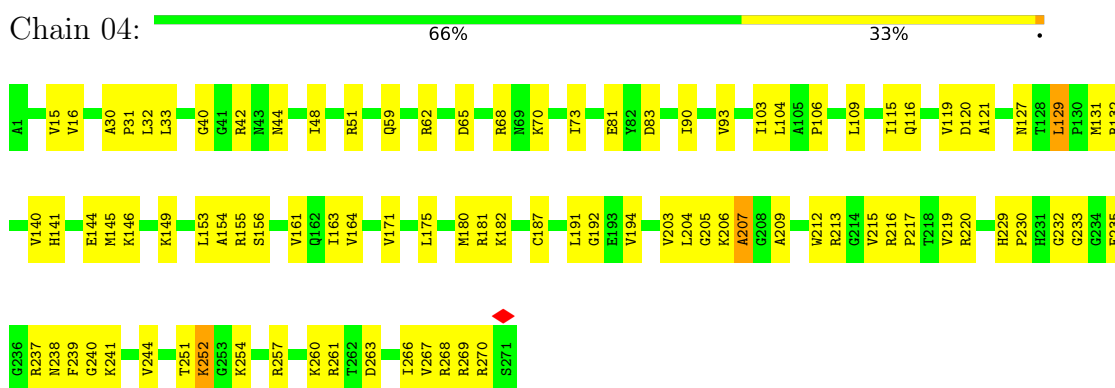
-
- The chemical structure of GCP (Guanosine Cyclic Phosphate) is shown. It consists of a guanine base (a purine ring system with an amino group at position 2) linked to a ribose sugar, which is in turn linked to a cyclic phosphate group. The structure is labeled with various atoms and bonds, including the amino group (H2N), the purine ring atoms (N1, N3, N7, N9), the ribose sugar atoms (C1', C2', C3', C4', C5'), and the phosphate group atoms (P1, P2, P3, P4, P5, P6, P7, P8, P9, P10, P11, P12, P13, P14, P15, P16, P17, P18, P19, P20, P21, P22, P23, P24, P25, P26, P27, P28, P29, P30, P31, P32, P33, P34, P35, P36, P37, P38, P39, P40, P41, P42, P43, P44, P45, P46, P47, P48, P49, P50, P51, P52, P53, P54, P55, P56, P57, P58, P59, P60, P61, P62, P63, P64, P65, P66, P67, P68, P69, P70, P71, P72, P73, P74, P75, P76, P77, P78, P79, P80, P81, P82, P83, P84, P85, P86, P87, P88, P89, P90, P91, P92, P93, P94, P95, P96, P97, P98, P99, P100, P101, P102, P103, P104, P105, P106, P107, P108, P109, P110, P111, P112, P113, P114, P115, P116, P117, P118, P119, P120, P121, P122, P123, P124, P125, P126, P127, P128, P129, P130, P131, P132, P133, P134, P135, P136, P137, P138, P139, P140, P141, P142, P143, P144, P145, P146, P147, P148, P149, P150, P151, P152, P153, P154, P155, P156, P157, P158, P159, P160, P161, P162, P163, P164, P165, P166, P167, P168, P169, P170, P171, P172, P173, P174, P175, P176, P177, P178, P179, P180, P181, P182, P183, P184, P185, P186, P187, P188, P189, P190, P191, P192, P193, P194, P195, P196, P197, P198, P199, P200, P201, P202, P203, P204, P205, P206, P207, P208, P209, P210, P211, P212, P213, P214, P215, P216, P217, P218, P219, P220, P221, P222, P223, P224, P225, P226, P227, P228, P229, P230, P231, P232, P233, P234, P235, P236, P237, P238, P239, P240, P241, P242, P243, P244, P245, P246, P247, P248, P249, P250, P251, P252, P253, P254, P255, P256, P257, P258, P259, P260, P261, P262, P263, P264, P265, P266, P267, P268, P269, P270, P271, P272, P273, P274, P275, P276, P277, P278, P279, P280, P281, P282, P283, P284, P285, P286, P287, P288, P289, P290, P291, P292, P293, P294, P295, P296, P297, P298, P299, P300, P301, P302, P303, P304, P305, P306, P307, P308, P309, P310, P311, P312, P313, P314, P315, P316, P317, P318, P319, P320, P321, P322, P323, P324, P325, P326, P327, P328, P329, P330, P331, P332, P333, P334, P335, P336, P337, P338, P339, P340, P341, P342, P343, P344, P345, P346, P347, P348, P349, P350, P351, P352, P353, P354, P355, P356, P357, P358, P359, P360, P361, P362, P363, P364, P365, P366, P367, P368, P369, P370, P371, P372, P373, P374, P375, P376, P377, P378, P379, P380, P381, P382, P383, P384, P385, P386, P387, P388, P389, P390, P391, P392, P393, P394, P395, P396, P397, P398, P399, P400, P401, P402, P403, P404, P405, P406, P407, P408, P409, P410, P411, P412, P413, P414, P415, P416, P417, P418, P419, P420, P421, P422, P423, P424, P425, P426, P427, P428, P429, P430, P431, P432, P433, P434, P435, P436, P437, P438, P439, P440, P441, P442, P443, P444, P445, P446, P447, P448, P449, P450, P451, P452, P453, P454, P455, P456, P457, P458, P459, P460, P461, P462, P463, P464, P465, P466, P467, P468, P469, P470, P471, P472, P473, P474, P475, P476, P477, P478, P479, P480, P481, P482, P483, P484, P485, P486, P487, P488, P489, P490, P491, P492, P493, P494, P495, P496, P497, P498, P499, P500, P501, P502, P503, P504, P505, P506, P507, P508, P509, P510, P511, P512, P513, P514, P515, P516, P517, P518, P519, P520, P521, P522, P523, P524, P525, P526, P527, P528, P529, P530, P531, P532, P533, P534, P535, P536, P537, P538, P539, P540, P541, P542, P543, P544, P545, P546, P547, P548, P549, P550, P551, P552, P553, P554, P555, P556, P557, P558, P559, P560, P561, P562, P563, P564, P565, P566, P567, P568, P569, P570, P571, P572, P573, P574, P575, P576, P577, P578, P579, P580, P581, P582, P583, P584, P585, P586, P587, P588, P589, P590, P591, P592, P593, P594, P595, P596, P597, P598, P599, P600, P601, P602, P603, P604, P605, P606, P607, P608, P609, P610, P611, P612, P613, P614, P615, P616, P617, P618, P619, P620, P621, P622, P623, P624, P625, P626, P627, P628, P629, P630, P631, P632, P633, P634, P635, P636, P637, P638, P639, P640, P641, P642, P643, P644, P645, P646, P647, P648, P649, P650, P651, P652, P653, P654, P655, P656, P657, P658, P659, P660, P661, P662, P663, P664, P665, P666, P667, P668, P669, P670, P671, P672, P673, P674, P675, P676, P677, P678, P679, P680, P681, P682, P683, P684, P685, P686, P687, P688, P689, P690, P691, P692, P693, P694, P695, P696, P697, P698, P699, P700, P701, P702, P703, P704, P705, P706, P707, P708, P709, P710, P711, P712, P713, P714, P715, P716, P717, P718, P719, P720, P721, P722, P723, P724, P725, P726, P727, P728, P729, P730, P731, P732, P733, P734, P735, P736, P737, P738, P739, P740, P741, P742, P743, P744, P745, P746, P747, P748, P749, P750, P751, P752, P753, P754, P755, P756, P757, P758, P759, P760, P761, P762, P763, P764, P765, P766, P767, P768, P769, P770, P771, P772, P773, P774, P775, P776, P777, P778, P779, P780, P781, P782, P783, P784, P785, P786, P787, P788, P789, P790, P791, P792, P793, P794, P795, P796, P797, P798, P799, P800, P801, P802, P803, P804, P805, P806, P807, P808

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

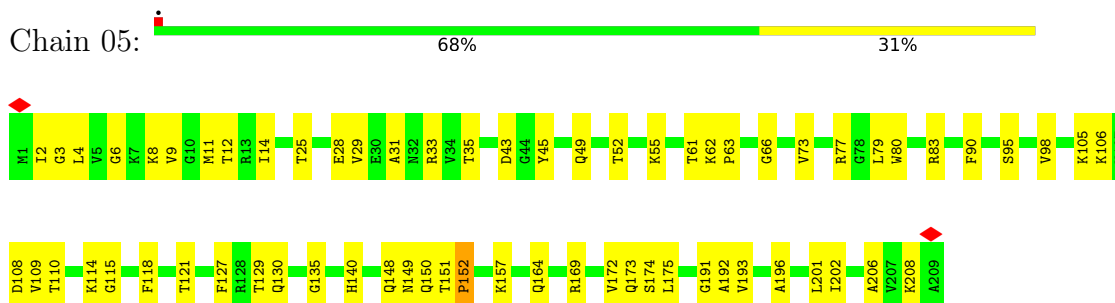
3 Residue-property plots

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

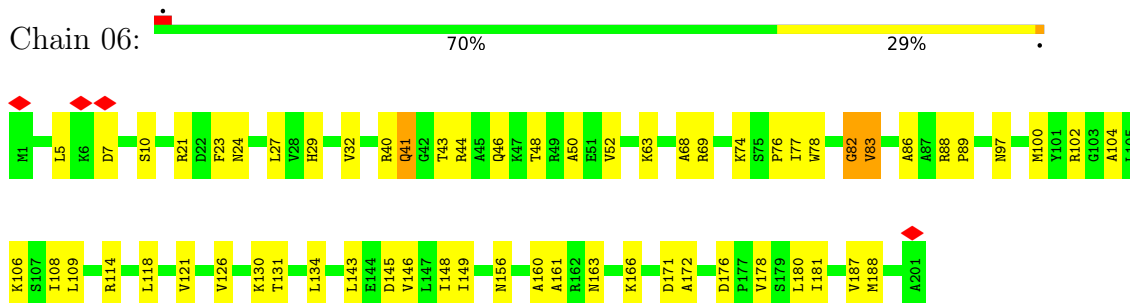
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

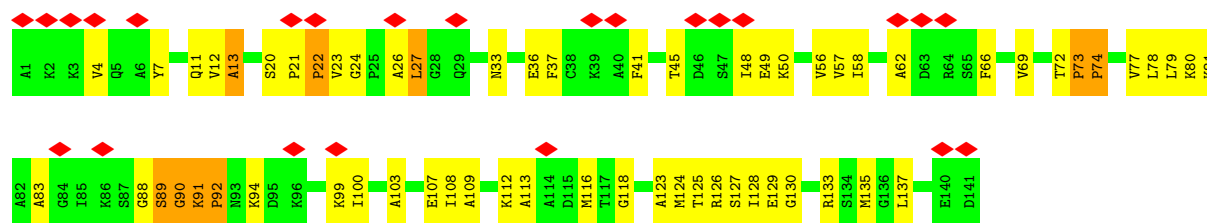


- Molecule 3: 50S ribosomal protein L4

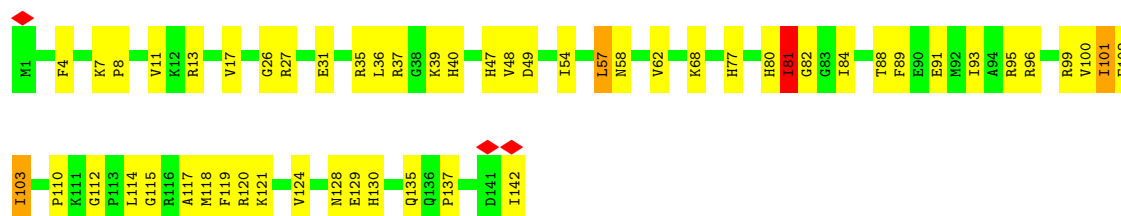


- Molecule 4: 50S ribosomal protein L5

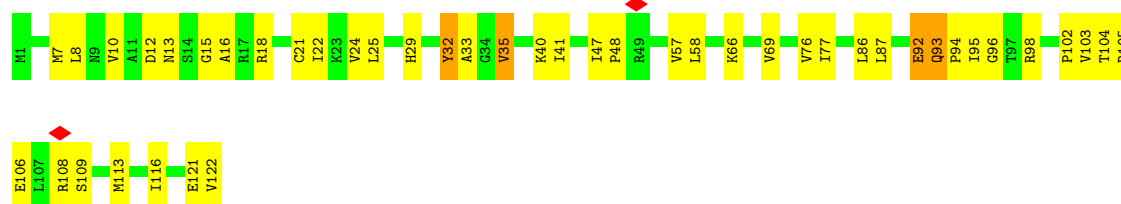




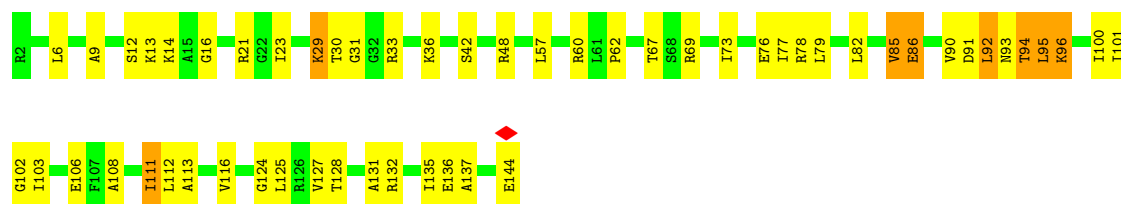
• Molecule 9: 50S ribosomal protein L13



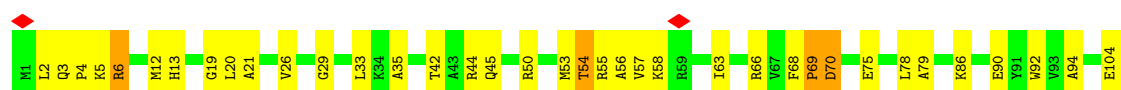
• Molecule 10: 50S ribosomal protein L14



• Molecule 11: 50S ribosomal protein L15



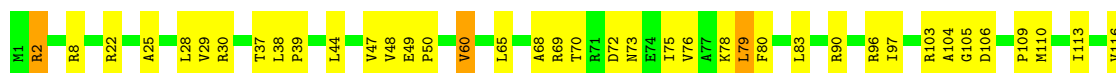
• Molecule 12: 50S ribosomal protein L16





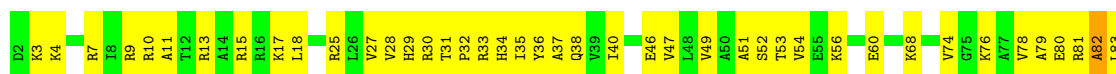
- Molecule 13: 50S ribosomal protein L17

Chain 16: 66% 31%



- Molecule 14: 50S ribosomal protein L18

Chain 17: 53% 46%



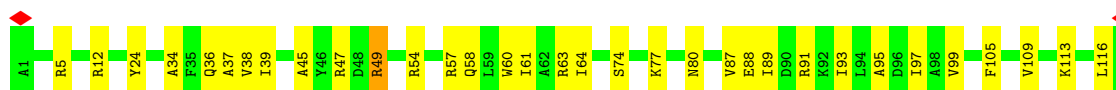
- Molecule 15: 50S ribosomal protein L19

Chain 18: 67% 32%



- Molecule 16: 50S ribosomal protein L20

Chain 19: 72% 27%

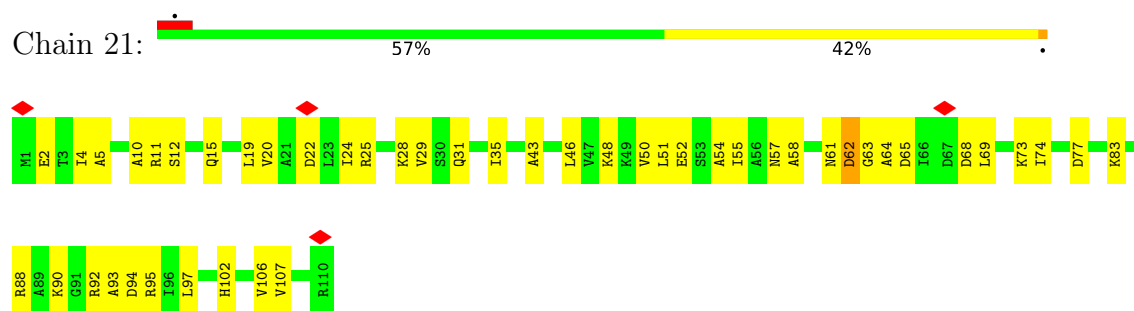


- Molecule 17: 50S ribosomal protein L21

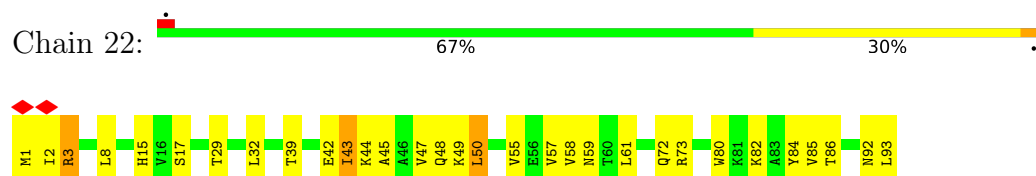
Chain 20: 73% 25%



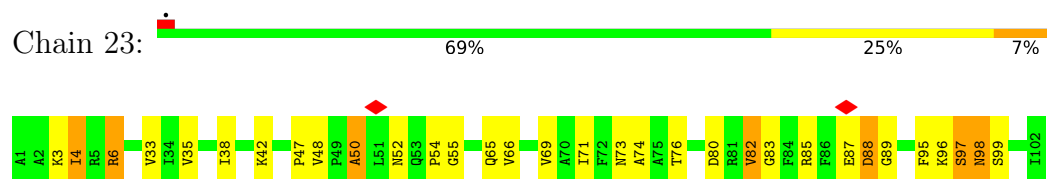
- Molecule 18: 50S ribosomal protein L22



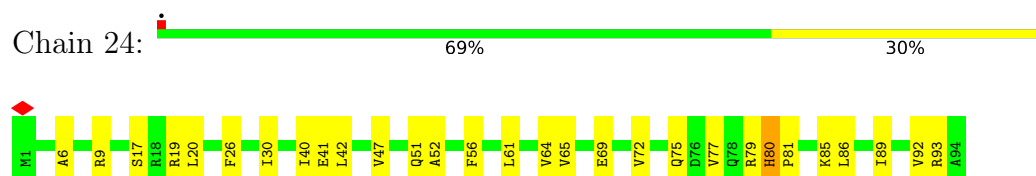
- Molecule 19: 50S ribosomal protein L23



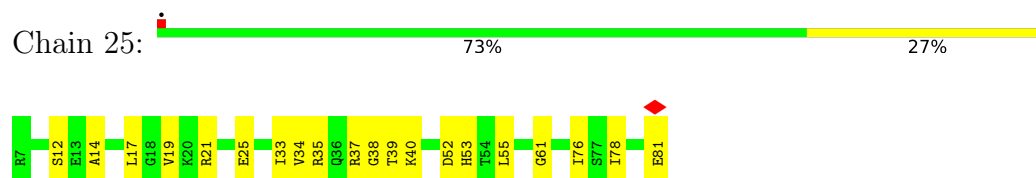
- Molecule 20: 50S ribosomal protein L24



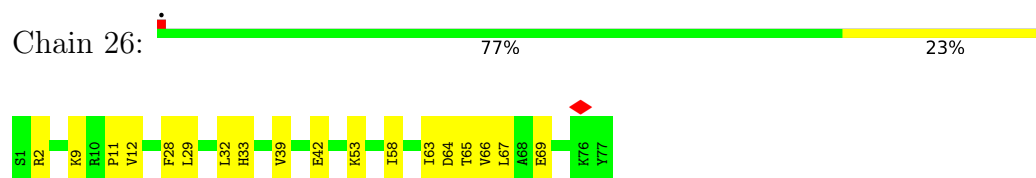
- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



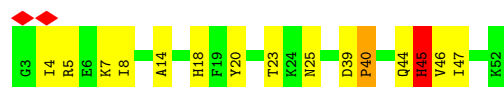
- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34

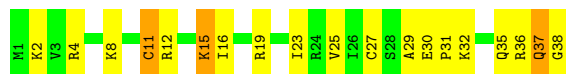


- Molecule 30: 50S ribosomal protein L35



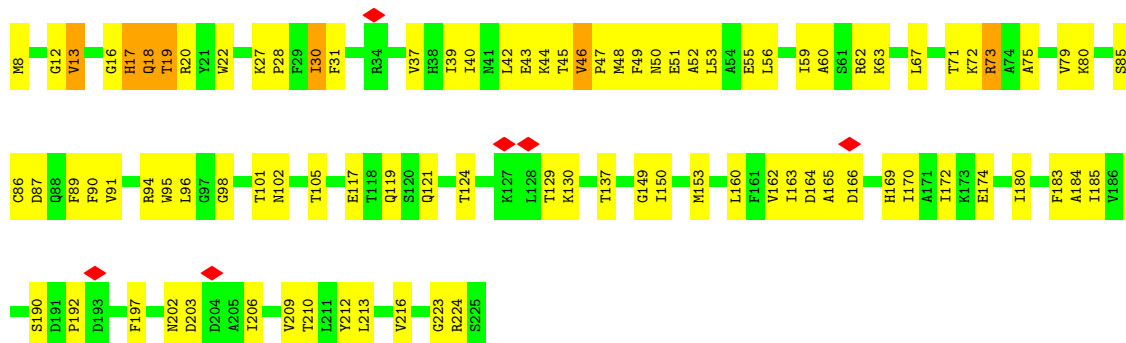
- Molecule 31: 50S ribosomal protein L36

Chain 34: 



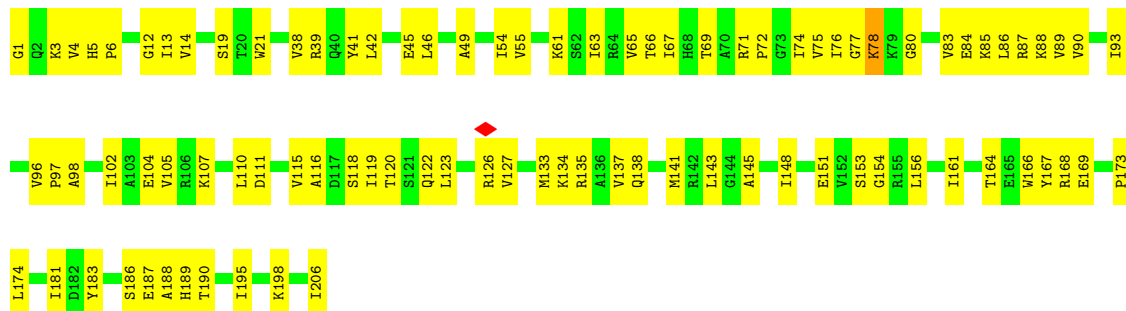
- Molecule 32: 30S ribosomal protein S2

Chain B: 



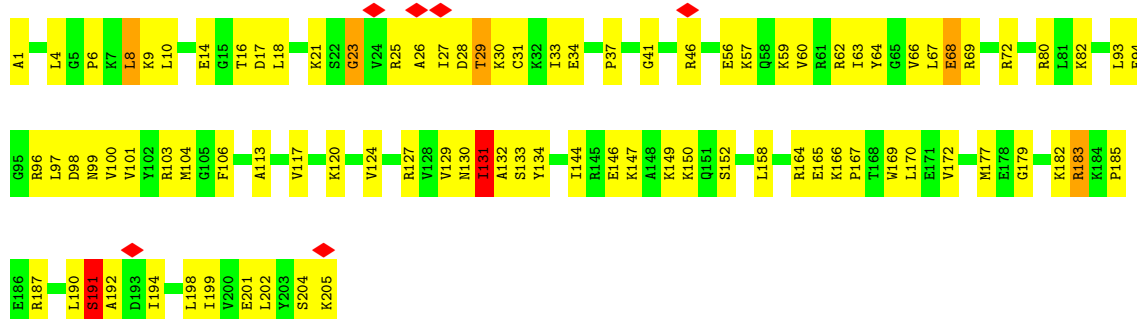
- Molecule 33: 30S ribosomal protein S3

Chain C: 

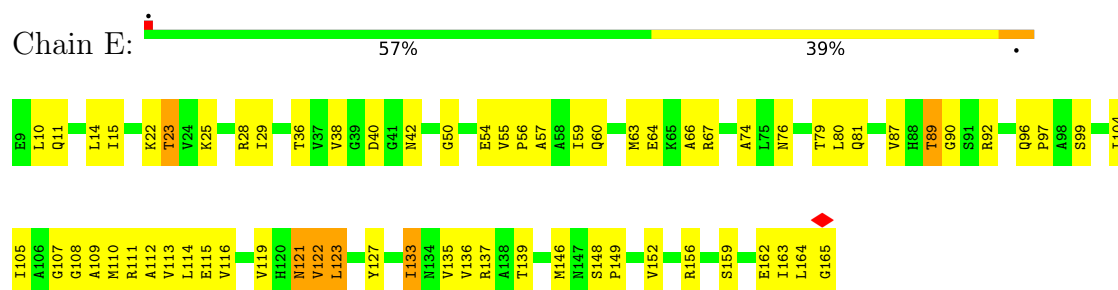


- Molecule 34: 30S ribosomal protein S4

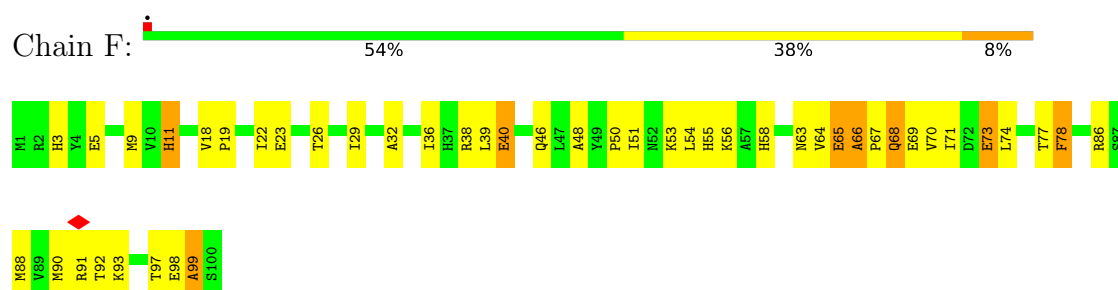
Chain D: 



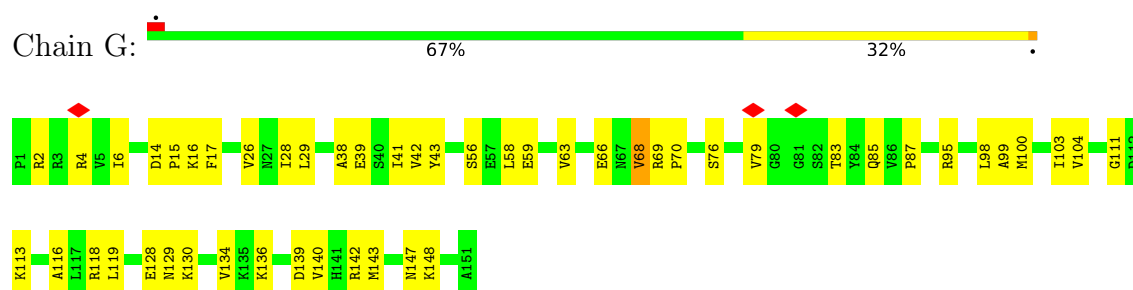
- Molecule 35: 30S ribosomal protein S5



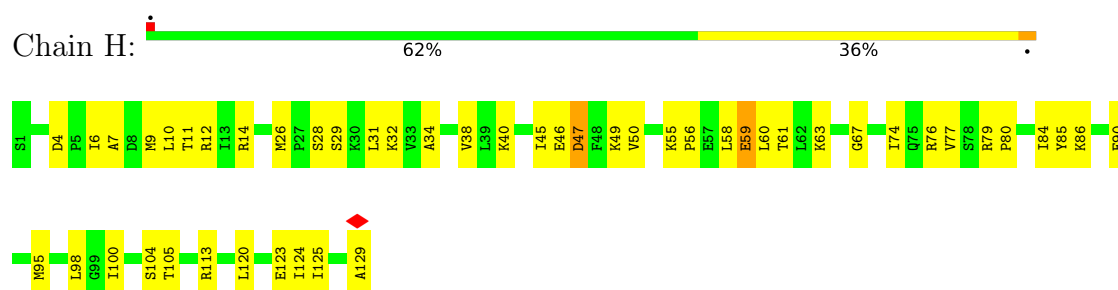
- Molecule 36: 30S ribosomal protein S6



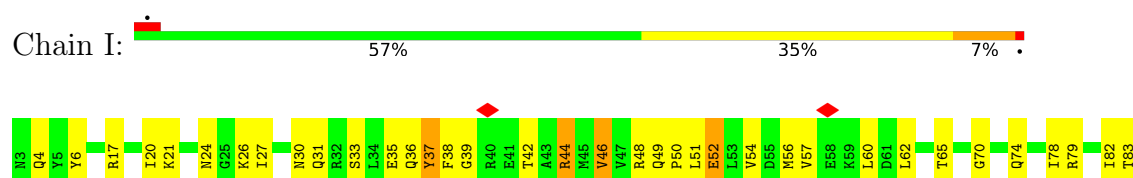
- Molecule 37: 30S ribosomal protein S7

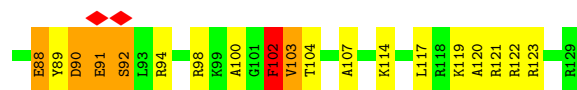


- Molecule 38: 30S ribosomal protein S8

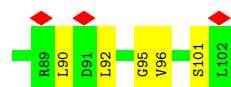


- Molecule 39: 30S ribosomal protein S9

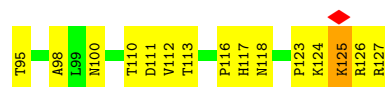
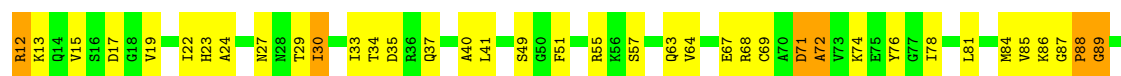




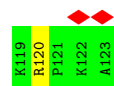
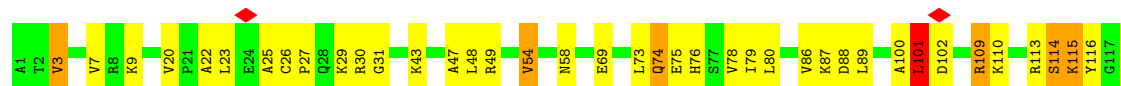
- Molecule 40: 30S ribosomal protein S10



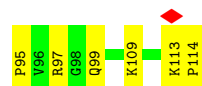
- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12

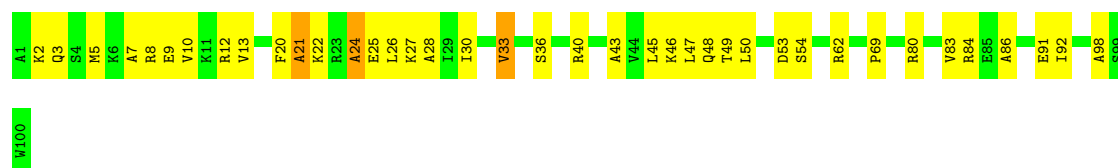


- Molecule 43: 30S ribosomal protein S13



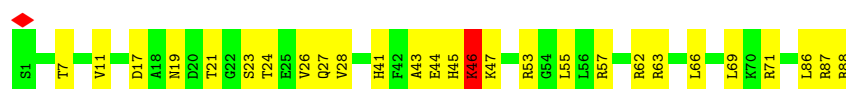
- Molecule 44: 30S ribosomal protein S14

Chain N: 



- Molecule 45: 30S ribosomal protein S15

Chain O: 



- Molecule 46: 30S ribosomal protein S16

Chain P: 



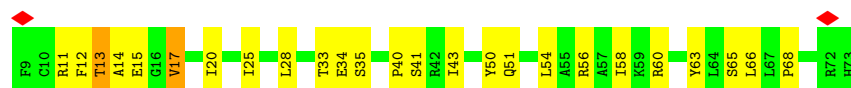
- Molecule 47: 30S ribosomal protein S17

Chain Q: 



- Molecule 48: 30S ribosomal protein S18

Chain R: 

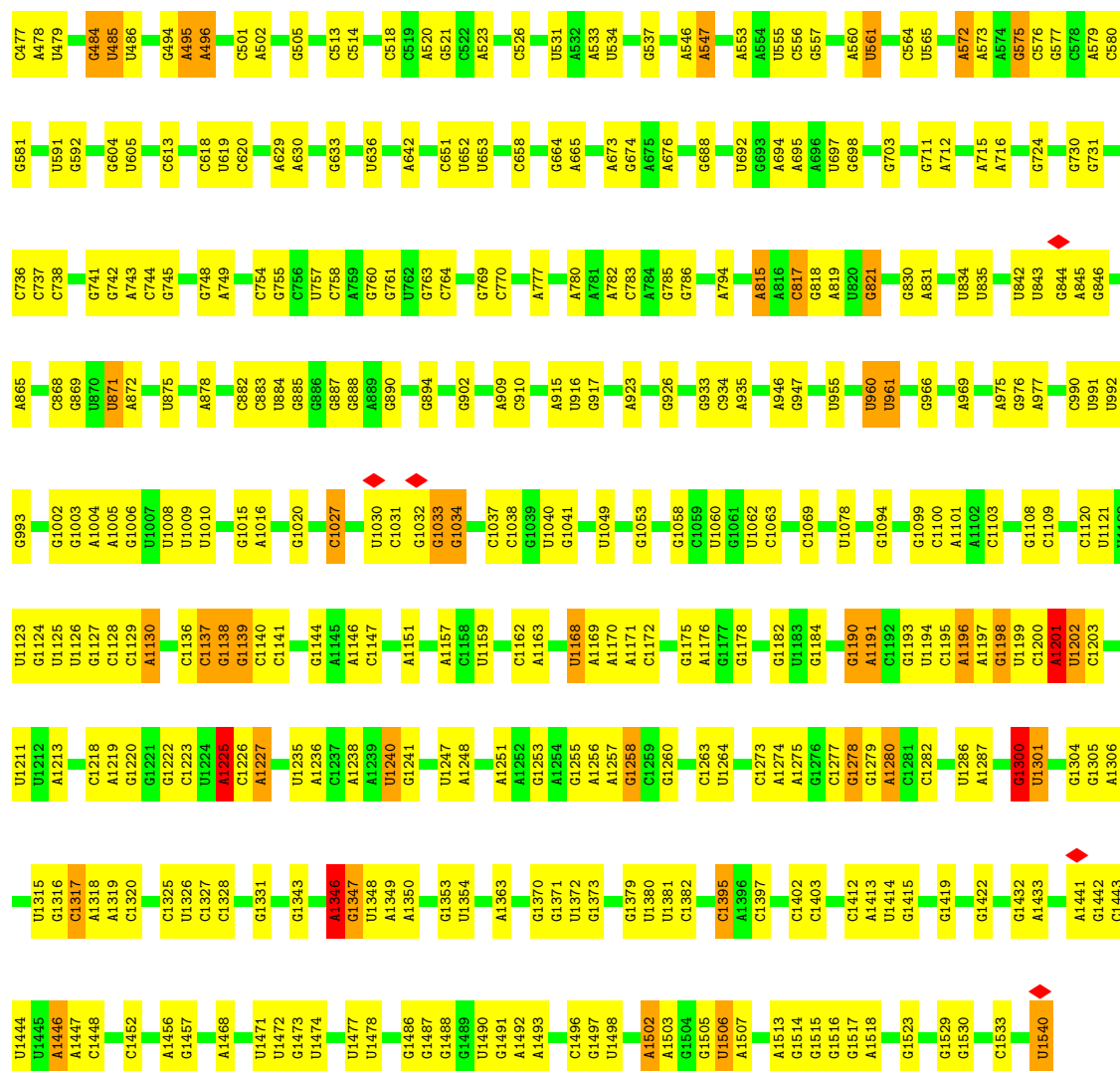


- Molecule 49: 30S ribosomal protein S19

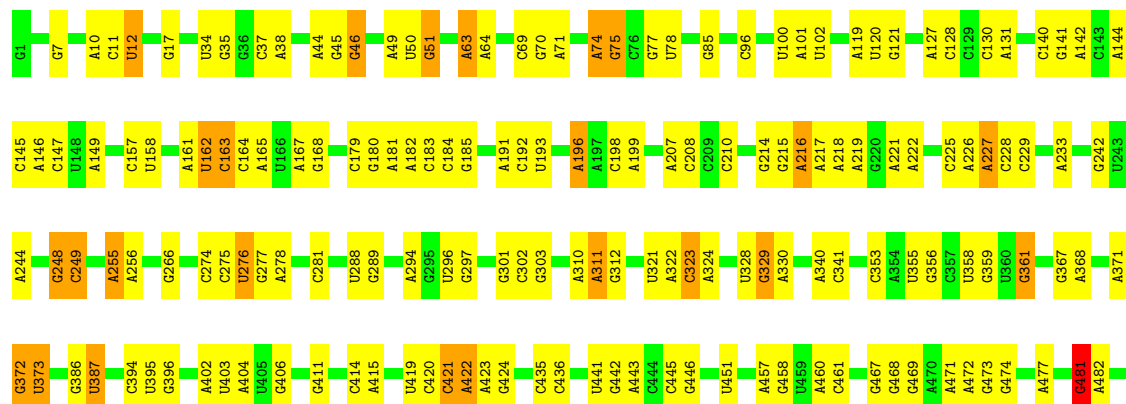
Chain S: 

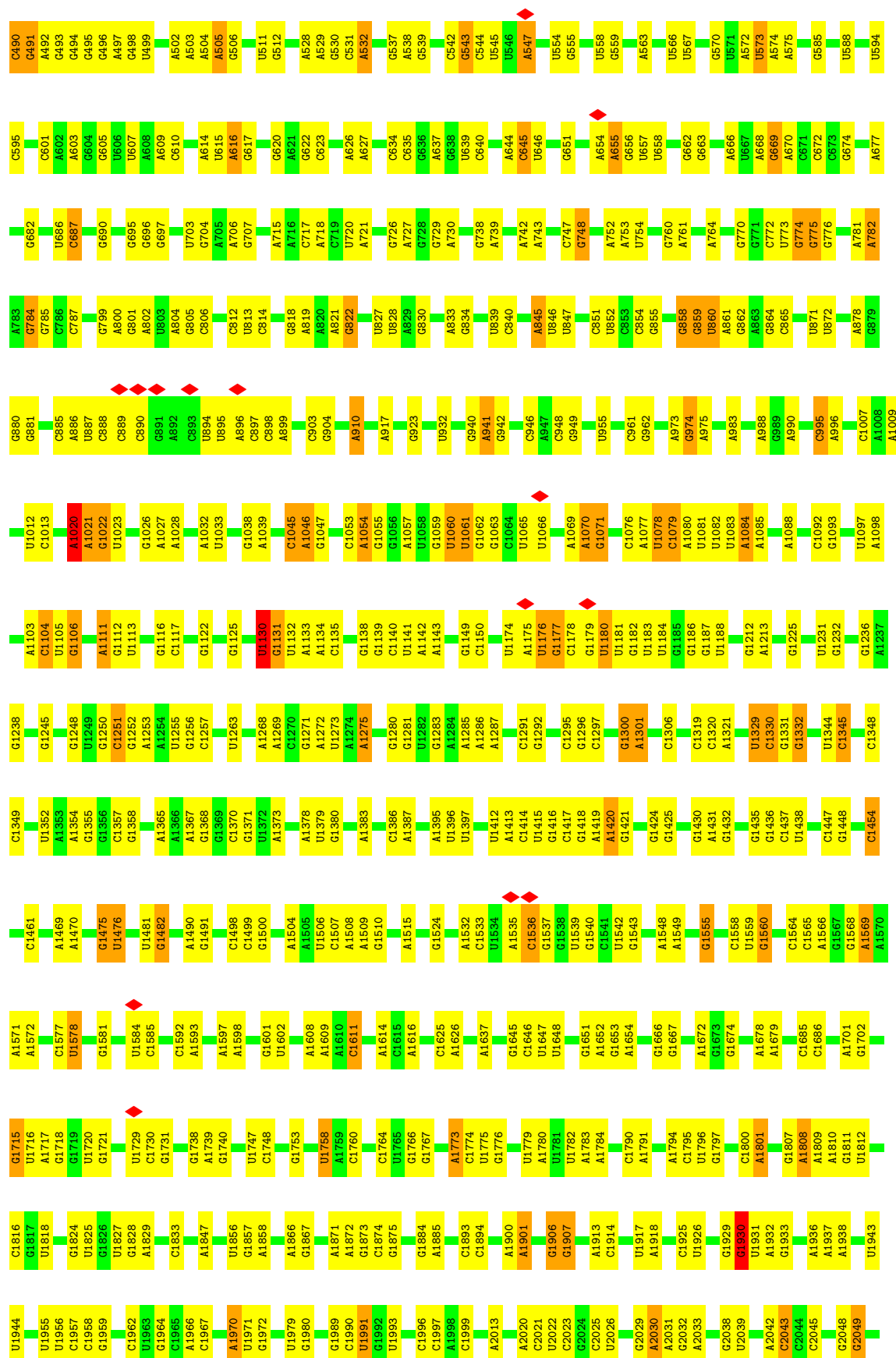


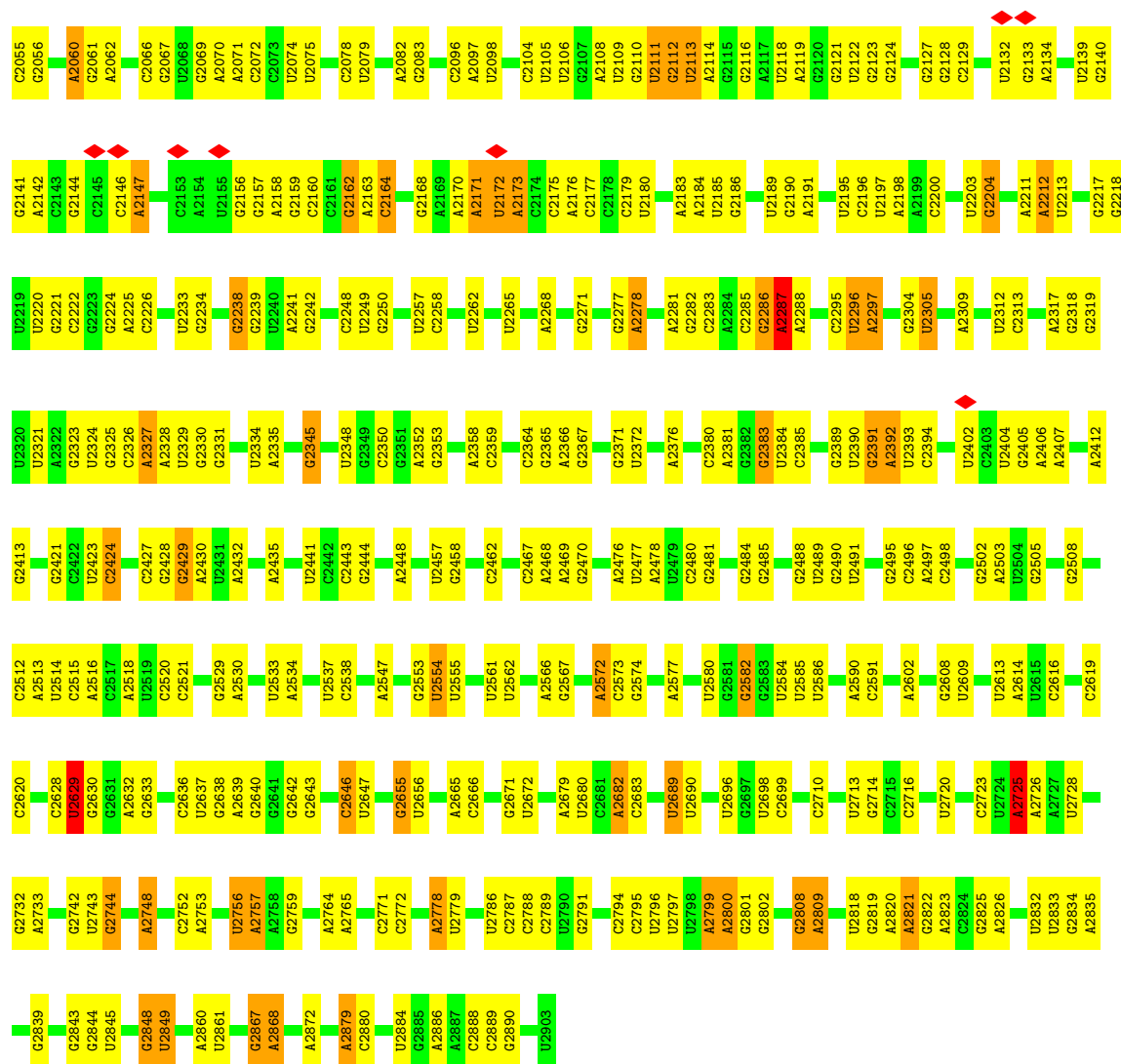
- Molecule 50: 30S ribosomal protein S20



● Molecule 54: 23S ribosomal RNA

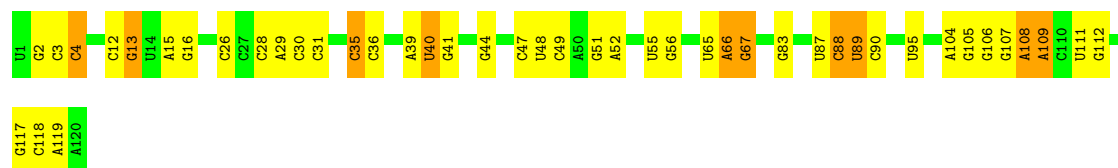






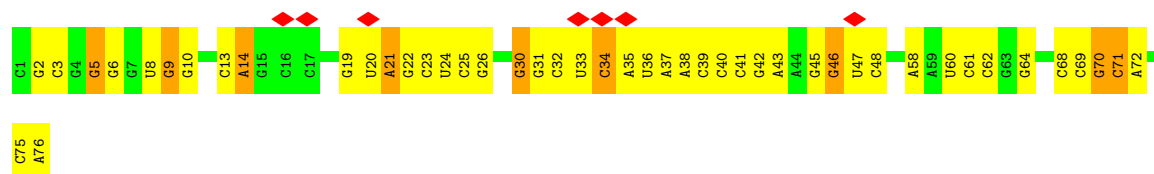
• Molecule 55: 5S ribosomal RNA

Chain 02: 62% 29% 8%

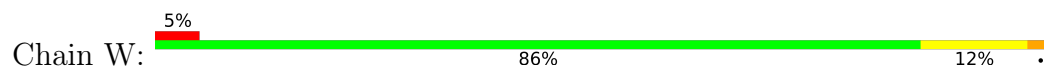


• Molecule 56: tRNA^{fMet}

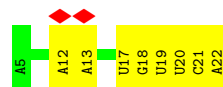
Chain X: 9% 39% 49% 12%



- Molecule 56: tRNA^{fMet}



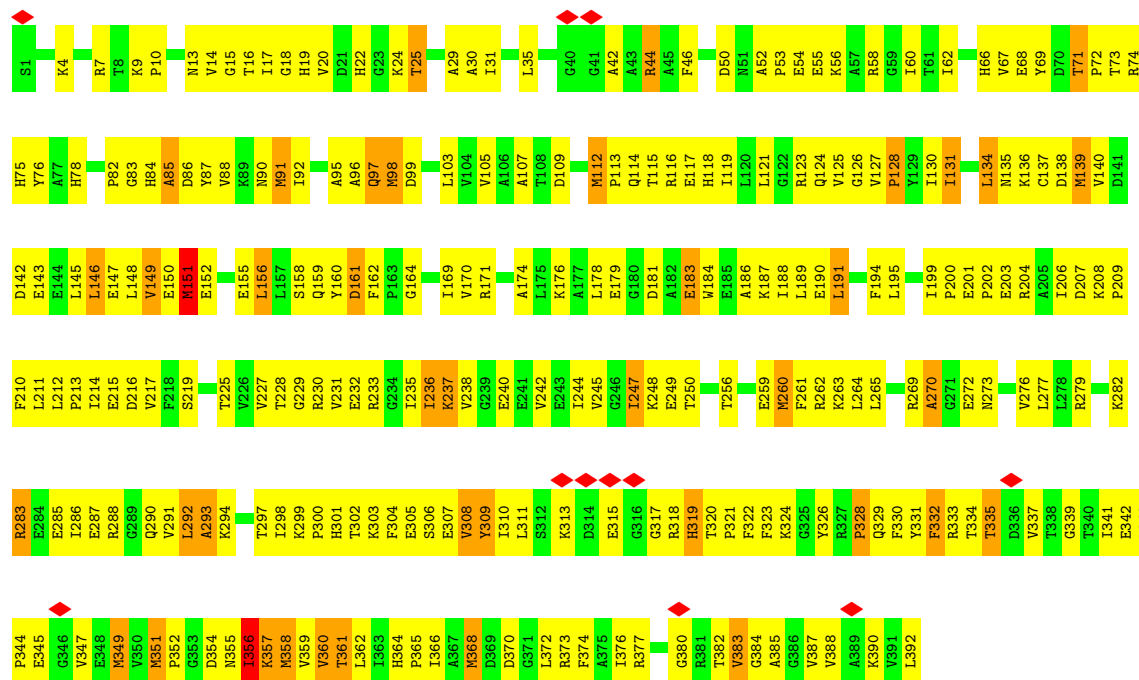
- Molecule 57: mRNA



- Molecule 58: Phe-tRNA^{Phe}



- Molecule 59: Elongation factor Tu 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	153597	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 ($e^-/\text{\AA}^2$)	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	17.168	Depositor
Minimum map value	-4.064	Depositor
Average map value	-0.393	Depositor
Map value standard deviation	1.187	Depositor
Recommended contour level	3.17	Depositor
Map size ($\text{\AA}$)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	04	0.31	0/2122	0.91	7/2852 (0.2%)
2	05	0.31	0/1586	0.85	1/2134 (0.0%)
3	06	0.30	0/1571	0.85	3/2113 (0.1%)
4	07	0.32	0/1435	0.87	4/1926 (0.2%)
5	08	0.32	0/1343	0.82	2/1816 (0.1%)
6	09	0.33	0/1122	1.04	7/1515 (0.5%)
7	10	0.38	0/1002	1.13	12/1350 (0.9%)
8	11	0.37	0/1046	1.04	7/1410 (0.5%)
9	12	0.31	0/1152	0.87	6/1551 (0.4%)
10	13	0.30	0/948	0.94	4/1268 (0.3%)
11	14	0.31	0/1054	1.00	5/1403 (0.4%)
12	15	0.30	0/1093	0.86	3/1460 (0.2%)
13	16	0.31	0/974	0.98	8/1301 (0.6%)
14	17	0.30	0/902	0.94	4/1209 (0.3%)
15	18	0.29	0/929	0.85	1/1242 (0.1%)
16	19	0.30	0/960	0.89	2/1278 (0.2%)
17	20	0.31	0/829	0.87	2/1107 (0.2%)
18	21	0.30	0/864	0.88	2/1156 (0.2%)
19	22	0.29	0/745	0.86	4/994 (0.4%)
20	23	0.29	0/788	0.91	3/1051 (0.3%)
21	24	0.31	0/766	0.86	2/1025 (0.2%)
22	25	0.29	0/582	0.78	1/769 (0.1%)
23	26	0.29	0/635	0.84	0/848
24	27	0.28	0/510	0.89	2/677 (0.3%)
25	28	0.29	0/453	0.81	1/605 (0.2%)
26	29	0.32	0/532	0.88	2/709 (0.3%)
27	30	0.30	0/450	0.79	1/599 (0.2%)
28	31	0.34	0/417	0.89	0/554
29	32	0.35	0/380	0.89	0/498
30	33	0.29	0/513	0.86	2/676 (0.3%)
31	34	0.30	0/303	0.79	0/397
32	B	0.32	0/1736	1.03	13/2338 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.33	0/1652	0.86	2/2225 (0.1%)
34	D	0.30	0/1665	0.92	9/2227 (0.4%)
35	E	0.33	0/1170	0.95	4/1573 (0.3%)
36	F	0.34	0/836	1.04	9/1128 (0.8%)
37	G	0.29	0/1196	0.93	3/1602 (0.2%)
38	H	0.31	0/989	0.94	1/1326 (0.1%)
39	I	0.32	0/1034	0.99	8/1375 (0.6%)
40	J	0.35	0/797	1.05	8/1077 (0.7%)
41	K	0.33	0/886	0.96	5/1195 (0.4%)
42	L	0.32	0/969	1.07	11/1300 (0.8%)
43	M	0.31	0/893	0.91	2/1193 (0.2%)
44	N	0.30	0/817	0.96	5/1088 (0.5%)
45	O	0.29	0/722	0.91	2/964 (0.2%)
46	P	0.31	0/659	0.90	1/884 (0.1%)
47	Q	0.30	0/658	0.95	3/881 (0.3%)
48	R	0.34	0/545	0.86	0/731
49	S	0.32	0/653	0.89	1/877 (0.1%)
50	T	0.30	0/671	1.01	5/888 (0.6%)
51	U	0.35	0/551	1.05	4/728 (0.5%)
52	03	1.61	3/1034 (0.3%)	1.10	4/1387 (0.3%)
53	A	0.41	0/36963	0.51	8/57662 (0.0%)
54	01	0.41	0/69796	0.52	9/108888 (0.0%)
55	02	0.42	0/2872	0.51	1/4479 (0.0%)
56	W	0.42	0/1832	0.48	0/2855
56	X	0.47	0/1832	0.55	0/2855
57	V	0.42	0/436	0.53	0/679
58	Y	0.43	0/1809	0.52	0/2819
59	Z	1.28	10/3085 (0.3%)	1.09	20/4173 (0.5%)
All	All	0.44	13/166764 (0.0%)	0.66	236/248890 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
54	01	0	3
59	Z	0	1
All	All	0	4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Z	151	MET	SD-CE	8.85	2.01	1.79
59	Z	260	MET	SD-CE	8.65	2.01	1.79
52	03	8	MET	SD-CE	8.56	2.00	1.79
59	Z	112	MET	SD-CE	8.27	2.00	1.79
59	Z	349	MET	SD-CE	8.17	2.00	1.79
59	Z	358	MET	SD-CE	7.85	1.99	1.79
59	Z	351	MET	SD-CE	7.64	1.98	1.79
59	Z	139	MET	SD-CE	7.61	1.98	1.79
52	03	218	MET	SD-CE	7.61	1.98	1.79
59	Z	368	MET	SD-CE	7.42	1.98	1.79
52	03	18	THR	CA-CB	6.85	1.61	1.53
59	Z	91	MET	SD-CE	6.60	1.96	1.79
59	Z	98	MET	SD-CE	6.57	1.96	1.79

All (236) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	L	114	SER	N-CA-C	-11.16	99.09	111.14
59	Z	71	THR	N-CA-C	-10.60	95.66	110.29
44	N	24	ALA	N-CA-C	-9.59	101.58	113.28
52	03	180	PHE	N-CA-C	-8.90	97.95	110.50
32	B	17	HIS	N-CA-C	8.88	119.96	108.24
32	B	30	ILE	N-CA-C	8.74	119.48	108.82
11	14	103	ILE	N-CA-C	8.63	118.71	110.42
11	14	95	LEU	N-CA-C	-8.55	101.46	112.23
7	10	117	LEU	N-CA-C	8.33	123.44	108.69
19	22	3	ARG	N-CA-C	-8.15	102.48	111.36
32	B	192	PRO	N-CA-C	-8.04	105.36	114.92
51	U	30	GLU	N-CA-C	-7.96	105.55	114.62
45	O	43	ALA	N-CA-C	-7.86	102.32	112.23
8	11	62	ALA	N-CA-C	-7.71	103.87	113.20
38	H	67	GLY	N-CA-C	-7.67	103.09	113.37
42	L	115	LYS	N-CA-C	-7.67	100.19	110.55
50	T	84	LYS	N-CA-C	-7.47	103.96	113.23
19	22	72	GLN	N-CA-C	-7.38	106.20	114.62
51	U	10	PRO	N-CA-C	7.35	122.84	112.26
21	24	80	HIS	N-CA-C	-7.35	100.50	109.83
9	12	81	ILE	N-CA-C	7.29	118.01	110.36
32	B	50	ASN	N-CA-C	-7.25	102.37	112.45
13	16	79	LEU	N-CA-C	-7.25	100.08	110.59
14	17	116	GLN	N-CA-C	7.23	120.19	108.63
16	19	49	ARG	N-CA-C	-7.22	104.08	113.17
36	F	66	ALA	N-CA-C	7.20	114.48	108.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	D	166	LYS	CA-C-N	7.20	128.84	119.84
34	D	166	LYS	C-N-CA	7.20	128.84	119.84
53	A	1190	G	C2'-C3'-O3'	7.10	120.15	109.50
50	T	7	LYS	N-CA-C	-7.10	104.50	113.02
54	01	1130	U	C2'-C3'-O3'	7.06	120.09	109.50
59	Z	115	THR	N-CA-C	-7.03	103.70	111.36
42	L	43	LYS	N-CA-C	7.00	125.29	109.81
3	06	41	GLN	N-CA-C	-6.93	103.82	112.90
20	23	89	GLY	N-CA-C	-6.92	106.08	114.66
10	13	32	TYR	N-CA-C	6.89	120.16	109.07
4	07	114	ARG	N-CA-C	-6.86	104.91	113.55
59	Z	146	LEU	N-CA-C	-6.86	103.81	111.28
44	N	48	GLN	N-CA-C	-6.83	105.50	114.31
59	Z	335	THR	N-CA-C	6.67	119.55	109.95
59	Z	383	VAL	N-CA-C	-6.66	106.51	111.90
26	29	48	GLN	N-CA-C	6.58	118.45	111.28
4	07	139	GLU	N-CA-C	6.57	118.10	111.07
39	I	46	VAL	N-CA-C	-6.53	103.42	112.50
13	16	105	GLY	N-CA-C	6.53	121.85	114.67
7	10	44	ALA	N-CA-C	-6.50	104.28	111.82
35	E	123	LEU	N-CA-C	-6.49	100.87	110.48
59	Z	162	PHE	N-CA-C	-6.49	100.77	110.24
59	Z	319	HIS	N-CA-C	-6.47	106.34	114.56
34	D	46	ARG	N-CA-C	-6.47	104.31	111.36
32	B	43	GLU	N-CA-C	-6.46	104.32	111.82
36	F	11	HIS	CA-C-N	6.40	127.84	119.84
36	F	11	HIS	C-N-CA	6.40	127.84	119.84
17	20	50	GLY	N-CA-C	-6.40	98.01	113.18
6	09	62	LEU	N-CA-C	-6.39	104.40	111.82
13	16	104	ALA	N-CA-C	6.38	117.93	110.97
36	F	39	LEU	N-CA-C	-6.37	102.74	112.99
39	I	104	THR	N-CA-C	-6.34	99.54	109.25
39	I	88	GLU	N-CA-C	-6.32	104.49	111.82
13	16	60	VAL	N-CA-C	-6.31	106.79	111.90
32	B	62	ARG	N-CA-C	-6.29	105.57	113.18
37	G	68	VAL	N-CA-C	-6.28	106.65	112.43
8	11	27	LEU	N-CA-C	-6.27	105.40	114.12
42	L	110	LYS	N-CA-C	-6.27	106.85	114.75
52	03	209	ILE	N-CA-C	6.23	116.86	110.82
41	K	125	LYS	N-CA-C	6.20	124.01	110.80
2	05	152	PRO	N-CA-C	-6.20	105.10	113.40
41	K	71	ASP	N-CA-C	-6.18	101.37	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	S	9	PHE	N-CA-C	6.18	119.22	110.50
43	M	36	ALA	N-CA-C	-6.18	105.78	113.38
6	09	13	GLY	N-CA-C	6.17	122.83	113.02
13	16	25	ALA	N-CA-C	-6.17	105.24	112.89
37	G	4	ARG	N-CA-C	6.15	118.96	110.35
8	11	91	LYS	CA-C-N	6.14	127.51	119.84
8	11	91	LYS	C-N-CA	6.14	127.51	119.84
1	04	132	ARG	N-CA-C	-6.10	105.01	112.88
20	23	96	LYS	N-CA-C	-6.10	100.91	110.36
52	03	167	LYS	N-CA-C	-6.09	105.72	113.02
40	J	77	VAL	N-CA-C	6.08	116.25	110.42
20	23	50	ALA	N-CA-C	6.07	117.89	109.15
44	N	49	THR	N-CA-C	-6.06	104.75	111.36
59	Z	361	THR	N-CA-C	-6.05	98.54	108.76
6	09	5	LEU	N-CA-C	6.02	117.65	110.19
39	I	92	SER	N-CA-C	-6.01	104.80	111.71
40	J	41	PRO	N-CA-C	6.01	121.37	113.86
8	11	73	PRO	CA-C-N	5.99	127.32	119.84
8	11	73	PRO	C-N-CA	5.99	127.32	119.84
32	B	185	ILE	N-CA-C	-5.95	101.04	108.89
37	G	29	LEU	N-CA-C	-5.93	107.03	114.56
59	Z	164	GLY	N-CA-C	5.92	120.05	112.83
51	U	23	GLU	N-CA-C	5.92	118.00	110.61
8	11	41	PHE	N-CA-C	5.91	117.40	111.07
42	L	74	GLN	N-CA-C	5.91	117.10	107.23
40	J	34	ALA	N-CA-C	5.90	123.38	110.80
47	Q	32	ILE	N-CA-C	5.89	116.63	111.56
6	09	65	ALA	N-CA-C	-5.88	105.59	112.89
59	Z	131	ILE	N-CA-C	-5.87	101.44	109.55
7	10	82	ILE	N-CA-C	5.87	116.74	108.17
13	16	78	LYS	N-CA-C	-5.85	104.86	112.23
59	Z	293	ALA	N-CA-C	5.84	118.57	109.52
7	10	43	LYS	N-CA-C	-5.83	105.27	112.90
18	21	2	GLU	N-CA-C	5.82	117.43	111.14
13	16	68	ALA	N-CA-C	-5.80	105.05	111.71
10	13	35	VAL	N-CA-C	5.79	116.25	110.23
53	A	1201	A	C2'-C3'-O3'	5.79	118.19	109.50
59	Z	345	GLU	N-CA-C	5.78	118.40	110.24
5	08	47	ASN	N-CA-C	-5.78	105.33	112.90
53	A	413	G	N9-C1'-C2'	5.76	120.64	112.00
40	J	42	LEU	CA-C-N	5.75	127.03	119.84
40	J	42	LEU	C-N-CA	5.75	127.03	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	E	137	ARG	N-CA-C	-5.73	106.29	113.28
15	18	15	ASP	N-CA-C	5.72	118.52	108.56
24	27	20	ASN	N-CA-C	-5.72	106.23	113.43
36	F	99	ALA	N-CA-C	5.72	122.97	110.80
34	D	8	LEU	N-CA-C	-5.71	106.18	114.12
1	04	40	GLY	N-CA-C	-5.70	107.46	115.32
55	02	66	A	C2'-C3'-O3'	-5.69	105.17	113.70
54	01	2629	U	N1-C1'-C2'	5.69	120.53	112.00
12	15	21	ALA	N-CA-C	5.67	117.39	110.41
54	01	1930	G	N9-C1'-C2'	5.67	120.50	112.00
14	17	84	GLU	N-CA-C	-5.66	106.05	113.12
36	F	78	PHE	N-CA-C	-5.64	106.75	113.97
59	Z	149	VAL	N-CA-C	-5.64	105.23	110.53
36	F	73	GLU	N-CA-C	-5.64	105.05	111.14
6	09	64	ALA	N-CA-C	-5.63	105.13	112.23
39	I	52	GLU	N-CA-C	-5.62	105.70	113.18
6	09	67	ALA	N-CA-C	-5.62	105.15	112.23
7	10	106	PHE	N-CA-C	5.62	118.04	111.02
30	33	63	TYR	N-CA-C	5.61	118.25	111.40
1	04	129	LEU	CA-C-N	5.61	125.62	119.90
1	04	129	LEU	C-N-CA	5.61	125.62	119.90
14	17	82	ALA	N-CA-C	-5.61	106.28	113.23
19	22	50	LEU	N-CA-C	5.60	119.86	113.19
41	K	100	ASN	N-CA-C	-5.60	106.12	113.12
12	15	54	THR	N-CA-C	-5.59	107.04	112.97
51	U	58	LYS	N-CA-C	-5.59	105.33	111.82
47	Q	69	THR	N-CA-C	-5.59	98.89	110.80
53	A	1300	G	N9-C1'-C2'	5.58	120.38	112.00
53	A	1346	A	N9-C1'-C2'	5.57	120.35	112.00
42	L	109	ARG	N-CA-C	-5.56	101.21	110.17
7	10	47	GLU	N-CA-C	-5.55	104.87	111.03
50	T	69	ASN	N-CA-C	-5.54	106.65	113.41
32	B	45	THR	N-CA-C	5.53	117.74	111.11
24	27	22	LEU	N-CA-C	-5.51	105.37	111.71
7	10	50	VAL	N-CA-C	5.50	120.14	112.50
27	30	9	ARG	N-CA-C	-5.48	105.33	112.23
7	10	42	ARG	N-CA-C	-5.48	106.60	113.28
54	01	2287	A	N9-C1'-C2'	5.46	120.20	112.00
35	E	87	VAL	N-CA-C	5.46	116.74	109.37
40	J	95	GLY	N-CA-C	-5.43	107.04	114.64
40	J	39	PRO	N-CA-C	5.40	118.98	110.50
7	10	6	GLN	N-CA-C	-5.40	104.94	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	Q	70	LYS	N-CA-C	5.40	117.23	110.91
39	I	37	TYR	N-CA-C	-5.39	104.82	111.40
34	D	4	LEU	N-CA-C	5.39	118.87	111.54
7	10	78	GLY	N-CA-C	5.39	123.33	112.34
1	04	213	ARG	N-CA-C	-5.38	105.07	111.69
45	O	46	LYS	N-CA-C	5.37	122.25	110.80
41	K	117	HIS	N-CA-C	-5.37	103.88	110.65
53	A	1301	U	N1-C1'-C2'	5.37	120.05	112.00
4	07	107	VAL	CB-CA-C	-5.36	108.66	114.35
10	13	95	ILE	N-CA-C	5.35	116.01	110.82
7	10	35	VAL	N-CA-C	-5.34	105.18	111.00
40	J	20	GLN	N-CA-C	-5.34	107.42	114.04
12	15	118	LYS	N-CA-C	-5.34	105.91	112.90
16	19	37	ALA	N-CA-C	-5.33	104.89	111.40
54	01	1020	A	C2'-C3'-O3'	5.32	117.48	109.50
7	10	45	GLY	N-CA-C	-5.32	107.72	114.16
9	12	62	VAL	N-CA-C	-5.31	104.27	110.05
26	29	62	LYS	N-CA-C	-5.31	106.58	113.16
39	I	102	PHE	N-CA-C	5.30	122.09	110.80
44	N	21	ALA	N-CA-C	-5.29	104.97	113.28
13	16	2	ARG	N-CA-C	5.28	118.48	111.30
42	L	25	ALA	N-CA-C	5.27	117.61	111.02
32	B	180	ILE	N-CA-C	5.27	113.64	107.89
39	I	44	ARG	N-CA-C	-5.27	106.90	113.38
34	D	131	ILE	N-CA-C	5.27	115.80	108.84
42	L	54	VAL	N-CA-C	5.27	115.70	108.12
17	20	51	VAL	N-CA-C	-5.26	97.52	108.88
9	12	119	PHE	N-CA-C	-5.26	107.24	113.97
21	24	52	ALA	N-CA-C	-5.24	105.65	111.36
59	Z	112	MET	CA-C-N	5.24	125.55	119.47
59	Z	112	MET	C-N-CA	5.24	125.55	119.47
59	Z	130	ILE	N-CA-C	5.24	115.91	107.73
33	C	154	GLY	N-CA-C	5.24	116.85	111.56
59	Z	360	VAL	N-CA-C	5.22	117.27	108.81
54	01	748	G	N9-C1'-C2'	5.22	119.83	112.00
22	25	40	LYS	N-CA-C	-5.20	105.31	110.97
35	E	116	VAL	N-CA-C	-5.19	108.44	113.53
11	14	137	ALA	N-CA-C	-5.19	106.19	112.88
42	L	101	LEU	N-CA-C	5.19	121.85	110.80
59	Z	216	ASP	N-CA-C	5.19	117.06	108.13
9	12	112	GLY	CA-C-N	5.19	126.32	119.84
9	12	112	GLY	C-N-CA	5.19	126.32	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	07	4	HIS	N-CA-C	-5.18	105.31	111.69
33	C	85	LYS	N-CA-C	-5.18	105.71	111.36
54	01	2725	A	N9-C1'-C2'	5.18	119.76	112.00
59	Z	29	ALA	N-CA-C	-5.17	105.55	111.14
9	12	103	ILE	N-CA-C	-5.17	107.37	111.81
54	01	2212	A	N9-C1'-C2'	5.16	119.74	112.00
1	04	237	ARG	N-CA-C	5.16	117.47	111.02
25	28	42	ALA	N-CA-C	-5.15	105.36	111.69
44	N	33	VAL	N-CA-C	5.12	120.00	109.34
46	P	45	GLU	N-CA-C	-5.12	99.65	108.56
43	M	14	ALA	N-CA-C	5.12	117.25	111.11
19	22	43	ILE	N-CA-C	-5.11	106.16	111.58
3	06	82	GLY	N-CA-C	5.11	125.29	113.18
32	B	46	VAL	CB-CA-C	-5.10	108.85	113.70
36	F	68	GLN	N-CA-C	5.09	118.59	112.38
1	04	207	ALA	N-CA-C	-5.09	105.81	112.23
42	L	9	LYS	CA-C-N	5.09	126.20	119.84
42	L	9	LYS	C-N-CA	5.09	126.20	119.84
10	13	109	SER	N-CA-C	5.09	116.97	110.61
11	14	60	ARG	N-CA-C	-5.09	107.73	114.04
14	17	68	LYS	N-CA-C	5.09	116.51	111.07
32	B	137	THR	N-CA-C	-5.08	105.38	112.45
52	03	52	ALA	N-CA-C	-5.08	106.92	113.01
59	Z	283	ARG	N-CA-C	5.08	116.50	111.07
3	06	171	ASP	N-CA-C	-5.07	102.27	110.32
53	A	130	A	N9-C1'-C2'	5.06	119.59	112.00
32	B	85	SER	N-CA-C	-5.06	105.85	111.36
50	T	79	THR	N-CA-C	-5.05	105.48	111.69
36	F	65	GLU	N-CA-C	-5.05	100.67	108.90
34	D	68	GLU	N-CA-C	5.04	117.16	111.11
32	B	13	VAL	N-CA-C	5.04	119.82	109.34
30	33	6	VAL	N-CA-C	-5.03	100.38	107.98
11	14	92	LEU	N-CA-C	-5.03	105.49	110.97
41	K	72	ALA	N-CA-C	-5.03	105.86	113.51
50	T	3	ILE	N-CA-C	5.03	114.51	107.37
54	01	481	G	N9-C1'-C2'	5.03	119.54	112.00
34	D	9	LYS	N-CA-C	-5.02	106.00	111.82
5	08	45	ALA	N-CA-C	5.01	121.47	110.80
53	A	1225	A	N9-C1'-C2'	5.01	119.51	112.00
6	09	122	LEU	N-CA-C	5.00	116.76	110.91
18	21	24	ILE	N-CA-C	5.00	119.75	109.34
34	D	147	LYS	N-CA-C	5.00	116.42	111.07

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
54	01	2629	U	Sidechain
54	01	2725	A	Sidechain
54	01	775	G	Sidechain
59	Z	309	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	04	2083	0	2157	91	0
2	05	1565	0	1616	55	0
3	06	1552	0	1619	50	0
4	07	1411	0	1447	56	0
5	08	1323	0	1374	32	0
6	09	1111	0	1148	45	0
7	10	989	0	1025	74	0
8	11	1032	0	1088	62	0
9	12	1129	0	1162	52	0
10	13	939	0	1012	40	0
11	14	1045	0	1117	48	0
12	15	1074	0	1157	35	0
13	16	961	0	1000	31	0
14	17	892	0	923	46	0
15	18	917	0	965	46	0
16	19	947	0	1022	29	0
17	20	816	0	839	24	0
18	21	857	0	922	28	0
19	22	739	0	807	26	0
20	23	780	0	834	26	0
21	24	753	0	780	23	0
22	25	575	0	592	14	0
23	26	625	0	655	10	0
24	27	509	0	543	17	0
25	28	449	0	491	16	0
26	29	523	0	524	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	30	444	0	461	15	0
28	31	410	0	440	12	0
29	32	377	0	418	15	0
30	33	504	0	574	15	0
31	34	302	0	343	21	0
32	B	1705	0	1732	70	0
33	C	1625	0	1699	67	0
34	D	1643	0	1710	78	0
35	E	1157	0	1199	54	0
36	F	818	0	808	45	0
37	G	1182	0	1240	43	0
38	H	979	0	1034	45	0
39	I	1022	0	1070	49	0
40	J	787	0	828	47	0
41	K	870	0	878	45	0
42	L	955	0	1019	44	0
43	M	884	0	944	42	0
44	N	805	0	847	34	0
45	O	714	0	737	23	0
46	P	649	0	666	43	0
47	Q	649	0	691	33	0
48	R	536	0	552	24	0
49	S	638	0	665	32	0
50	T	665	0	714	17	0
51	U	545	0	579	36	0
52	03	1027	0	1092	159	0
53	A	33012	0	16618	358	0
54	01	62317	0	31346	690	0
55	02	2568	0	1303	38	0
56	W	1640	0	836	4	0
56	X	1640	0	837	34	0
57	V	388	0	196	4	0
58	Y	1619	0	821	13	0
59	Z	3029	0	3043	332	0
60	01	263	0	0	0	0
60	02	6	0	0	0	0
60	12	1	0	0	0	0
60	25	1	0	0	0	0
60	A	107	0	0	0	0
60	N	1	0	0	0	0
60	V	2	0	0	0	0
60	W	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	Z	1	0	0	0	0
61	29	1	0	0	0	0
61	34	1	0	0	0	0
62	W	10	0	10	0	0
63	Y	11	0	8	3	0
64	Z	32	0	14	1	0
All	All	154139	0	104791	3254	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 13.

All (3254) 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)
59:Z:151:MET:CE	59:Z:151:MET:SD	2.01	1.46
52:03:181:ASP:HB2	52:03:184:LYS:HD3	1.19	1.19
59:Z:212:LEU:HD11	59:Z:229:GLY:HA3	1.32	1.08
35:E:80:LEU:HD13	35:E:122:VAL:HG11	1.31	1.08
59:Z:344:PRO:HG2	59:Z:347:VAL:HG21	1.36	1.06
54:01:2277:G:H2'	54:01:2278:A:H5''	1.41	1.03
59:Z:4:LYS:HG3	59:Z:264:LEU:HD22	1.38	1.03
11:14:111:ILE:H	11:14:111:ILE:HD12	1.22	1.03
36:F:3:HIS:H	36:F:92:THR:HG22	1.23	1.02
59:Z:124:GLN:HE22	59:Z:385:ALA:HB2	1.23	1.02
59:Z:245:VAL:HA	59:Z:250:THR:HG22	1.41	1.02
54:01:821:A:H5''	54:01:822:G:H5''	1.41	1.02
39:I:20:ILE:HD11	39:I:60:LEU:HD22	1.43	1.00
52:03:42:VAL:HG22	52:03:216:THR:HG22	1.44	1.00
1:04:153:LEU:HD13	1:04:175:LEU:HD21	1.42	0.99
7:10:48:ALA:HB3	7:10:51:TYR:HE1	1.28	0.98
52:03:22:ASP:HB2	52:03:25:GLU:HG3	1.45	0.98
54:01:45:G:H5''	54:01:46:G:H5'	1.46	0.96
59:Z:214:ILE:HG23	59:Z:227:VAL:HG23	1.48	0.96
41:K:19:VAL:HG11	41:K:84:MET:HE3	1.46	0.95
1:04:106:PRO:HD2	1:04:109:LEU:HD22	1.48	0.95
6:09:63:ALA:HA	6:09:66:ASN:HD22	1.31	0.95
59:Z:321:PRO:HG2	59:Z:349:MET:HE2	1.48	0.95
1:04:175:LEU:HD11	1:04:181:ARG:HH12	1.32	0.94
12:15:12:MET:HA	54:01:910:A:H62	1.30	0.94
1:04:154:ALA:HB2	1:04:161:VAL:HG23	1.48	0.94
8:11:91:LYS:HB3	8:11:94:LYS:HB2	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:M:15:VAL:HG23	43:M:16:ILE:HD12	1.49	0.94
40:J:66:GLU:HG2	44:N:98:ALA:HB2	1.45	0.94
17:20:14:VAL:HG23	17:20:18:GLN:HE21	1.31	0.94
15:18:59:THR:HG22	15:18:72:VAL:HG12	1.49	0.93
39:I:83:THR:HG21	39:I:102:PHE:HB3	1.50	0.93
52:03:200:LYS:HD2	52:03:201:PRO:HD2	1.51	0.93
53:A:405:U:H3'	53:A:406:G:H5'	1.49	0.92
59:Z:332:PHE:O	59:Z:333:ARG:HG2	1.69	0.92
33:C:71:ARG:HD3	33:C:74:ILE:HD12	1.51	0.92
42:L:23:LEU:HD22	42:L:58:ASN:HD22	1.35	0.92
7:10:2:ALA:HB3	7:10:6:GLN:HG3	1.52	0.91
52:03:23:ILE:HG22	52:03:186:LYS:HD2	1.52	0.91
59:Z:311:LEU:HD12	59:Z:315:GLU:HG2	1.51	0.90
20:23:85:ARG:HD3	20:23:87:GLU:HG3	1.52	0.90
32:B:18:GLN:HG2	32:B:187:ASP:OD2	1.72	0.90
46:P:67:ILE:H	46:P:67:ILE:HD12	1.37	0.90
54:01:1906:G:H2'	54:01:1907:G:H5''	1.49	0.90
54:01:1077:A:H2'	54:01:1078:U:H5'	1.54	0.90
49:S:5:LYS:HE2	49:S:6:LYS:HE3	1.51	0.90
6:09:72:ILE:HB	6:09:108:VAL:HG22	1.54	0.90
7:10:3:LEU:HD12	7:10:5:LEU:H	1.36	0.89
7:10:87:GLU:HG2	7:10:95:LEU:HD12	1.53	0.88
37:G:111:GLY:HA2	37:G:118:ARG:HD3	1.56	0.88
39:I:33:SER:HB3	39:I:36:GLN:HG2	1.56	0.88
7:10:48:ALA:HB3	7:10:51:TYR:CE1	2.09	0.87
59:Z:305:GLU:HB2	59:Z:392:LEU:HD21	1.55	0.87
21:24:75:GLN:HB2	21:24:92:VAL:HG23	1.56	0.87
54:01:1300:G:H4'	54:01:1301:A:H5'	1.55	0.87
53:A:484:G:H4'	53:A:485:U:H5''	1.56	0.87
54:01:215:G:H4'	54:01:216:A:H4'	1.57	0.86
15:18:52:ARG:HH21	54:01:2720:U:H5''	1.41	0.86
52:03:4:LEU:HA	52:03:8:MET:SD	2.16	0.85
1:04:175:LEU:HD11	1:04:181:ARG:NH1	1.91	0.85
14:17:51:ALA:HB3	14:17:78:VAL:HG22	1.57	0.85
43:M:7:ASN:ND2	43:M:9:PRO:HD3	1.92	0.84
51:U:66:ARG:HH21	53:A:1099:G:H4'	1.41	0.84
56:X:31:G:H2'	56:X:32:C:H5'	1.58	0.84
52:03:50:ILE:HG21	52:03:201:PRO:HG2	1.60	0.84
52:03:194:VAL:O	52:03:198:LYS:HG3	1.78	0.84
34:D:120:LYS:HE2	34:D:130:ASN:HD21	1.41	0.84
1:04:164:VAL:HG21	1:04:180:MET:HE1	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:K:23:HIS:HB3	41:K:30:ILE:HG23	1.60	0.83
59:Z:116:ARG:HD3	59:Z:156:LEU:HD21	1.60	0.83
52:03:50:ILE:HD13	52:03:59:VAL:HG23	1.59	0.83
10:13:121:GLU:HG2	10:13:122:VAL:HG23	1.61	0.83
19:22:2:ILE:HD11	54:01:144:A:H4'	1.60	0.83
52:03:31:LYS:HE2	52:03:31:LYS:HA	1.61	0.83
59:Z:357:LYS:HD2	59:Z:358:MET:N	1.91	0.83
38:H:29:SER:HB3	38:H:32:LYS:HG2	1.60	0.82
53:A:664:G:H22	53:A:741:G:H1	1.26	0.82
59:Z:248:LYS:HE3	59:Z:290:GLN:OE1	1.79	0.82
6:09:72:ILE:HD12	6:09:108:VAL:HG13	1.61	0.82
59:Z:297:THR:HG23	59:Z:298:ILE:HG13	1.60	0.82
52:03:30:LEU:HD12	52:03:31:LYS:HE3	1.59	0.82
12:15:53:MET:HE3	12:15:63:ILE:HG21	1.60	0.82
6:09:84:ALA:HA	6:09:91:PHE:H	1.44	0.82
1:04:16:VAL:HB	1:04:203:VAL:HG22	1.61	0.81
59:Z:237:LYS:HE2	59:Z:240:GLU:HB2	1.60	0.81
54:01:121:G:H4'	54:01:149:A:H5'	1.62	0.81
20:23:42:LYS:HE2	54:01:499:U:H5''	1.63	0.81
41:K:87:GLY:H	41:K:113:THR:HG22	1.44	0.81
59:Z:311:LEU:HB2	59:Z:315:GLU:OE1	1.79	0.81
13:16:22:ARG:HG3	13:16:70:THR:HA	1.63	0.80
49:S:5:LYS:HG3	49:S:6:LYS:HG2	1.63	0.80
5:08:140:ILE:HD12	5:08:141:GLY:N	1.95	0.80
52:03:4:LEU:HD22	52:03:8:MET:HB2	1.60	0.80
59:Z:247:ILE:HG22	59:Z:364:HIS:HB3	1.63	0.80
13:16:65:LEU:HG	13:16:69:ARG:HH22	1.45	0.80
41:K:85:VAL:HG21	51:U:16:ARG:HH22	1.45	0.80
59:Z:323:PHE:CE1	59:Z:349:MET:HG2	2.16	0.80
9:12:31:GLU:HG2	9:12:142:ILE:HG12	1.62	0.80
59:Z:97:GLN:HB3	59:Z:230:ARG:HD2	1.64	0.79
43:M:76:ILE:HG22	43:M:80:MET:HE2	1.64	0.79
22:25:39:THR:H	54:01:2331:G:H4'	1.48	0.79
52:03:38:PHE:CE2	52:03:40:GLU:HG2	2.17	0.79
5:08:21:GLN:HE21	5:08:36:LEU:HB2	1.45	0.78
52:03:33:LEU:HD13	52:03:220:ALA:H	1.47	0.78
54:01:2277:G:C2'	54:01:2278:A:H5''	2.12	0.78
54:01:1053:C:H2'	54:01:1054:A:H5''	1.63	0.78
52:03:195:ALA:HA	52:03:198:LYS:HD3	1.63	0.78
59:Z:19:HIS:HB3	59:Z:22:HIS:CE1	2.19	0.78
59:Z:324:LYS:HE3	59:Z:342:GLU:HA	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:3:C:H2'	55:02:4:C:H5''	1.65	0.78
52:03:183:ASP:O	52:03:187:GLU:HG2	1.84	0.78
53:A:960:U:H4'	53:A:961:U:O5'	1.83	0.77
39:I:98:ARG:HG3	39:I:103:VAL:HG21	1.64	0.77
32:B:71:THR:HG22	32:B:72:LYS:H	1.48	0.77
40:J:59:LYS:HE2	40:J:62:ARG:HH21	1.49	0.77
51:U:24:LYS:HG2	51:U:25:ALA:H	1.49	0.77
40:J:20:GLN:O	40:J:24:GLU:HG3	1.84	0.77
39:I:50:PRO:O	39:I:54:VAL:HG22	1.85	0.77
51:U:13:VAL:HG13	51:U:15:LEU:HG	1.67	0.77
56:X:13:C:H2'	56:X:14:A:H5''	1.67	0.77
2:05:151:THR:HB	2:05:152:PRO:HD3	1.67	0.77
53:A:1137:C:H5'	53:A:1138:G:H5'	1.67	0.77
1:04:252:LYS:HZ3	1:04:252:LYS:HB2	1.50	0.76
52:03:5:THR:H	52:03:8:MET:CG	1.97	0.76
52:03:204:ALA:C	52:03:205:LYS:HE2	2.11	0.76
17:20:49:ILE:HD12	17:20:52:PRO:HA	1.67	0.76
32:B:46:VAL:HB	32:B:47:PRO:HD3	1.65	0.76
39:I:44:ARG:H	39:I:44:ARG:HD2	1.50	0.76
11:14:111:ILE:H	11:14:111:ILE:CD1	1.98	0.76
40:J:59:LYS:HE2	40:J:62:ARG:NH2	2.00	0.76
52:03:9:ARG:O	52:03:13:GLU:HG3	1.85	0.76
52:03:200:LYS:HD2	52:03:201:PRO:CD	2.16	0.76
52:03:170:ILE:HD12	52:03:170:ILE:N	2.00	0.76
59:Z:206:ILE:HD12	59:Z:207:ASP:N	2.00	0.76
21:24:9:ARG:HG2	21:24:41:GLU:HB2	1.67	0.76
36:F:3:HIS:N	36:F:92:THR:HG22	2.00	0.76
36:F:64:VAL:HG22	36:F:65:GLU:N	2.01	0.76
52:03:194:VAL:HA	52:03:197:LYS:NZ	2.00	0.76
52:03:166:ASP:OD2	52:03:168:ASN:HB2	1.85	0.76
7:10:23:LEU:HB3	7:10:87:GLU:OE1	1.85	0.76
59:Z:214:ILE:HG12	59:Z:227:VAL:HG21	1.68	0.76
9:12:27:ARG:HH22	54:01:1142:A:H4'	1.52	0.75
37:G:139:ASP:O	37:G:143:MET:HG2	1.86	0.75
50:T:80:ALA:HA	50:T:83:ASN:HD21	1.51	0.75
45:O:45:HIS:O	45:O:47:LYS:N	2.20	0.75
54:01:1936:A:H2	54:01:1943:U:H3	1.32	0.75
54:01:2286:G:H5''	54:01:2287:A:OP1	1.86	0.75
54:01:2156:G:H2'	54:01:2157:G:H5'	1.68	0.75
30:33:18:LYS:HG3	54:01:651:G:H5'	1.66	0.75
54:01:1779:U:H5	54:01:1784:A:N7	1.83	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:7:ARG:NH2	59:Z:269:ARG:HD3	2.01	0.75
1:04:93:VAL:HG11	1:04:115:ILE:HD11	1.69	0.75
36:F:36:ILE:HA	36:F:64:VAL:HG23	1.68	0.75
54:01:2800:A:H3'	54:01:2801:G:H5'	1.69	0.75
59:Z:259:GLU:HG2	59:Z:264:LEU:HA	1.66	0.75
10:13:35:VAL:HG22	10:13:69:VAL:HG12	1.69	0.75
38:H:95:MET:SD	38:H:129:ALA:HB1	2.27	0.74
21:24:72:VAL:HG12	21:24:93:ARG:HA	1.69	0.74
52:03:181:ASP:HB2	52:03:184:LYS:CD	2.10	0.74
53:A:1201:A:H1'	53:A:1202:U:OP2	1.85	0.74
7:10:103:ASN:HA	7:10:107:GLU:HB3	1.69	0.74
52:03:209:ILE:HD12	52:03:210:LYS:N	2.01	0.74
5:08:9:VAL:HA	5:08:48:THR:HG22	1.70	0.74
34:D:60:VAL:HG21	34:D:199:ILE:HD11	1.70	0.74
36:F:86:ARG:HD3	48:R:63:TYR:O	1.88	0.74
52:03:69:THR:HA	52:03:176:GLY:HA2	1.70	0.74
8:11:21:PRO:HB2	8:11:22:PRO:HD3	1.69	0.74
20:23:82:VAL:HG12	20:23:83:GLY:H	1.52	0.74
43:M:6:ILE:HG13	43:M:7:ASN:H	1.51	0.74
4:07:114:ARG:HH11	43:M:70:ARG:HD2	1.52	0.74
59:Z:323:PHE:HE1	59:Z:349:MET:HG2	1.51	0.74
12:15:6:ARG:O	12:15:6:ARG:HD3	1.86	0.73
59:Z:362:LEU:HD13	59:Z:364:HIS:H	1.53	0.73
13:16:44:LEU:HD23	13:16:113:ILE:HD13	1.68	0.73
19:22:39:THR:O	19:22:43:ILE:HG13	1.87	0.73
49:S:27:LYS:HG2	49:S:28:LYS:H	1.53	0.73
54:01:1906:G:C2'	54:01:1907:G:H5''	2.17	0.73
42:L:109:ARG:NH1	53:A:537:G:H5''	2.03	0.73
33:C:67:ILE:HB	33:C:102:ILE:HG22	1.71	0.73
41:K:124:LYS:HE2	53:A:1523:G:H5''	1.69	0.73
10:13:21:CYS:HA	10:13:41:ILE:HG22	1.71	0.73
9:12:7:LYS:O	9:12:11:VAL:HG23	1.89	0.73
52:03:42:VAL:CG2	52:03:216:THR:HG22	2.19	0.73
59:Z:212:LEU:HD11	59:Z:229:GLY:CA	2.17	0.73
9:12:58:ASN:HD21	9:12:128:ASN:HB2	1.53	0.72
38:H:10:LEU:HD22	38:H:74:ILE:HD11	1.68	0.72
13:16:37:THR:HG22	13:16:110:MET:HE1	1.71	0.72
32:B:31:PHE:HB2	32:B:39:ILE:HB	1.69	0.72
59:Z:374:PHE:HE2	59:Z:376:ILE:HD11	1.52	0.72
59:Z:143:GLU:O	59:Z:147:GLU:HG3	1.90	0.72
34:D:131:ILE:H	34:D:131:ILE:HD12	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:10:LEU:HD12	35:E:11:GLN:N	2.05	0.72
39:I:51:LEU:HD11	39:I:62:LEU:HD11	1.71	0.72
37:G:56:SER:HB3	37:G:59:GLU:HG2	1.71	0.72
43:M:28:ARG:HH21	43:M:62:PHE:HB2	1.54	0.72
37:G:143:MET:HE1	56:X:30:G:H21	1.54	0.72
40:J:40:ILE:HB	40:J:73:LEU:HB2	1.72	0.72
34:D:120:LYS:CE	34:D:130:ASN:HD21	2.03	0.71
52:O3:53:ARG:O	56:X:62:C:H4'	1.89	0.71
59:Z:260:MET:CE	59:Z:272:GLU:HG3	2.18	0.71
11:14:85:VAL:HG12	11:14:94:THR:HG22	1.72	0.71
54:O1:2297:A:N1	54:O1:2321:U:H5	1.88	0.71
18:21:77:ASP:OD1	18:21:102:HIS:HB2	1.89	0.71
30:33:61:LEU:HD12	30:33:61:LEU:O	1.89	0.71
41:K:34:THR:HG22	41:K:40:ALA:HA	1.71	0.71
54:O1:1020:A:H1'	54:O1:1021:A:OP2	1.90	0.71
59:Z:15:GLY:HA2	59:Z:78:HIS:CE1	2.26	0.71
6:O9:78:VAL:HG21	6:O9:103:VAL:HG22	1.72	0.71
33:C:69:THR:HG21	33:C:75:VAL:HG21	1.72	0.71
43:M:6:ILE:HG13	43:M:7:ASN:N	2.05	0.71
59:Z:287:GLU:H	59:Z:290:GLN:NE2	1.89	0.71
38:H:77:VAL:HG12	38:H:84:ILE:HD12	1.71	0.71
59:Z:151:MET:O	59:Z:155:GLU:HG3	1.90	0.71
59:Z:206:ILE:HG21	59:Z:269:ARG:NH1	2.06	0.71
33:C:107:LYS:HB3	33:C:143:LEU:HD21	1.73	0.71
52:O3:7:ARG:O	52:O3:11:ILE:HG13	1.90	0.71
53:A:572:A:H5''	53:A:917:G:H4'	1.72	0.71
36:F:64:VAL:HG22	36:F:65:GLU:H	1.56	0.70
54:O1:1807:G:H2'	54:O1:1808:A:H5'	1.73	0.70
43:M:97:ARG:HB2	43:M:99:GLN:HE22	1.56	0.70
55:O2:55:U:O2'	55:O2:56:G:H5'	1.90	0.70
29:32:34:ARG:HD3	54:O1:467:G:OP2	1.91	0.70
36:F:29:ILE:HG21	36:F:64:VAL:HG21	1.73	0.70
59:Z:308:VAL:HB	59:Z:358:MET:HE1	1.73	0.70
12:15:78:LEU:HD23	12:15:79:ALA:N	2.07	0.70
19:22:1:MET:HE2	19:22:3:ARG:HB2	1.74	0.70
50:T:43:LYS:HB2	50:T:86:ALA:HB2	1.73	0.70
59:Z:92:ILE:HD11	59:Z:121:LEU:HD22	1.72	0.70
59:Z:237:LYS:H	59:Z:237:LYS:HD3	1.57	0.70
59:Z:264:LEU:HD23	59:Z:265:LEU:N	2.07	0.70
18:21:88:ARG:HG3	18:21:94:ASP:OD2	1.91	0.70
48:R:41:SER:HB3	48:R:51:GLN:HE21	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:91:MET:HE1	59:Z:121:LEU:HB2	1.73	0.70
59:Z:96:ALA:HA	59:Z:125:VAL:HG21	1.72	0.70
4:07:87:LYS:HD2	54:01:2313:C:H5''	1.74	0.70
7:10:59:LEU:HD21	54:01:1047:G:H8	1.57	0.70
39:I:46:VAL:HA	39:I:49:GLN:HG3	1.74	0.70
42:L:87:LYS:HE3	53:A:526:C:OP2	1.92	0.70
51:U:8:ASN:HB3	51:U:9:GLU:OE1	1.92	0.70
59:Z:148:LEU:O	59:Z:148:LEU:HD13	1.92	0.70
38:H:100:ILE:HD12	38:H:100:ILE:O	1.92	0.69
13:16:103:ARG:HD2	13:16:106:ASP:OD1	1.91	0.69
46:P:20:VAL:HG23	46:P:35:ARG:HA	1.74	0.69
4:07:48:LEU:HD11	4:07:147:ARG:HH12	1.58	0.69
33:C:96:VAL:HB	33:C:97:PRO:HD2	1.75	0.69
59:Z:17:ILE:HB	59:Z:118:HIS:HD2	1.57	0.69
7:10:54:VAL:HG22	7:10:83:ALA:HB1	1.73	0.69
34:D:21:LYS:HE3	53:A:429:U:O2'	1.92	0.69
58:Y:44:G:H1'	58:Y:45:U:H2'	1.74	0.69
33:C:19:SER:HB3	33:C:21:TRP:HE1	1.55	0.69
41:K:63:GLN:O	41:K:67:GLU:HG3	1.93	0.69
54:01:435:C:H2'	54:01:436:C:H5'	1.73	0.69
54:01:1801:A:H5''	54:01:2203:U:H2'	1.73	0.69
59:Z:341:ILE:HD12	59:Z:358:MET:HG3	1.74	0.69
47:Q:58:VAL:HG22	47:Q:59:GLU:H	1.58	0.69
56:X:9:G:H21	56:X:45:G:H3'	1.58	0.69
11:14:132:ARG:O	11:14:136:GLU:HG3	1.93	0.69
14:17:35:ILE:HD12	14:17:102:ARG:HB3	1.74	0.69
19:22:61:LEU:HD11	19:22:82:LYS:HD3	1.74	0.69
41:K:88:PRO:HG2	41:K:89:GLY:H	1.58	0.69
53:A:29:U:O2'	53:A:30:U:H5'	1.93	0.69
54:01:962:G:H21	54:01:2250:G:H1	1.39	0.69
54:01:2682:A:H61	54:01:2728:U:H1'	1.56	0.69
59:Z:217:VAL:HG12	59:Z:283:ARG:HE	1.58	0.69
35:E:54:GLU:HG2	35:E:56:PRO:HD2	1.75	0.69
1:04:252:LYS:HB2	1:04:252:LYS:NZ	2.07	0.68
18:21:90:LYS:HB2	18:21:92:ARG:NH1	2.08	0.68
36:F:97:THR:O	36:F:98:GLU:HG2	1.93	0.68
59:Z:318:ARG:NH2	59:Z:322:PHE:HB3	2.09	0.68
7:10:117:LEU:HD23	7:10:120:ALA:HA	1.73	0.68
54:01:1141:U:H4'	54:01:1142:A:O4'	1.93	0.68
59:Z:25:THR:HG22	59:Z:46:PHE:CE1	2.27	0.68
6:09:15:LEU:HD21	6:09:56:ALA:HB1	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S:18:VAL:O	49:S:22:VAL:HG23	1.94	0.68
16:19:88:GLU:OE1	17:20:52:PRO:HB3	1.92	0.68
4:07:109:ARG:HH12	43:M:2:ARG:HD3	1.58	0.68
54:01:1611:C:H5'	54:01:1611:C:H6	1.57	0.68
5:08:51:PHE:HZ	5:08:71:LEU:HD22	1.57	0.68
52:03:40:GLU:CD	52:03:217:THR:HB	2.19	0.68
42:L:26:CYS:SG	42:L:29:LYS:HD3	2.33	0.68
4:07:104:THR:HG21	26:29:22:MET:SD	2.33	0.68
46:P:48:GLU:HG3	46:P:49:GLY:H	1.57	0.68
7:10:3:LEU:CD1	7:10:5:LEU:H	2.06	0.68
31:34:2:LYS:HG3	31:34:4:ARG:HH12	1.59	0.68
46:P:2:VAL:HG23	46:P:65:ALA:HA	1.74	0.68
59:Z:215:GLU:OE1	59:Z:229:GLY:HA2	1.94	0.68
33:C:161:ILE:HD12	33:C:161:ILE:O	1.93	0.68
35:E:133:ILE:HD12	35:E:133:ILE:H	1.59	0.68
52:03:37:LYS:HB2	54:01:2127:G:H5'	1.76	0.68
54:01:198:C:O2'	54:01:199:A:H5'	1.94	0.68
36:F:19:PRO:O	36:F:23:GLU:HG3	1.95	0.67
40:J:6:ILE:HG22	40:J:8:ILE:HG13	1.76	0.67
59:Z:16:THR:HG23	59:Z:78:HIS:CE1	2.29	0.67
59:Z:203:GLU:C	59:Z:204:ARG:HD2	2.19	0.67
2:05:149:ASN:HB3	54:01:2572:A:OP2	1.95	0.67
54:01:784:G:H5'	54:01:785:G:OP1	1.94	0.67
41:K:71:ASP:HA	41:K:74:LYS:HG3	1.76	0.67
47:Q:4:ILE:HD12	47:Q:4:ILE:O	1.95	0.67
54:01:2287:A:O2'	54:01:2288:A:H2'	1.95	0.67
11:14:124:GLY:H	11:14:144:GLU:HA	1.60	0.67
53:A:1200:C:H5''	53:A:1201:A:H3'	1.77	0.67
8:11:130:GLY:HA2	8:11:133:ARG:NH1	2.10	0.67
34:D:131:ILE:HD12	34:D:131:ILE:N	2.09	0.67
59:Z:148:LEU:O	59:Z:152:GLU:HG2	1.94	0.67
59:Z:150:GLU:HG3	59:Z:169:ILE:HG21	1.77	0.67
59:Z:214:ILE:CG2	59:Z:227:VAL:HG23	2.23	0.67
40:J:41:PRO:CB	53:A:1151:A:H1'	2.24	0.67
43:M:3:ILE:HD11	43:M:18:LEU:HD22	1.76	0.67
56:X:41:C:H2'	56:X:42:G:C8	2.30	0.67
59:Z:237:LYS:CE	59:Z:240:GLU:HB2	2.24	0.67
2:05:49:GLN:NE2	2:05:79:LEU:HD13	2.09	0.67
8:11:74:PRO:HB2	8:11:77:VAL:HG22	1.77	0.67
8:11:88:GLY:HA3	54:01:1063:G:O2'	1.95	0.67
11:14:9:ALA:HB3	11:14:12:SER:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:10:LEU:HD23	40:J:10:LEU:H	1.59	0.67
59:Z:214:ILE:HG12	59:Z:227:VAL:CG2	2.25	0.67
14:17:76:LYS:O	14:17:80:GLU:HG3	1.95	0.66
54:01:192:C:H2'	54:01:193:U:H5'	1.75	0.66
59:Z:219:SER:HB2	59:Z:283:ARG:HD3	1.77	0.66
7:10:27:VAL:CG1	7:10:83:ALA:HB3	2.25	0.66
34:D:144:ILE:HD13	34:D:177:MET:HB3	1.76	0.66
52:03:185:LEU:HA	52:03:188:ASN:HD22	1.60	0.66
15:18:7:LEU:O	15:18:7:LEU:HD23	1.96	0.66
40:J:41:PRO:HB2	53:A:1151:A:H1'	1.77	0.66
42:L:109:ARG:HB2	42:L:118:VAL:HG21	1.77	0.66
53:A:1197:A:H2'	53:A:1198:G:H5'	1.77	0.66
54:01:1539:U:H2'	54:01:1540:G:H8	1.60	0.66
58:Y:16:U:H2'	58:Y:17:C:H4'	1.76	0.66
59:Z:114:GLN:OE1	59:Z:117:GLU:HB3	1.95	0.66
3:06:63:LYS:HD2	54:01:2444:G:OP2	1.95	0.66
32:B:44:LYS:O	32:B:47:PRO:HD2	1.95	0.66
35:E:148:SER:HB2	35:E:149:PRO:HD2	1.77	0.66
8:11:56:VAL:HG22	8:11:57:VAL:N	2.11	0.66
52:03:48:LEU:HD13	52:03:59:VAL:HG21	1.77	0.66
1:04:175:LEU:CD1	1:04:181:ARG:HH12	2.07	0.66
10:13:113:MET:SD	10:13:116:ILE:HD11	2.35	0.66
34:D:57:LYS:HD3	34:D:202:LEU:HD13	1.76	0.66
53:A:70:U:H5''	53:A:71:A:OP1	1.94	0.66
59:Z:152:GLU:HA	59:Z:155:GLU:OE1	1.96	0.66
10:13:58:LEU:HD11	10:13:86:LEU:HD22	1.78	0.66
46:P:79:ASN:HB2	46:P:82:ALA:OXT	1.96	0.66
53:A:1540:U:O2	53:A:1540:U:H3'	1.94	0.66
54:01:1045:C:H5'	54:01:1046:A:H5''	1.77	0.66
59:Z:264:LEU:HD23	59:Z:264:LEU:C	2.21	0.66
34:D:33:ILE:HG13	34:D:34:GLU:N	2.11	0.66
39:I:24:ASN:HD22	39:I:26:LYS:HE3	1.61	0.66
46:P:8:ARG:HB3	46:P:28:ARG:CZ	2.26	0.66
51:U:16:ARG:HB2	51:U:19:LYS:HD3	1.78	0.66
52:03:186:LYS:O	52:03:190:GLU:HG3	1.97	0.65
59:Z:85:ALA:O	59:Z:88:VAL:HG23	1.96	0.65
8:11:56:VAL:HG22	8:11:57:VAL:H	1.61	0.65
16:19:93:ILE:HD12	17:20:13:ARG:HB2	1.77	0.65
18:21:4:ILE:HG22	18:21:106:VAL:HG22	1.77	0.65
33:C:13:ILE:HG22	33:C:14:VAL:HG23	1.78	0.65
37:G:85:GLN:HB2	37:G:147:ASN:OD1	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:63:THR:O	52:03:160:GLN:HG3	1.96	0.65
54:01:2572:A:OP1	54:01:2574:G:H4'	1.97	0.65
1:04:229:HIS:ND1	1:04:230:PRO:HD2	2.11	0.65
7:10:23:LEU:HD13	7:10:118:ILE:HB	1.77	0.65
7:10:57:ASN:HB2	7:10:62:ARG:CD	2.27	0.65
53:A:130:A:O2'	53:A:264:C:H5'	1.96	0.65
56:X:21:A:H61	56:X:46:G:H2'	1.60	0.65
38:H:9:MET:HG3	38:H:26:MET:SD	2.36	0.65
38:H:14:ARG:HD2	53:A:875:U:O2'	1.97	0.65
2:05:135:GLY:HA2	54:01:743:A:OP1	1.97	0.65
52:03:51:ASP:OD2	52:03:54:LYS:HG3	1.97	0.65
54:01:704:G:H2'	54:01:726:G:H22	1.62	0.65
59:Z:156:LEU:HD13	59:Z:159:GLN:HE21	1.62	0.65
11:14:95:LEU:HD11	11:14:125:LEU:HD21	1.78	0.65
22:25:17:LEU:HD21	22:25:37:ARG:NH2	2.11	0.65
54:01:275:C:H3'	54:01:276:U:H5''	1.78	0.65
54:01:1373:A:H5'	54:01:2212:A:H1'	1.77	0.65
54:01:1715:G:HO2'	54:01:1716:U:H6	1.45	0.65
43:M:21:ILE:HB	43:M:24:VAL:HG12	1.78	0.65
52:03:15:VAL:HG11	52:03:222:VAL:HG22	1.77	0.65
9:12:101:ILE:HD12	9:12:101:ILE:N	2.12	0.65
16:19:45:ALA:O	16:19:49:ARG:HG3	1.97	0.65
31:34:11:CYS:SG	31:34:12:ARG:N	2.70	0.65
41:K:126:ARG:NH2	53:A:692:U:H5''	2.12	0.65
47:Q:67:SER:OG	47:Q:70:LYS:HB3	1.97	0.65
54:01:310:A:O2'	54:01:311:A:H5''	1.97	0.65
8:11:103:ALA:O	8:11:107:GLU:HG3	1.97	0.64
16:19:49:ARG:HG2	16:19:49:ARG:HH11	1.62	0.64
29:32:10:LEU:HD23	54:01:770:G:H5''	1.77	0.64
52:03:177:LYS:HE2	52:03:177:LYS:HA	1.79	0.64
59:Z:31:ILE:O	59:Z:35:LEU:HD23	1.97	0.64
49:S:17:LYS:HB2	49:S:17:LYS:NZ	2.12	0.64
49:S:19:GLU:O	49:S:23:GLU:HG2	1.96	0.64
54:01:858:G:H5'	54:01:859:G:OP2	1.98	0.64
1:04:146:LYS:HB2	1:04:149:LYS:HB2	1.80	0.64
8:11:45:THR:HG22	8:11:50:LYS:HG2	1.80	0.64
36:F:18:VAL:HG21	36:F:58:HIS:CD2	2.33	0.64
49:S:28:LYS:HB3	49:S:29:PRO:HD2	1.79	0.64
53:A:505:G:H5'	53:A:534:U:H2'	1.80	0.64
59:Z:309:TYR:HB2	59:Z:355:ASN:OD1	1.97	0.64
4:07:56:LEU:HD13	4:07:88:VAL:HG23	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:20:76:LYS:HB2	17:20:85:LYS:HB3	1.79	0.64
48:R:25:ILE:HG21	48:R:66:LEU:HB3	1.80	0.64
54:01:1900:A:H1'	54:01:1970:A:H2'	1.79	0.64
54:01:2834:G:H2'	54:01:2879:A:H61	1.63	0.64
59:Z:30:ALA:HA	59:Z:178:LEU:HD13	1.79	0.64
59:Z:262:ARG:HH11	59:Z:262:ARG:HG3	1.62	0.64
31:34:36:ARG:O	31:34:36:ARG:HD3	1.98	0.64
47:Q:13:SER:H	47:Q:21:VAL:HG13	1.61	0.64
47:Q:69:THR:HG22	47:Q:70:LYS:H	1.62	0.64
53:A:1218:C:H2'	53:A:1219:A:C8	2.32	0.64
54:01:554:U:H2'	54:01:555:G:O4'	1.97	0.64
59:Z:84:HIS:O	59:Z:86:ASP:N	2.31	0.64
59:Z:116:ARG:CD	59:Z:156:LEU:HD21	2.28	0.64
8:11:48:ILE:HG13	8:11:49:GLU:H	1.63	0.64
15:18:52:ARG:HG2	15:18:52:ARG:HH11	1.63	0.64
59:Z:76:TYR:CZ	59:Z:195:LEU:HG	2.33	0.64
59:Z:142:ASP:OD2	59:Z:145:LEU:HG	1.97	0.64
54:01:1179:G:C5	54:01:1180:U:H1'	2.32	0.64
54:01:2144:G:H1'	54:01:2147:A:H61	1.63	0.64
35:E:133:ILE:O	35:E:136:VAL:HG12	1.97	0.64
54:01:1396:U:H5''	54:01:1397:U:OP2	1.98	0.64
59:Z:124:GLN:NE2	59:Z:385:ALA:HB2	2.05	0.64
8:11:24:GLY:O	8:11:27:LEU:HD23	1.98	0.63
14:17:11:ALA:O	14:17:15:ARG:HG2	1.98	0.63
14:17:80:GLU:O	14:17:84:GLU:HG3	1.97	0.63
32:B:202:ASN:HD22	32:B:203:ASP:H	1.43	0.63
54:01:2156:G:C2'	54:01:2157:G:H5'	2.27	0.63
59:Z:142:ASP:CG	59:Z:145:LEU:HG	2.23	0.63
6:09:132:PHE:HB2	6:09:140:ALA:HB3	1.79	0.63
7:10:57:ASN:HD22	7:10:62:ARG:HG2	1.62	0.63
59:Z:145:LEU:O	59:Z:149:VAL:HG23	1.98	0.63
7:10:118:ILE:N	7:10:119:PRO:CD	2.59	0.63
10:13:13:ASN:ND2	10:13:98:ARG:HB2	2.13	0.63
55:02:66:A:H5''	55:02:67:G:OP1	1.98	0.63
11:14:57:LEU:HD22	30:33:53:ASP:HB3	1.81	0.63
51:U:9:GLU:HB2	51:U:10:PRO:HD3	1.80	0.63
59:Z:211:LEU:HD12	59:Z:293:ALA:HB2	1.81	0.63
59:Z:236:ILE:HD12	59:Z:236:ILE:O	1.97	0.63
59:Z:304:PHE:C	59:Z:392:LEU:HD23	2.24	0.63
2:05:8:LYS:HB2	2:05:201:LEU:HD11	1.79	0.63
7:10:61:ARG:HB3	54:01:1046:A:H4'	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:76:ASN:HB2	35:E:81:GLN:HE22	1.62	0.63
56:W:6:G:O2'	56:W:7:G:H5'	1.99	0.63
7:10:3:LEU:HD12	7:10:5:LEU:N	2.13	0.63
34:D:170:LEU:HD12	34:D:170:LEU:O	1.98	0.63
59:Z:142:ASP:HB3	59:Z:145:LEU:HD11	1.80	0.63
39:I:98:ARG:HG3	39:I:103:VAL:CG2	2.29	0.62
52:03:40:GLU:OE2	52:03:218:MET:HG3	1.98	0.62
59:Z:95:ALA:HA	59:Z:98:MET:HB2	1.80	0.62
1:04:116:GLN:NE2	1:04:121:ALA:HA	2.13	0.62
10:13:10:VAL:HG21	10:13:16:ALA:HB3	1.81	0.62
53:A:1432:G:H1'	53:A:1468:A:N6	2.14	0.62
54:01:310:A:C2'	54:01:311:A:H5''	2.29	0.62
59:Z:82:PRO:HG3	59:Z:90:ASN:HB2	1.80	0.62
59:Z:306:SER:O	59:Z:357:LYS:HB2	1.99	0.62
59:Z:370:ASP:OD1	59:Z:390:LYS:HA	1.98	0.62
5:08:34:ARG:HE	5:08:70:LEU:HD13	1.62	0.62
7:10:59:LEU:HD21	54:01:1047:G:C8	2.33	0.62
9:12:26:GLY:HA3	54:01:1140:C:H5'	1.81	0.62
10:13:66:LYS:NZ	10:13:66:LYS:HB3	2.14	0.62
35:E:114:LEU:O	35:E:119:VAL:HG22	1.98	0.62
36:F:86:ARG:NH1	53:A:673:A:H4'	2.14	0.62
37:G:68:VAL:HG21	37:G:103:ILE:HD11	1.79	0.62
40:J:52:LEU:HD21	40:J:59:LYS:HD2	1.80	0.62
44:N:45:LEU:HG	49:S:12:LEU:HD21	1.81	0.62
52:03:41:SER:HB2	52:03:177:LYS:HE2	1.80	0.62
53:A:327:A:O2'	53:A:328:C:H4'	1.98	0.62
53:A:1306:A:N6	53:A:1331:G:H1'	2.14	0.62
54:01:1213:A:N6	54:01:1236:G:H1'	2.13	0.62
54:01:1509:A:H2'	54:01:1510:G:C8	2.34	0.62
1:04:257:ARG:NH2	1:04:266:ILE:HD12	2.13	0.62
5:08:118:ALA:O	5:08:120:ILE:N	2.32	0.62
54:01:974:G:H1'	54:01:975:A:C8	2.34	0.62
54:01:2391:G:H2'	54:01:2424:C:H41	1.62	0.62
55:02:3:C:C2'	55:02:4:C:H5''	2.28	0.62
59:Z:136:LYS:HB3	59:Z:139:MET:HG3	1.81	0.62
21:24:17:SER:O	21:24:20:LEU:HD23	2.00	0.62
26:29:44:PHE:CD2	26:29:45:THR:HG23	2.35	0.62
35:E:133:ILE:HD12	35:E:133:ILE:N	2.14	0.62
37:G:113:LYS:HE2	37:G:113:LYS:HA	1.82	0.62
40:J:57:VAL:O	40:J:58:ASN:HB2	1.98	0.62
47:Q:18:LYS:NZ	47:Q:18:LYS:HB2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:50:ILE:CD1	52:03:59:VAL:HG23	2.28	0.62
54:01:215:G:C4'	54:01:216:A:H4'	2.28	0.62
59:Z:152:GLU:HA	59:Z:155:GLU:CD	2.25	0.62
32:B:224:ARG:HB2	32:B:224:ARG:NH2	2.14	0.62
54:01:2391:G:H2'	54:01:2424:C:N4	2.14	0.62
59:Z:357:LYS:NZ	59:Z:359:VAL:HG23	2.13	0.62
7:10:118:ILE:H	7:10:119:PRO:CD	2.12	0.62
35:E:76:ASN:HB2	35:E:81:GLN:NE2	2.15	0.62
54:01:2553:G:H3'	54:01:2554:U:H5''	1.82	0.62
59:Z:214:ILE:HD13	59:Z:286:ILE:HD11	1.81	0.62
15:18:38:ARG:HH21	15:18:38:ARG:HG3	1.64	0.62
54:01:1139:G:O2'	54:01:1140:C:H5'	1.99	0.62
59:Z:321:PRO:HB3	59:Z:351:MET:HA	1.81	0.62
12:15:42:THR:OG1	12:15:45:GLN:HG3	2.00	0.62
15:18:92:ARG:HD3	54:01:1753:G:H5''	1.82	0.62
40:J:57:VAL:HG22	40:J:58:ASN:H	1.65	0.62
41:K:84:MET:HG2	41:K:110:THR:OG1	2.00	0.62
42:L:31:GLY:HA3	42:L:54:VAL:CG1	2.30	0.62
52:03:4:LEU:HD22	52:03:8:MET:CB	2.30	0.62
54:01:1701:A:H2'	54:01:1702:G:H5'	1.80	0.62
1:04:70:LYS:HE3	1:04:73:ILE:HD12	1.82	0.61
4:07:91:ARG:HA	4:07:95:MET:HB3	1.82	0.61
34:D:37:PRO:HD2	34:D:41:GLY:HA3	1.81	0.61
54:01:1810:A:H2'	54:01:1811:G:O4'	2.00	0.61
59:Z:69:TYR:HE1	59:Z:78:HIS:HB2	1.65	0.61
8:11:100:ILE:N	8:11:100:ILE:HD12	2.15	0.61
9:12:17:VAL:HG23	9:12:137:PRO:HB2	1.81	0.61
10:13:76:VAL:H	15:18:72:VAL:HG22	1.65	0.61
15:18:20:ARG:HD3	15:18:112:ARG:HH12	1.65	0.61
31:34:15:LYS:HB2	31:34:15:LYS:NZ	2.15	0.61
44:N:26:LEU:HD23	44:N:26:LEU:O	2.00	0.61
2:05:108:ASP:OD2	2:05:206:ALA:HA	1.99	0.61
38:H:28:SER:HB3	38:H:56:PRO:HB2	1.82	0.61
59:Z:156:LEU:HD13	59:Z:159:GLN:NE2	2.15	0.61
13:16:47:VAL:C	13:16:50:PRO:HD2	2.26	0.61
23:26:11:PRO:HB3	23:26:29:LEU:HD23	1.82	0.61
32:B:117:GLU:O	32:B:121:GLN:HG2	2.01	0.61
40:J:57:VAL:HG22	40:J:58:ASN:N	2.15	0.61
46:P:51:ARG:O	46:P:52:LEU:HD12	2.00	0.61
59:Z:206:ILE:HD12	59:Z:207:ASP:H	1.66	0.61
20:23:97:SER:O	20:23:98:ASN:HB3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:06:176:ASP:OD2	3:06:178:VAL:HG12	2.01	0.61
33:C:19:SER:HB3	33:C:21:TRP:NE1	2.14	0.61
33:C:156:LEU:HD12	33:C:156:LEU:O	2.00	0.61
49:S:49:ALA:HB1	49:S:56:HIS:HB3	1.83	0.61
52:03:16:ASP:OD2	52:03:19:LYS:HB2	2.00	0.61
3:06:29:HIS:HA	3:06:32:VAL:HG12	1.82	0.61
14:17:37:ALA:HB2	14:17:106:LEU:HD11	1.81	0.61
33:C:38:VAL:O	33:C:42:LEU:HD13	2.01	0.61
53:A:1033:G:H2'	53:A:1034:G:C4'	2.30	0.61
3:06:48:THR:HG23	3:06:86:ALA:HB3	1.82	0.61
3:06:104:ALA:O	3:06:108:ILE:HG13	2.00	0.61
4:07:140:ILE:HD12	4:07:140:ILE:N	2.15	0.61
7:10:29:ASP:HB2	7:10:56:ARG:HH12	1.65	0.61
8:11:74:PRO:HG3	54:01:1060:U:OP1	2.00	0.61
42:L:113:ARG:HH11	42:L:113:ARG:HG2	1.65	0.61
43:M:15:VAL:HG23	43:M:16:ILE:CD1	2.29	0.61
59:Z:354:ASP:HB3	59:Z:356:ILE:HG12	1.83	0.61
1:04:48:ILE:HD11	1:04:51:ARG:HA	1.82	0.61
7:10:73:LYS:HB3	7:10:117:LEU:HD21	1.82	0.61
28:31:47:ILE:HD12	28:31:47:ILE:N	2.16	0.61
32:B:165:ALA:HB3	32:B:190:SER:HB3	1.83	0.61
32:B:202:ASN:ND2	32:B:203:ASP:H	1.99	0.61
54:01:1071:G:OP1	54:01:1071:G:H3'	2.00	0.61
54:01:2233:U:H2'	54:01:2234:G:C8	2.36	0.61
7:10:87:GLU:OE2	7:10:95:LEU:HB2	2.01	0.60
52:03:202:THR:HB	52:03:203:GLN:OE1	2.01	0.60
5:08:154:GLU:OE2	5:08:156:TYR:HB2	2.00	0.60
38:H:49:LYS:HB2	38:H:59:GLU:HG2	1.83	0.60
53:A:352:C:H4'	53:A:354:G:OP1	2.01	0.60
53:A:769:G:H4'	53:A:1513:A:H4'	1.82	0.60
53:A:1379:G:O2'	53:A:1380:U:H5'	2.00	0.60
54:01:1367:A:H2'	54:01:1368:G:H5'	1.82	0.60
59:Z:191:LEU:HD12	59:Z:191:LEU:C	2.26	0.60
31:34:36:ARG:HD3	31:34:36:ARG:C	2.27	0.60
34:D:131:ILE:HG22	34:D:133:SER:H	1.67	0.60
59:Z:357:LYS:HZ2	59:Z:359:VAL:HG23	1.66	0.60
10:13:35:VAL:HG11	10:13:106:GLU:HB2	1.82	0.60
33:C:133:MET:HE3	33:C:167:TYR:HB2	1.82	0.60
49:S:68:HIS:HB3	49:S:72:GLU:HG3	1.82	0.60
52:03:40:GLU:HB3	52:03:217:THR:OG1	2.01	0.60
52:03:203:GLN:C	52:03:205:LYS:HE3	2.25	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:62:ARG:HH11	1:04:62:ARG:HG3	1.65	0.60
5:08:98:LYS:NZ	5:08:103:ASN:HD22	1.99	0.60
8:11:127:SER:HA	54:01:1080:A:H1'	1.84	0.60
11:14:23:ILE:HD12	11:14:23:ILE:N	2.17	0.60
35:E:23:THR:HA	35:E:28:ARG:HA	1.82	0.60
40:J:66:GLU:CG	44:N:98:ALA:HB2	2.26	0.60
8:11:4:VAL:HA	8:11:7:TYR:CE1	2.36	0.60
33:C:39:ARG:HG3	33:C:54:ILE:HD11	1.84	0.60
40:J:53:ILE:HG23	53:A:1060:U:H4'	1.83	0.60
5:08:132:LEU:HD12	5:08:132:LEU:O	2.02	0.60
44:N:7:ALA:O	44:N:10:VAL:HG12	2.01	0.60
44:N:36:SER:HA	44:N:40:ARG:HD3	1.82	0.60
50:T:80:ALA:HA	50:T:83:ASN:ND2	2.17	0.60
54:01:1023:U:O2'	54:01:1122:G:H5'	2.01	0.60
54:01:2134:A:N6	54:01:2157:G:H4'	2.16	0.60
59:Z:10:PRO:HD2	59:Z:74:ARG:HA	1.82	0.60
4:07:140:ILE:HD12	4:07:140:ILE:H	1.67	0.60
11:14:76:GLU:C	11:14:77:ILE:HD12	2.27	0.60
15:18:51:ASN:O	54:01:2845:U:H5''	2.02	0.60
20:23:4:ILE:HD12	20:23:4:ILE:N	2.17	0.60
9:12:35:ARG:HA	9:12:40:HIS:HD2	1.67	0.60
34:D:96:ARG:O	34:D:100:VAL:HG23	2.02	0.60
52:03:200:LYS:HE3	52:03:204:ALA:HB3	1.84	0.60
53:A:273:U:H2'	53:A:274:A:H5'	1.83	0.60
59:Z:351:MET:HG2	59:Z:354:ASP:OD1	2.02	0.60
6:09:12:LEU:HD12	6:09:13:GLY:N	2.17	0.60
31:34:8:LYS:HB2	31:34:8:LYS:NZ	2.16	0.60
33:C:137:VAL:HG21	33:C:167:TYR:HD2	1.67	0.60
47:Q:16:MET:HG3	47:Q:19:SER:OG	2.02	0.60
54:01:1979:U:O2'	54:01:1980:G:H5'	2.02	0.60
54:01:2849:U:H4'	54:01:2868:A:C2	2.37	0.60
34:D:131:ILE:HG12	53:A:620:C:C2	2.37	0.59
1:04:215:VAL:HG12	1:04:216:ARG:H	1.67	0.59
7:10:11:ILE:O	7:10:15:VAL:HG23	2.02	0.59
8:11:4:VAL:HA	8:11:7:TYR:HE1	1.68	0.59
16:19:49:ARG:CZ	17:20:72:VAL:HG13	2.33	0.59
35:E:80:LEU:HD13	35:E:122:VAL:CG1	2.19	0.59
37:G:15:PRO:HB2	39:I:44:ARG:NH1	2.17	0.59
43:M:8:ILE:HD12	43:M:8:ILE:N	2.17	0.59
52:03:56:ASP:HB2	52:03:203:GLN:HE21	1.67	0.59
53:A:304:U:O2'	53:A:305:G:H5'	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1273:C:H2'	53:A:1274:A:O4'	2.02	0.59
59:Z:143:GLU:HA	59:Z:146:LEU:HB2	1.83	0.59
5:08:51:PHE:CZ	5:08:71:LEU:HD22	2.35	0.59
44:N:25:GLU:HA	44:N:28:ALA:HB3	1.82	0.59
54:01:2238:G:N3	54:01:2238:G:H2'	2.17	0.59
54:01:2537:U:H2'	54:01:2538:C:C6	2.36	0.59
4:07:139:GLU:H	4:07:139:GLU:CD	2.11	0.59
40:J:67:ILE:HG13	40:J:67:ILE:O	2.02	0.59
54:01:278:A:H2'	54:01:278:A:N3	2.18	0.59
58:Y:14:A:H2'	58:Y:15:G:O4'	2.01	0.59
20:23:3:LYS:C	20:23:4:ILE:HD12	2.27	0.59
26:29:22:MET:HE3	26:29:24:ILE:HG21	1.83	0.59
33:C:120:THR:HG23	33:C:188:ALA:HB2	1.83	0.59
38:H:49:LYS:HB2	38:H:59:GLU:CG	2.31	0.59
53:A:354:G:H2'	53:A:355:C:H5'	1.83	0.59
54:01:1565:C:O2'	54:01:1566:A:H2'	2.02	0.59
59:Z:324:LYS:CE	59:Z:342:GLU:HA	2.32	0.59
8:11:20:SER:HB3	8:11:21:PRO:HD3	1.84	0.59
11:14:96:LYS:HB2	11:14:96:LYS:NZ	2.18	0.59
27:30:24:VAL:HG13	27:30:25:THR:H	1.66	0.59
48:R:20:ILE:HG21	48:R:54:LEU:HA	1.85	0.59
52:03:219:GLY:O	54:01:2176:A:H5'	2.03	0.59
54:01:329:G:O4'	54:01:477:A:H1'	2.02	0.59
56:X:25:C:H2'	56:X:26:G:H8	1.67	0.59
59:Z:9:LYS:HE3	59:Z:72:PRO:HA	1.84	0.59
9:12:117:ALA:HA	9:12:120:ARG:HH21	1.66	0.59
41:K:71:ASP:O	41:K:72:ALA:HB3	2.01	0.59
47:Q:58:VAL:HG21	47:Q:74:LEU:HD11	1.85	0.59
54:01:558:U:H2'	54:01:559:G:H8	1.68	0.59
54:01:973:A:H5'	54:01:1188:U:H1'	1.85	0.59
54:01:1083:U:H2'	54:01:1085:A:OP2	2.03	0.59
1:04:216:ARG:HH11	1:04:216:ARG:HG3	1.67	0.59
2:05:9:VAL:O	15:18:4:ILE:HD11	2.02	0.59
49:S:17:LYS:HB2	49:S:17:LYS:HZ3	1.68	0.59
3:06:21:ARG:HH21	3:06:106:LYS:HE2	1.68	0.59
6:09:73:ASN:HD22	6:09:76:GLU:HA	1.66	0.59
16:19:91:ARG:HH11	16:19:91:ARG:HG3	1.68	0.59
17:20:14:VAL:HG21	17:20:98:ILE:HG13	1.85	0.59
53:A:225:C:H2'	53:A:226:G:H5''	1.84	0.59
54:01:1666:G:C2'	54:01:1667:G:H5'	2.33	0.59
54:01:2638:G:H1'	54:01:2778:A:N6	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:215:GLU:CD	59:Z:229:GLY:HA2	2.28	0.59
59:Z:244:ILE:HG21	59:Z:290:GLN:OE1	2.03	0.59
15:18:13:LYS:HE3	15:18:76:HIS:HA	1.85	0.59
20:23:33:VAL:HG13	20:23:66:VAL:HG22	1.84	0.59
20:23:80:ASP:OD2	20:23:95:PHE:HB3	2.02	0.59
21:24:51:GLN:OE1	21:24:86:LEU:HD11	2.03	0.59
31:34:36:ARG:HD3	31:34:37:GLN:HG2	1.83	0.59
40:J:26:VAL:HG13	40:J:36:VAL:HG11	1.84	0.59
46:P:6:LEU:HB3	46:P:17:TYR:HB3	1.85	0.59
53:A:1256:A:H1'	53:A:1258:G:C4	2.37	0.59
59:Z:91:MET:HE1	59:Z:121:LEU:CB	2.31	0.59
59:Z:318:ARG:HH21	59:Z:322:PHE:HB3	1.67	0.59
3:06:24:ASN:ND2	3:06:27:LEU:HB2	2.16	0.58
9:12:135:GLN:NE2	54:01:7:G:H1'	2.18	0.58
27:30:54:ILE:HG23	27:30:56:LYS:H	1.68	0.58
45:O:28:VAL:HG11	45:O:66:LEU:HD21	1.85	0.58
54:01:100:U:H4'	54:01:101:A:O4'	2.02	0.58
54:01:2111:U:H3	54:01:2147:A:H1'	1.67	0.58
59:Z:324:LYS:HZ1	59:Z:342:GLU:CA	2.15	0.58
1:04:145:MET:HE1	1:04:181:ARG:HE	1.68	0.58
15:18:3:ILE:N	15:18:3:ILE:HD12	2.18	0.58
59:Z:248:LYS:HE3	59:Z:290:GLN:CD	2.28	0.58
18:21:83:LYS:HG2	18:21:95:ARG:HH11	1.68	0.58
19:22:2:ILE:CD1	54:01:144:A:H4'	2.32	0.58
34:D:1:ALA:HA	34:D:67:LEU:HD11	1.86	0.58
43:M:84:CYS:O	43:M:88:LEU:HD13	2.02	0.58
53:A:882:C:O2'	53:A:883:C:H5'	2.03	0.58
54:01:2029:G:O6	54:01:2032:G:H5''	2.02	0.58
54:01:2282:G:H4'	54:01:2389:G:O2'	2.02	0.58
59:Z:148:LEU:HD13	59:Z:148:LEU:C	2.28	0.58
59:Z:332:PHE:N	59:Z:332:PHE:CD1	2.71	0.58
52:03:42:VAL:HG11	52:03:214:ILE:HD13	1.83	0.58
54:01:1872:A:H2'	54:01:1873:G:O4'	2.04	0.58
55:02:3:C:C3'	55:02:4:C:H5''	2.33	0.58
59:Z:299:LYS:HD2	59:Z:301:HIS:CE1	2.38	0.58
20:23:65:GLN:HE21	54:01:328:U:H4'	1.69	0.58
22:25:61:GLY:HA2	22:25:81:GLU:H	1.69	0.58
43:M:28:ARG:NH2	43:M:62:PHE:HB2	2.17	0.58
53:A:1441:A:H2'	53:A:1442:G:H5'	1.84	0.58
54:01:2391:G:H4'	54:01:2392:A:OP1	2.03	0.58
59:Z:303:LYS:HG3	59:Z:392:LEU:HB2	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:17:29:HIS:HB3	14:17:36:TYR:HB2	1.86	0.58
18:21:51:LEU:O	18:21:55:ILE:HG13	2.03	0.58
20:23:71:ILE:HD11	20:23:82:VAL:HG22	1.85	0.58
53:A:273:U:C2'	53:A:274:A:H5'	2.34	0.58
56:X:13:C:C2'	56:X:14:A:H5''	2.32	0.58
59:Z:307:GLU:CD	59:Z:308:VAL:N	2.60	0.58
1:04:252:LYS:HD3	54:01:1901:A:H4'	1.86	0.58
11:14:77:ILE:HD12	11:14:77:ILE:N	2.19	0.58
15:18:52:ARG:NH2	54:01:2720:U:H5''	2.16	0.58
29:32:3:ARG:HE	29:32:4:THR:H	1.49	0.58
38:H:63:LYS:NZ	38:H:63:LYS:HB3	2.19	0.58
51:U:36:PHE:C	51:U:38:GLU:H	2.11	0.58
52:03:65:LEU:HD11	52:03:175:ILE:HA	1.85	0.58
59:Z:69:TYR:CE1	59:Z:78:HIS:HB2	2.39	0.58
1:04:156:SER:OG	54:01:1818:U:H5'	2.02	0.58
2:05:62:LYS:HB2	2:05:63:PRO:HD3	1.84	0.58
14:17:40:ILE:HG12	14:17:47:VAL:HG12	1.86	0.58
15:18:2:ASN:O	15:18:6:GLN:HG3	2.04	0.58
42:L:101:LEU:HD12	42:L:101:LEU:H	1.68	0.58
43:M:7:ASN:HD22	43:M:9:PRO:HD3	1.68	0.58
47:Q:19:SER:HB3	47:Q:70:LYS:NZ	2.18	0.58
47:Q:60:ILE:CG2	47:Q:72:TRP:HB3	2.34	0.58
47:Q:73:THR:HG22	47:Q:74:LEU:N	2.18	0.58
54:01:511:U:H2'	54:01:512:G:H5'	1.84	0.58
4:07:58:ALA:O	4:07:139:GLU:HG2	2.04	0.58
7:10:34:THR:HB	7:10:37:LYS:HE2	1.86	0.58
24:27:1:MET:HA	24:27:4:LYS:HE2	1.86	0.58
29:32:30:VAL:O	29:32:34:ARG:HG2	2.04	0.58
31:34:25:VAL:HB	31:34:35:GLN:HG2	1.85	0.58
44:N:80:ARG:HG3	44:N:80:ARG:HH11	1.68	0.58
45:O:17:ASP:OD2	45:O:19:ASN:HB2	2.04	0.58
46:P:14:ARG:HH12	53:A:618:C:H1'	1.69	0.58
54:01:1373:A:C5'	54:01:2212:A:H1'	2.34	0.58
54:01:1783:A:H5'	54:01:2608:G:H4'	1.85	0.58
59:Z:25:THR:HG21	59:Z:50:ASP:OD2	2.03	0.58
59:Z:152:GLU:HA	59:Z:155:GLU:CG	2.34	0.58
59:Z:351:MET:SD	59:Z:351:MET:N	2.73	0.58
20:23:71:ILE:CD1	20:23:82:VAL:HG22	2.33	0.58
41:K:24:ALA:HA	41:K:29:THR:HG22	1.84	0.58
42:L:113:ARG:HB2	42:L:118:VAL:HB	1.85	0.58
46:P:31:ARG:NH1	46:P:31:ARG:HB3	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:703:U:H2'	54:01:704:G:O4'	2.03	0.58
54:01:1601:G:O2'	54:01:1602:U:H5'	2.03	0.58
1:04:216:ARG:CG	1:04:217:PRO:HD2	2.34	0.57
3:06:149:ILE:HD11	3:06:172:ALA:HA	1.86	0.57
52:03:27:ILE:HG13	52:03:182:ALA:HB1	1.84	0.57
54:01:1105:U:C2'	54:01:1106:G:H5''	2.34	0.57
59:Z:215:GLU:HG2	59:Z:228:THR:OG1	2.04	0.57
59:Z:283:ARG:HH11	59:Z:283:ARG:HG3	1.69	0.57
4:07:116:LEU:HD13	4:07:175:PRO:HB2	1.86	0.57
8:11:91:LYS:CB	8:11:94:LYS:HE2	2.34	0.57
12:15:45:GLN:NE2	54:01:2485:G:H5''	2.18	0.57
53:A:1170:A:H2'	53:A:1171:A:O4'	2.04	0.57
54:01:226:A:H2'	54:01:227:A:O4'	2.03	0.57
59:Z:305:GLU:HB2	59:Z:392:LEU:CD2	2.33	0.57
1:04:104:LEU:HD11	1:04:155:ARG:HG2	1.85	0.57
34:D:23:GLY:HA3	53:A:409:U:OP1	2.05	0.57
41:K:111:ASP:HB3	51:U:3:ILE:HA	1.86	0.57
46:P:20:VAL:HG22	46:P:21:VAL:N	2.19	0.57
53:A:555:U:H2'	53:A:556:C:C6	2.40	0.57
27:30:24:VAL:HG13	27:30:25:THR:N	2.20	0.57
45:O:23:SER:O	45:O:27:GLN:HG3	2.05	0.57
53:A:16:A:O2'	53:A:17:U:H5'	2.04	0.57
54:01:2732:G:O2'	54:01:2733:A:H5'	2.03	0.57
59:Z:310:ILE:HB	59:Z:352:PRO:HA	1.86	0.57
1:04:129:LEU:N	1:04:129:LEU:HD23	2.19	0.57
7:10:118:ILE:H	7:10:119:PRO:HD2	1.70	0.57
52:03:175:ILE:HB	52:03:188:ASN:HB3	1.86	0.57
53:A:79:G:O2'	53:A:80:A:H5'	2.04	0.57
54:01:668:A:H2'	54:01:670:A:H62	1.69	0.57
54:01:1858:A:H1'	54:01:1885:A:C2	2.39	0.57
59:Z:236:ILE:HA	59:Z:240:GLU:OE1	2.05	0.57
3:06:46:GLN:CB	3:06:83:VAL:HG11	2.35	0.57
53:A:85:U:H5''	53:A:86:G:H5'	1.86	0.57
59:Z:307:GLU:OE2	59:Z:355:ASN:HA	2.04	0.57
9:12:101:ILE:HD12	9:12:101:ILE:H	1.68	0.57
52:03:40:GLU:HB2	52:03:178:VAL:HG11	1.86	0.57
54:01:742:A:H2'	54:01:743:A:C8	2.40	0.57
54:01:1105:U:H2'	54:01:1106:G:H5''	1.85	0.57
59:Z:332:PHE:HB3	59:Z:374:PHE:HB3	1.85	0.57
5:08:101:VAL:HG22	5:08:115:GLN:OE1	2.04	0.57
7:10:54:VAL:HG23	7:10:84:TYR:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:16:38:LEU:HB3	13:16:39:PRO:HD3	1.85	0.57
14:17:4:LYS:HE3	14:17:7:ARG:HH21	1.69	0.57
38:H:84:ILE:HG21	38:H:124:ILE:HD11	1.86	0.57
38:H:105:THR:HB	38:H:120:LEU:CD1	2.35	0.57
52:03:51:ASP:HB3	52:03:54:LYS:HB2	1.86	0.57
54:01:1176:U:H2'	54:01:1177:G:C8	2.40	0.57
54:01:2432:A:H1'	56:X:75:C:O4'	2.04	0.57
14:17:3:LYS:HE2	55:02:47:C:OP2	2.04	0.57
21:24:26:PHE:HE2	21:24:89:ILE:HG13	1.69	0.57
25:28:40:THR:OG1	25:28:41:PRO:HD2	2.04	0.57
29:32:26:ASN:CG	54:01:682:G:H5'	2.29	0.57
30:33:14:LYS:HD3	30:33:22:LYS:HE2	1.87	0.57
32:B:67:LEU:HD21	32:B:91:VAL:HG23	1.87	0.57
37:G:16:LYS:HG2	37:G:17:PHE:HD1	1.70	0.57
54:01:2179:C:H2'	54:01:2180:U:C6	2.40	0.57
4:07:114:ARG:NH1	43:M:70:ARG:HD2	2.19	0.57
35:E:156:ARG:C	35:E:156:ARG:HD3	2.29	0.57
54:01:1380:G:H1'	54:01:1569:A:N6	2.19	0.57
59:Z:260:MET:HE1	59:Z:272:GLU:HG3	1.84	0.57
7:10:53:ARG:HB3	7:10:55:VAL:HG13	1.86	0.56
28:31:4:ILE:HD12	28:31:4:ILE:N	2.20	0.56
37:G:70:PRO:HG3	37:G:98:LEU:HD23	1.87	0.56
54:01:615:U:H5''	54:01:616:A:OP2	2.03	0.56
3:06:149:ILE:CG2	3:06:188:MET:HG2	2.35	0.56
6:09:103:VAL:HG21	6:09:132:PHE:CZ	2.40	0.56
6:09:133:GLN:HE21	6:09:136:SER:HA	1.70	0.56
21:24:9:ARG:CG	21:24:41:GLU:HB2	2.35	0.56
21:24:26:PHE:CZ	21:24:42:LEU:HD11	2.40	0.56
33:C:102:ILE:HD12	33:C:102:ILE:O	2.04	0.56
35:E:15:ILE:HD12	35:E:15:ILE:N	2.19	0.56
35:E:165:GLY:HA2	38:H:113:ARG:HD2	1.87	0.56
36:F:32:ALA:HB1	36:F:70:VAL:HG21	1.85	0.56
46:P:25:ARG:NH1	46:P:25:ARG:HB2	2.20	0.56
51:U:32:ARG:HG2	51:U:33:ARG:HG2	1.87	0.56
54:01:2848:G:O2'	54:01:2867:G:N2	2.38	0.56
56:X:71:C:H2'	56:X:72:A:C8	2.39	0.56
59:Z:119:ILE:HD13	59:Z:156:LEU:HD12	1.87	0.56
1:04:42:ARG:HH12	54:01:690:G:H21	1.53	0.56
6:09:44:ILE:O	6:09:48:GLU:HG2	2.05	0.56
8:11:130:GLY:HA2	8:11:133:ARG:HH12	1.70	0.56
18:21:31:GLN:O	18:21:35:ILE:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:34:36:ARG:O	31:34:37:GLN:HB2	2.05	0.56
32:B:102:ASN:HD21	32:B:105:THR:HG21	1.69	0.56
33:C:13:ILE:N	33:C:13:ILE:HD12	2.20	0.56
35:E:105:ILE:HD11	35:E:123:LEU:HD23	1.87	0.56
38:H:80:PRO:HG2	53:A:878:A:C5'	2.35	0.56
40:J:50:THR:HG22	40:J:62:ARG:HD3	1.87	0.56
43:M:28:ARG:O	43:M:32:ILE:HG12	2.06	0.56
43:M:47:LEU:HD23	43:M:48:SER:O	2.06	0.56
43:M:47:LEU:HD21	43:M:51:GLN:HB2	1.86	0.56
52:03:27:ILE:CG1	52:03:182:ALA:HB1	2.35	0.56
53:A:29:U:HO2'	53:A:30:U:H5'	1.70	0.56
53:A:224:U:H2'	53:A:225:C:C6	2.39	0.56
54:01:255:A:H2'	54:01:256:A:O4'	2.05	0.56
18:21:22:ASP:HA	18:21:25:ARG:NH1	2.20	0.56
40:J:6:ILE:HB	40:J:76:ILE:HB	1.86	0.56
42:L:88:ASP:HB3	42:L:89:LEU:HD12	1.87	0.56
47:Q:58:VAL:HG22	47:Q:59:GLU:N	2.18	0.56
54:01:11:C:H2'	54:01:12:U:H5''	1.88	0.56
54:01:1827:U:C2'	54:01:1828:G:H5'	2.35	0.56
7:10:118:ILE:HG22	7:10:119:PRO:HD3	1.86	0.56
13:16:2:ARG:O	13:16:2:ARG:HD3	2.05	0.56
41:K:124:LYS:HE3	53:A:780:A:H5''	1.88	0.56
44:N:86:ALA:HB1	44:N:91:GLU:HB2	1.88	0.56
48:R:54:LEU:O	48:R:58:ILE:HG12	2.06	0.56
50:T:66:ILE:HG23	50:T:70:LYS:HB3	1.87	0.56
52:03:41:SER:N	52:03:178:VAL:HG13	2.21	0.56
53:A:78:A:H2'	53:A:79:G:O4'	2.05	0.56
54:01:1827:U:O2'	54:01:1828:G:H5'	2.05	0.56
59:Z:373:ARG:CA	59:Z:387:VAL:HG23	2.36	0.56
11:14:62:PRO:HB2	30:33:29:ARG:HH11	1.69	0.56
36:F:86:ARG:HH12	53:A:673:A:H4'	1.70	0.56
54:01:441:U:O2'	54:01:442:G:H5'	2.06	0.56
59:Z:142:ASP:O	59:Z:145:LEU:HD12	2.06	0.56
59:Z:311:LEU:HD12	59:Z:315:GLU:CG	2.31	0.56
14:17:56:LYS:O	14:17:60:GLU:HG3	2.05	0.56
36:F:29:ILE:HD13	36:F:64:VAL:HG11	1.87	0.56
36:F:64:VAL:CG2	36:F:65:GLU:N	2.69	0.56
41:K:81:LEU:HD12	41:K:81:LEU:O	2.06	0.56
52:03:4:LEU:HB3	52:03:8:MET:HG3	1.87	0.56
54:01:473:G:O2'	54:01:474:G:H5'	2.05	0.56
54:01:1097:U:H2'	54:01:1098:A:H5'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2220:U:H2'	54:01:2221:G:H8	1.70	0.56
63:Y:101:PHE:N	59:Z:260:MET:HA	2.20	0.56
1:04:182:LYS:HE3	1:04:267:VAL:HG22	1.87	0.56
4:07:90:LEU:HD12	4:07:90:LEU:O	2.05	0.56
7:10:27:VAL:HG12	7:10:83:ALA:HB3	1.88	0.56
34:D:120:LYS:HE2	34:D:130:ASN:ND2	2.18	0.56
52:03:47:ASN:CG	52:03:170:ILE:HG13	2.31	0.56
52:03:170:ILE:HD12	52:03:170:ILE:H	1.70	0.56
54:01:161:A:H3'	54:01:162:U:H5''	1.88	0.56
54:01:1138:G:H2'	54:01:1139:G:O4'	2.06	0.56
1:04:215:VAL:HG12	1:04:216:ARG:N	2.20	0.56
2:05:173:GLN:NE2	54:01:2772:C:H5'	2.21	0.56
6:09:73:ASN:ND2	6:09:76:GLU:HA	2.20	0.56
32:B:73:ARG:HH22	32:B:94:ARG:HH22	1.51	0.56
35:E:121:ASN:O	35:E:122:VAL:HG22	2.06	0.56
52:03:49:GLY:HA2	52:03:210:LYS:NZ	2.20	0.56
59:Z:138:ASP:HB2	59:Z:176:LYS:NZ	2.20	0.56
59:Z:332:PHE:CE2	59:Z:366:ILE:HD13	2.41	0.56
4:07:143:ASP:C	4:07:144:LYS:HD2	2.31	0.56
20:23:35:VAL:HB	20:23:38:ILE:HG13	1.87	0.56
34:D:37:PRO:HD2	34:D:41:GLY:CA	2.36	0.56
37:G:76:SER:OG	37:G:83:THR:HG22	2.06	0.56
53:A:575:G:O2'	53:A:821:G:H5'	2.06	0.56
54:01:2163:A:H2'	54:01:2164:C:H5'	1.86	0.56
1:04:207:ALA:HB2	54:01:1790:C:O2'	2.06	0.55
2:05:105:LYS:NZ	2:05:105:LYS:HB2	2.21	0.55
7:10:14:GLU:O	7:10:18:VAL:HG23	2.06	0.55
7:10:56:ARG:HE	7:10:83:ALA:HB2	1.72	0.55
8:11:99:LYS:C	8:11:100:ILE:HD12	2.31	0.55
25:28:13:ILE:HD12	54:01:988:A:C8	2.40	0.55
52:03:20:GLN:HG3	52:03:223:ALA:HB3	1.88	0.55
1:04:149:LYS:HD3	54:01:2204:G:H4'	1.87	0.55
24:27:2:LYS:HD2	54:01:78:U:OP2	2.06	0.55
28:31:47:ILE:HD12	28:31:47:ILE:H	1.70	0.55
32:B:75:ALA:O	32:B:79:VAL:HG23	2.06	0.55
52:03:46:VAL:C	52:03:170:ILE:HG23	2.31	0.55
54:01:1932:A:H2'	54:01:1933:G:O4'	2.06	0.55
54:01:2808:G:H5'	54:01:2809:A:OP1	2.06	0.55
59:Z:55:GLU:HG2	59:Z:60:ILE:O	2.06	0.55
4:07:77:LYS:HB2	4:07:77:LYS:NZ	2.21	0.55
19:22:73:ARG:N	19:22:73:ARG:HD2	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:30:8:THR:HG21	54:01:2020:A:H5'	1.87	0.55
29:32:12:ARG:NE	29:32:44:VAL:HG21	2.22	0.55
35:E:163:ILE:C	35:E:163:ILE:HD12	2.30	0.55
36:F:67:PRO:HG2	36:F:70:VAL:CG2	2.36	0.55
52:03:39:VAL:HG22	52:03:179:ASP:OD2	2.07	0.55
54:01:1357:C:H2'	54:01:1358:G:O4'	2.06	0.55
59:Z:329:GLN:N	59:Z:329:GLN:CD	2.65	0.55
2:05:164:GLN:HE22	54:01:2822:G:H5''	1.71	0.55
11:14:29:LYS:HG2	11:14:30:THR:HG23	1.88	0.55
11:14:85:VAL:CG1	11:14:94:THR:HG22	2.37	0.55
53:A:744:C:H2'	53:A:745:G:C8	2.41	0.55
59:Z:19:HIS:ND1	59:Z:112:MET:HG3	2.22	0.55
59:Z:159:GLN:NE2	59:Z:160:TYR:CG	2.74	0.55
9:12:31:GLU:HG2	9:12:142:ILE:CG1	2.36	0.55
32:B:67:LEU:HB3	32:B:160:LEU:HD12	1.88	0.55
54:01:1380:G:H1'	54:01:1569:A:H61	1.72	0.55
54:01:1666:G:H2'	54:01:1667:G:H5'	1.88	0.55
54:01:2389:G:H5''	54:01:2390:U:O4'	2.07	0.55
54:01:2462:C:H1'	54:01:2491:U:O4	2.07	0.55
4:07:115:GLY:HA3	4:07:177:ARG:HB2	1.89	0.55
8:11:118:GLY:HA3	8:11:124:MET:SD	2.46	0.55
34:D:131:ILE:HG22	34:D:133:SER:N	2.22	0.55
48:R:34:GLU:HB3	51:U:18:PHE:CZ	2.41	0.55
51:U:66:ARG:HG3	53:A:1099:G:O4'	2.06	0.55
6:09:63:ALA:HA	6:09:66:ASN:ND2	2.13	0.55
34:D:158:LEU:HD23	34:D:158:LEU:O	2.07	0.55
44:N:20:PHE:O	44:N:21:ALA:HB3	2.06	0.55
47:Q:11:VAL:HG11	47:Q:20:ILE:HD11	1.89	0.55
52:03:4:LEU:HB3	52:03:9:ARG:HG3	1.89	0.55
52:03:27:ILE:HD12	52:03:182:ALA:C	2.31	0.55
52:03:194:VAL:C	52:03:198:LYS:HG3	2.31	0.55
54:01:420:C:O2'	54:01:421:C:H5'	2.07	0.55
3:06:163:ASN:HB2	54:01:322:A:OP2	2.07	0.55
9:12:8:PRO:HG3	9:12:48:VAL:HG13	1.89	0.55
9:12:95:ARG:HG2	9:12:96:ARG:HG3	1.88	0.55
18:21:90:LYS:HB2	18:21:92:ARG:HH12	1.71	0.55
52:03:51:ASP:CB	52:03:54:LYS:HD2	2.36	0.55
53:A:31:G:N2	53:A:47:C:H5''	2.22	0.55
34:D:94:GLU:HA	34:D:99:ASN:ND2	2.21	0.55
42:L:69:GLU:HG2	53:A:521:G:H4'	1.88	0.55
5:08:155:PRO:HG3	54:01:2530:A:N6	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:09:84:ALA:HB2	6:09:90:LEU:HD12	1.89	0.55
8:11:21:PRO:CB	8:11:22:PRO:HD3	2.36	0.55
14:17:49:VAL:CG1	14:17:81:ARG:HG3	2.37	0.55
15:18:52:ARG:HG2	15:18:52:ARG:NH1	2.20	0.55
18:21:29:VAL:HG23	18:21:69:LEU:O	2.07	0.55
45:O:62:ARG:NH2	54:O1:715:A:H4'	2.22	0.55
45:O:71:ARG:HH11	45:O:71:ARG:HG3	1.70	0.55
59:Z:186:ALA:O	59:Z:190:GLU:HG3	2.07	0.55
8:11:124:MET:O	8:11:127:SER:HB3	2.06	0.54
14:17:108:ASP:O	14:17:112:GLU:HG3	2.07	0.54
18:21:28:LYS:HE2	18:21:31:GLN:OE1	2.07	0.54
32:B:27:LYS:N	32:B:28:PRO:CD	2.71	0.54
52:03:194:VAL:HA	52:03:197:LYS:HZ2	1.72	0.54
53:A:769:G:O2'	53:A:770:C:H5'	2.07	0.54
54:01:2139:U:H2'	54:01:2140:G:C8	2.42	0.54
6:09:40:THR:HB	6:09:43:ASN:HD22	1.72	0.54
8:11:33:ASN:HB2	8:11:36:GLU:HG3	1.88	0.54
19:22:57:VAL:HG22	19:22:58:VAL:N	2.23	0.54
31:34:8:LYS:HB2	31:34:8:LYS:HZ2	1.71	0.54
53:A:128:G:O2'	53:A:129:A:H5'	2.07	0.54
53:A:955:U:H3	53:A:1225:A:H61	1.55	0.54
54:01:402:A:H2'	54:01:403:U:H5'	1.89	0.54
59:Z:9:LYS:CE	59:Z:72:PRO:HA	2.37	0.54
59:Z:119:ILE:CD1	59:Z:156:LEU:HD12	2.37	0.54
1:04:119:VAL:HG23	6:09:91:PHE:CE1	2.42	0.54
2:05:12:THR:HG21	15:18:4:ILE:HG23	1.90	0.54
22:25:21:ARG:HD3	22:25:25:GLU:OE2	2.08	0.54
26:29:16:CYS:SG	26:29:37:CYS:HB3	2.47	0.54
33:C:78:LYS:HB2	33:C:78:LYS:NZ	2.22	0.54
35:E:54:GLU:HB3	35:E:57:ALA:HB3	1.89	0.54
42:L:86:VAL:HG21	42:L:89:LEU:HD13	1.89	0.54
47:Q:6:THR:C	47:Q:7:LEU:HD12	2.32	0.54
52:03:60:ARG:HD2	52:03:164:ARG:HD3	1.89	0.54
59:Z:237:LYS:HE2	59:Z:240:GLU:CB	2.34	0.54
59:Z:260:MET:SD	59:Z:272:GLU:OE2	2.66	0.54
1:04:239:PHE:O	1:04:241:LYS:HG3	2.07	0.54
21:24:77:VAL:HG23	21:24:89:ILE:HG12	1.89	0.54
47:Q:73:THR:HG22	47:Q:74:LEU:H	1.73	0.54
53:A:1506:U:O2'	53:A:1507:A:H5'	2.07	0.54
1:04:140:VAL:HG12	1:04:191:LEU:HD23	1.89	0.54
13:16:30:ARG:NH1	13:16:75:ILE:HD11	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:19:91:ARG:HG3	16:19:91:ARG:NH1	2.23	0.54
22:25:33:ILE:HD11	22:25:78:ILE:HD11	1.90	0.54
33:C:174:LEU:HB2	53:A:1108:G:OP1	2.07	0.54
36:F:64:VAL:CG2	36:F:65:GLU:H	2.19	0.54
52:03:8:MET:HA	52:03:11:ILE:HD12	1.90	0.54
53:A:477:C:H2'	53:A:478:A:C8	2.42	0.54
53:A:1225:A:H5'	53:A:1226:C:OP2	2.07	0.54
55:02:35:C:H2'	55:02:36:C:H5'	1.89	0.54
59:Z:84:HIS:HB3	59:Z:87:TYR:CD2	2.43	0.54
15:18:3:ILE:HD12	15:18:3:ILE:H	1.72	0.54
37:G:28:ILE:HG22	37:G:28:ILE:O	2.08	0.54
53:A:1197:A:C2'	53:A:1198:G:H5'	2.37	0.54
7:10:34:THR:O	7:10:37:LYS:HG2	2.07	0.54
12:15:19:GLY:C	12:15:20:LEU:HD12	2.33	0.54
12:15:75:GLU:HB3	12:15:90:GLU:HG3	1.90	0.54
36:F:51:ILE:HD11	48:R:65:SER:HB2	1.90	0.54
39:I:119:LYS:O	39:I:120:ALA:HB3	2.08	0.54
52:03:23:ILE:HG22	52:03:186:LYS:CD	2.31	0.54
54:01:1893:C:H2'	54:01:1894:C:H5'	1.89	0.54
54:01:2183:A:H2'	54:01:2184:A:C8	2.42	0.54
54:01:2638:G:H1'	54:01:2778:A:H61	1.73	0.54
59:Z:44:ARG:NH2	59:Z:44:ARG:HG2	2.23	0.54
30:33:54:LEU:O	30:33:58:ILE:HG13	2.08	0.54
42:L:88:ASP:HB2	53:A:523:A:N1	2.23	0.54
53:A:711:G:O2'	53:A:712:A:H5'	2.07	0.54
53:A:946:A:H2'	53:A:947:G:C8	2.43	0.54
53:A:1236:A:H4'	53:A:1304:G:H4'	1.90	0.54
54:01:717:C:H2'	54:01:718:A:H5'	1.88	0.54
54:01:1344:U:H3'	54:01:1345:C:H5'	1.89	0.54
54:01:1506:U:H2'	54:01:1507:C:C6	2.43	0.54
1:04:15:VAL:HG22	1:04:205:GLY:HA3	1.90	0.54
16:19:36:GLN:HA	16:19:39:ILE:HG22	1.90	0.54
32:B:44:LYS:O	32:B:48:MET:HG2	2.08	0.54
41:K:12:ARG:N	41:K:12:ARG:HD2	2.23	0.54
46:P:5:ARG:HB2	53:A:376:G:H5''	1.89	0.54
52:03:51:ASP:OD1	52:03:53:ARG:HB2	2.07	0.54
53:A:212:G:H2'	53:A:213:G:H8	1.73	0.54
55:02:65:U:H3'	55:02:108:A:H61	1.73	0.54
5:08:104:LEU:HD21	5:08:130:ILE:HD11	1.90	0.54
22:25:19:VAL:HG13	22:25:34:VAL:HG22	1.89	0.54
33:C:190:THR:HG21	33:C:195:ILE:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1827:U:H2'	54:01:1828:G:H5'	1.88	0.54
54:01:2066:C:O2'	54:01:2067:G:H5'	2.08	0.54
59:Z:210:PHE:CD1	59:Z:236:ILE:HG23	2.43	0.54
59:Z:311:LEU:H	59:Z:311:LEU:HD23	1.73	0.54
9:12:68:LYS:HD3	54:01:1022:G:N7	2.22	0.53
12:15:13:HIS:HE1	54:01:2265:U:H4'	1.72	0.53
13:16:72:ASP:OD2	13:16:75:ILE:HG12	2.08	0.53
13:16:79:LEU:HD23	13:16:83:LEU:HB2	1.89	0.53
17:20:14:VAL:HG23	17:20:18:GLN:NE2	2.13	0.53
29:32:24:THR:HG23	29:32:27:GLY:H	1.73	0.53
32:B:90:PHE:CE1	32:B:149:GLY:HA3	2.43	0.53
51:U:25:ALA:HA	51:U:28:LEU:HB3	1.90	0.53
52:03:49:GLY:N	52:03:208:TYR:O	2.39	0.53
54:01:2163:A:H2'	54:01:2163:A:N3	2.23	0.53
54:01:2224:G:H4'	54:01:2226:C:C2	2.43	0.53
54:01:2655:G:O2'	54:01:2656:U:H5	1.92	0.53
56:X:31:G:C2'	56:X:32:C:H5'	2.33	0.53
59:Z:370:ASP:HA	59:Z:388:VAL:CG1	2.37	0.53
9:12:93:ILE:HD13	9:12:100:VAL:HG21	1.89	0.53
26:29:11:GLU:HA	26:29:25:ARG:HA	1.89	0.53
28:31:20:TYR:OH	54:01:2348:U:H5'	2.08	0.53
34:D:187:ARG:HD2	34:D:190:LEU:HD11	1.88	0.53
37:G:129:ASN:HA	37:G:134:VAL:HG11	1.89	0.53
54:01:1796:U:H2'	54:01:1797:G:H8	1.73	0.53
54:01:2808:G:H2'	54:01:2890:G:C6	2.42	0.53
59:Z:233:ARG:HB3	59:Z:233:ARG:NH1	2.23	0.53
1:04:59:GLN:HA	54:01:1568:G:H5'	1.90	0.53
2:05:114:LYS:HE2	2:05:196:ALA:HB2	1.91	0.53
6:09:3:VAL:HG12	6:09:36:ALA:HB1	1.91	0.53
7:10:33:VAL:HG12	54:01:1055:G:H5''	1.91	0.53
11:14:48:ARG:HD3	54:01:666:A:H4'	1.90	0.53
50:T:2:ASN:OD1	50:T:3:ILE:N	2.39	0.53
52:03:63:THR:HG22	52:03:163:TYR:HE1	1.73	0.53
53:A:245:U:O2'	53:A:246:A:H5'	2.08	0.53
53:A:868:C:H2'	53:A:869:G:O4'	2.08	0.53
53:A:1497:G:O2'	53:A:1498:U:H5'	2.09	0.53
54:01:804:A:H2'	54:01:806:C:C4	2.43	0.53
54:01:1539:U:H2'	54:01:1540:G:C8	2.43	0.53
55:02:51:G:H2'	55:02:52:A:O4'	2.09	0.53
56:X:40:C:H2'	56:X:41:C:C6	2.43	0.53
59:Z:84:HIS:HB3	59:Z:87:TYR:HD2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:152:GLU:HA	59:Z:155:GLU:HG3	1.91	0.53
8:11:37:PHE:HA	8:11:66:PHE:HZ	1.73	0.53
18:21:58:ALA:HA	18:21:62:ASP:OD1	2.08	0.53
49:S:72:GLU:OE2	53:A:1320:C:H4'	2.09	0.53
52:03:50:ILE:HD13	52:03:59:VAL:CG2	2.35	0.53
54:01:1672:A:C2	54:01:2582:G:H5'	2.43	0.53
22:25:25:GLU:HG3	54:01:923:G:H4'	1.91	0.53
23:26:9:LYS:HE2	23:26:53:LYS:HE2	1.91	0.53
32:B:71:THR:O	32:B:72:LYS:HB2	2.09	0.53
43:M:21:ILE:HB	43:M:24:VAL:CG1	2.38	0.53
46:P:43:ALA:HB1	46:P:46:LYS:HE3	1.91	0.53
54:01:594:U:H2'	54:01:595:C:C6	2.44	0.53
54:01:1979:U:C2'	54:01:1980:G:H5'	2.39	0.53
54:01:2134:A:C6	54:01:2157:G:H4'	2.44	0.53
59:Z:84:HIS:O	59:Z:87:TYR:N	2.35	0.53
59:Z:245:VAL:O	59:Z:291:VAL:HG12	2.07	0.53
20:23:52:ASN:CG	20:23:54:PRO:HD3	2.34	0.53
34:D:131:ILE:H	34:D:131:ILE:CD1	2.20	0.53
34:D:172:VAL:HA	34:D:179:GLY:HA2	1.89	0.53
37:G:63:VAL:O	37:G:66:GLU:HG2	2.09	0.53
39:I:49:GLN:N	39:I:50:PRO:HD2	2.23	0.53
44:N:30:ILE:CG2	44:N:43:ALA:HB2	2.38	0.53
52:03:23:ILE:HG23	52:03:189:LEU:HD23	1.90	0.53
53:A:760:G:H2'	53:A:761:G:H5'	1.91	0.53
53:A:1305:G:H22	53:A:1331:G:H2'	1.74	0.53
54:01:2286:G:H4'	54:01:2287:A:O4'	2.09	0.53
56:X:21:A:N6	56:X:46:G:H2'	2.24	0.53
59:Z:176:LYS:HA	59:Z:179:GLU:OE1	2.09	0.53
1:04:209:ALA:HA	1:04:212:TRP:CE2	2.44	0.53
2:05:25:THR:HG21	2:05:193:VAL:HG22	1.90	0.53
2:05:129:THR:HG23	2:05:140:HIS:O	2.09	0.53
8:11:48:ILE:HG13	8:11:49:GLU:N	2.22	0.53
9:12:35:ARG:HB2	9:12:54:ILE:HD11	1.90	0.53
16:19:24:TYR:HE1	54:01:17:G:H4'	1.74	0.53
34:D:10:LEU:HD13	34:D:62:ARG:HD2	1.90	0.53
35:E:111:ARG:O	35:E:115:GLU:HG2	2.09	0.53
48:R:11:ARG:NH1	48:R:15:GLU:HB3	2.24	0.53
48:R:33:THR:HG23	48:R:35:SER:H	1.71	0.53
54:01:1076:C:H2'	54:01:1077:A:C8	2.42	0.53
59:Z:203:GLU:O	59:Z:204:ARG:HD2	2.09	0.53
13:16:65:LEU:HG	13:16:69:ARG:NH2	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:18:51:ASN:O	15:18:52:ARG:HD2	2.08	0.53
17:20:49:ILE:CD1	17:20:52:PRO:HA	2.39	0.53
19:22:8:LEU:HD23	19:22:50:LEU:HD21	1.91	0.53
40:J:22:THR:O	40:J:26:VAL:HG23	2.09	0.53
41:K:116:PRO:HB3	53:A:676:A:H1'	1.91	0.53
54:01:704:G:H1'	54:01:727:A:N6	2.24	0.53
54:01:2114:A:N3	54:01:2114:A:H2'	2.24	0.53
54:01:2297:A:N6	54:01:2319:G:H1'	2.24	0.53
54:01:2788:C:H2'	54:01:2789:C:C6	2.44	0.53
59:Z:231:VAL:HB	59:Z:270:ALA:HA	1.91	0.53
59:Z:237:LYS:HD3	59:Z:240:GLU:HB2	1.90	0.53
4:07:40:GLY:HA2	4:07:84:ILE:HD11	1.90	0.53
6:09:5:LEU:CD2	6:09:13:GLY:HA3	2.38	0.53
18:21:15:GLN:O	18:21:19:LEU:HD13	2.09	0.53
20:23:48:VAL:HG22	20:23:50:ALA:H	1.74	0.53
21:24:30:ILE:HG13	21:24:40:ILE:HG13	1.91	0.53
22:25:55:LEU:HD12	22:25:76:ILE:HD12	1.91	0.53
33:C:120:THR:HG23	33:C:188:ALA:CB	2.39	0.53
33:C:141:MET:HE2	33:C:169:GLU:HG3	1.90	0.53
34:D:201:GLU:O	53:A:8:A:N6	2.37	0.53
40:J:8:ILE:HB	40:J:74:VAL:HB	1.91	0.53
53:A:730:G:H2'	53:A:731:G:H5'	1.91	0.53
54:01:394:C:H2'	54:01:395:U:O4'	2.09	0.53
9:12:37:ARG:HH21	9:12:37:ARG:HG3	1.74	0.53
14:17:18:LEU:HD21	14:17:25:ARG:HB3	1.91	0.53
17:20:74:ILE:N	17:20:74:ILE:HD12	2.24	0.53
33:C:12:GLY:C	33:C:13:ILE:HD12	2.34	0.53
33:C:87:ARG:HH11	33:C:87:ARG:HG3	1.74	0.53
40:J:7:ARG:HB3	40:J:101:SER:HB2	1.90	0.53
53:A:1412:C:H2'	53:A:1413:A:C8	2.44	0.53
54:01:481:G:H1'	54:01:506:G:N2	2.25	0.53
54:01:898:C:H2'	54:01:899:A:O4'	2.09	0.53
59:Z:299:LYS:HE3	59:Z:301:HIS:NE2	2.23	0.53
59:Z:357:LYS:HD2	59:Z:358:MET:H	1.72	0.53
59:Z:370:ASP:HA	59:Z:388:VAL:HG12	1.89	0.53
11:14:13:LYS:HE3	54:01:1245:G:OP1	2.09	0.52
13:16:39:PRO:HG2	54:01:1651:G:H4'	1.91	0.52
27:30:24:VAL:HG22	27:30:26:SER:H	1.75	0.52
32:B:46:VAL:HA	32:B:49:PHE:CE1	2.45	0.52
34:D:1:ALA:O	34:D:67:LEU:HD11	2.09	0.52
44:N:30:ILE:O	44:N:30:ILE:HG22	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1370:G:O2'	53:A:1371:G:H5'	2.08	0.52
53:A:1487:G:O2'	53:A:1488:G:H5'	2.09	0.52
54:01:941:A:H2'	54:01:942:G:O4'	2.09	0.52
54:01:1645:G:H5''	54:01:1646:C:H5'	1.90	0.52
54:01:1715:G:O2'	54:01:1716:U:H6	1.91	0.52
54:01:2834:G:H2'	54:01:2879:A:N6	2.24	0.52
59:Z:209:PRO:HB3	59:Z:294:LYS:HE2	1.91	0.52
59:Z:210:PHE:CG	59:Z:236:ILE:HG23	2.43	0.52
1:04:153:LEU:HD21	1:04:181:ARG:HH22	1.74	0.52
6:09:55:GLU:HA	6:09:58:LEU:HD12	1.92	0.52
6:09:84:ALA:HB1	6:09:90:LEU:HA	1.91	0.52
39:I:70:GLY:O	39:I:74:GLN:HG3	2.09	0.52
52:03:181:ASP:O	52:03:184:LYS:HB2	2.09	0.52
53:A:1138:G:H3'	53:A:1138:G:N3	2.24	0.52
55:02:3:C:H3'	55:02:4:C:H5''	1.91	0.52
1:04:106:PRO:HG2	1:04:109:LEU:HB2	1.91	0.52
3:06:149:ILE:HG21	3:06:188:MET:HG2	1.91	0.52
12:15:5:LYS:C	12:15:6:ARG:HG3	2.34	0.52
14:17:31:THR:HG23	55:02:29:A:OP2	2.10	0.52
19:22:80:TRP:CZ3	19:22:82:LYS:HB3	2.45	0.52
36:F:3:HIS:H	36:F:92:THR:CG2	2.10	0.52
47:Q:11:VAL:CG1	47:Q:20:ILE:HD11	2.40	0.52
51:U:57:LYS:HE2	51:U:57:LYS:HA	1.90	0.52
55:02:30:C:H2'	55:02:31:C:H5'	1.91	0.52
59:Z:373:ARG:HA	59:Z:387:VAL:HG23	1.90	0.52
9:12:110:PRO:O	9:12:115:GLY:HA3	2.09	0.52
11:14:111:ILE:HD12	11:14:111:ILE:N	2.06	0.52
16:19:49:ARG:NH2	17:20:72:VAL:HG13	2.25	0.52
32:B:202:ASN:ND2	32:B:203:ASP:N	2.58	0.52
34:D:29:THR:C	34:D:30:LYS:HD2	2.34	0.52
35:E:159:SER:HB2	35:E:162:GLU:HB2	1.91	0.52
54:01:1917:U:C2'	54:01:1918:A:H5'	2.40	0.52
59:Z:356:ILE:O	59:Z:357:LYS:HB3	2.09	0.52
2:05:98:VAL:O	2:05:98:VAL:HG22	2.08	0.52
6:09:26:ALA:O	6:09:31:VAL:HG23	2.10	0.52
54:01:704:G:H2'	54:01:726:G:N2	2.25	0.52
54:01:1077:A:C2'	54:01:1078:U:H5'	2.35	0.52
54:01:2168:G:H2'	54:01:2168:G:N3	2.24	0.52
54:01:2248:C:C2'	54:01:2249:U:H5'	2.40	0.52
54:01:2843:G:O2'	54:01:2844:G:H5'	2.10	0.52
2:05:33:ARG:HA	2:05:95:SER:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:05:151:THR:CB	2:05:152:PRO:HD3	2.39	0.52
14:17:94:ARG:HD3	54:01:2376:A:N6	2.25	0.52
26:29:56:ARG:HH22	49:S:68:HIS:HE1	1.57	0.52
43:M:113:LYS:N	43:M:114:PRO:HD2	2.25	0.52
51:U:35:GLU:O	51:U:36:PHE:HB2	2.08	0.52
53:A:354:G:C2'	53:A:355:C:H5'	2.39	0.52
53:A:1128:C:O2'	53:A:1129:C:H5'	2.10	0.52
54:01:288:U:H2'	54:01:289:G:C8	2.45	0.52
54:01:2285:C:O2'	54:01:2287:A:H1'	2.08	0.52
54:01:2629:U:O2'	54:01:2630:G:H5''	2.09	0.52
55:02:30:C:C2'	55:02:31:C:H5'	2.39	0.52
1:04:220:ARG:HD2	54:01:1827:U:OP2	2.09	0.52
7:10:15:VAL:HG13	7:10:69:PHE:CE2	2.45	0.52
8:11:78:LEU:HD21	8:11:108:ILE:HG21	1.92	0.52
9:12:36:LEU:HD22	9:12:121:LYS:HB2	1.92	0.52
10:13:76:VAL:HG12	15:18:72:VAL:HG22	1.91	0.52
11:14:85:VAL:HG21	11:14:90:VAL:HG22	1.92	0.52
21:24:86:LEU:HD13	21:24:89:ILE:HD11	1.91	0.52
23:26:65:THR:O	23:26:69:GLU:HG3	2.10	0.52
32:B:22:TRP:CD1	32:B:22:TRP:H	2.27	0.52
37:G:6:ILE:HD12	37:G:6:ILE:O	2.10	0.52
51:U:9:GLU:HB2	51:U:10:PRO:CD	2.38	0.52
52:03:54:LYS:HB3	52:03:56:ASP:OD1	2.10	0.52
53:A:219:U:H2'	53:A:220:G:C8	2.45	0.52
55:02:106:G:H2'	55:02:107:G:O4'	2.10	0.52
59:Z:112:MET:HE3	59:Z:113:PRO:HD3	1.90	0.52
4:07:48:LEU:HD11	4:07:147:ARG:NH1	2.23	0.52
7:10:118:ILE:N	7:10:119:PRO:HD2	2.24	0.52
32:B:60:ALA:HB3	32:B:223:GLY:HA3	1.92	0.52
37:G:76:SER:HB2	37:G:85:GLN:OE1	2.10	0.52
51:U:16:ARG:CZ	51:U:19:LYS:HE2	2.40	0.52
53:A:82:G:H2'	53:A:83:C:O4'	2.10	0.52
54:01:49:A:H5'	54:01:51:G:O4'	2.10	0.52
54:01:1386:C:H2'	54:01:1387:A:C8	2.45	0.52
55:02:118:C:H2'	55:02:119:A:C8	2.45	0.52
59:Z:4:LYS:CG	59:Z:264:LEU:HD22	2.27	0.52
59:Z:151:MET:HG2	59:Z:152:GLU:N	2.23	0.52
59:Z:217:VAL:HG21	59:Z:287:GLU:HA	1.92	0.52
1:04:216:ARG:HG2	1:04:217:PRO:HD2	1.92	0.52
1:04:220:ARG:HD3	54:01:1827:U:H5	1.74	0.52
8:11:79:LEU:O	8:11:83:ALA:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:16:73:ASN:HA	13:16:76:VAL:HG12	1.90	0.52
13:16:103:ARG:HH11	54:01:1287:A:H5'	1.74	0.52
33:C:71:ARG:O	33:C:75:VAL:HG23	2.10	0.52
35:E:107:GLY:HA3	53:A:9:G:H5'	1.92	0.52
48:R:11:ARG:HG2	48:R:12:PHE:N	2.24	0.52
50:T:82:ILE:O	50:T:86:ALA:N	2.43	0.52
52:03:40:GLU:HB3	52:03:217:THR:CB	2.40	0.52
53:A:181:A:N6	53:A:194:C:H2'	2.25	0.52
53:A:1397:C:H42	57:V:22:A:H2'	1.74	0.52
54:01:2286:G:H5'	54:01:2287:A:C1'	2.40	0.52
54:01:2366:A:H2'	54:01:2367:G:O4'	2.10	0.52
59:Z:156:LEU:HD13	59:Z:156:LEU:O	2.10	0.52
2:05:14:ILE:HG23	15:18:11:GLN:HE22	1.75	0.52
4:07:102:LEU:O	4:07:107:VAL:HG23	2.10	0.52
18:21:74:ILE:HG23	18:21:74:ILE:O	2.10	0.52
24:27:2:LYS:HE2	54:01:102:U:H1'	1.91	0.52
38:H:80:PRO:HG2	53:A:878:A:H5'	1.91	0.52
45:O:71:ARG:NH2	53:A:754:C:H5'	2.25	0.52
46:P:33:ILE:N	46:P:33:ILE:HD12	2.24	0.52
53:A:376:G:O2'	53:A:377:G:H5'	2.10	0.52
53:A:1168:U:H5''	53:A:1169:A:OP2	2.09	0.52
54:01:1213:A:H62	54:01:1236:G:H1'	1.74	0.52
54:01:2196:C:O2'	54:01:2197:U:H5'	2.10	0.52
54:01:2248:C:H2'	54:01:2249:U:H5'	1.92	0.52
54:01:2679:A:O2'	54:01:2680:U:H5'	2.10	0.52
56:X:70:G:H2'	56:X:71:C:O4'	2.10	0.52
59:Z:324:LYS:HZ1	59:Z:342:GLU:C	2.17	0.52
7:10:26:VAL:HB	7:10:82:ILE:HG23	1.91	0.51
32:B:96:LEU:HD22	53:A:1103:C:H5''	1.92	0.51
44:N:30:ILE:HG22	44:N:43:ALA:HB2	1.92	0.51
53:A:782:A:H2'	53:A:783:C:H5'	1.92	0.51
54:01:2112:G:H2'	54:01:2113:U:H5'	1.92	0.51
59:Z:145:LEU:HD12	59:Z:146:LEU:N	2.25	0.51
59:Z:230:ARG:HA	59:Z:273:ASN:HA	1.92	0.51
59:Z:256:THR:HG22	59:Z:279:ARG:HE	1.76	0.51
10:13:105:ARG:NH1	10:13:108:ARG:HH21	2.07	0.51
15:18:63:ILE:HA	15:18:68:GLY:HA2	1.92	0.51
18:21:46:LEU:O	18:21:50:VAL:HG23	2.11	0.51
33:C:1:GLY:HA3	53:A:1060:U:H5	1.74	0.51
34:D:10:LEU:HD22	34:D:62:ARG:NH1	2.25	0.51
36:F:50:PRO:HG3	36:F:55:HIS:CE1	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:11:THR:HA	38:H:14:ARG:NH1	2.24	0.51
54:01:1027:A:C2	54:01:2488:G:H5'	2.45	0.51
54:01:1827:U:H2'	54:01:1828:G:C5'	2.40	0.51
2:05:43:ASP:HB3	2:05:45:TYR:CE1	2.44	0.51
4:07:28:PRO:HB2	4:07:168:LEU:HD22	1.92	0.51
22:25:38:GLY:HA2	54:01:2330:G:H21	1.76	0.51
24:27:49:ASP:O	24:27:53:VAL:HG23	2.11	0.51
40:J:8:ILE:HG21	40:J:25:ILE:CD1	2.40	0.51
52:03:197:LYS:NZ	52:03:197:LYS:HB2	2.25	0.51
52:03:200:LYS:CE	52:03:204:ALA:HB3	2.39	0.51
52:03:204:ALA:O	52:03:205:LYS:HE2	2.10	0.51
53:A:250:A:H4'	53:A:251:G:O5'	2.10	0.51
53:A:1005:A:H2'	53:A:1006:G:O4'	2.09	0.51
54:01:1420:A:H5'	54:01:1421:G:OP2	2.11	0.51
54:01:2428:G:H5''	54:01:2429:G:OP1	2.10	0.51
55:02:104:A:H2'	55:02:105:G:O4'	2.10	0.51
58:Y:73:A:O2'	58:Y:74:C:H5'	2.11	0.51
59:Z:288:ARG:HG2	59:Z:288:ARG:HH11	1.76	0.51
4:07:7:TYR:O	4:07:12:VAL:HG23	2.10	0.51
11:14:78:ARG:HB3	11:14:113:ALA:HB3	1.93	0.51
12:15:55:ARG:HD3	54:01:2469:A:H4'	1.92	0.51
14:17:52:SER:OG	14:17:54:VAL:HG12	2.10	0.51
30:33:28:LEU:O	30:33:28:LEU:HD23	2.09	0.51
35:E:14:LEU:HA	35:E:36:THR:HG22	1.91	0.51
35:E:113:VAL:HG13	35:E:114:LEU:HD13	1.92	0.51
54:01:669:G:H2'	54:01:669:G:N3	2.26	0.51
54:01:1053:C:C2'	54:01:1054:A:H5''	2.37	0.51
54:01:2185:U:H2'	54:01:2186:G:H8	1.76	0.51
57:V:17:U:O2'	57:V:18:G:H5'	2.11	0.51
59:Z:237:LYS:CD	59:Z:240:GLU:HB2	2.40	0.51
59:Z:262:ARG:HG3	59:Z:262:ARG:NH1	2.26	0.51
3:06:41:GLN:HG3	3:06:43:THR:HG23	1.91	0.51
8:11:78:LEU:HD11	8:11:108:ILE:CG2	2.41	0.51
8:11:91:LYS:HB3	8:11:94:LYS:HE2	1.92	0.51
31:34:36:ARG:O	31:34:37:GLN:CB	2.59	0.51
32:B:224:ARG:CB	32:B:224:ARG:HH21	2.24	0.51
37:G:2:ARG:HB3	53:A:933:G:OP2	2.10	0.51
41:K:22:ILE:HD13	41:K:95:THR:HG23	1.93	0.51
43:M:52:ILE:HG22	43:M:56:ARG:NH1	2.25	0.51
54:01:760:G:H2'	54:01:761:A:H5'	1.92	0.51
54:01:1637:A:H5'	54:01:1760:C:O2'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:X:42:G:O2'	56:X:43:A:H5'	2.11	0.51
59:Z:324:LYS:NZ	59:Z:343:LEU:N	2.58	0.51
9:12:58:ASN:HD21	9:12:128:ASN:CB	2.21	0.51
35:E:156:ARG:HH12	38:H:100:ILE:HG23	1.75	0.51
38:H:74:ILE:HG23	38:H:74:ILE:O	2.09	0.51
52:03:41:SER:CA	52:03:178:VAL:HG13	2.40	0.51
52:03:54:LYS:HD3	52:03:57:GLN:NE2	2.25	0.51
54:01:538:A:H2'	54:01:539:G:O4'	2.10	0.51
59:Z:187:LYS:HA	59:Z:190:GLU:HG3	1.92	0.51
59:Z:337:VAL:HG11	59:Z:362:LEU:HD22	1.93	0.51
1:04:235:GLU:H	1:04:238:ASN:ND2	2.07	0.51
5:08:144:ALA:HB1	5:08:163:TYR:HE1	1.76	0.51
6:09:133:GLN:HA	6:09:139:PHE:HD1	1.75	0.51
14:17:31:THR:HG23	14:17:32:PRO:HD2	1.93	0.51
17:20:35:PHE:HB2	17:20:59:ILE:HB	1.92	0.51
19:22:50:LEU:HD12	19:22:50:LEU:N	2.25	0.51
35:E:135:VAL:O	35:E:139:THR:HG23	2.11	0.51
37:G:58:LEU:H	37:G:58:LEU:HD12	1.76	0.51
37:G:119:LEU:C	37:G:119:LEU:HD23	2.36	0.51
43:M:39:ALA:O	43:M:42:VAL:HG22	2.11	0.51
46:P:31:ARG:HH21	53:A:230:G:H5'	1.75	0.51
46:P:36:VAL:HG23	46:P:53:ASP:HB3	1.93	0.51
52:03:163:TYR:HB2	52:03:171:ILE:HD11	1.92	0.51
54:01:69:C:O2'	54:01:70:G:H5'	2.10	0.51
54:01:1475:G:O2'	54:01:1476:U:H6	1.92	0.51
54:01:2799:A:C2'	54:01:2800:A:H5'	2.41	0.51
59:Z:138:ASP:OD2	59:Z:176:LYS:HE3	2.10	0.51
59:Z:269:ARG:HH21	59:Z:269:ARG:HG3	1.75	0.51
5:08:3:VAL:HG21	54:01:2748:A:H5'	1.93	0.51
8:11:123:ALA:HA	8:11:126:ARG:NH1	2.26	0.51
29:32:34:ARG:NH2	29:32:39:ARG:HD2	2.26	0.51
30:33:61:LEU:HD13	30:33:64:ALA:HB3	1.93	0.51
33:C:46:LEU:HB3	33:C:49:ALA:HB3	1.93	0.51
38:H:12:ARG:HD3	38:H:26:MET:HB3	1.93	0.51
39:I:27:ILE:N	39:I:27:ILE:HD12	2.25	0.51
42:L:30:ARG:HD3	42:L:101:LEU:HD21	1.91	0.51
45:O:21:THR:HG21	53:A:658:C:H1'	1.91	0.51
46:P:67:ILE:HD12	46:P:67:ILE:N	2.17	0.51
51:U:34:ARG:HB3	51:U:36:PHE:CE2	2.46	0.51
54:01:2170:A:H2'	54:01:2171:A:O4'	2.09	0.51
59:Z:112:MET:HE3	59:Z:113:PRO:CD	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:116:GLN:HE21	1:04:121:ALA:HA	1.74	0.51
1:04:144:GLU:HB2	1:04:187:CYS:HB3	1.92	0.51
19:22:43:ILE:O	19:22:47:VAL:HG23	2.10	0.51
33:C:107:LYS:HD2	33:C:110:LEU:HD12	1.92	0.51
50:T:4:LYS:HG3	53:A:332:G:OP1	2.11	0.51
52:03:214:ILE:C	52:03:214:ILE:HD12	2.36	0.51
54:01:310:A:H2'	54:01:311:A:H5''	1.92	0.51
54:01:1330:C:O2'	54:01:1331:G:H5'	2.11	0.51
54:01:1874:C:H2'	54:01:1875:G:O4'	2.11	0.51
59:Z:211:LEU:HB3	59:Z:233:ARG:HG2	1.93	0.51
59:Z:302:THR:HG23	59:Z:365:PRO:HA	1.93	0.51
7:10:65:GLU:O	7:10:68:PRO:HD2	2.10	0.51
9:12:49:ASP:OD2	9:12:121:LYS:HE3	2.11	0.51
9:12:114:LEU:HG	9:12:118:MET:HE3	1.93	0.51
10:13:24:VAL:HG13	10:13:33:ALA:HB2	1.92	0.51
36:F:48:ALA:HB1	48:R:68:PRO:HG3	1.92	0.51
52:03:38:PHE:HZ	52:03:217:THR:HG21	1.76	0.51
52:03:195:ALA:O	52:03:198:LYS:HB2	2.10	0.51
53:A:1301:U:O2	53:A:1301:U:H2'	2.11	0.51
54:01:657:U:H2'	54:01:658:U:C6	2.46	0.51
5:08:71:LEU:O	5:08:75:VAL:HG23	2.11	0.50
21:24:56:PHE:CE1	21:24:61:LEU:HD21	2.46	0.50
27:30:7:PRO:HD2	54:01:1263:U:O2'	2.11	0.50
33:C:6:PRO:HD2	33:C:183:TYR:CD2	2.46	0.50
41:K:17:ASP:HA	41:K:78:ILE:HG23	1.94	0.50
46:P:43:ALA:O	46:P:44:SER:HB2	2.10	0.50
47:Q:17:GLU:OE2	53:A:255:G:H1'	2.11	0.50
52:03:22:ASP:HB2	52:03:25:GLU:CG	2.31	0.50
52:03:51:ASP:HB3	52:03:54:LYS:HD2	1.92	0.50
54:01:1297:C:OP1	54:01:2710:C:H4'	2.10	0.50
54:01:2195:U:O2'	54:01:2196:C:H5'	2.12	0.50
54:01:2345:G:N3	54:01:2381:A:H2'	2.26	0.50
55:02:87:U:H5''	55:02:88:C:OP2	2.12	0.50
59:Z:208:LYS:HB2	59:Z:233:ARG:HB2	1.92	0.50
11:14:101:ILE:HG13	11:14:102:GLY:N	2.26	0.50
21:24:42:LEU:HD13	21:24:47:VAL:HG21	1.94	0.50
38:H:46:GLU:O	38:H:61:THR:HB	2.10	0.50
41:K:55:ARG:HH22	56:X:40:C:H5'	1.76	0.50
42:L:22:ALA:O	42:L:26:CYS:SG	2.69	0.50
50:T:27:MET:O	50:T:31:ILE:HG13	2.11	0.50
52:03:177:LYS:H	52:03:180:PHE:HE2	1.56	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1144:G:H21	53:A:1146:A:H62	1.59	0.50
54:01:2467:C:H2'	54:01:2468:A:O4'	2.10	0.50
1:04:30:ALA:HB3	1:04:31:PRO:HD3	1.94	0.50
2:05:12:THR:CG2	15:18:4:ILE:HG23	2.41	0.50
21:24:79:ARG:HG3	21:24:86:LEU:HD23	1.92	0.50
26:29:64:PHE:CE2	26:29:66:ILE:HG23	2.47	0.50
36:F:11:HIS:CE1	36:F:54:LEU:HD23	2.46	0.50
36:F:64:VAL:HG22	36:F:65:GLU:O	2.12	0.50
52:03:210:LYS:O	52:03:211:LYS:HG3	2.12	0.50
54:01:543:G:H5'	54:01:543:G:H8	1.75	0.50
54:01:1103:A:H3'	54:01:1104:C:H5''	1.93	0.50
54:01:2508:G:H1	54:01:2580:U:H3	1.60	0.50
55:02:88:C:H4'	55:02:89:U:OP1	2.10	0.50
63:Y:101:PHE:CD2	59:Z:66:HIS:HB2	2.47	0.50
59:Z:24:LYS:HB2	64:Z:402:GCP:O2B	2.11	0.50
59:Z:309:TYR:OH	59:Z:311:LEU:HA	2.10	0.50
3:06:50:ALA:HB2	54:01:801:G:C8	2.47	0.50
4:07:148:VAL:HG12	4:07:148:VAL:O	2.12	0.50
8:11:50:LYS:HB2	8:11:50:LYS:NZ	2.27	0.50
10:13:32:TYR:OH	54:01:1996:C:H5	1.92	0.50
33:C:3:LYS:HE3	53:A:1191:A:H5''	1.94	0.50
40:J:53:ILE:HG13	44:N:84:ARG:NE	2.27	0.50
40:J:57:VAL:O	40:J:58:ASN:CB	2.59	0.50
49:S:10:ILE:HG21	49:S:40:PHE:CE2	2.46	0.50
51:U:16:ARG:HH21	51:U:19:LYS:HG2	1.75	0.50
53:A:1140:C:H2'	53:A:1141:C:C6	2.47	0.50
53:A:1318:A:H2'	53:A:1319:A:H5'	1.93	0.50
54:01:191:A:H2'	54:01:192:C:C6	2.47	0.50
54:01:490:C:H4'	54:01:491:G:OP2	2.10	0.50
54:01:503:A:H4'	54:01:505:A:H5''	1.93	0.50
54:01:706:A:H2'	54:01:707:G:O4'	2.11	0.50
54:01:2104:C:H2'	54:01:2105:U:C6	2.46	0.50
54:01:2158:A:H4'	54:01:2159:G:O4'	2.11	0.50
54:01:2469:A:H2'	54:01:2470:G:O4'	2.11	0.50
54:01:2628:C:H3'	54:01:2629:U:H5'	1.92	0.50
1:04:44:ASN:ND2	54:01:1812:U:H1'	2.26	0.50
5:08:174:LYS:O	5:08:175:LYS:HG3	2.11	0.50
8:11:79:LEU:HD13	8:11:137:LEU:HD12	1.93	0.50
13:16:28:LEU:HD23	13:16:48:VAL:HG21	1.92	0.50
26:29:56:ARG:HH22	49:S:68:HIS:CE1	2.29	0.50
38:H:50:VAL:HG22	38:H:50:VAL:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:N:5:MET:HE3	44:N:62:ARG:HH21	1.75	0.50
47:Q:58:VAL:CG2	47:Q:74:LEU:HD11	2.41	0.50
49:S:14:LEU:O	49:S:18:VAL:HG23	2.11	0.50
54:01:799:G:H5''	54:01:800:A:H2'	1.93	0.50
54:01:1601:G:C2'	54:01:1602:U:H5'	2.41	0.50
59:Z:282:LYS:HB2	59:Z:285:GLU:CG	2.42	0.50
7:10:23:LEU:HD13	7:10:118:ILE:CG1	2.41	0.50
35:E:96:GLN:HG3	35:E:97:PRO:HD2	1.94	0.50
39:I:17:ARG:HH22	53:A:1129:C:H5''	1.77	0.50
48:R:12:PHE:O	48:R:14:ALA:N	2.44	0.50
53:A:494:G:O2'	53:A:496:A:H1'	2.10	0.50
53:A:1222:G:O2'	53:A:1223:C:H5'	2.11	0.50
53:A:1497:G:C2'	53:A:1498:U:H5'	2.41	0.50
54:01:419:U:H2'	54:01:420:C:C6	2.45	0.50
54:01:1078:U:H4'	54:01:1079:C:H5''	1.94	0.50
58:Y:59:U:H2'	58:Y:60:U:O4'	2.12	0.50
59:Z:159:GLN:NE2	59:Z:160:TYR:CD2	2.74	0.50
3:06:97:ASN:HD22	3:06:97:ASN:N	2.10	0.50
12:15:4:PRO:HG3	12:15:68:PHE:HE2	1.76	0.50
34:D:26:ALA:C	34:D:27:ILE:HD12	2.37	0.50
41:K:71:ASP:O	41:K:72:ALA:CB	2.58	0.50
42:L:23:LEU:HD22	42:L:58:ASN:ND2	2.16	0.50
46:P:31:ARG:CB	46:P:31:ARG:HH11	2.24	0.50
46:P:51:ARG:C	46:P:52:LEU:HD12	2.37	0.50
54:01:774:G:N2	54:01:787:C:O2'	2.45	0.50
54:01:1319:C:O2'	54:01:1320:C:H5'	2.11	0.50
54:01:2642:G:O2'	54:01:2643:G:H5'	2.12	0.50
59:Z:370:ASP:OD1	59:Z:388:VAL:HG12	2.11	0.50
3:06:126:VAL:HG13	3:06:156:ASN:OD1	2.11	0.50
4:07:127:TYR:HE2	4:07:129:MET:HE2	1.76	0.50
4:07:130:GLY:HA3	54:01:2305:U:H5''	1.94	0.50
32:B:56:LEU:HD13	32:B:216:VAL:HG13	1.94	0.50
32:B:162:VAL:HG12	32:B:164:ASP:H	1.77	0.50
35:E:163:ILE:HD12	35:E:164:LEU:N	2.27	0.50
42:L:113:ARG:HG2	42:L:113:ARG:NH1	2.27	0.50
53:A:697:U:H2'	53:A:698:G:H5'	1.94	0.50
4:07:141:ASP:HB2	4:07:144:LYS:HD3	1.94	0.50
14:17:17:LYS:HZ1	54:01:2380:C:H5'	1.76	0.50
25:28:50:VAL:O	25:28:54:VAL:HG22	2.12	0.50
29:32:34:ARG:CZ	29:32:39:ARG:HD2	2.42	0.50
35:E:108:GLY:O	35:E:109:ALA:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:G:26:VAL:HG22	37:G:42:VAL:HG21	1.93	0.50
40:J:22:THR:O	40:J:25:ILE:HG22	2.12	0.50
43:M:27:THR:HG21	53:A:1328:C:OP1	2.11	0.50
45:O:44:GLU:C	45:O:46:LYS:H	2.19	0.50
46:P:8:ARG:HH11	46:P:8:ARG:HG3	1.77	0.50
47:Q:5:ARG:HD3	53:A:636:U:H5''	1.94	0.50
54:01:2097:A:H2'	54:01:2098:U:O4'	2.11	0.50
54:01:2512:C:H2'	54:01:2513:A:O4'	2.12	0.50
2:05:52:THR:HG22	2:05:80:TRP:CZ3	2.46	0.49
12:15:69:PRO:O	12:15:70:ASP:OD1	2.30	0.49
23:26:63:ILE:O	23:26:67:LEU:HD13	2.12	0.49
27:30:14:MET:SD	54:01:2045:C:H5''	2.52	0.49
34:D:27:ILE:HD12	34:D:27:ILE:N	2.26	0.49
37:G:56:SER:H	37:G:59:GLU:HG3	1.76	0.49
37:G:119:LEU:HD23	37:G:119:LEU:O	2.12	0.49
38:H:86:LYS:HD2	38:H:90:GLU:HG2	1.93	0.49
42:L:87:LYS:HE3	53:A:526:C:P	2.52	0.49
43:M:97:ARG:HB2	43:M:99:GLN:NE2	2.26	0.49
47:Q:28:VAL:HG22	47:Q:29:LYS:N	2.26	0.49
52:03:40:GLU:O	52:03:178:VAL:HG22	2.12	0.49
53:A:35:G:H2'	53:A:36:C:C6	2.47	0.49
53:A:871:U:H5''	53:A:872:A:OP2	2.12	0.49
53:A:1211:U:H4'	53:A:1213:A:N3	2.26	0.49
54:01:1045:C:H5'	54:01:1046:A:C5'	2.42	0.49
54:01:2743:U:H3'	54:01:2744:G:H5''	1.94	0.49
7:10:34:THR:O	7:10:38:MET:HG3	2.12	0.49
11:14:21:ARG:HH21	11:14:21:ARG:HG2	1.78	0.49
14:17:18:LEU:CD2	14:17:25:ARG:HB3	2.42	0.49
17:20:24:LYS:HA	17:20:94:THR:OG1	2.12	0.49
31:34:23:ILE:HD13	54:01:1032:A:H1'	1.93	0.49
35:E:63:MET:O	35:E:67:ARG:HD3	2.11	0.49
35:E:92:ARG:HB2	35:E:127:TYR:HB2	1.93	0.49
54:01:1507:C:H2'	54:01:1508:A:C4'	2.43	0.49
54:01:1717:A:H2'	54:01:1718:G:O4'	2.12	0.49
55:02:35:C:C2'	55:02:36:C:H5'	2.42	0.49
59:Z:287:GLU:OE2	59:Z:290:GLN:NE2	2.37	0.49
7:10:43:LYS:O	7:10:46:ARG:HB3	2.13	0.49
8:11:112:LYS:O	8:11:116:MET:HG2	2.11	0.49
18:21:88:ARG:HH12	54:01:2013:A:H2	1.60	0.49
19:22:80:TRP:HZ3	19:22:82:LYS:HB3	1.77	0.49
35:E:60:GLN:O	35:E:64:GLU:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:U:66:ARG:NE	51:U:66:ARG:HA	2.26	0.49
53:A:1033:G:H2'	53:A:1034:G:H5''	1.93	0.49
54:01:288:U:H2'	54:01:289:G:H8	1.75	0.49
59:Z:121:LEU:O	59:Z:125:VAL:HG12	2.11	0.49
59:Z:170:VAL:HG21	59:Z:191:LEU:HA	1.93	0.49
4:07:30:VAL:HA	4:07:157:THR:HA	1.94	0.49
10:13:76:VAL:HG12	15:18:72:VAL:CG2	2.42	0.49
15:18:13:LYS:NZ	15:18:80:VAL:HG23	2.28	0.49
17:20:49:ILE:HB	17:20:51:VAL:O	2.11	0.49
24:27:39:GLN:HB3	24:27:41:HIS:CE1	2.48	0.49
27:30:10:SER:O	27:30:14:MET:HG3	2.11	0.49
44:N:80:ARG:HG3	44:N:80:ARG:NH1	2.27	0.49
52:03:42:VAL:HG13	52:03:215:SER:O	2.12	0.49
52:03:43:ASP:HA	52:03:174:THR:HA	1.94	0.49
52:03:165:ASN:HA	52:03:171:ILE:HA	1.93	0.49
53:A:90:C:H2'	53:A:91:U:C5	2.47	0.49
53:A:1516:G:H2'	53:A:1518:A:OP2	2.12	0.49
54:01:146:A:H2'	54:01:147:C:C6	2.46	0.49
54:01:1130:U:O2'	54:01:1131:G:OP1	2.25	0.49
54:01:1251:C:O2'	54:01:1252:G:H3'	2.11	0.49
54:01:1564:C:H2'	54:01:1565:C:O4'	2.13	0.49
54:01:1956:U:H2'	54:01:1957:C:H5'	1.94	0.49
54:01:2048:G:H2'	54:01:2049:G:H5''	1.94	0.49
56:X:13:C:C3'	56:X:14:A:H5''	2.43	0.49
10:13:7:MET:HB3	10:13:18:ARG:HD2	1.94	0.49
51:U:16:ARG:NH2	51:U:19:LYS:HE2	2.28	0.49
53:A:56:U:H2'	53:A:57:G:C8	2.48	0.49
53:A:112:G:O2'	53:A:113:G:H5'	2.13	0.49
54:01:1435:G:O2'	54:01:1436:G:H5'	2.11	0.49
54:01:1782:U:H3	54:01:2586:U:H3	1.61	0.49
54:01:2220:U:H2'	54:01:2221:G:C8	2.47	0.49
54:01:2834:G:O2'	54:01:2835:A:H5'	2.12	0.49
59:Z:60:ILE:HG13	59:Z:62:ILE:HG23	1.94	0.49
59:Z:282:LYS:H	59:Z:285:GLU:CD	2.19	0.49
1:04:116:GLN:H	1:04:127:ASN:HD22	1.60	0.49
4:07:77:LYS:HB2	4:07:77:LYS:HZ2	1.78	0.49
27:30:9:ARG:HG3	27:30:9:ARG:HH21	1.76	0.49
36:F:66:ALA:HB1	36:F:67:PRO:HD2	1.95	0.49
46:P:70:ARG:NH1	53:A:452:A:H1'	2.28	0.49
52:03:170:ILE:HB	52:03:172:HIS:HE1	1.78	0.49
53:A:1162:C:H2'	53:A:1163:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1256:A:H1'	53:A:1258:G:C5	2.48	0.49
54:01:1133:A:H4'	54:01:1134:A:H5''	1.94	0.49
54:01:2318:G:H2'	54:01:2319:G:O4'	2.12	0.49
54:01:2756:U:H4'	54:01:2757:A:OP1	2.13	0.49
55:02:65:U:H3'	55:02:108:A:N6	2.28	0.49
59:Z:282:LYS:O	59:Z:285:GLU:HG3	2.13	0.49
59:Z:299:LYS:HB2	59:Z:300:PRO:HD2	1.94	0.49
6:09:51:ARG:HG2	6:09:55:GLU:OE1	2.13	0.49
7:10:57:ASN:HB2	7:10:62:ARG:HD3	1.94	0.49
9:12:81:ILE:HD11	54:01:2514:U:C5'	2.42	0.49
9:12:84:ILE:HG23	9:12:84:ILE:O	2.12	0.49
9:12:93:ILE:CD1	9:12:100:VAL:HG21	2.42	0.49
32:B:67:LEU:HD12	32:B:153:MET:HE1	1.93	0.49
34:D:16:THR:HG22	34:D:17:ASP:N	2.27	0.49
35:E:89:THR:O	35:E:89:THR:HG22	2.12	0.49
39:I:119:LYS:HD3	53:A:1350:A:OP2	2.12	0.49
47:Q:46:HIS:HB2	47:Q:70:LYS:HE2	1.93	0.49
53:A:205:A:H2'	53:A:206:C:O4'	2.11	0.49
53:A:206:C:H2'	53:A:207:C:O4'	2.11	0.49
54:01:572:A:H5''	54:01:573:U:OP2	2.13	0.49
54:01:2128:G:H21	54:01:2173:A:H1'	1.78	0.49
54:01:2323:G:H2'	54:01:2324:U:O4'	2.12	0.49
54:01:2443:C:O2'	54:01:2444:G:H5'	2.13	0.49
54:01:2818:U:H2'	54:01:2819:G:C8	2.48	0.49
59:Z:30:ALA:CA	59:Z:178:LEU:HD13	2.42	0.49
1:04:42:ARG:HG2	1:04:42:ARG:HH11	1.78	0.49
1:04:260:LYS:HA	1:04:263:ASP:OD2	2.13	0.49
4:07:3:LEU:HD21	4:07:100:GLU:HA	1.94	0.49
9:12:117:ALA:HA	9:12:120:ARG:NH2	2.28	0.49
13:16:37:THR:HG22	13:16:110:MET:CE	2.41	0.49
13:16:60:VAL:HG13	54:01:1454:C:O2'	2.13	0.49
13:16:90:ARG:NH2	13:16:116:VAL:HG11	2.28	0.49
14:17:15:ARG:NE	14:17:93:ASP:OD2	2.45	0.49
17:20:93:PHE:HE2	17:20:95:ASP:OD2	1.95	0.49
28:31:14:ALA:HB2	28:31:46:VAL:HG21	1.94	0.49
34:D:62:ARG:HG3	34:D:62:ARG:HH11	1.78	0.49
34:D:164:ARG:HG2	34:D:165:GLU:H	1.78	0.49
38:H:4:ASP:OD2	38:H:7:ALA:HB2	2.13	0.49
39:I:91:GLU:HA	39:I:94:ARG:HB2	1.95	0.49
42:L:109:ARG:HH12	53:A:537:G:H5''	1.74	0.49
44:N:20:PHE:C	44:N:22:LYS:H	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1758:U:C5	54:01:2696:U:H5'	2.48	0.49
54:01:2358:A:H2'	54:01:2359:C:O4'	2.13	0.49
54:01:2825:G:H2'	54:01:2826:A:H5'	1.95	0.49
56:X:47:U:H5''	56:X:48:C:H5'	1.93	0.49
59:Z:282:LYS:HB2	59:Z:285:GLU:HG3	1.95	0.49
59:Z:308:VAL:CB	59:Z:358:MET:HE1	2.43	0.49
4:07:173:ASP:O	4:07:174:PHE:C	2.55	0.49
8:11:4:VAL:HG22	8:11:7:TYR:OH	2.13	0.49
13:16:103:ARG:NH1	54:01:1287:A:H5'	2.28	0.49
21:24:80:HIS:HB2	21:24:85:LYS:HG3	1.94	0.49
32:B:162:VAL:HB	32:B:184:ALA:HB2	1.94	0.49
34:D:59:LYS:O	34:D:63:ILE:HG13	2.13	0.49
46:P:31:ARG:HB2	53:A:310:G:H5''	1.94	0.49
47:Q:19:SER:HB3	47:Q:70:LYS:HZ1	1.78	0.49
52:03:39:VAL:HG12	52:03:177:LYS:HD3	1.93	0.49
52:03:166:ASP:OD1	52:03:169:GLY:N	2.45	0.49
54:01:340:A:H2'	54:01:341:C:O4'	2.12	0.49
54:01:687:C:H5'	54:01:687:C:H6	1.78	0.49
54:01:1906:G:C3'	54:01:1907:G:H5''	2.43	0.49
55:02:13:G:O2'	55:02:15:A:H2'	2.12	0.49
59:Z:191:LEU:HD12	59:Z:191:LEU:O	2.12	0.49
59:Z:287:GLU:CD	59:Z:290:GLN:HE21	2.19	0.49
59:Z:324:LYS:HZ2	59:Z:343:LEU:N	2.10	0.49
1:04:220:ARG:NH1	1:04:220:ARG:HB2	2.28	0.49
31:34:4:ARG:HH22	54:01:2477:U:H2'	1.78	0.49
34:D:64:TYR:CD2	34:D:93:LEU:HD13	2.48	0.49
48:R:11:ARG:HD2	53:A:845:A:O2'	2.13	0.49
48:R:56:ARG:O	48:R:60:ARG:HG3	2.12	0.49
52:03:42:VAL:HG13	52:03:215:SER:C	2.37	0.49
52:03:65:LEU:HD22	52:03:188:ASN:OD1	2.13	0.49
53:A:1033:G:H2'	53:A:1034:G:C5'	2.42	0.49
53:A:1157:A:N6	53:A:1178:G:H1'	2.28	0.49
53:A:1162:C:H2'	53:A:1163:A:C8	2.47	0.49
54:01:1507:C:H2'	54:01:1508:A:H4'	1.95	0.49
54:01:1625:C:H2'	54:01:1626:A:O4'	2.13	0.49
4:07:39:VAL:HG13	4:07:40:GLY:N	2.28	0.48
5:08:104:LEU:HD11	5:08:147:LEU:HD22	1.95	0.48
6:09:78:VAL:O	6:09:144:VAL:HG13	2.13	0.48
10:13:48:PRO:HG3	53:A:1422:G:H5'	1.94	0.48
11:14:42:SER:OG	54:01:672:C:H5	1.96	0.48
15:18:38:ARG:HG3	15:18:38:ARG:NH2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:25:12:SER:OG	54:01:2262:U:H5	1.96	0.48
26:29:2:LYS:HB2	26:29:5:ILE:HD11	1.95	0.48
33:C:72:PRO:HG3	33:C:104:GLU:OE1	2.12	0.48
40:J:37:ARG:HB3	40:J:74:VAL:O	2.13	0.48
42:L:80:LEU:HB2	42:L:101:LEU:HD13	1.96	0.48
46:P:36:VAL:HG13	46:P:36:VAL:O	2.13	0.48
52:03:7:ARG:HG3	52:03:11:ILE:HD11	1.93	0.48
54:01:1370:C:H2'	54:01:1371:G:O4'	2.13	0.48
54:01:2217:G:O2'	54:01:2218:G:H5'	2.13	0.48
59:Z:121:LEU:HD21	59:Z:377:ARG:HD2	1.93	0.48
3:06:102:ARG:O	3:06:106:LYS:HG3	2.13	0.48
9:12:77:HIS:CE1	9:12:80:HIS:H	2.31	0.48
12:15:26:VAL:HG13	12:15:104:GLU:HG2	1.95	0.48
14:17:49:VAL:HG13	14:17:81:ARG:HG3	1.94	0.48
18:21:73:LYS:HB2	18:21:106:VAL:HB	1.94	0.48
19:22:8:LEU:HD13	24:27:21:LEU:HB3	1.93	0.48
33:C:89:VAL:O	33:C:93:ILE:HG13	2.11	0.48
36:F:51:ILE:HG23	36:F:86:ARG:HH21	1.78	0.48
38:H:6:ILE:HD11	38:H:31:LEU:HD23	1.95	0.48
38:H:55:LYS:HE3	53:A:653:U:H1'	1.94	0.48
41:K:22:ILE:HD13	41:K:95:THR:CG2	2.43	0.48
53:A:736:C:H2'	53:A:737:C:C6	2.48	0.48
53:A:1016:A:H4'	53:A:1218:C:H4'	1.95	0.48
54:01:1720:U:H2'	54:01:1721:G:O4'	2.13	0.48
54:01:1824:G:O2'	54:01:1825:U:H5'	2.14	0.48
54:01:1958:C:O2'	54:01:1959:G:H5'	2.13	0.48
54:01:2025:C:H2'	54:01:2026:U:C6	2.48	0.48
8:11:78:LEU:HD11	8:11:108:ILE:HG22	1.94	0.48
11:14:73:ILE:HD12	11:14:106:GLU:OE1	2.14	0.48
16:19:60:TRP:O	16:19:64:ILE:HG13	2.13	0.48
20:23:97:SER:O	20:23:98:ASN:CB	2.60	0.48
34:D:144:ILE:HD12	34:D:144:ILE:N	2.29	0.48
34:D:204:SER:HB2	53:A:8:A:H62	1.77	0.48
35:E:164:LEU:C	35:E:164:LEU:HD12	2.38	0.48
44:N:26:LEU:HD22	44:N:47:LEU:HD13	1.95	0.48
49:S:79:TYR:CZ	53:A:1226:C:H4'	2.48	0.48
51:U:31:VAL:O	51:U:31:VAL:HG22	2.13	0.48
52:03:30:LEU:CD1	52:03:31:LYS:HE3	2.36	0.48
52:03:205:LYS:HE2	52:03:205:LYS:N	2.29	0.48
53:A:560:A:H4'	53:A:561:U:H5'	1.95	0.48
53:A:1432:G:H1'	53:A:1468:A:H62	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:225:C:H2'	54:01:226:A:O4'	2.12	0.48
54:01:445:C:C2'	54:01:446:G:H5'	2.43	0.48
54:01:696:G:O2'	54:01:697:G:H5'	2.13	0.48
54:01:1555:G:H8	54:01:1555:G:H5'	1.78	0.48
54:01:2725:A:O2'	54:01:2726:A:C8	2.66	0.48
59:Z:44:ARG:HG2	59:Z:44:ARG:HH21	1.77	0.48
59:Z:247:ILE:HD11	59:Z:287:GLU:OE1	2.13	0.48
2:05:202:ILE:N	2:05:202:ILE:HD12	2.28	0.48
3:06:149:ILE:HG23	3:06:188:MET:HA	1.96	0.48
7:10:23:LEU:HD13	7:10:118:ILE:CB	2.41	0.48
8:11:23:VAL:CG1	8:11:26:ALA:HB3	2.43	0.48
9:12:57:LEU:O	9:12:58:ASN:HB2	2.13	0.48
12:15:57:VAL:HG11	12:15:105:MET:SD	2.53	0.48
14:17:34:HIS:HA	14:17:53:THR:OG1	2.12	0.48
29:32:12:ARG:HG3	29:32:12:ARG:HH21	1.78	0.48
33:C:198:LYS:HE3	53:A:1058:G:OP1	2.13	0.48
44:N:9:GLU:O	44:N:13:VAL:HG23	2.14	0.48
46:P:19:VAL:HG13	46:P:36:VAL:O	2.12	0.48
49:S:48:ILE:O	49:S:59:VAL:HG22	2.14	0.48
53:A:235:C:H2'	53:A:236:A:C8	2.48	0.48
53:A:458:U:H2'	53:A:459:A:C8	2.47	0.48
54:01:196:A:H2'	54:01:196:A:N3	2.28	0.48
54:01:492:A:H2'	54:01:493:G:O4'	2.13	0.48
54:01:1181:U:H2'	54:01:1182:G:C8	2.49	0.48
54:01:1469:A:H2'	54:01:1470:A:C8	2.49	0.48
54:01:1917:U:O2'	54:01:1918:A:H5'	2.12	0.48
54:01:2328:A:H2'	54:01:2329:U:C6	2.49	0.48
54:01:2743:U:H2'	54:01:2744:G:O4'	2.14	0.48
56:X:33:U:H2'	56:X:35:A:OP2	2.13	0.48
59:Z:217:VAL:CG1	59:Z:283:ARG:HE	2.27	0.48
4:07:73:VAL:HG22	4:07:78:ILE:HD11	1.95	0.48
6:09:30:LEU:HB3	6:09:36:ALA:HB3	1.96	0.48
10:13:10:VAL:HG21	10:13:16:ALA:CB	2.42	0.48
24:27:9:LYS:O	24:27:13:GLU:HG2	2.13	0.48
33:C:110:LEU:HD21	33:C:145:ALA:HB2	1.95	0.48
36:F:92:THR:OG1	36:F:93:LYS:N	2.46	0.48
46:P:14:ARG:HE	46:P:42:ILE:CD1	2.25	0.48
47:Q:4:ILE:HD12	47:Q:4:ILE:C	2.37	0.48
53:A:1037:C:H2'	53:A:1038:C:C6	2.47	0.48
54:01:164:C:H2'	54:01:165:A:O4'	2.13	0.48
54:01:277:G:H1'	54:01:361:G:O6	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1273:U:H4'	54:01:1275:A:OP1	2.13	0.48
59:Z:215:GLU:OE2	59:Z:229:GLY:HA2	2.13	0.48
59:Z:341:ILE:HD13	59:Z:360:VAL:CG2	2.44	0.48
1:04:83:ASP:HB2	1:04:90:ILE:HD13	1.93	0.48
4:07:40:GLY:HA2	4:07:84:ILE:CD1	2.44	0.48
4:07:58:ALA:HB1	4:07:139:GLU:HB3	1.95	0.48
7:10:33:VAL:HG23	7:10:35:VAL:H	1.79	0.48
35:E:59:ILE:HD12	35:E:60:GLN:N	2.28	0.48
42:L:89:LEU:HD12	42:L:89:LEU:N	2.28	0.48
43:M:16:ILE:HD12	43:M:16:ILE:N	2.28	0.48
49:S:27:LYS:CG	49:S:28:LYS:H	2.22	0.48
50:T:42:ASP:HB2	50:T:45:ALA:HB3	1.96	0.48
53:A:335:C:H2'	53:A:336:A:C8	2.48	0.48
54:01:974:G:H2'	54:01:974:G:N3	2.29	0.48
54:01:2141:G:H2'	54:01:2142:A:H8	1.79	0.48
54:01:2832:U:H1'	54:01:2834:G:C4	2.47	0.48
4:07:151:LEU:C	4:07:151:LEU:HD12	2.39	0.48
8:11:123:ALA:HA	8:11:126:ARG:HH12	1.77	0.48
16:19:57:ARG:O	16:19:61:ILE:HG13	2.14	0.48
20:23:52:ASN:OD1	20:23:54:PRO:HD3	2.13	0.48
21:24:6:ALA:HB1	21:24:40:ILE:HG23	1.94	0.48
39:I:51:LEU:HB3	39:I:56:MET:HB2	1.95	0.48
42:L:88:ASP:CB	53:A:523:A:H61	2.26	0.48
46:P:59:HIS:O	46:P:63:GLN:HG2	2.14	0.48
53:A:17:U:H2'	53:A:18:C:C6	2.49	0.48
53:A:715:A:H2'	53:A:716:A:C8	2.48	0.48
54:01:2162:G:H2'	54:01:2163:A:H8	1.78	0.48
54:01:2327:A:H2'	54:01:2328:A:C8	2.49	0.48
59:Z:370:ASP:OD1	59:Z:390:LYS:CA	2.62	0.48
6:09:84:ALA:HA	6:09:91:PHE:N	2.22	0.48
7:10:94:ARG:HB3	7:10:97:LYS:CG	2.44	0.48
11:14:62:PRO:HG2	30:33:24:LYS:HB3	1.95	0.48
25:28:5:LYS:HB2	25:28:57:GLU:HG3	1.95	0.48
34:D:6:PRO:HG2	53:A:428:G:OP2	2.13	0.48
41:K:41:LEU:HD12	41:K:78:ILE:HD11	1.96	0.48
51:U:64:ALA:C	51:U:66:ARG:H	2.22	0.48
52:03:36:ALA:HB2	52:03:218:MET:SD	2.54	0.48
53:A:501:C:H2'	53:A:502:A:C8	2.48	0.48
53:A:1395:C:H6	53:A:1395:C:H5'	1.78	0.48
54:01:482:A:H1'	54:01:498:G:N2	2.29	0.48
54:01:1857:G:H1'	54:01:1885:A:N6	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:67:VAL:HG22	59:Z:78:HIS:HB3	1.95	0.48
59:Z:370:ASP:CG	59:Z:390:LYS:HA	2.38	0.48
3:06:77:ILE:HG13	3:06:78:TRP:HD1	1.79	0.48
9:12:27:ARG:HG2	9:12:27:ARG:HH11	1.79	0.48
11:14:96:LYS:HB2	11:14:101:ILE:HD11	1.94	0.48
12:15:20:LEU:HD23	21:24:81:PRO:HG2	1.96	0.48
19:22:73:ARG:HH21	19:22:73:ARG:HG2	1.79	0.48
38:H:124:ILE:O	38:H:124:ILE:HG13	2.14	0.48
41:K:22:ILE:HG21	41:K:95:THR:HG21	1.95	0.48
45:O:46:LYS:HG2	45:O:46:LYS:O	2.14	0.48
45:O:55:LEU:HD21	54:01:715:A:C2	2.49	0.48
45:O:71:ARG:HH21	53:A:754:C:H5'	1.77	0.48
54:01:296:U:H2'	54:01:297:G:C8	2.48	0.48
54:01:1532:A:H2	54:01:1539:U:H3	1.62	0.48
54:01:1796:U:H2'	54:01:1797:G:C8	2.48	0.48
12:15:3:GLN:HE21	12:15:92:TRP:HE1	1.61	0.48
14:17:106:LEU:HD23	14:17:106:LEU:C	2.39	0.48
18:21:5:ALA:HB3	18:21:54:ALA:HB2	1.95	0.48
18:21:20:VAL:HG21	18:21:43:ALA:HB3	1.96	0.48
39:I:39:GLY:HA2	39:I:44:ARG:HB2	1.95	0.48
44:N:92:ILE:N	44:N:92:ILE:HD12	2.29	0.48
53:A:89:U:H2'	53:A:90:C:O4'	2.14	0.48
53:A:1443:C:H2'	53:A:1444:U:O4'	2.14	0.48
59:Z:19:HIS:HB3	59:Z:22:HIS:ND1	2.28	0.48
59:Z:318:ARG:HG2	59:Z:318:ARG:HH11	1.78	0.48
59:Z:362:LEU:C	59:Z:362:LEU:HD12	2.39	0.48
12:15:4:PRO:HG2	12:15:70:ASP:HA	1.95	0.47
15:18:13:LYS:HG2	15:18:76:HIS:ND1	2.29	0.47
28:31:8:ILE:HD12	28:31:8:ILE:C	2.39	0.47
32:B:102:ASN:ND2	32:B:105:THR:CG2	2.77	0.47
34:D:101:VAL:HG13	34:D:106:PHE:HB2	1.96	0.47
40:J:52:LEU:HB2	44:N:80:ARG:HD2	1.95	0.47
44:N:47:LEU:HD12	44:N:50:LEU:HD12	1.95	0.47
52:03:24:ASN:N	52:03:186:LYS:HE2	2.29	0.47
53:A:163:C:H2'	53:A:164:G:O4'	2.13	0.47
53:A:371:A:H2'	53:A:372:C:O4'	2.14	0.47
53:A:1502:A:C8	53:A:1505:G:N2	2.81	0.47
54:01:130:C:H2'	54:01:131:A:O4'	2.14	0.47
54:01:2121:G:H2'	54:01:2122:U:O4'	2.14	0.47
3:06:46:GLN:HB3	3:06:83:VAL:HG11	1.96	0.47
3:06:109:LEU:HD11	3:06:180:LEU:HD13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:57:ASN:ND2	7:10:62:ARG:HG2	2.27	0.47
33:C:84:GLU:O	33:C:88:LYS:HG2	2.14	0.47
33:C:134:LYS:O	33:C:138:GLN:HG3	2.14	0.47
37:G:142:ARG:HB3	56:X:41:C:H4'	1.96	0.47
42:L:113:ARG:HH21	42:L:120:ARG:HH11	1.62	0.47
42:L:114:SER:CB	53:A:35:G:H21	2.27	0.47
45:O:7:THR:O	45:O:11:VAL:HG23	2.14	0.47
54:01:1999:C:H5''	54:01:2723:C:O2'	2.13	0.47
54:01:2515:C:O2'	54:01:2516:A:H5'	2.14	0.47
54:01:2590:A:O2'	54:01:2591:C:H5'	2.14	0.47
59:Z:332:PHE:CZ	59:Z:366:ILE:HD13	2.50	0.47
1:04:120:ASP:HB2	6:09:91:PHE:CE1	2.50	0.47
3:06:145:ASP:HA	3:06:166:LYS:HB3	1.95	0.47
14:17:4:LYS:CE	14:17:7:ARG:HH21	2.26	0.47
22:25:14:ALA:HB1	54:01:2271:G:OP1	2.14	0.47
26:29:16:CYS:SG	26:29:20:ASN:HB3	2.53	0.47
33:C:122:GLN:O	33:C:127:VAL:HG12	2.14	0.47
36:F:3:HIS:HB2	36:F:92:THR:HA	1.96	0.47
41:K:33:ILE:HG13	41:K:69:CYS:SG	2.53	0.47
41:K:41:LEU:CD1	41:K:78:ILE:HD11	2.44	0.47
43:M:94:LEU:HB3	43:M:95:PRO:HD2	1.95	0.47
45:O:24:THR:HG21	45:O:69:LEU:HB2	1.95	0.47
46:P:78:VAL:O	46:P:78:VAL:HG22	2.14	0.47
52:03:177:LYS:N	52:03:180:PHE:CD2	2.82	0.47
54:01:367:G:H2'	54:01:368:A:O4'	2.13	0.47
54:01:537:G:H22	54:01:555:G:H2'	1.79	0.47
54:01:2172:U:OP1	54:01:2173:A:H5'	2.15	0.47
58:Y:52:G:H5'	59:Z:326:TYR:CD1	2.49	0.47
2:05:31:ALA:HB1	2:05:95:SER:OG	2.14	0.47
7:10:59:LEU:HB3	7:10:62:ARG:CB	2.44	0.47
8:11:74:PRO:HB2	8:11:77:VAL:CG2	2.44	0.47
19:22:8:LEU:HD13	24:27:21:LEU:CB	2.44	0.47
32:B:19:THR:OG1	32:B:20:ARG:N	2.42	0.47
34:D:183:ARG:HH11	34:D:183:ARG:HG3	1.78	0.47
35:E:74:ALA:O	35:E:146:MET:HE3	2.14	0.47
36:F:38:ARG:HH21	36:F:40:GLU:HG3	1.79	0.47
36:F:74:LEU:HD21	36:F:78:PHE:CE2	2.49	0.47
36:F:91:ARG:HG3	53:A:737:C:OP1	2.14	0.47
40:J:53:ILE:HG12	53:A:1060:U:H5''	1.96	0.47
41:K:85:VAL:HG21	51:U:16:ARG:NH2	2.23	0.47
53:A:406:G:O2'	53:A:407:U:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:163:C:H2'	54:01:164:C:O4'	2.14	0.47
54:01:296:U:H2'	54:01:297:G:H8	1.79	0.47
54:01:889:C:H2'	54:01:890:C:O4'	2.14	0.47
59:Z:233:ARG:HB3	59:Z:233:ARG:HH11	1.78	0.47
10:13:40:LYS:HE3	54:01:2561:U:O3'	2.14	0.47
12:15:3:GLN:HE21	12:15:92:TRP:NE1	2.12	0.47
14:17:49:VAL:HG21	14:17:82:ALA:HA	1.94	0.47
25:28:29:ARG:HG2	25:28:29:ARG:HH21	1.80	0.47
32:B:8:MET:N	32:B:46:VAL:HG21	2.29	0.47
48:R:28:LEU:HG	48:R:58:ILE:HD13	1.95	0.47
48:R:41:SER:CB	48:R:51:GLN:HE21	2.25	0.47
52:03:166:ASP:CG	52:03:168:ASN:H	2.22	0.47
53:A:219:U:H2'	53:A:220:G:H8	1.80	0.47
53:A:1175:G:H2'	53:A:1176:A:C8	2.50	0.47
54:01:1701:A:C2'	54:01:1702:G:H5'	2.45	0.47
3:06:134:LEU:HD21	3:06:161:ALA:HB2	1.97	0.47
20:23:47:PRO:HD3	20:23:55:GLY:HA2	1.96	0.47
32:B:46:VAL:HA	32:B:49:PHE:HE1	1.78	0.47
32:B:91:VAL:HG11	32:B:95:TRP:HD1	1.80	0.47
32:B:209:VAL:O	32:B:213:LEU:HD13	2.15	0.47
32:B:224:ARG:NH2	32:B:224:ARG:CB	2.78	0.47
33:C:69:THR:O	33:C:105:VAL:HG12	2.14	0.47
34:D:94:GLU:HB3	34:D:185:PRO:HG2	1.96	0.47
44:N:8:ARG:HG2	44:N:12:ARG:NH1	2.29	0.47
53:A:225:C:C3'	53:A:226:G:H5''	2.44	0.47
53:A:1402:C:H2'	53:A:1403:C:O4'	2.14	0.47
53:A:1477:U:H2'	53:A:1478:U:C6	2.50	0.47
54:01:511:U:C2'	54:01:512:G:H5'	2.45	0.47
54:01:528:A:C2	54:01:2042:A:H2'	2.48	0.47
54:01:859:G:HO2'	54:01:860:U:H6	1.60	0.47
59:Z:212:LEU:HD12	59:Z:213:PRO:N	2.28	0.47
59:Z:313:LYS:HB2	59:Z:319:HIS:HB3	1.97	0.47
59:Z:330:PHE:CZ	59:Z:360:VAL:HG21	2.49	0.47
1:04:216:ARG:HG3	1:04:216:ARG:NH1	2.30	0.47
2:05:55:LYS:HD2	2:05:77:ARG:HA	1.96	0.47
2:05:83:ARG:HG3	2:05:83:ARG:HH21	1.78	0.47
3:06:69:ARG:HD3	54:01:674:G:H1'	1.95	0.47
5:08:9:VAL:O	5:08:9:VAL:HG13	2.14	0.47
7:10:117:LEU:CD2	7:10:120:ALA:HA	2.43	0.47
8:11:78:LEU:HD13	8:11:112:LYS:HD3	1.97	0.47
9:12:81:ILE:HG23	9:12:82:GLY:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:15:56:ALA:HB2	12:15:119:LEU:HD12	1.96	0.47
12:15:86:LYS:HE3	54:01:955:U:OP1	2.14	0.47
16:19:49:ARG:HG2	16:19:49:ARG:NH1	2.29	0.47
19:22:29:THR:OG1	19:22:86:THR:HG22	2.14	0.47
32:B:202:ASN:HD22	32:B:203:ASP:N	2.09	0.47
33:C:116:ALA:HB1	33:C:186:SER:OG	2.14	0.47
38:H:10:LEU:HD12	38:H:76:ARG:HB2	1.96	0.47
39:I:26:LYS:C	39:I:27:ILE:HD12	2.40	0.47
39:I:35:GLU:HA	39:I:39:GLY:HA3	1.97	0.47
40:J:40:ILE:HD13	53:A:1125:U:C6	2.50	0.47
40:J:41:PRO:HB2	53:A:1151:A:C1'	2.44	0.47
42:L:79:ILE:C	42:L:79:ILE:HD12	2.39	0.47
50:T:77:ASN:O	50:T:81:GLN:HG2	2.14	0.47
53:A:86:G:H4'	53:A:87:C:C5	2.50	0.47
53:A:337:G:H2'	53:A:338:A:C8	2.50	0.47
53:A:1123:U:O2'	53:A:1124:G:H5'	2.14	0.47
53:A:1306:A:H62	53:A:1331:G:H1'	1.79	0.47
54:01:167:A:H2'	54:01:168:G:O4'	2.14	0.47
54:01:1231:U:H2'	54:01:1232:G:H8	1.79	0.47
54:01:1558:C:O4'	54:01:1560:G:C8	2.67	0.47
54:01:1652:A:H2'	54:01:1653:G:O4'	2.14	0.47
54:01:2281:A:O2'	54:01:2282:G:H5'	2.14	0.47
55:02:12:C:O4'	55:02:12:C:O2	2.32	0.47
59:Z:142:ASP:O	59:Z:146:LEU:HD23	2.14	0.47
59:Z:183:GLU:C	59:Z:183:GLU:CD	2.83	0.47
59:Z:212:LEU:HB3	59:Z:292:LEU:HB3	1.96	0.47
59:Z:215:GLU:O	59:Z:288:ARG:HD2	2.14	0.47
59:Z:242:VAL:HG21	59:Z:292:LEU:HD11	1.96	0.47
59:Z:303:LYS:HG3	59:Z:392:LEU:CB	2.45	0.47
1:04:106:PRO:CD	1:04:109:LEU:HD22	2.34	0.47
5:08:85:LYS:HG3	5:08:131:VAL:HG22	1.96	0.47
8:11:72:THR:HG23	8:11:73:PRO:HD2	1.95	0.47
13:16:110:MET:HE2	13:16:110:MET:HA	1.96	0.47
27:30:28:SER:OG	27:30:39:ARG:HD2	2.14	0.47
37:G:147:ASN:ND2	41:K:55:ARG:HD3	2.30	0.47
50:T:70:LYS:HE2	53:A:261:U:OP2	2.15	0.47
52:03:11:ILE:HG23	52:03:33:LEU:HD22	1.97	0.47
52:03:40:GLU:C	52:03:178:VAL:HG13	2.40	0.47
53:A:1137:C:H4'	53:A:1138:G:C2	2.50	0.47
54:01:1348:C:H2'	54:01:1349:C:H5'	1.97	0.47
59:Z:14:VAL:HG11	59:Z:195:LEU:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:16:VAL:CB	1:04:203:VAL:HG22	2.39	0.47
1:04:219:VAL:HG21	54:01:782:A:N7	2.30	0.47
23:26:58:ILE:HG12	23:26:66:VAL:HG21	1.97	0.47
24:27:23:ARG:O	24:27:25:GLN:N	2.48	0.47
34:D:26:ALA:CB	34:D:27:ILE:HD12	2.45	0.47
38:H:84:ILE:CG2	38:H:124:ILE:HD11	2.45	0.47
48:R:17:VAL:O	48:R:17:VAL:HG13	2.15	0.47
53:A:1305:G:N2	53:A:1331:G:H2'	2.30	0.47
54:01:1331:G:O2'	54:01:1332:G:H5''	2.15	0.47
54:01:1808:A:H3'	54:01:1809:A:C8	2.50	0.47
59:Z:13:ASN:ND2	59:Z:99:ASP:OD2	2.45	0.47
59:Z:332:PHE:HB3	59:Z:374:PHE:CB	2.45	0.47
59:Z:373:ARG:N	59:Z:387:VAL:HG23	2.28	0.47
2:05:172:VAL:HG11	2:05:175:LEU:HD21	1.97	0.47
4:07:131:VAL:HG22	4:07:151:LEU:HD12	1.96	0.47
9:12:27:ARG:NH2	54:01:1142:A:H4'	2.25	0.47
25:28:23:LEU:HD11	25:28:53:MET:SD	2.55	0.47
27:30:42:ILE:HG22	27:30:48:TYR:HB2	1.96	0.47
36:F:46:GLN:HA	36:F:56:LYS:HA	1.97	0.47
42:L:86:VAL:HG23	42:L:87:LYS:N	2.30	0.47
42:L:100:ALA:O	42:L:101:LEU:O	2.32	0.47
51:U:33:ARG:NH1	51:U:34:ARG:HG2	2.30	0.47
52:03:27:ILE:HG13	52:03:28:ALA:N	2.30	0.47
52:03:189:LEU:O	52:03:193:LEU:HG	2.15	0.47
52:03:194:VAL:HG12	52:03:198:LYS:HD2	1.97	0.47
54:01:414:C:H2'	54:01:415:A:C8	2.49	0.47
54:01:974:G:H1'	54:01:975:A:H8	1.77	0.47
54:01:1149:G:H2'	54:01:1150:C:C6	2.49	0.47
54:01:2553:G:H2'	54:01:2554:U:H4'	1.97	0.47
59:Z:54:GLU:HG3	59:Z:58:ARG:HD3	1.97	0.47
1:04:145:MET:CE	1:04:181:ARG:HE	2.28	0.46
1:04:267:VAL:HG12	1:04:268:ARG:NH1	2.29	0.46
2:05:129:THR:HG22	2:05:130:GLN:O	2.15	0.46
6:09:16:GLY:HA2	6:09:47:PHE:CE2	2.50	0.46
31:34:2:LYS:HG3	31:34:4:ARG:NH1	2.26	0.46
34:D:205:LYS:HB3	53:A:8:A:C6	2.50	0.46
41:K:49:SER:HA	41:K:68:ARG:NH1	2.30	0.46
50:T:66:ILE:CG2	50:T:70:LYS:HB3	2.45	0.46
52:03:50:ILE:HG22	52:03:204:ALA:CB	2.45	0.46
53:A:405:U:C3'	53:A:406:G:H5'	2.34	0.46
54:01:2296:U:H5''	54:01:2297:A:OP1	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:19:HIS:CD2	59:Z:114:GLN:HB3	2.49	0.46
59:Z:67:VAL:CG2	59:Z:78:HIS:HB3	2.45	0.46
59:Z:107:ALA:HB2	59:Z:134:LEU:HD12	1.97	0.46
59:Z:126:GLY:O	59:Z:128:PRO:HD3	2.14	0.46
1:04:204:LEU:HB3	1:04:209:ALA:HB3	1.98	0.46
9:12:101:ILE:H	9:12:101:ILE:CD1	2.29	0.46
15:18:52:ARG:H	15:18:56:SER:HB3	1.81	0.46
18:21:57:ASN:OD1	18:21:61:ASN:ND2	2.46	0.46
24:27:4:LYS:HA	24:27:7:ARG:HH12	1.79	0.46
33:C:45:GLU:HG2	33:C:86:LEU:HD21	1.95	0.46
35:E:40:ASP:OD2	35:E:42:ASN:HB3	2.15	0.46
43:M:6:ILE:CG1	43:M:7:ASN:H	2.22	0.46
43:M:97:ARG:HH11	43:M:97:ARG:HG3	1.80	0.46
52:03:217:THR:O	54:01:2175:C:H1'	2.15	0.46
53:A:280:C:O2'	53:A:281:G:P	2.74	0.46
2:05:121:THR:HB	2:05:127:PHE:CD2	2.49	0.46
32:B:49:PHE:HA	32:B:52:ALA:HB3	1.97	0.46
32:B:206:ILE:O	32:B:210:THR:HG23	2.15	0.46
33:C:76:ILE:HA	33:C:83:VAL:HG23	1.97	0.46
38:H:85:TYR:CD1	38:H:123:GLU:HB2	2.51	0.46
41:K:49:SER:OG	41:K:68:ARG:HD3	2.15	0.46
42:L:114:SER:HB3	53:A:35:G:H21	1.79	0.46
44:N:2:LYS:HD2	53:A:1049:U:H2'	1.97	0.46
52:03:50:ILE:HD12	52:03:57:GLN:O	2.16	0.46
53:A:67:C:H2'	53:A:68:G:C8	2.50	0.46
53:A:181:A:H61	53:A:194:C:H2'	1.79	0.46
53:A:737:C:H2'	53:A:738:C:C6	2.51	0.46
54:01:1856:U:H2'	54:01:1857:G:O4'	2.15	0.46
54:01:2257:U:O2'	54:01:2258:C:H5'	2.14	0.46
59:Z:236:ILE:HG22	59:Z:240:GLU:OE1	2.15	0.46
12:15:33:LEU:HD13	12:15:117:PHE:HB3	1.96	0.46
14:17:27:VAL:HG21	14:17:40:ILE:HD12	1.97	0.46
46:P:4:ILE:HD12	46:P:67:ILE:HG13	1.96	0.46
26:29:26:SER:OG	26:29:28:VAL:HG23	2.16	0.46
28:31:5:ARG:NH1	28:31:25:ASN:HB2	2.31	0.46
40:J:10:LEU:HD23	40:J:10:LEU:N	2.30	0.46
53:A:1062:U:H2'	53:A:1063:C:C6	2.50	0.46
53:A:1471:U:O2'	53:A:1472:U:H5'	2.15	0.46
54:01:917:A:H5''	54:01:2268:A:N6	2.29	0.46
59:Z:186:ALA:HA	59:Z:189:LEU:HD12	1.96	0.46
1:04:44:ASN:ND2	54:01:1812:U:Cl'	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:14:77:ILE:HD13	11:14:108:ALA:HB1	1.97	0.46
11:14:101:ILE:HG13	11:14:102:GLY:H	1.80	0.46
33:C:153:SER:HB3	33:C:164:THR:HG22	1.97	0.46
35:E:104:ILE:HG23	35:E:104:ILE:O	2.15	0.46
37:G:39:GLU:OE1	39:I:42:THR:HG22	2.15	0.46
49:S:30:LEU:HB2	49:S:48:ILE:HG22	1.96	0.46
53:A:210:C:H4'	53:A:211:G:C2	2.51	0.46
53:A:579:A:H2'	53:A:580:C:C6	2.50	0.46
53:A:1278:G:OP1	53:A:1279:G:H5'	2.15	0.46
53:A:1490:U:O2'	53:A:1491:G:H5'	2.15	0.46
54:01:395:U:H2'	54:01:396:G:C8	2.50	0.46
54:01:1773:A:C2'	54:01:1774:C:H5'	2.46	0.46
55:02:30:C:H2'	55:02:31:C:O4'	2.16	0.46
59:Z:96:ALA:HA	59:Z:125:VAL:CG2	2.43	0.46
59:Z:377:ARG:HH22	59:Z:380:GLY:C	2.23	0.46
8:11:23:VAL:HG12	8:11:26:ALA:HB3	1.98	0.46
13:16:97:ILE:HD13	13:16:113:ILE:HG13	1.97	0.46
15:18:17:PRO:O	15:18:19:PHE:HD1	1.99	0.46
18:21:93:ALA:HB2	54:01:1614:A:C2	2.50	0.46
19:22:61:LEU:HD12	19:22:61:LEU:O	2.15	0.46
24:27:6:LEU:HD13	24:27:56:LEU:HD22	1.97	0.46
29:32:19:ARG:HG2	29:32:19:ARG:HH21	1.79	0.46
53:A:742:G:O2'	53:A:743:A:H5'	2.15	0.46
53:A:1235:U:O2'	53:A:1305:G:H5'	2.15	0.46
54:01:1111:A:C2	54:01:1112:G:H1'	2.50	0.46
54:01:1357:C:C2'	54:01:1358:G:H5'	2.46	0.46
54:01:2078:C:O2'	54:01:2079:U:H5'	2.16	0.46
54:01:2554:U:H2'	54:01:2555:U:C6	2.51	0.46
11:14:82:LEU:HD11	11:14:90:VAL:HG21	1.98	0.46
14:17:10:ARG:HD3	54:01:2295:C:OP2	2.15	0.46
14:17:18:LEU:HD23	14:17:25:ARG:HD3	1.97	0.46
23:26:63:ILE:HG23	23:26:64:ASP:N	2.31	0.46
33:C:42:LEU:HD21	33:C:65:VAL:HG11	1.97	0.46
34:D:28:ASP:CG	34:D:29:THR:H	2.24	0.46
34:D:202:LEU:HD23	34:D:202:LEU:C	2.41	0.46
36:F:74:LEU:HA	36:F:77:THR:OG1	2.16	0.46
48:R:40:PRO:HG2	48:R:43:ILE:HG12	1.98	0.46
52:03:11:ILE:CG2	52:03:33:LEU:HD22	2.45	0.46
54:01:1257:C:O5'	54:01:1257:C:H6	1.98	0.46
54:01:1801:A:H5''	54:01:2203:U:C2'	2.45	0.46
54:01:2070:A:H2'	54:01:2071:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2383:G:O2'	54:01:2384:U:H5'	2.15	0.46
56:X:69:C:H2'	56:X:70:G:H5'	1.97	0.46
59:Z:123:ARG:NE	59:Z:161:ASP:OD1	2.48	0.46
1:04:48:ILE:O	1:04:48:ILE:HG23	2.16	0.46
4:07:7:TYR:OH	4:07:29:ARG:HB3	2.16	0.46
4:07:140:ILE:H	4:07:140:ILE:CD1	2.28	0.46
18:21:65:ASP:OD2	18:21:68:ASP:HB2	2.15	0.46
34:D:56:GLU:HG2	34:D:198:LEU:HD12	1.97	0.46
34:D:127:ARG:HH21	53:A:619:U:H4'	1.81	0.46
39:I:123:ARG:HG3	39:I:123:ARG:HH21	1.81	0.46
46:P:70:ARG:HH11	53:A:452:A:H1'	1.81	0.46
48:R:51:GLN:OE1	48:R:54:LEU:HD23	2.16	0.46
50:T:54:GLN:N	50:T:55:PRO:HD2	2.31	0.46
53:A:31:G:H21	53:A:47:C:H5''	1.81	0.46
53:A:629:A:H2'	53:A:630:A:O4'	2.16	0.46
54:01:372:G:HO2'	54:01:373:U:H6	1.62	0.46
54:01:1437:C:H2'	54:01:1438:U:C6	2.51	0.46
54:01:2484:G:O2'	54:01:2485:G:H5'	2.15	0.46
59:Z:319:HIS:CD2	59:Z:320:THR:OG1	2.69	0.46
59:Z:321:PRO:CG	59:Z:349:MET:HB3	2.46	0.46
59:Z:324:LYS:HA	59:Z:343:LEU:HD12	1.98	0.46
1:04:206:LYS:HD2	54:01:729:G:OP2	2.16	0.46
4:07:45:ASP:HB2	4:07:48:LEU:HB2	1.98	0.46
7:10:2:ALA:HB3	7:10:6:GLN:CG	2.36	0.46
7:10:94:ARG:O	7:10:97:LYS:HG2	2.16	0.46
15:18:90:ALA:HB2	15:18:112:ARG:HA	1.96	0.46
37:G:38:ALA:O	37:G:42:VAL:HG23	2.16	0.46
37:G:100:MET:O	37:G:104:VAL:HG23	2.16	0.46
39:I:79:ARG:HG2	39:I:79:ARG:HH11	1.81	0.46
40:J:53:ILE:HD12	40:J:63:ASP:OD2	2.15	0.46
42:L:49:ARG:NE	42:L:88:ASP:OD2	2.49	0.46
52:03:16:ASP:OD2	52:03:19:LYS:CB	2.63	0.46
53:A:77:A:H2'	53:A:78:A:C8	2.51	0.46
53:A:1473:G:O2'	53:A:1474:U:H5'	2.16	0.46
54:01:2489:U:O2'	54:01:2490:G:H5'	2.16	0.46
59:Z:230:ARG:HD3	59:Z:232:GLU:OE2	2.15	0.46
2:05:149:ASN:OD1	2:05:150:GLN:N	2.44	0.45
8:11:56:VAL:HG23	8:11:69:VAL:O	2.16	0.45
13:16:117:ASP:O	13:16:118:ARG:HB2	2.16	0.45
22:25:35:ARG:HG2	22:25:35:ARG:HH11	1.81	0.45
35:E:38:VAL:HG22	35:E:66:ALA:HB1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:R:50:TYR:O	48:R:54:LEU:N	2.48	0.45
53:A:29:U:C2'	53:A:30:U:H5'	2.45	0.45
53:A:411:A:C4	53:A:413:G:H1'	2.51	0.45
53:A:424:G:O2'	53:A:425:G:H5'	2.16	0.45
53:A:484:G:C4'	53:A:485:U:H5''	2.37	0.45
53:A:1202:U:H2'	53:A:1203:C:H5'	1.97	0.45
53:A:1353:G:O2'	53:A:1354:U:H5'	2.16	0.45
54:01:2190:G:H2'	54:01:2191:A:C8	2.50	0.45
55:02:2:G:H2'	55:02:3:C:C6	2.50	0.45
55:02:108:A:H5'	55:02:109:A:O5'	2.16	0.45
59:Z:13:ASN:HB2	59:Z:99:ASP:OD2	2.16	0.45
59:Z:329:GLN:N	59:Z:329:GLN:NE2	2.63	0.45
3:06:41:GLN:NE2	54:01:442:G:O4'	2.50	0.45
5:08:126:THR:HG22	5:08:127:GLN:N	2.31	0.45
10:13:15:GLY:O	10:13:47:ILE:HG12	2.16	0.45
12:15:50:ARG:HH21	12:15:50:ARG:HG2	1.82	0.45
25:28:29:ARG:NE	54:01:1183:U:H5''	2.30	0.45
29:32:29:GLN:NE2	54:01:210:C:OP1	2.49	0.45
34:D:8:LEU:HB3	53:A:430:A:OP1	2.17	0.45
38:H:85:TYR:CE1	38:H:123:GLU:HB2	2.51	0.45
43:M:14:ALA:CB	43:M:33:LEU:HD21	2.45	0.45
43:M:109:LYS:HD2	53:A:1227:A:OP2	2.17	0.45
53:A:1033:G:C3'	53:A:1034:G:H5''	2.46	0.45
54:01:37:C:H4'	54:01:451:U:OP1	2.16	0.45
54:01:2286:G:H5'	54:01:2287:A:H1'	1.99	0.45
2:05:173:GLN:HE21	54:01:2772:C:H5'	1.81	0.45
7:10:111:ALA:O	7:10:114:GLU:HG2	2.16	0.45
8:11:118:GLY:HA2	54:01:1082:U:H5'	1.98	0.45
10:13:66:LYS:HB3	10:13:66:LYS:HZ3	1.80	0.45
11:14:79:LEU:HD12	11:14:112:LEU:HD12	1.97	0.45
16:19:34:ALA:O	16:19:38:VAL:HG23	2.16	0.45
32:B:166:ASP:HB2	32:B:190:SER:OG	2.17	0.45
34:D:97:LEU:O	34:D:101:VAL:HG23	2.16	0.45
35:E:133:ILE:H	35:E:133:ILE:CD1	2.27	0.45
40:J:14:ASP:OD1	40:J:16:ARG:HG2	2.16	0.45
43:M:85:TYR:O	43:M:89:ARG:HG2	2.15	0.45
48:R:12:PHE:CG	48:R:13:THR:N	2.84	0.45
53:A:946:A:H2'	53:A:947:G:H8	1.81	0.45
53:A:1349:A:H2'	53:A:1350:A:O4'	2.17	0.45
54:01:467:G:O2'	54:01:468:G:H5'	2.16	0.45
54:01:542:C:H2'	54:01:543:G:H5''	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2743:U:C3'	54:01:2744:G:H5''	2.45	0.45
56:X:68:C:H2'	56:X:69:C:O4'	2.15	0.45
9:12:13:ARG:HH21	9:12:13:ARG:HG3	1.81	0.45
9:12:37:ARG:NH2	9:12:110:PRO:HG3	2.31	0.45
15:18:74:GLN:HB2	15:18:77:SER:HB2	1.97	0.45
16:19:5:ARG:NH1	54:01:585:G:N7	2.64	0.45
25:28:8:GLN:NE2	25:28:23:LEU:HD13	2.32	0.45
33:C:76:ILE:HB	33:C:80:GLY:HA2	1.97	0.45
39:I:90:ASP:O	39:I:92:SER:N	2.50	0.45
48:R:25:ILE:C	48:R:25:ILE:HD12	2.41	0.45
53:A:49:U:O4	53:A:365:U:H5	1.98	0.45
54:01:634:C:H2'	54:01:635:C:C6	2.52	0.45
54:01:717:C:C2'	54:01:718:A:H5'	2.46	0.45
54:01:760:G:H4'	54:01:1776:G:OP1	2.16	0.45
54:01:948:C:H6	54:01:948:C:O5'	1.98	0.45
54:01:2533:U:H2'	54:01:2534:A:O4'	2.16	0.45
54:01:2655:G:O2'	54:01:2656:U:C5	2.69	0.45
58:Y:23:A:H2'	58:Y:24:G:C8	2.52	0.45
59:Z:155:GLU:O	59:Z:158:SER:HB2	2.16	0.45
4:07:101:ARG:HG3	4:07:105:ILE:HD11	1.97	0.45
5:08:16:VAL:HG11	5:08:49:LEU:HD21	1.98	0.45
9:12:47:HIS:CE1	9:12:48:VAL:HG23	2.52	0.45
15:18:77:SER:O	15:18:80:VAL:HG22	2.16	0.45
17:20:7:SER:OG	17:20:22:LEU:HD22	2.17	0.45
20:23:95:PHE:O	20:23:99:SER:HA	2.16	0.45
32:B:102:ASN:HD21	32:B:105:THR:CG2	2.29	0.45
32:B:169:HIS:CE1	32:B:170:ILE:HG23	2.52	0.45
38:H:80:PRO:HG2	53:A:878:A:H5''	1.97	0.45
45:O:63:ARG:NE	45:O:87:ARG:HH12	2.15	0.45
47:Q:64:ARG:HD2	53:A:264:C:H4'	1.97	0.45
50:T:67:HIS:C	50:T:69:ASN:H	2.24	0.45
52:03:42:VAL:HG22	52:03:216:THR:CG2	2.30	0.45
53:A:335:C:H2'	53:A:336:A:H8	1.81	0.45
53:A:1225:A:H2'	53:A:1225:A:N3	2.30	0.45
54:01:445:C:O2'	54:01:446:G:H5'	2.16	0.45
54:01:1111:A:H2	54:01:1112:G:H1'	1.82	0.45
54:01:2698:U:H2'	54:01:2699:C:C6	2.51	0.45
59:Z:74:ARG:HH22	59:Z:200:PRO:HA	1.80	0.45
59:Z:304:PHE:N	59:Z:304:PHE:CD1	2.85	0.45
59:Z:383:VAL:HG23	59:Z:384:GLY:N	2.31	0.45
1:04:244:VAL:CA	1:04:251:THR:HG22	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:06:5:LEU:HD13	3:06:10:SER:O	2.16	0.45
6:09:6:LEU:HD11	6:09:37:VAL:HG23	1.98	0.45
13:16:96:ARG:HH11	13:16:116:VAL:HG13	1.81	0.45
21:24:19:ARG:NH2	55:02:95:U:OP2	2.49	0.45
33:C:141:MET:HG3	33:C:169:GLU:HG2	1.99	0.45
42:L:109:ARG:HH11	53:A:537:G:H5''	1.79	0.45
51:U:36:PHE:C	51:U:38:GLU:N	2.75	0.45
52:03:5:THR:H	52:03:8:MET:HG3	1.79	0.45
53:A:1171:A:H2'	53:A:1172:C:C6	2.51	0.45
54:01:655:A:H4'	54:01:656:G:H5'	1.98	0.45
54:01:772:C:O2'	54:01:773:U:H5'	2.16	0.45
54:01:1499:C:H2'	54:01:1500:G:H8	1.82	0.45
54:01:2404:U:H2'	54:01:2405:G:O4'	2.16	0.45
54:01:2808:G:H2'	54:01:2890:G:O6	2.16	0.45
59:Z:288:ARG:HG2	59:Z:288:ARG:NH1	2.31	0.45
59:Z:323:PHE:CD1	59:Z:349:MET:HG2	2.51	0.45
7:10:54:VAL:HG22	7:10:54:VAL:O	2.16	0.45
8:11:124:MET:O	8:11:128:ILE:HG12	2.16	0.45
9:12:35:ARG:HD3	9:12:40:HIS:CD2	2.52	0.45
10:13:105:ARG:HH11	10:13:108:ARG:HH21	1.63	0.45
14:17:99:TYR:CE2	14:17:104:GLN:HG3	2.51	0.45
15:18:31:VAL:HG12	15:18:38:ARG:O	2.17	0.45
17:20:83:TYR:CZ	54:01:1187:G:H5''	2.52	0.45
27:30:11:LYS:HZ1	54:01:2616:C:P	2.39	0.45
39:I:121:ARG:HG3	53:A:1348:U:H4'	1.98	0.45
42:L:23:LEU:HD23	42:L:29:LYS:NZ	2.32	0.45
50:T:34:VAL:HG11	50:T:78:LEU:HD21	1.99	0.45
52:03:40:GLU:HB3	52:03:217:THR:HB	1.99	0.45
52:03:65:LEU:HB2	52:03:159:GLY:O	2.17	0.45
53:A:70:U:H4'	53:A:71:A:H8	1.82	0.45
54:01:880:G:H2'	54:01:881:G:H8	1.81	0.45
54:01:1555:G:H5'	54:01:1555:G:C8	2.52	0.45
54:01:1766:G:O2'	54:01:1767:G:H5'	2.16	0.45
54:01:2795:C:H2'	54:01:2796:U:O4'	2.17	0.45
54:01:2818:U:H2'	54:01:2819:G:H8	1.82	0.45
55:02:88:C:C4'	55:02:89:U:OP1	2.65	0.45
59:Z:225:THR:O	59:Z:277:LEU:HD12	2.17	0.45
59:Z:282:LYS:C	59:Z:285:GLU:HG3	2.42	0.45
1:04:266:ILE:HG21	1:04:269:ARG:HD2	1.98	0.45
5:08:98:LYS:HZ1	5:08:103:ASN:HD22	1.64	0.45
8:11:72:THR:CG2	8:11:73:PRO:HD2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:13:25:LEU:CD2	54:01:2562:U:H4'	2.46	0.45
10:13:58:LEU:CD1	10:13:86:LEU:HD22	2.46	0.45
11:14:23:ILE:HD13	17:20:84:ARG:NH1	2.32	0.45
13:16:8:ARG:HG3	13:16:8:ARG:HH21	1.82	0.45
14:17:33:ARG:HG2	14:17:34:HIS:CD2	2.52	0.45
14:17:79:ALA:O	14:17:83:LEU:HG	2.17	0.45
22:25:55:LEU:CD1	22:25:76:ILE:HD12	2.47	0.45
44:N:2:LYS:O	44:N:5:MET:N	2.44	0.45
49:S:9:PHE:CD2	53:A:1318:A:H4'	2.51	0.45
52:03:4:LEU:HD22	52:03:8:MET:CG	2.46	0.45
52:03:194:VAL:HA	52:03:197:LYS:HZ1	1.78	0.45
53:A:253:A:H2'	53:A:254:G:C8	2.52	0.45
53:A:990:C:H2'	53:A:991:U:O4'	2.17	0.45
53:A:1040:U:H2'	53:A:1041:G:H8	1.82	0.45
53:A:1325:C:O2'	53:A:1326:U:H5'	2.16	0.45
54:01:372:G:O2'	54:01:373:U:C6	2.69	0.45
54:01:616:A:H2'	54:01:617:G:O4'	2.17	0.45
54:01:894:U:O2'	54:01:895:U:H5'	2.16	0.45
54:01:1475:G:O2'	54:01:1476:U:P	2.74	0.45
54:01:1481:U:H2'	54:01:1482:G:H4'	1.98	0.45
54:01:1678:A:H2'	54:01:1679:A:O4'	2.16	0.45
54:01:2233:U:H2'	54:01:2234:G:H8	1.79	0.45
2:05:2:ILE:HD13	2:05:90:PHE:CE2	2.52	0.45
8:11:74:PRO:O	8:11:77:VAL:HG22	2.17	0.45
13:16:49:GLU:OE1	54:01:2839:G:H4'	2.17	0.45
17:20:16:GLU:CD	17:20:100:GLY:HA2	2.42	0.45
33:C:118:SER:O	33:C:122:GLN:HG3	2.17	0.45
34:D:98:ASP:HB3	34:D:132:ALA:HB1	1.98	0.45
41:K:63:GLN:HG3	41:K:98:ALA:HB2	1.99	0.45
43:M:6:ILE:CG1	43:M:7:ASN:N	2.76	0.45
49:S:59:VAL:HG23	49:S:59:VAL:O	2.17	0.45
52:03:21:TYR:CD2	52:03:222:VAL:HG13	2.52	0.45
54:01:886:A:H2'	54:01:886:A:N3	2.31	0.45
54:01:1412:U:H2'	54:01:1413:A:C8	2.51	0.45
59:Z:54:GLU:CG	59:Z:58:ARG:HD3	2.47	0.45
1:04:261:ARG:HH11	1:04:261:ARG:HG3	1.82	0.45
2:05:208:LYS:HE3	54:01:2771:C:O2'	2.17	0.45
3:06:76:PRO:HA	3:06:82:GLY:HA2	1.99	0.45
8:11:109:ALA:O	8:11:113:ALA:N	2.50	0.45
9:12:39:LYS:HD2	54:01:1007:C:OP1	2.17	0.45
12:15:66:ARG:NH1	12:15:104:GLU:OE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:18:13:LYS:HZ2	15:18:80:VAL:HG23	1.80	0.45
24:27:55:THR:HG21	54:01:77:G:O4'	2.16	0.45
25:28:10:ARG:HH21	25:28:10:ARG:HG3	1.81	0.45
26:29:49:ARG:O	26:29:53:THR:OG1	2.35	0.45
31:34:23:ILE:HD12	31:34:38:GLY:OXT	2.17	0.45
40:J:53:ILE:HG12	53:A:1060:U:C5'	2.47	0.45
54:01:74:A:H4'	54:01:75:G:O5'	2.16	0.45
54:01:639:U:H2'	54:01:640:C:C6	2.52	0.45
54:01:839:U:H2'	54:01:840:C:C6	2.52	0.45
54:01:1291:C:O2'	54:01:1292:G:H5'	2.16	0.45
54:01:2639:A:H2'	54:01:2640:G:O4'	2.17	0.45
59:Z:109:ASP:HB3	59:Z:112:MET:SD	2.57	0.45
59:Z:324:LYS:NZ	59:Z:342:GLU:C	2.75	0.45
5:08:126:THR:HG22	5:08:127:GLN:H	1.81	0.44
10:13:8:LEU:O	10:13:18:ARG:HD3	2.16	0.44
11:14:14:LYS:HB3	54:01:662:G:H4'	2.00	0.44
11:14:93:ASN:O	11:14:94:THR:CB	2.65	0.44
14:17:15:ARG:HH21	14:17:95:SER:HA	1.82	0.44
25:28:9:THR:HG22	25:28:53:MET:O	2.16	0.44
30:33:5:THR:HG23	30:33:61:LEU:HA	1.98	0.44
42:L:23:LEU:HB2	42:L:58:ASN:ND2	2.32	0.44
45:O:45:HIS:C	45:O:47:LYS:H	2.21	0.44
48:R:25:ILE:HA	48:R:28:LEU:HB3	1.99	0.44
53:A:392:C:H2'	53:A:393:A:C8	2.53	0.44
53:A:815:A:H4'	53:A:817:C:C4	2.52	0.44
53:A:1008:U:H2'	53:A:1009:U:O4'	2.17	0.44
54:01:903:C:H2'	54:01:904:G:H8	1.83	0.44
54:01:2122:U:H2'	54:01:2123:G:O4'	2.18	0.44
54:01:2297:A:N1	54:01:2321:U:C5	2.78	0.44
54:01:2577:A:H2'	54:01:2614:A:N6	2.32	0.44
59:Z:19:HIS:ND1	59:Z:112:MET:CB	2.80	0.44
59:Z:208:LYS:HE3	59:Z:209:PRO:HD2	1.99	0.44
4:07:15:LEU:HD13	4:07:28:PRO:HD2	1.98	0.44
7:10:88:HIS:HB2	7:10:89:PRO:HD3	1.99	0.44
12:15:44:ARG:HG2	12:15:44:ARG:HH21	1.82	0.44
15:18:5:LYS:O	15:18:9:GLN:HG2	2.17	0.44
20:23:6:ARG:N	54:01:85:G:OP1	2.43	0.44
29:32:3:ARG:HG3	29:32:4:THR:N	2.32	0.44
29:32:12:ARG:HG3	29:32:12:ARG:NH2	2.32	0.44
31:34:16:ILE:HD13	31:34:25:VAL:HG22	1.99	0.44
40:J:40:ILE:HD12	40:J:73:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:74:GLN:C	42:L:76:HIS:H	2.25	0.44
42:L:115:LYS:O	42:L:116:TYR:HB2	2.17	0.44
52:03:184:LYS:O	52:03:187:GLU:HB2	2.18	0.44
53:A:206:C:O2'	53:A:207:C:H5'	2.17	0.44
53:A:1201:A:C1'	53:A:1202:U:OP2	2.60	0.44
54:01:1183:U:H2'	54:01:1184:U:C6	2.52	0.44
54:01:2185:U:H2'	54:01:2186:G:C8	2.52	0.44
54:01:2393:U:H2'	54:01:2394:C:O4'	2.17	0.44
54:01:2520:C:O2'	54:01:2521:C:H5'	2.18	0.44
54:01:2786:U:H2'	54:01:2787:C:C6	2.51	0.44
55:02:30:C:H2'	55:02:31:C:C5'	2.48	0.44
56:X:38:A:H2'	56:X:39:C:O4'	2.17	0.44
59:Z:233:ARG:HH11	59:Z:233:ARG:CB	2.31	0.44
59:Z:332:PHE:O	59:Z:333:ARG:CG	2.54	0.44
1:04:163:ILE:HG23	1:04:171:VAL:CG1	2.48	0.44
5:08:72:ASN:O	5:08:76:ILE:HG12	2.16	0.44
8:11:73:PRO:HA	8:11:74:PRO:HD3	1.90	0.44
8:11:77:VAL:HA	8:11:80:LYS:HE2	1.99	0.44
32:B:119:GLN:O	32:B:124:THR:N	2.51	0.44
33:C:151:GLU:HG3	33:C:166:TRP:HB3	1.99	0.44
34:D:8:LEU:HD21	34:D:31:CYS:HB3	1.98	0.44
35:E:113:VAL:HG13	35:E:114:LEU:CD1	2.47	0.44
39:I:48:ARG:O	39:I:52:GLU:HG2	2.17	0.44
53:A:1395:C:H5'	53:A:1395:C:C6	2.52	0.44
54:01:528:A:C2	54:01:2043:C:H4'	2.52	0.44
54:01:859:G:O2'	54:01:860:U:P	2.75	0.44
55:02:88:C:H5''	55:02:89:U:OP1	2.18	0.44
57:V:20:U:H2'	57:V:21:C:C6	2.53	0.44
58:Y:15:G:H2'	58:Y:16:U:H5'	2.00	0.44
59:Z:74:ARG:NH2	59:Z:199:ILE:O	2.48	0.44
59:Z:366:ILE:O	59:Z:368:MET:HG2	2.18	0.44
5:08:10:VAL:HA	5:08:11:PRO:HD3	1.85	0.44
6:09:110:VAL:HG22	6:09:111:ALA:N	2.32	0.44
7:10:118:ILE:HD13	7:10:118:ILE:HA	1.84	0.44
10:13:40:LYS:HD2	10:13:57:VAL:HG12	2.00	0.44
14:17:28:VAL:CG2	14:17:106:LEU:HD13	2.48	0.44
16:19:47:ARG:HG2	16:19:47:ARG:HH21	1.83	0.44
34:D:150:LYS:HB3	34:D:177:MET:HE2	1.99	0.44
51:U:39:LYS:N	51:U:40:PRO:CD	2.81	0.44
53:A:398:U:H2'	53:A:399:G:C8	2.52	0.44
54:01:127:A:H5''	54:01:128:C:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:494:G:O2'	54:01:495:G:H5'	2.18	0.44
54:01:720:U:H2'	54:01:721:A:C8	2.53	0.44
54:01:1424:G:H2'	54:01:1425:G:O4'	2.16	0.44
54:01:2048:G:C3'	54:01:2049:G:H5''	2.47	0.44
56:X:30:G:H2'	56:X:31:G:C8	2.53	0.44
59:Z:116:ARG:HD2	59:Z:160:TYR:HE2	1.81	0.44
9:12:101:ILE:N	9:12:101:ILE:CD1	2.80	0.44
12:15:29:GLY:HA2	12:15:106:ASP:HB2	1.98	0.44
17:20:49:ILE:HD12	17:20:52:PRO:CA	2.41	0.44
18:21:48:LYS:O	18:21:52:GLU:HG3	2.16	0.44
32:B:101:THR:HG22	32:B:174:GLU:CD	2.42	0.44
35:E:22:LYS:HB3	35:E:29:ILE:CG2	2.48	0.44
35:E:110:MET:HG3	35:E:139:THR:HG21	1.99	0.44
39:I:88:GLU:HG2	39:I:89:TYR:N	2.32	0.44
45:O:23:SER:OG	45:O:26:VAL:HG23	2.18	0.44
49:S:52:ASN:OD1	49:S:53:GLY:N	2.39	0.44
52:03:29:LEU:HD12	52:03:32:GLU:HG3	2.00	0.44
53:A:1120:C:H2'	53:A:1121:U:C6	2.53	0.44
54:01:543:G:H2'	54:01:544:C:O4'	2.18	0.44
54:01:547:A:H3'	54:01:547:A:N3	2.33	0.44
54:01:889:C:O2'	54:01:890:C:H5'	2.18	0.44
54:01:1020:A:C1'	54:01:1021:A:OP2	2.64	0.44
59:Z:91:MET:SD	59:Z:121:LEU:HD13	2.58	0.44
3:06:63:LYS:NZ	54:01:2060:A:H3'	2.32	0.44
4:07:147:ARG:HG2	4:07:147:ARG:HH11	1.82	0.44
6:09:84:ALA:CB	6:09:90:LEU:HA	2.47	0.44
7:10:67:THR:N	7:10:68:PRO:CD	2.81	0.44
15:18:6:GLN:HA	15:18:9:GLN:HG2	2.00	0.44
20:23:73:ASN:ND2	20:23:76:THR:HG23	2.32	0.44
41:K:126:ARG:O	51:U:34:ARG:NH2	2.50	0.44
42:L:30:ARG:HD2	42:L:78:VAL:HG11	1.98	0.44
45:O:87:ARG:O	45:O:88:ARG:C	2.61	0.44
46:P:14:ARG:HE	46:P:42:ILE:HD12	1.83	0.44
52:03:49:GLY:HA2	52:03:210:LYS:HZ1	1.81	0.44
53:A:216:U:H2'	53:A:217:C:C6	2.52	0.44
53:A:225:C:C2'	53:A:226:G:H5''	2.46	0.44
53:A:1139:G:H5''	53:A:1140:C:H5	1.81	0.44
53:A:1346:A:H2'	53:A:1346:A:N3	2.33	0.44
54:01:471:A:H2'	54:01:472:A:O4'	2.18	0.44
54:01:1989:G:H2'	54:01:1990:C:O4'	2.18	0.44
54:01:2074:U:H2'	54:01:2075:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2553:G:H2'	54:01:2554:U:C4'	2.47	0.44
55:02:13:G:H21	55:02:16:G:H1'	1.83	0.44
55:02:111:U:H2'	55:02:112:G:H8	1.83	0.44
56:X:36:U:H2'	56:X:37:A:O4'	2.18	0.44
59:Z:16:THR:HG23	59:Z:78:HIS:NE2	2.32	0.44
2:05:118:PHE:HB2	54:01:2823:A:OP1	2.18	0.44
4:07:134:GLN:HB3	4:07:149:ARG:O	2.17	0.44
8:11:56:VAL:CG2	8:11:57:VAL:H	2.29	0.44
8:11:135:MET:HE2	8:11:135:MET:HA	2.00	0.44
11:14:95:LEU:CD2	11:14:100:ILE:HD11	2.48	0.44
11:14:116:VAL:HG13	11:14:116:VAL:O	2.18	0.44
19:22:15:HIS:HE1	19:22:17:SER:HB3	1.82	0.44
25:28:24:LEU:HD23	25:28:24:LEU:C	2.43	0.44
29:32:44:VAL:HG13	29:32:44:VAL:O	2.18	0.44
33:C:55:VAL:HB	33:C:66:THR:HB	2.00	0.44
35:E:112:ALA:HA	35:E:115:GLU:HG2	2.00	0.44
43:M:11:HIS:HA	43:M:43:LYS:HD2	1.98	0.44
52:03:5:THR:N	52:03:8:MET:SD	2.91	0.44
52:03:170:ILE:HG12	54:01:2177:C:O2'	2.18	0.44
53:A:887:G:H2'	53:A:888:G:H5'	2.00	0.44
53:A:1127:G:H5'	53:A:1280:A:O2'	2.17	0.44
53:A:1256:A:H4'	53:A:1258:G:O4'	2.17	0.44
54:01:248:G:O5'	54:01:249:C:H5'	2.17	0.44
54:01:1038:G:H2'	54:01:1039:A:C8	2.53	0.44
54:01:1060:U:H4'	54:01:1061:U:O5'	2.17	0.44
59:Z:52:ALA:O	59:Z:56:LYS:HG2	2.17	0.44
59:Z:83:GLY:HA2	59:Z:118:HIS:CE1	2.53	0.44
59:Z:377:ARG:HG2	59:Z:382:THR:HA	1.98	0.44
2:05:11:MET:O	54:01:2682:A:H5'	2.18	0.44
19:22:59:ASN:HB2	19:22:84:TYR:HB2	2.00	0.44
24:27:41:HIS:CG	54:01:96:C:H4'	2.53	0.44
32:B:86:CYS:SG	32:B:87:ASP:N	2.90	0.44
33:C:86:LEU:O	33:C:90:VAL:HG23	2.18	0.44
33:C:187:GLU:HG3	33:C:189:HIS:CE1	2.52	0.44
34:D:106:PHE:CG	34:D:144:ILE:HD11	2.53	0.44
35:E:107:GLY:HA2	53:A:8:A:H1'	2.00	0.44
36:F:67:PRO:HG2	36:F:70:VAL:HG23	2.00	0.44
38:H:4:ASP:HB2	38:H:80:PRO:HG3	1.99	0.44
40:J:42:LEU:HA	40:J:43:PRO:HD2	1.72	0.44
52:03:7:ARG:HB3	54:01:2129:C:OP1	2.18	0.44
53:A:403:C:O2'	53:A:404:G:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1032:G:H3'	53:A:1032:G:N3	2.33	0.44
53:A:1326:U:H2'	53:A:1327:C:C6	2.53	0.44
53:A:1346:A:O2'	53:A:1347:G:H4'	2.17	0.44
54:01:1092:C:H2'	54:01:1093:G:H5'	2.00	0.44
54:01:1857:G:H1'	54:01:1885:A:H62	1.82	0.44
59:Z:211:LEU:CD1	59:Z:293:ALA:HB2	2.47	0.44
59:Z:248:LYS:HE2	59:Z:285:GLU:O	2.18	0.44
4:07:58:ALA:HB1	4:07:139:GLU:CB	2.48	0.44
7:10:45:GLY:HA2	7:10:49:GLY:HA2	2.00	0.44
14:17:7:ARG:HD2	14:17:97:PHE:CZ	2.53	0.44
14:17:74:VAL:O	14:17:78:VAL:HG23	2.17	0.44
21:24:19:ARG:HH22	55:02:95:U:P	2.41	0.44
31:34:32:LYS:HE3	54:01:2478:A:H5'	1.99	0.44
34:D:59:LYS:HE3	34:D:194:ILE:HG22	2.00	0.44
36:F:69:GLU:O	36:F:73:GLU:HG3	2.17	0.44
37:G:41:ILE:HG23	37:G:116:ALA:HA	1.99	0.44
38:H:95:MET:O	38:H:98:LEU:HG	2.18	0.44
43:M:97:ARG:HG3	43:M:97:ARG:NH1	2.33	0.44
53:A:357:G:O2'	53:A:358:U:H5'	2.18	0.44
54:01:1097:U:C2'	54:01:1098:A:H5'	2.47	0.44
1:04:81:GLU:HB2	1:04:90:ILE:HG13	1.99	0.43
6:09:46:PHE:O	6:09:50:ARG:HB2	2.18	0.43
7:10:97:LYS:HE3	7:10:129:LEU:HD12	1.99	0.43
10:13:40:LYS:HD2	10:13:57:VAL:CG1	2.48	0.43
12:15:54:THR:O	12:15:54:THR:HG22	2.17	0.43
12:15:66:ARG:HG3	12:15:66:ARG:HH11	1.83	0.43
16:19:57:ARG:HG2	16:19:57:ARG:HH11	1.82	0.43
30:33:34:LYS:HD2	54:01:2391:G:OP2	2.17	0.43
37:G:136:LYS:O	37:G:140:VAL:HG23	2.18	0.43
38:H:34:ALA:O	38:H:38:VAL:HG23	2.18	0.43
39:I:90:ASP:C	39:I:92:SER:H	2.26	0.43
42:L:20:VAL:HG23	42:L:20:VAL:O	2.18	0.43
50:T:50:PHE:HA	50:T:53:MET:HG3	1.99	0.43
53:A:694:A:C2'	53:A:695:A:H5'	2.48	0.43
53:A:1277:C:H2'	53:A:1278:G:H5''	2.00	0.43
54:01:435:C:C2'	54:01:436:C:H5'	2.44	0.43
54:01:497:A:H2'	54:01:498:G:O4'	2.17	0.43
54:01:532:A:H2'	54:01:532:A:N3	2.33	0.43
54:01:2489:U:C2'	54:01:2490:G:H5'	2.47	0.43
59:Z:103:LEU:HG	59:Z:105:VAL:HG23	2.00	0.43
59:Z:238:VAL:HG13	59:Z:256:THR:C	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:260:MET:HE3	59:Z:272:GLU:HG3	1.98	0.43
59:Z:331:TYR:HA	59:Z:335:THR:O	2.18	0.43
4:07:67:THR:N	4:07:85:GLY:O	2.50	0.43
4:07:97:GLU:HG2	26:29:9:TYR:OH	2.18	0.43
9:12:47:HIS:ND1	9:12:48:VAL:HG23	2.33	0.43
17:20:72:VAL:O	17:20:74:ILE:HD12	2.18	0.43
20:23:82:VAL:HG12	20:23:83:GLY:N	2.27	0.43
21:24:65:VAL:O	21:24:65:VAL:HG13	2.18	0.43
23:26:2:ARG:C	23:26:32:LEU:HD11	2.43	0.43
33:C:168:ARG:HD2	33:C:168:ARG:C	2.42	0.43
37:G:58:LEU:HD12	37:G:58:LEU:N	2.33	0.43
39:I:122:ARG:HD2	53:A:1343:G:O2'	2.18	0.43
41:K:86:LYS:HB2	41:K:112:VAL:HG23	2.00	0.43
49:S:30:LEU:HD13	49:S:48:ILE:HG22	1.99	0.43
52:03:61:GLY:C	52:03:163:TYR:CE2	2.95	0.43
53:A:909:A:H2'	53:A:910:C:O4'	2.17	0.43
53:A:1382:C:O2	56:X:34:C:H5''	2.18	0.43
54:01:207:A:H2'	54:01:208:C:O4'	2.18	0.43
54:01:1054:A:H2'	54:01:1055:G:C8	2.54	0.43
54:01:1773:A:H2'	54:01:1774:C:H5'	1.99	0.43
54:01:1866:A:H2'	54:01:1867:G:O4'	2.18	0.43
54:01:2584:U:H2'	54:01:2585:U:H2'	2.00	0.43
56:X:58:A:H1'	56:X:60:U:OP2	2.19	0.43
59:Z:357:LYS:CD	59:Z:358:MET:N	2.74	0.43
1:04:229:HIS:ND1	1:04:230:PRO:CD	2.80	0.43
10:13:92:GLU:O	10:13:93:GLN:C	2.61	0.43
11:14:131:ALA:O	11:14:135:ILE:HG13	2.18	0.43
17:20:54:VAL:HG12	17:20:55:ASP:N	2.34	0.43
20:23:85:ARG:HD3	20:23:87:GLU:CG	2.36	0.43
28:31:18:HIS:HB3	28:31:39:ASP:OD1	2.18	0.43
32:B:47:PRO:O	32:B:51:GLU:HG3	2.18	0.43
41:K:35:ASP:OD2	41:K:37:GLN:HB2	2.18	0.43
49:S:27:LYS:HG2	49:S:28:LYS:N	2.28	0.43
52:03:55:SER:HA	52:03:58:ASN:ND2	2.34	0.43
53:A:464:U:H2'	53:A:466:A:OP2	2.17	0.43
54:01:687:C:H5'	54:01:687:C:C6	2.53	0.43
54:01:1609:A:H1'	54:01:1616:A:O4'	2.18	0.43
54:01:2632:A:O2'	54:01:2633:G:H5'	2.19	0.43
54:01:2888:C:H2'	54:01:2889:C:C6	2.53	0.43
56:W:47:U:H3'	56:W:48:C:C5'	2.48	0.43
59:Z:97:GLN:CB	59:Z:230:ARG:HD2	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:264:LEU:C	59:Z:264:LEU:CD2	2.91	0.43
3:06:46:GLN:HB3	3:06:83:VAL:HG21	2.01	0.43
3:06:52:VAL:O	3:06:74:LYS:HE3	2.18	0.43
3:06:97:ASN:N	3:06:97:ASN:ND2	2.67	0.43
4:07:126:ASN:OD1	4:07:156:THR:HG23	2.18	0.43
8:11:125:THR:O	8:11:129:GLU:HG3	2.18	0.43
12:15:69:PRO:HA	12:15:94:ALA:HB2	2.00	0.43
18:21:61:ASN:OD1	54:01:496:G:H1'	2.18	0.43
19:22:44:LYS:O	19:22:48:GLN:HG2	2.18	0.43
32:B:63:LYS:HA	32:B:63:LYS:HD2	1.80	0.43
33:C:206:ILE:OXT	33:C:206:ILE:HG12	2.18	0.43
34:D:33:ILE:HG13	34:D:34:GLU:H	1.79	0.43
42:L:48:LEU:HB2	53:A:520:A:OP1	2.19	0.43
49:S:54:ARG:HG2	49:S:54:ARG:HH11	1.83	0.43
52:03:19:LYS:HD3	52:03:21:TYR:HE1	1.83	0.43
52:03:44:VAL:HG12	52:03:46:VAL:HG23	2.00	0.43
52:03:171:ILE:C	52:03:172:HIS:ND1	2.77	0.43
53:A:70:U:H4'	53:A:71:A:O5'	2.18	0.43
53:A:1540:U:O2	53:A:1540:U:C3'	2.64	0.43
54:01:607:U:O4	54:01:620:G:H5'	2.18	0.43
54:01:1301:A:H2'	54:01:1301:A:N3	2.33	0.43
54:01:2682:A:O2'	54:01:2683:C:H5'	2.18	0.43
59:Z:137:CYS:HB2	59:Z:184:TRP:CZ3	2.54	0.43
59:Z:149:VAL:HA	59:Z:152:GLU:CG	2.48	0.43
1:04:216:ARG:HG3	1:04:217:PRO:HD2	2.00	0.43
3:06:88:ARG:HB3	3:06:89:PRO:HD2	2.00	0.43
5:08:97:VAL:HG23	5:08:124:CYS:SG	2.59	0.43
6:09:70:GLU:HG2	6:09:71:LYS:HG3	2.00	0.43
14:17:31:THR:CG2	14:17:32:PRO:HD2	2.48	0.43
31:34:29:ALA:O	31:34:31:PRO:HD3	2.18	0.43
32:B:98:GLY:O	32:B:102:ASN:HB3	2.19	0.43
33:C:39:ARG:HG3	33:C:54:ILE:CD1	2.48	0.43
41:K:88:PRO:CG	41:K:89:GLY:H	2.30	0.43
44:N:53:ASP:O	44:N:54:SER:OG	2.30	0.43
51:U:24:LYS:CG	51:U:25:ALA:H	2.26	0.43
53:A:830:G:O2'	53:A:831:A:H5'	2.18	0.43
53:A:1193:G:O2'	53:A:1194:U:H5'	2.19	0.43
54:01:558:U:H2'	54:01:559:G:C8	2.49	0.43
54:01:845:A:H3'	54:01:845:A:N3	2.33	0.43
54:01:1597:A:O3'	54:01:1598:A:H8	2.02	0.43
54:01:1790:C:H2'	54:01:1791:A:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1857:G:N2	54:01:1884:G:H2'	2.33	0.43
54:01:2116:G:H1	54:01:2171:A:H61	1.64	0.43
54:01:2497:A:H8	54:01:2497:A:OP2	2.02	0.43
59:Z:372:LEU:HB3	59:Z:388:VAL:CG2	2.48	0.43
1:04:93:VAL:HG21	1:04:103:ILE:CD1	2.49	0.43
1:04:235:GLU:H	1:04:238:ASN:HD22	1.66	0.43
1:04:270:ARG:CB	1:04:270:ARG:NH1	2.82	0.43
1:04:270:ARG:NH1	1:04:270:ARG:HB3	2.34	0.43
6:09:59:ALA:HA	6:09:62:LEU:HD12	1.99	0.43
7:10:79:PRO:O	7:10:80:THR:OG1	2.36	0.43
8:11:109:ALA:HA	8:11:112:LYS:NZ	2.33	0.43
10:13:103:VAL:HG23	10:13:122:VAL:OXT	2.19	0.43
11:14:30:THR:O	11:14:33:ARG:HG2	2.17	0.43
12:15:4:PRO:HG3	12:15:68:PHE:CE2	2.53	0.43
15:18:20:ARG:HD3	15:18:112:ARG:NH1	2.31	0.43
22:25:52:ASP:O	22:25:53:HIS:HB2	2.18	0.43
24:27:2:LYS:CE	54:01:102:U:H1'	2.48	0.43
24:27:42:LEU:O	24:27:46:VAL:HG23	2.18	0.43
32:B:71:THR:HG22	32:B:72:LYS:N	2.24	0.43
52:03:56:ASP:OD2	52:03:203:GLN:HG2	2.19	0.43
53:A:591:U:H2'	53:A:592:G:H8	1.84	0.43
53:A:915:A:H2'	53:A:916:U:H5'	2.00	0.43
53:A:1009:U:H2'	53:A:1010:U:H6	1.83	0.43
53:A:1033:G:H3'	53:A:1034:G:H5''	2.00	0.43
53:A:1441:A:C2'	53:A:1442:G:H5'	2.49	0.43
54:01:145:C:H2'	54:01:146:A:C8	2.53	0.43
54:01:2480:C:H2'	54:01:2481:G:O4'	2.19	0.43
59:Z:181:ASP:OD2	59:Z:184:TRP:HD1	2.02	0.43
4:07:84:ILE:HG21	54:01:2312:U:H5'	2.01	0.43
7:10:67:THR:HB	7:10:68:PRO:HD3	2.01	0.43
8:11:126:ARG:HA	8:11:129:GLU:HG3	2.00	0.43
10:13:69:VAL:HG22	10:13:77:ILE:HB	2.01	0.43
13:16:79:LEU:O	13:16:80:PHE:HB2	2.19	0.43
20:23:47:PRO:HB3	20:23:55:GLY:H	1.82	0.43
30:33:3:ILE:HG21	30:33:62:PRO:HG2	2.01	0.43
33:C:87:ARG:HD2	33:C:87:ARG:O	2.19	0.43
35:E:25:LYS:HG2	53:A:923:A:OP1	2.19	0.43
43:M:18:LEU:HD12	43:M:33:LEU:HD11	2.01	0.43
44:N:27:LYS:HE2	53:A:1317:C:OP2	2.18	0.43
44:N:62:ARG:HH12	44:N:69:PRO:HD3	1.83	0.43
45:O:41:HIS:CE1	45:O:45:HIS:ND1	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:P:8:ARG:HD3	46:P:17:TYR:CE1	2.54	0.43
47:Q:13:SER:HB3	47:Q:21:VAL:HG11	2.00	0.43
52:03:194:VAL:O	52:03:198:LYS:N	2.51	0.43
53:A:1125:U:H2'	53:A:1126:U:H2'	2.01	0.43
54:01:63:A:O2'	54:01:64:A:H5'	2.19	0.43
54:01:387:U:H6	54:01:387:U:H5'	1.84	0.43
54:01:1283:G:H1'	54:01:1329:U:O2	2.19	0.43
54:01:1779:U:OP2	54:01:1784:A:N6	2.49	0.43
54:01:2105:U:H2'	54:01:2106:U:O4'	2.19	0.43
54:01:2111:U:N3	54:01:2147:A:H1'	2.32	0.43
54:01:2537:U:H2'	54:01:2538:C:H6	1.83	0.43
59:Z:123:ARG:CZ	59:Z:161:ASP:OD1	2.67	0.43
59:Z:227:VAL:HG13	59:Z:276:VAL:HB	2.01	0.43
59:Z:299:LYS:NZ	59:Z:301:HIS:CD2	2.87	0.43
59:Z:328:PRO:HD2	59:Z:339:GLY:O	2.18	0.43
1:04:32:LEU:C	1:04:33:LEU:HD12	2.43	0.43
3:06:97:ASN:HB2	3:06:100:MET:HG3	2.00	0.43
5:08:91:VAL:HG12	5:08:159:LYS:NZ	2.34	0.43
7:10:30:SER:O	54:01:1054:A:H4'	2.19	0.43
16:19:63:ARG:HH11	16:19:63:ARG:HG3	1.84	0.43
16:19:109:VAL:HG12	16:19:113:LYS:HE2	1.99	0.43
19:22:29:THR:HG23	19:22:85:VAL:O	2.19	0.43
25:28:11:SER:OG	25:28:13:ILE:HG13	2.17	0.43
34:D:66:VAL:HG12	34:D:67:LEU:N	2.33	0.43
39:I:30:ASN:O	39:I:31:GLN:HB2	2.19	0.43
42:L:31:GLY:HA3	42:L:54:VAL:HG11	1.98	0.43
46:P:20:VAL:CG2	46:P:21:VAL:N	2.82	0.43
49:S:35:ARG:HD2	49:S:51:HIS:O	2.19	0.43
52:03:6:LYS:HG3	52:03:7:ARG:H	1.84	0.43
53:A:393:A:O2'	53:A:394:G:H5'	2.18	0.43
53:A:604:G:H2'	53:A:605:U:O4'	2.19	0.43
53:A:884:U:H4'	53:A:885:G:H5''	2.01	0.43
53:A:1002:G:H2'	53:A:1003:G:O4'	2.18	0.43
54:01:622:G:O2'	54:01:623:C:H5'	2.19	0.43
54:01:644:A:H2'	54:01:645:C:O4'	2.19	0.43
54:01:851:C:H2'	54:01:852:U:C6	2.54	0.43
54:01:2364:C:H2'	54:01:2365:G:O4'	2.18	0.43
1:04:141:HIS:CD2	1:04:194:VAL:HG22	2.54	0.43
1:04:141:HIS:ND1	1:04:192:GLY:O	2.52	0.43
2:05:109:VAL:HG23	2:05:175:LEU:HD12	2.01	0.43
5:08:173:ALA:C	5:08:175:LYS:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:29:ASP:H	7:10:56:ARG:HH22	1.67	0.43
14:17:35:ILE:HG23	14:17:74:VAL:HG21	2.00	0.43
32:B:89:PHE:HB3	32:B:149:GLY:O	2.18	0.43
34:D:97:LEU:HB2	34:D:134:TYR:HB3	2.00	0.43
37:G:14:ASP:HB3	37:G:17:PHE:O	2.19	0.43
39:I:6:TYR:CE2	53:A:1147:C:H4'	2.54	0.43
39:I:117:LEU:HD12	39:I:117:LEU:N	2.34	0.43
44:N:26:LEU:HD11	44:N:46:LYS:HB3	2.00	0.43
53:A:113:G:H1'	53:A:354:G:H5'	2.00	0.43
53:A:673:A:H2'	53:A:674:G:C8	2.54	0.43
53:A:1486:G:H2'	53:A:1487:G:O4'	2.18	0.43
54:01:274:C:H2'	54:01:275:C:O4'	2.18	0.43
54:01:302:C:H2'	54:01:303:G:H8	1.84	0.43
54:01:372:G:C2'	54:01:373:U:OP2	2.67	0.43
54:01:570:G:H2'	54:01:2030:A:N7	2.33	0.43
54:01:1367:A:C2'	54:01:1368:G:H5'	2.49	0.43
54:01:1430:G:H2'	54:01:1431:A:O4'	2.19	0.43
54:01:2665:A:O2'	54:01:2666:C:H5'	2.19	0.43
59:Z:151:MET:CE	59:Z:151:MET:CG	2.94	0.43
1:04:219:VAL:HG21	54:01:782:A:C8	2.54	0.43
3:06:46:GLN:HB2	3:06:83:VAL:HG11	2.01	0.43
7:10:34:THR:HG21	54:01:1057:A:H1'	2.00	0.43
14:17:101:GLY:HA3	55:02:49:C:OP1	2.19	0.43
15:18:105:LYS:O	15:18:108:ARG:HG2	2.18	0.43
23:26:39:VAL:HG11	23:26:42:GLU:OE1	2.19	0.43
25:28:41:PRO:HA	25:28:44:ARG:HB2	2.00	0.43
34:D:14:GLU:HG3	34:D:18:LEU:HD11	2.01	0.43
39:I:17:ARG:NH2	53:A:1129:C:H5''	2.33	0.43
52:03:24:ASN:ND2	52:03:186:LYS:HE3	2.34	0.43
52:03:24:ASN:HD22	52:03:24:ASN:HA	1.62	0.43
54:01:601:C:O2'	54:01:605:G:H5''	2.19	0.43
54:01:1925:C:O2'	54:01:1926:U:H5'	2.19	0.43
54:01:2082:A:H2'	54:01:2083:G:O4'	2.18	0.43
54:01:2317:A:H2'	54:01:2318:G:O4'	2.19	0.43
55:02:26:C:O2	55:02:117:G:H1'	2.19	0.43
59:Z:299:LYS:CE	59:Z:301:HIS:NE2	2.82	0.43
2:05:9:VAL:O	2:05:9:VAL:HG12	2.19	0.42
3:06:68:ALA:HA	54:01:1255:U:C6	2.54	0.42
3:06:102:ARG:HH21	3:06:102:ARG:HB2	1.84	0.42
4:07:107:VAL:HB	4:07:108:PRO:HD3	2.00	0.42
7:10:13:ALA:O	7:10:17:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:20:38:VAL:O	17:20:54:VAL:HG23	2.18	0.42
32:B:94:ARG:HG3	53:A:1100:C:OP2	2.18	0.42
34:D:103:ARG:HB3	34:D:170:LEU:HD21	2.01	0.42
53:A:469:C:H2'	53:A:470:C:O4'	2.19	0.42
53:A:1027:C:H6	53:A:1027:C:O5'	2.01	0.42
53:A:1195:C:H5''	53:A:1196:A:OP2	2.19	0.42
54:01:502:A:H2'	54:01:503:A:H5'	1.99	0.42
54:01:1917:U:H2'	54:01:1918:A:H5'	2.00	0.42
54:01:2671:G:H2'	54:01:2672:U:C6	2.53	0.42
54:01:2752:C:H2'	54:01:2753:A:O4'	2.19	0.42
59:Z:18:GLY:H	59:Z:118:HIS:CD2	2.36	0.42
59:Z:211:LEU:HD11	59:Z:291:VAL:HG21	2.01	0.42
59:Z:383:VAL:CG2	59:Z:384:GLY:N	2.82	0.42
1:04:83:ASP:HB2	1:04:90:ILE:CD1	2.48	0.42
2:05:28:GLU:HG3	2:05:28:GLU:O	2.19	0.42
3:06:143:LEU:HB3	3:06:146:VAL:HG11	2.01	0.42
7:10:26:VAL:HB	7:10:82:ILE:HD12	2.01	0.42
7:10:56:ARG:NE	7:10:83:ALA:HB2	2.34	0.42
8:11:12:VAL:HG12	8:11:13:ALA:H	1.84	0.42
9:12:89:PHE:HE1	9:12:100:VAL:HG11	1.84	0.42
10:13:93:GLN:HA	10:13:94:PRO:HD2	1.76	0.42
33:C:76:ILE:HG13	33:C:77:GLY:N	2.33	0.42
33:C:173:PRO:O	33:C:181:ILE:HD11	2.19	0.42
39:I:114:LYS:HB2	39:I:117:LEU:HD22	2.02	0.42
44:N:2:LYS:HD2	53:A:1049:U:O2'	2.20	0.42
45:O:53:ARG:HH11	45:O:53:ARG:HG2	1.84	0.42
49:S:62:THR:HG22	49:S:63:ASP:N	2.33	0.42
51:U:22:CYS:SG	51:U:23:GLU:HG3	2.59	0.42
51:U:33:ARG:HH11	51:U:34:ARG:HG2	1.83	0.42
54:01:1106:G:H5'	54:01:1106:G:H8	1.84	0.42
54:01:2159:G:H2'	54:01:2160:C:O4'	2.19	0.42
54:01:2799:A:H2'	54:01:2800:A:H5'	2.01	0.42
54:01:2801:G:H2'	54:01:2802:G:C8	2.55	0.42
59:Z:138:ASP:HA	59:Z:184:TRP:CZ2	2.54	0.42
2:05:66:GLY:HA3	54:01:2787:C:H5'	2.01	0.42
6:09:5:LEU:HD21	6:09:13:GLY:HA3	2.02	0.42
9:12:99:ARG:O	9:12:103:ILE:HG13	2.19	0.42
14:17:13:ARG:HD3	54:01:2335:A:OP1	2.18	0.42
24:27:17:GLU:OE2	24:27:54:LYS:HG2	2.18	0.42
27:30:30:ASP:HB3	27:30:34:GLY:H	1.83	0.42
28:31:44:GLN:O	28:31:45:HIS:ND1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:183:PHE:HD1	32:B:197:PHE:HB2	1.84	0.42
33:C:122:GLN:HE22	33:C:135:ARG:NH1	2.18	0.42
34:D:56:GLU:HG2	34:D:198:LEU:HB2	1.99	0.42
35:E:104:ILE:HA	35:E:121:ASN:O	2.19	0.42
36:F:18:VAL:O	36:F:22:ILE:HG13	2.20	0.42
40:J:12:ALA:HB2	40:J:96:VAL:HG22	2.01	0.42
45:O:71:ARG:HG3	45:O:71:ARG:NH1	2.32	0.42
46:P:42:ILE:HG22	53:A:449:G:O2'	2.19	0.42
46:P:67:ILE:H	46:P:67:ILE:CD1	2.15	0.42
52:O3:22:ASP:CB	52:O3:25:GLU:HG3	2.31	0.42
53:A:77:A:H2'	53:A:78:A:H8	1.83	0.42
53:A:421:U:O2'	53:A:422:C:OP1	2.35	0.42
54:O1:373:U:O2'	54:O1:423:A:H1'	2.19	0.42
54:O1:402:A:C2'	54:O1:403:U:H5'	2.49	0.42
54:O1:1092:C:C2'	54:O1:1093:G:H5'	2.49	0.42
54:O1:1509:A:H2'	54:O1:1510:G:H8	1.82	0.42
54:O1:1536:C:H4'	54:O1:1537:G:C2	2.54	0.42
54:O1:2352:A:H2'	54:O1:2353:G:H5'	2.01	0.42
59:Z:68:GLU:HB3	59:Z:261:PHE:CZ	2.54	0.42
59:Z:71:THR:C	59:Z:73:THR:H	2.26	0.42
59:Z:92:ILE:HD11	59:Z:121:LEU:HD13	2.00	0.42
59:Z:116:ARG:HD2	59:Z:156:LEU:HD11	2.00	0.42
59:Z:131:ILE:HD12	59:Z:194:PHE:HB3	2.01	0.42
59:Z:140:VAL:HG23	59:Z:146:LEU:HD21	2.02	0.42
1:O4:62:ARG:HD3	1:O4:90:ILE:HD11	2.01	0.42
7:10:31:ARG:HB2	7:10:109:LYS:HD2	2.01	0.42
9:12:35:ARG:HA	9:12:40:HIS:CD2	2.52	0.42
11:14:96:LYS:HB2	11:14:96:LYS:HZ2	1.83	0.42
31:34:4:ARG:NH2	54:O1:2477:U:H2'	2.34	0.42
33:C:111:ASP:O	33:C:115:VAL:HG23	2.19	0.42
40:J:8:ILE:HD13	40:J:25:ILE:HD11	2.01	0.42
42:L:73:LEU:N	42:L:73:LEU:HD12	2.34	0.42
53:A:1219:A:H2'	53:A:1220:G:C8	2.55	0.42
54:O1:738:G:O2'	54:O1:739:A:H5'	2.19	0.42
54:O1:903:C:H2'	54:O1:904:G:C8	2.54	0.42
58:Y:58:A:H1'	58:Y:60:U:H5	1.85	0.42
59:Z:321:PRO:HB2	59:Z:349:MET:HB3	2.00	0.42
59:Z:324:LYS:HZ1	59:Z:342:GLU:HA	1.82	0.42
12:15:50:ARG:HA	12:15:53:MET:HE2	2.02	0.42
19:22:80:TRP:CD1	19:22:80:TRP:H	2.37	0.42
32:B:53:LEU:HD23	32:B:56:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:C:1:GLY:HA3	53:A:1060:U:C5	2.54	0.42
33:C:63:ILE:HG22	33:C:98:ALA:HA	2.00	0.42
35:E:152:VAL:HG21	38:H:98:LEU:HB2	2.01	0.42
36:F:9:MET:HE1	36:F:51:ILE:HD13	2.01	0.42
37:G:79:VAL:O	37:G:79:VAL:HG12	2.19	0.42
44:N:24:ALA:O	44:N:28:ALA:N	2.50	0.42
46:P:53:ASP:O	46:P:57:ILE:HG13	2.20	0.42
52:03:50:ILE:CG2	52:03:201:PRO:HG2	2.41	0.42
53:A:1372:U:H2'	53:A:1373:G:O4'	2.18	0.42
54:01:995:C:H6	54:01:995:C:H5'	1.84	0.42
54:01:1028:A:N6	54:01:1125:G:H2'	2.34	0.42
54:01:1747:U:H2'	54:01:1748:C:C6	2.54	0.42
59:Z:332:PHE:N	59:Z:332:PHE:HD1	2.16	0.42
4:07:72:SER:OG	4:07:79:ARG:HA	2.20	0.42
4:07:130:GLY:HA2	4:07:152:ASP:HA	2.02	0.42
8:11:89:SER:HB3	8:11:135:MET:HA	2.02	0.42
9:12:114:LEU:HG	9:12:118:MET:CE	2.49	0.42
11:14:95:LEU:HD23	11:14:100:ILE:HD11	2.02	0.42
14:17:9:ARG:HH11	14:17:9:ARG:HG3	1.84	0.42
18:21:29:VAL:HG21	18:21:69:LEU:HD23	2.00	0.42
20:23:87:GLU:O	20:23:88:ASP:HB2	2.18	0.42
21:24:42:LEU:C	21:24:42:LEU:HD12	2.44	0.42
28:31:7:LYS:HA	28:31:23:THR:HA	2.01	0.42
39:I:37:TYR:HD2	39:I:38:PHE:CD1	2.37	0.42
39:I:98:ARG:NH2	53:A:1178:G:N7	2.68	0.42
40:J:57:VAL:CG2	40:J:58:ASN:N	2.83	0.42
41:K:127:ARG:HD3	51:U:34:ARG:HH22	1.84	0.42
51:U:57:LYS:HE2	51:U:57:LYS:CA	2.49	0.42
52:03:186:LYS:O	52:03:190:GLU:CG	2.67	0.42
53:A:430:A:H2'	53:A:431:A:H5'	2.01	0.42
53:A:1315:U:H2'	53:A:1316:G:O4'	2.20	0.42
54:01:184:C:H2'	54:01:185:G:C8	2.55	0.42
54:01:421:C:C2'	54:01:422:A:OP2	2.67	0.42
54:01:1300:G:H4'	54:01:1301:A:C5'	2.37	0.42
54:01:1354:A:H2'	54:01:1355:G:O4'	2.19	0.42
54:01:1930:G:HO2'	54:01:1931:U:H5	1.65	0.42
54:01:2286:G:C5'	54:01:2287:A:O4'	2.67	0.42
54:01:2421:G:H2'	56:X:76:A:N6	2.33	0.42
56:X:26:G:N3	56:X:26:G:H2'	2.35	0.42
2:05:157:LYS:HA	54:01:2619:C:H5''	2.01	0.42
7:10:8:LYS:O	7:10:12:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:94:ARG:HB3	7:10:97:LYS:HG2	2.01	0.42
8:11:90:GLY:C	8:11:92:PRO:HD3	2.45	0.42
9:12:88:THR:OG1	9:12:91:GLU:HG3	2.20	0.42
13:16:113:ILE:HG23	13:16:113:ILE:O	2.19	0.42
19:22:45:ALA:O	19:22:49:LYS:HD3	2.19	0.42
26:29:2:LYS:HB2	26:29:5:ILE:CD1	2.50	0.42
32:B:18:GLN:OE1	32:B:18:GLN:HA	2.13	0.42
34:D:68:GLU:HB3	53:A:546:A:P	2.59	0.42
36:F:5:GLU:HA	36:F:63:ASN:HA	2.01	0.42
37:G:15:PRO:HB2	39:I:44:ARG:HH11	1.84	0.42
37:G:68:VAL:HG23	37:G:99:ALA:HB1	2.02	0.42
37:G:85:GLN:HE22	56:X:32:C:H5''	1.84	0.42
41:K:126:ARG:HB3	51:U:33:ARG:CZ	2.49	0.42
42:L:47:ALA:O	42:L:48:LEU:HD12	2.20	0.42
46:P:4:ILE:HD13	46:P:57:ILE:HG23	2.01	0.42
47:Q:8:GLN:NE2	47:Q:59:GLU:OE2	2.52	0.42
49:S:30:LEU:HD12	49:S:30:LEU:N	2.35	0.42
51:U:34:ARG:HD2	51:U:36:PHE:CZ	2.55	0.42
52:03:200:LYS:HA	52:03:201:PRO:HD3	1.87	0.42
53:A:438:U:C2'	53:A:439:U:OP2	2.67	0.42
54:01:864:G:O2'	54:01:865:C:H5'	2.20	0.42
54:01:1070:A:H2'	54:01:1097:U:OP1	2.19	0.42
54:01:2221:G:O2'	54:01:2222:C:H5'	2.19	0.42
58:Y:28:G:O2'	58:Y:29:G:H5'	2.20	0.42
59:Z:311:LEU:H	59:Z:311:LEU:CD2	2.32	0.42
1:04:62:ARG:HG3	1:04:62:ARG:NH1	2.31	0.42
3:06:23:PHE:N	3:06:114:ARG:HH22	2.18	0.42
3:06:118:LEU:HD11	3:06:188:MET:SD	2.59	0.42
9:12:129:GLU:OE2	9:12:130:HIS:O	2.37	0.42
16:19:24:TYR:CE1	54:01:17:G:H4'	2.54	0.42
16:19:54:ARG:O	16:19:58:GLN:HG2	2.19	0.42
18:21:10:ALA:O	18:21:12:SER:N	2.50	0.42
20:23:73:ASN:O	20:23:74:ALA:HB3	2.18	0.42
21:24:64:VAL:HG22	21:24:69:GLU:HG2	2.01	0.42
33:C:119:ILE:O	33:C:123:LEU:HG	2.20	0.42
34:D:113:ALA:O	34:D:117:VAL:HG23	2.20	0.42
39:I:98:ARG:HH11	39:I:103:VAL:HG21	1.85	0.42
41:K:15:VAL:HG12	41:K:76:TYR:HB3	2.02	0.42
41:K:118:ASN:HD22	41:K:118:ASN:HA	1.61	0.42
52:03:31:LYS:HE2	52:03:31:LYS:CA	2.40	0.42
52:03:44:VAL:CG2	52:03:175:ILE:HG23	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1202:U:C2'	53:A:1203:C:H5'	2.49	0.42
54:01:2162:G:H2'	54:01:2163:A:C8	2.55	0.42
58:Y:3:C:O2'	58:Y:4:C:H5'	2.19	0.42
8:11:91:LYS:CG	8:11:94:LYS:HE2	2.50	0.42
13:16:2:ARG:HD2	54:01:2822:G:O6	2.20	0.42
16:19:80:ASN:HD22	16:19:116:LEU:CD1	2.32	0.42
27:30:8:THR:HG21	54:01:2020:A:C5'	2.50	0.42
34:D:31:CYS:SG	34:D:33:ILE:HB	2.60	0.42
35:E:25:LYS:HD2	53:A:1069:C:OP1	2.20	0.42
38:H:28:SER:HB2	38:H:58:LEU:HB2	2.01	0.42
39:I:78:ILE:O	39:I:82:ILE:HG13	2.19	0.42
53:A:556:C:O2'	53:A:557:G:H5'	2.19	0.42
53:A:744:C:H2'	53:A:745:G:H8	1.85	0.42
53:A:1456:A:H2'	53:A:1457:G:O4'	2.20	0.42
54:01:1186:G:H2'	54:01:1187:G:O4'	2.20	0.42
54:01:1417:C:H2'	54:01:1418:G:O4'	2.20	0.42
54:01:1447:C:H2'	54:01:1448:G:H8	1.84	0.42
54:01:1542:U:H2'	54:01:1543:G:O4'	2.18	0.42
54:01:2066:C:C2'	54:01:2067:G:H5'	2.50	0.42
54:01:2123:G:H2'	54:01:2124:G:C8	2.54	0.42
59:Z:16:THR:H	59:Z:78:HIS:CE1	2.37	0.42
59:Z:55:GLU:CG	59:Z:62:ILE:HG12	2.50	0.42
59:Z:145:LEU:HA	59:Z:148:LEU:HB3	2.01	0.42
10:13:22:ILE:HD11	10:13:40:LYS:HG3	2.02	0.42
20:23:66:VAL:O	20:23:69:VAL:HG22	2.20	0.42
25:28:35:VAL:HG22	25:28:37:ARG:NH1	2.35	0.42
25:28:52:PHE:CD2	55:02:83:G:H4'	2.55	0.42
27:30:39:ARG:HD3	54:01:2886:A:N1	2.34	0.42
30:33:24:LYS:HD3	30:33:46:LYS:HE3	2.02	0.42
32:B:162:VAL:HG12	32:B:163:ILE:N	2.35	0.42
32:B:162:VAL:HG21	32:B:172:ILE:HG12	2.02	0.42
33:C:86:LEU:HA	33:C:89:VAL:HG22	2.01	0.42
43:M:14:ALA:HB1	43:M:33:LEU:HD21	2.01	0.42
54:01:157:C:H2'	54:01:158:U:O4'	2.20	0.42
54:01:528:A:N1	54:01:2042:A:H2'	2.35	0.42
54:01:948:C:H2'	54:01:949:G:H8	1.84	0.42
54:01:2038:G:H2'	54:01:2039:U:O4'	2.20	0.42
56:W:6:G:C2'	56:W:7:G:H5'	2.49	0.42
58:Y:68:C:H2'	58:Y:69:G:H8	1.85	0.42
2:05:3:GLY:C	2:05:4:LEU:HD12	2.45	0.41
2:05:106:LYS:HD3	2:05:174:SER:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:135:GLN:HE22	54:01:7:G:H1'	1.85	0.41
11:14:78:ARG:NH2	54:01:626:A:N3	2.68	0.41
14:17:25:ARG:HH21	14:17:25:ARG:HG2	1.85	0.41
16:19:12:ARG:HH21	16:19:12:ARG:HG3	1.85	0.41
32:B:129:THR:HG22	32:B:130:LYS:N	2.35	0.41
34:D:1:ALA:HA	53:A:547:A:OP2	2.20	0.41
34:D:169:TRP:O	34:D:182:LYS:HB2	2.20	0.41
37:G:76:SER:HB3	56:X:33:U:H5''	2.01	0.41
37:G:87:PRO:HG3	37:G:148:LYS:HA	2.02	0.41
39:I:60:LEU:HD12	39:I:60:LEU:O	2.20	0.41
53:A:495:A:H4'	53:A:496:A:OP1	2.19	0.41
53:A:834:U:H2'	53:A:835:U:C6	2.55	0.41
53:A:1247:U:O2'	53:A:1248:A:H5'	2.20	0.41
54:01:37:C:O2'	54:01:38:A:H5'	2.19	0.41
54:01:917:A:H5''	54:01:2268:A:H61	1.85	0.41
54:01:940:G:H3'	54:01:941:A:H5''	2.02	0.41
54:01:2146:C:H4'	54:01:2147:A:C5	2.55	0.41
54:01:2412:A:H2'	54:01:2413:G:O4'	2.19	0.41
59:Z:235:ILE:HG22	59:Z:269:ARG:CB	2.50	0.41
59:Z:249:GLU:CD	59:Z:249:GLU:N	2.78	0.41
59:Z:302:THR:HG22	59:Z:362:LEU:HD11	2.02	0.41
3:06:44:ARG:NH2	54:01:1248:G:OP1	2.46	0.41
6:09:16:GLY:HA2	6:09:47:PHE:HE2	1.85	0.41
6:09:73:ASN:HB2	6:09:108:VAL:HG23	2.02	0.41
6:09:111:ALA:HB3	6:09:114:GLU:OE1	2.21	0.41
6:09:122:LEU:HD22	6:09:128:HIS:CG	2.55	0.41
23:26:33:HIS:HE1	54:01:2200:C:H4'	1.85	0.41
34:D:29:THR:O	34:D:29:THR:HG22	2.20	0.41
35:E:123:LEU:HD13	53:A:7:A:C8	2.54	0.41
36:F:18:VAL:HB	36:F:19:PRO:HD3	2.02	0.41
52:03:21:TYR:HD2	52:03:222:VAL:HG13	1.83	0.41
53:A:377:G:O2'	53:A:378:G:H5'	2.20	0.41
53:A:513:C:H2'	53:A:514:C:C6	2.55	0.41
53:A:1414:U:H2'	53:A:1415:G:H8	1.85	0.41
53:A:1446:A:O2'	53:A:1447:A:H5'	2.20	0.41
54:01:609:A:H2'	54:01:610:C:O4'	2.21	0.41
54:01:962:G:N2	54:01:2250:G:H1	2.12	0.41
54:01:1300:G:C4'	54:01:1301:A:H5'	2.38	0.41
54:01:1386:C:H2'	54:01:1387:A:H8	1.84	0.41
54:01:1577:C:H2'	54:01:1578:U:O4'	2.19	0.41
54:01:1775:U:H2'	54:01:1776:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:39:A:H2'	55:02:40:U:C6	2.55	0.41
59:Z:170:VAL:HG12	59:Z:171:ARG:O	2.20	0.41
59:Z:324:LYS:HD2	59:Z:343:LEU:H	1.85	0.41
1:04:131:MET:CE	1:04:187:CYS:HB2	2.49	0.41
1:04:270:ARG:CB	1:04:270:ARG:HH11	2.34	0.41
2:05:52:THR:HG22	2:05:80:TRP:HZ3	1.85	0.41
3:06:131:THR:HG22	3:06:160:ALA:O	2.20	0.41
11:14:91:ASP:CG	11:14:92:LEU:H	2.28	0.41
12:15:2:LEU:N	12:15:2:LEU:HD12	2.35	0.41
13:16:2:ARG:O	13:16:2:ARG:CD	2.69	0.41
18:21:97:LEU:HD12	18:21:97:LEU:N	2.36	0.41
28:31:39:ASP:HA	28:31:40:PRO:HD2	1.87	0.41
32:B:16:GLY:HA2	32:B:40:ILE:HG13	2.02	0.41
34:D:183:ARG:HG3	34:D:183:ARG:NH1	2.35	0.41
42:L:88:ASP:HB2	53:A:523:A:H61	1.85	0.41
53:A:381:C:H2'	53:A:382:A:O4'	2.20	0.41
53:A:396:C:C3'	53:A:397:A:H5''	2.50	0.41
53:A:580:C:H2'	53:A:581:G:O4'	2.21	0.41
53:A:763:G:H2'	53:A:764:C:C6	2.54	0.41
53:A:865:A:H5'	53:A:1078:U:O4	2.20	0.41
54:01:460:A:H2'	54:01:461:C:O4'	2.19	0.41
54:01:1548:A:H2'	54:01:1549:A:C8	2.54	0.41
54:01:2636:C:H2'	54:01:2637:U:C6	2.55	0.41
54:01:2860:A:H2'	54:01:2861:U:H5'	2.02	0.41
59:Z:305:GLU:N	59:Z:392:LEU:HD23	2.35	0.41
59:Z:337:VAL:CG1	59:Z:362:LEU:HD22	2.50	0.41
59:Z:364:HIS:HA	59:Z:365:PRO:HD2	1.83	0.41
2:05:77:ARG:HH21	2:05:77:ARG:HG3	1.85	0.41
2:05:192:ALA:HB1	54:01:2680:U:H1'	2.02	0.41
15:18:8:GLU:HG2	15:18:54:LEU:HD23	2.03	0.41
15:18:77:SER:HA	15:18:78:PRO:HD3	1.91	0.41
16:19:87:VAL:HG12	16:19:89:ILE:H	1.84	0.41
24:27:28:LEU:O	24:27:32:ALA:N	2.52	0.41
31:34:19:ARG:HG2	54:01:2756:U:OP2	2.20	0.41
33:C:61:LYS:O	33:C:97:PRO:HD2	2.20	0.41
34:D:69:ARG:CD	34:D:72:ARG:HH21	2.34	0.41
40:J:22:THR:HA	40:J:25:ILE:HG22	2.02	0.41
47:Q:18:LYS:HB2	47:Q:18:LYS:HZ3	1.86	0.41
49:S:10:ILE:C	49:S:10:ILE:HD12	2.45	0.41
53:A:67:C:H2'	53:A:68:G:H8	1.85	0.41
53:A:1255:G:O2'	53:A:1258:G:H1'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1300:G:C2'	53:A:1301:U:OP2	2.68	0.41
53:A:1493:A:O2'	57:V:19:U:H1'	2.21	0.41
53:A:1514:G:O2'	53:A:1515:G:H5'	2.20	0.41
54:01:854:C:O2'	54:01:855:G:H5'	2.21	0.41
54:01:1507:C:C2'	54:01:1508:A:H4'	2.51	0.41
54:01:2457:U:O2'	54:01:2458:G:H5'	2.20	0.41
58:Y:76:A:O2'	63:Y:101:PHE:C	2.62	0.41
59:Z:201:GLU:HA	59:Z:202:PRO:HD2	1.91	0.41
3:06:148:ILE:HD13	3:06:187:VAL:CG1	2.50	0.41
4:07:139:GLU:CD	4:07:139:GLU:N	2.77	0.41
6:09:1:MET:HB3	6:09:3:VAL:HG23	2.02	0.41
6:09:5:LEU:HD22	6:09:13:GLY:HA3	2.03	0.41
7:10:59:LEU:HB3	7:10:62:ARG:HB2	2.03	0.41
9:12:102:GLU:HG3	9:12:124:VAL:HG21	2.02	0.41
10:13:41:ILE:C	10:13:41:ILE:HD12	2.46	0.41
10:13:102:PRO:HB3	10:13:121:GLU:HB3	2.02	0.41
11:14:69:ARG:HG3	11:14:69:ARG:HH11	1.85	0.41
14:17:17:LYS:NZ	54:01:2380:C:H5'	2.35	0.41
32:B:30:ILE:C	32:B:30:ILE:HD12	2.45	0.41
32:B:94:ARG:CG	53:A:1100:C:OP2	2.69	0.41
33:C:41:TYR:HE2	33:C:89:VAL:HG21	1.85	0.41
33:C:137:VAL:HG13	33:C:148:ILE:HG23	2.03	0.41
38:H:12:ARG:CD	38:H:26:MET:HB3	2.51	0.41
39:I:37:TYR:HD2	39:I:38:PHE:HD1	1.68	0.41
39:I:123:ARG:HG3	39:I:123:ARG:NH2	2.35	0.41
40:J:86:ALA:O	40:J:90:LEU:HD12	2.21	0.41
41:K:111:ASP:OD1	41:K:113:THR:HG23	2.20	0.41
42:L:74:GLN:O	42:L:76:HIS:N	2.54	0.41
46:P:61:VAL:HG22	46:P:67:ILE:HD11	2.02	0.41
47:Q:13:SER:HB3	47:Q:21:VAL:CG1	2.49	0.41
54:01:182:A:O2'	54:01:183:C:H5'	2.21	0.41
54:01:1182:G:H2'	54:01:1183:U:O4'	2.21	0.41
54:01:1592:C:H2'	54:01:1593:A:C8	2.55	0.41
54:01:2128:G:H2'	54:01:2129:C:O4'	2.21	0.41
55:02:48:U:H2'	55:02:49:C:C6	2.54	0.41
59:Z:16:THR:N	59:Z:78:HIS:CE1	2.88	0.41
59:Z:136:LYS:HB3	59:Z:139:MET:CG	2.49	0.41
59:Z:146:LEU:HD12	59:Z:171:ARG:NH1	2.35	0.41
2:05:110:THR:HG21	2:05:169:ARG:HE	1.86	0.41
3:06:40:ARG:HD2	54:01:443:A:C5	2.56	0.41
3:06:121:VAL:HG22	3:06:188:MET:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:07:99:PHE:O	4:07:103:ILE:HG12	2.20	0.41
4:07:128:SER:O	54:01:2304:G:H4'	2.20	0.41
5:08:98:LYS:HZ2	5:08:103:ASN:HD22	1.68	0.41
6:09:124:THR:HG22	6:09:125:THR:N	2.35	0.41
10:13:29:HIS:O	10:13:29:HIS:ND1	2.54	0.41
15:18:50:ARG:NH2	15:18:52:ARG:NH1	2.69	0.41
32:B:60:ALA:CB	32:B:223:GLY:HA3	2.50	0.41
32:B:183:PHE:CD1	32:B:197:PHE:HB2	2.55	0.41
32:B:212:TYR:O	32:B:216:VAL:HG23	2.20	0.41
34:D:100:VAL:O	34:D:104:MET:HG2	2.21	0.41
34:D:129:VAL:HA	53:A:619:U:O2	2.21	0.41
41:K:126:ARG:HH22	53:A:692:U:H5''	1.83	0.41
46:P:68:SER:OG	46:P:71:VAL:HG23	2.21	0.41
47:Q:45:VAL:HG21	47:Q:60:ILE:HD13	2.03	0.41
52:03:38:PHE:CZ	52:03:217:THR:HG21	2.54	0.41
53:A:399:G:H2'	53:A:400:C:C6	2.56	0.41
53:A:1108:G:H2'	53:A:1109:C:H5'	2.03	0.41
54:01:1080:A:H2'	54:01:1081:U:O4'	2.21	0.41
54:01:1990:C:H2'	54:01:1991:U:O4'	2.20	0.41
54:01:2070:A:O2'	54:01:2071:A:H5'	2.20	0.41
54:01:2495:G:C2'	54:01:2496:C:H5'	2.50	0.41
54:01:2689:U:O2	54:01:2713:U:H5''	2.20	0.41
56:X:5:G:H2'	56:X:6:G:C8	2.56	0.41
59:Z:74:ARG:HH22	59:Z:200:PRO:CA	2.33	0.41
59:Z:149:VAL:HA	59:Z:152:GLU:CD	2.46	0.41
10:13:76:VAL:H	15:18:72:VAL:CG2	2.34	0.41
23:26:12:VAL:HG23	23:26:28:PHE:HB2	2.03	0.41
30:33:44:ARG:N	30:33:45:PRO:HD2	2.35	0.41
32:B:18:GLN:O	32:B:37:VAL:HG23	2.21	0.41
35:E:79:THR:OG1	35:E:80:LEU:N	2.54	0.41
37:G:39:GLU:HB3	37:G:43:TYR:CE2	2.56	0.41
38:H:104:SER:HB2	38:H:125:ILE:HD11	2.02	0.41
47:Q:30:HIS:HA	47:Q:31:PRO:HD3	1.92	0.41
47:Q:82:VAL:HG22	47:Q:82:VAL:OXT	2.21	0.41
52:03:170:ILE:N	52:03:170:ILE:CD1	2.72	0.41
53:A:107:G:H2'	53:A:108:G:O4'	2.21	0.41
53:A:171:A:H2'	53:A:172:A:C8	2.56	0.41
53:A:222:C:O2'	53:A:223:A:H5'	2.21	0.41
53:A:448:A:H3'	53:A:449:G:C8	2.56	0.41
53:A:748:G:H2'	53:A:749:A:H8	1.86	0.41
53:A:757:U:H2'	53:A:758:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1316:G:H2'	53:A:1317:C:H5''	2.03	0.41
54:01:358:U:H2'	54:01:359:G:O4'	2.20	0.41
54:01:542:C:H2'	54:01:543:G:C5'	2.51	0.41
54:01:2371:G:O2'	54:01:2372:U:H5'	2.20	0.41
59:Z:116:ARG:HD2	59:Z:160:TYR:CE2	2.55	0.41
59:Z:188:ILE:O	59:Z:191:LEU:HG	2.21	0.41
1:04:129:LEU:HD23	1:04:129:LEU:H	1.83	0.41
2:05:35:THR:HG22	2:05:73:VAL:HG21	2.03	0.41
3:06:163:ASN:ND2	54:01:323:C:H5''	2.36	0.41
5:08:138:GLN:HE22	54:01:2759:G:H21	1.67	0.41
7:10:59:LEU:HB3	7:10:62:ARG:HB3	2.03	0.41
12:15:3:GLN:HA	12:15:4:PRO:HD3	1.90	0.41
13:16:29:VAL:HG13	13:16:83:LEU:CD1	2.51	0.41
14:17:40:ILE:HG23	14:17:46:GLU:O	2.21	0.41
15:18:2:ASN:HA	15:18:5:LYS:HB3	2.03	0.41
15:18:20:ARG:HB3	15:18:21:PRO:HD2	2.03	0.41
34:D:16:THR:HG22	34:D:17:ASP:H	1.86	0.41
37:G:128:GLU:HG3	37:G:130:LYS:HE2	2.02	0.41
38:H:10:LEU:CD2	38:H:74:ILE:HD11	2.43	0.41
44:N:20:PHE:O	44:N:21:ALA:CB	2.68	0.41
52:03:6:LYS:O	52:03:10:VAL:HG23	2.21	0.41
53:A:244:U:C6	53:A:894:G:N2	2.89	0.41
53:A:280:C:HO2'	53:A:281:G:P	2.43	0.41
53:A:785:G:O2'	53:A:786:G:H5'	2.21	0.41
54:01:813:U:O2'	54:01:1225:G:H1'	2.21	0.41
54:01:2742:G:O2'	54:01:2743:U:H5'	2.20	0.41
59:Z:235:ILE:O	59:Z:236:ILE:HG23	2.21	0.41
59:Z:360:VAL:CG1	59:Z:361:THR:N	2.83	0.41
1:04:32:LEU:O	1:04:33:LEU:HD12	2.21	0.41
1:04:65:ASP:OD2	1:04:68:ARG:HD2	2.21	0.41
2:05:83:ARG:HG3	2:05:83:ARG:NH2	2.36	0.41
4:07:19:PHE:HB2	4:07:21:TYR:CZ	2.56	0.41
4:07:109:ARG:NH1	43:M:2:ARG:HH11	2.19	0.41
7:10:55:VAL:HA	54:01:1084:A:H5''	2.03	0.41
8:11:78:LEU:HA	8:11:81:LYS:HG2	2.03	0.41
9:12:4:PHE:CD2	16:19:99:VAL:HG11	2.56	0.41
10:13:7:MET:HE3	10:13:18:ARG:HG3	2.02	0.41
11:14:127:VAL:HG12	11:14:128:THR:N	2.36	0.41
12:15:5:LYS:O	12:15:6:ARG:HG3	2.20	0.41
14:17:38:GLN:HE21	14:17:40:ILE:HD11	1.86	0.41
16:19:74:SER:OG	16:19:77:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:28:9:THR:HG22	25:28:53:MET:C	2.46	0.41
30:33:63:TYR:CE2	54:01:242:G:H5''	2.56	0.41
31:34:27:CYS:SG	31:34:30:GLU:N	2.93	0.41
34:D:25:ARG:HD3	34:D:27:ILE:O	2.20	0.41
34:D:82:LYS:HG3	53:A:5:U:O4	2.20	0.41
35:E:105:ILE:CD1	35:E:123:LEU:HD23	2.51	0.41
36:F:9:MET:HE1	36:F:51:ILE:CD1	2.50	0.41
36:F:73:GLU:O	36:F:77:THR:HG23	2.21	0.41
37:G:41:ILE:HD11	53:A:1240:U:O4'	2.21	0.41
39:I:4:GLN:HA	39:I:21:LYS:HG2	2.01	0.41
40:J:15:HIS:HA	40:J:18:ILE:HG22	2.03	0.41
40:J:28:THR:O	40:J:28:THR:HG22	2.20	0.41
40:J:41:PRO:HB3	53:A:1151:A:H1'	2.01	0.41
40:J:57:VAL:CG2	40:J:58:ASN:H	2.31	0.41
41:K:27:ASN:HA	41:K:57:SER:OG	2.20	0.41
41:K:51:PHE:CE2	41:K:64:VAL:HG11	2.55	0.41
42:L:20:VAL:HG21	53:A:553:A:H5''	2.02	0.41
45:O:57:ARG:HG2	45:O:57:ARG:HH11	1.86	0.41
46:P:33:ILE:HD12	46:P:33:ILE:H	1.86	0.41
46:P:79:ASN:C	46:P:81:ALA:H	2.29	0.41
47:Q:39:ARG:HH11	47:Q:39:ARG:HG3	1.85	0.41
53:A:88:U:H2'	53:A:89:U:C6	2.56	0.41
53:A:350:G:H2'	53:A:351:G:C8	2.56	0.41
53:A:1199:U:H2'	53:A:1200:C:H5'	2.02	0.41
54:01:184:C:H2'	54:01:185:G:H8	1.86	0.41
54:01:214:G:O2'	54:01:215:G:H5'	2.21	0.41
54:01:1079:C:H2'	54:01:1080:A:O4'	2.20	0.41
54:01:1116:G:O2'	54:01:1117:C:H5'	2.20	0.41
54:01:1268:A:H2'	54:01:1269:A:O4'	2.20	0.41
54:01:1431:A:O2'	54:01:1432:G:H5'	2.21	0.41
54:01:1794:A:H2'	54:01:1795:C:C6	2.55	0.41
54:01:2637:U:H2'	54:01:2638:G:O4'	2.20	0.41
56:W:69:C:H2'	56:W:70:G:C8	2.56	0.41
59:Z:333:ARG:O	59:Z:334:THR:HG23	2.20	0.41
59:Z:362:LEU:HD13	59:Z:364:HIS:N	2.29	0.41
1:04:120:ASP:HB2	6:09:91:PHE:HE1	1.86	0.41
3:06:40:ARG:HD2	54:01:443:A:C6	2.55	0.41
8:11:56:VAL:CG2	8:11:57:VAL:N	2.79	0.41
15:18:21:PRO:HD3	15:18:49:ILE:HD12	2.03	0.41
21:24:75:GLN:CB	21:24:92:VAL:HG23	2.38	0.41
32:B:42:LEU:O	32:B:46:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:C:4:VAL:HG22	33:C:5:HIS:N	2.35	0.41
34:D:191:SER:O	34:D:192:ALA:HB3	2.21	0.41
38:H:40:LYS:HG3	38:H:47:ASP:HA	2.03	0.41
39:I:65:THR:HG21	53:A:1130:A:OP1	2.21	0.41
39:I:70:GLY:HA3	53:A:1371:G:O3'	2.20	0.41
52:O3:45:ALA:HB3	52:O3:213:SER:OG	2.21	0.41
53:A:147:G:H2'	53:A:148:G:C8	2.56	0.41
53:A:1015:G:O2'	53:A:1016:A:H5'	2.21	0.41
53:A:1251:A:O2'	53:A:1370:G:H5'	2.21	0.41
54:O1:662:G:O2'	54:O1:663:G:H5'	2.20	0.41
54:O1:871:U:H2'	54:O1:872:U:C6	2.55	0.41
54:O1:940:G:H2'	54:O1:941:A:C4'	2.51	0.41
54:O1:1685:C:H2'	54:O1:1686:C:C6	2.56	0.41
54:O1:2241:A:O2'	54:O1:2242:G:H5'	2.21	0.41
54:O1:2646:C:H2'	54:O1:2647:U:O4'	2.21	0.41
59:Z:9:LYS:HB2	59:Z:75:HIS:HB2	2.03	0.41
59:Z:44:ARG:HD3	59:Z:44:ARG:HA	1.95	0.41
59:Z:135:ASN:HD21	59:Z:174:ALA:HB3	1.86	0.41
2:O5:11:MET:HE3	2:O5:191:GLY:O	2.22	0.40
2:O5:149:ASN:CG	2:O5:150:GLN:H	2.28	0.40
3:O6:48:THR:O	3:O6:52:VAL:HG23	2.21	0.40
3:O6:130:LYS:HA	54:O1:321:U:OP2	2.21	0.40
3:O6:149:ILE:HG23	3:O6:188:MET:HG2	2.03	0.40
7:10:38:MET:O	7:10:42:ARG:HB2	2.20	0.40
8:11:7:TYR:HA	8:11:58:ILE:O	2.20	0.40
9:12:115:GLY:HA2	9:12:118:MET:HG2	2.03	0.40
36:F:22:ILE:O	36:F:26:THR:HG22	2.21	0.40
36:F:78:PHE:HD1	36:F:78:PHE:HA	1.81	0.40
37:G:56:SER:H	37:G:59:GLU:CG	2.34	0.40
43:M:3:ILE:HD11	43:M:21:ILE:HD11	2.03	0.40
46:P:25:ARG:CB	46:P:25:ARG:HH11	2.33	0.40
50:T:6:ALA:C	50:T:8:LYS:H	2.28	0.40
52:O3:170:ILE:HG22	52:O3:172:HIS:CE1	2.56	0.40
53:A:1263:C:H2'	53:A:1264:U:C6	2.56	0.40
53:A:1432:G:H2'	53:A:1433:A:OP2	2.21	0.40
54:O1:217:A:H2'	54:O1:218:A:O4'	2.20	0.40
54:O1:355:U:H2'	54:O1:356:G:H8	1.86	0.40
54:O1:753:A:O2'	54:O1:754:U:H5'	2.21	0.40
54:O1:1280:G:O2'	54:O1:1281:G:H5'	2.21	0.40
54:O1:1962:C:O2'	54:O1:1964:G:OP2	2.39	0.40
56:X:23:C:H2'	56:X:24:U:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:256:THR:OG1	59:Z:277:LEU:HG	2.20	0.40
59:Z:304:PHE:HA	59:Z:392:LEU:H	1.86	0.40
2:05:115:GLY:N	54:01:2821:A:OP2	2.51	0.40
5:08:140:ILE:HD12	5:08:140:ILE:C	2.44	0.40
6:09:81:ALA:HB1	6:09:149:GLU:HB2	2.03	0.40
7:10:7:ASP:O	7:10:11:ILE:HG12	2.22	0.40
9:12:81:ILE:CG2	9:12:82:GLY:N	2.85	0.40
10:13:12:ASP:HB2	10:13:96:GLY:HA3	2.02	0.40
12:15:35:ALA:HB1	12:15:126:ILE:HD12	2.03	0.40
19:22:92:ASN:O	19:22:93:LEU:HG	2.21	0.40
32:B:55:GLU:O	32:B:59:ILE:HG12	2.21	0.40
34:D:146:GLU:HA	34:D:149:LYS:HE2	2.03	0.40
45:O:86:LEU:C	45:O:86:LEU:HD12	2.47	0.40
49:S:17:LYS:HG2	49:S:30:LEU:HD23	2.03	0.40
52:03:10:VAL:HG12	52:03:14:LYS:HE2	2.02	0.40
52:03:23:ILE:C	52:03:186:LYS:HE2	2.46	0.40
53:A:651:C:H2'	53:A:652:U:C6	2.56	0.40
54:01:44:A:H2'	54:01:45:G:O4'	2.22	0.40
54:01:861:A:H2'	54:01:862:G:O4'	2.21	0.40
54:01:1295:C:H2'	54:01:1296:G:H8	1.85	0.40
54:01:1739:A:H2'	54:01:1740:G:O4'	2.21	0.40
55:02:28:C:H2'	55:02:29:A:C8	2.56	0.40
59:Z:242:VAL:CG2	59:Z:292:LEU:HD11	2.50	0.40
1:04:216:ARG:NH2	54:01:781:A:OP1	2.55	0.40
2:05:25:THR:HG21	2:05:193:VAL:CG2	2.51	0.40
3:06:181:ILE:HD13	11:14:6:LEU:HD11	2.03	0.40
7:10:29:ASP:H	7:10:56:ARG:NH2	2.19	0.40
10:13:104:THR:HG22	10:13:105:ARG:N	2.36	0.40
11:14:29:LYS:O	11:14:30:THR:OG1	2.22	0.40
11:14:85:VAL:O	11:14:86:GLU:HB2	2.21	0.40
15:18:3:ILE:H	15:18:3:ILE:CD1	2.32	0.40
16:19:105:PHE:O	16:19:109:VAL:HG23	2.21	0.40
32:B:91:VAL:HG11	32:B:95:TRP:CD1	2.56	0.40
33:C:87:ARG:HG3	33:C:87:ARG:NH1	2.36	0.40
34:D:124:VAL:HG13	34:D:124:VAL:O	2.21	0.40
35:E:104:ILE:O	35:E:111:ARG:NH1	2.55	0.40
37:G:99:ALA:O	37:G:103:ILE:HG13	2.22	0.40
38:H:29:SER:HB3	38:H:32:LYS:CG	2.42	0.40
39:I:90:ASP:C	39:I:92:SER:N	2.78	0.40
41:K:123:PRO:HG2	51:U:33:ARG:HB3	2.03	0.40
43:M:48:SER:O	43:M:52:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S:5:LYS:HG3	49:S:6:LYS:N	2.36	0.40
52:03:201:PRO:HB2	52:03:204:ALA:HB2	2.02	0.40
53:A:1222:G:C2'	53:A:1223:C:H5'	2.51	0.40
54:01:566:U:O2'	54:01:567:U:H5'	2.20	0.40
54:01:677:A:O2'	54:01:2071:A:H5'	2.21	0.40
54:01:813:U:H2'	54:01:814:C:C6	2.56	0.40
54:01:833:A:H2'	54:01:834:G:C8	2.56	0.40
54:01:1893:C:C2'	54:01:1894:C:H5'	2.50	0.40
54:01:1956:U:C2'	54:01:1957:C:H5'	2.51	0.40
54:01:2116:G:H1	54:01:2171:A:N6	2.19	0.40
59:Z:19:HIS:O	59:Z:24:LYS:NZ	2.54	0.40
59:Z:311:LEU:HD23	59:Z:311:LEU:N	2.34	0.40
1:04:121:ALA:HB1	1:04:127:ASN:HB3	2.04	0.40
1:04:131:MET:HG3	1:04:187:CYS:O	2.22	0.40
1:04:270:ARG:HH11	1:04:270:ARG:HB2	1.86	0.40
2:05:6:GLY:HA3	2:05:29:VAL:HG22	2.03	0.40
11:14:67:THR:HG21	54:01:244:A:H5''	2.03	0.40
11:14:77:ILE:CD1	11:14:108:ALA:HB1	2.52	0.40
15:18:3:ILE:N	15:18:3:ILE:CD1	2.84	0.40
16:19:95:ALA:O	16:19:99:VAL:HG23	2.21	0.40
19:22:39:THR:OG1	19:22:42:GLU:HG3	2.22	0.40
28:31:47:ILE:H	28:31:47:ILE:CD1	2.35	0.40
32:B:16:GLY:HA3	32:B:39:ILE:HA	2.04	0.40
35:E:55:VAL:N	35:E:56:PRO:HD2	2.36	0.40
36:F:67:PRO:HG2	36:F:70:VAL:HB	2.03	0.40
36:F:68:GLN:HA	36:F:71:ILE:HG22	2.04	0.40
38:H:79:ARG:HB2	38:H:80:PRO:HD2	2.03	0.40
39:I:44:ARG:HD2	39:I:44:ARG:N	2.25	0.40
40:J:8:ILE:HG21	40:J:25:ILE:HD11	2.02	0.40
44:N:83:VAL:HG13	44:N:84:ARG:N	2.36	0.40
47:Q:18:LYS:HG2	47:Q:18:LYS:O	2.20	0.40
48:R:12:PHE:C	48:R:14:ALA:H	2.30	0.40
52:03:41:SER:HB2	52:03:177:LYS:CE	2.47	0.40
53:A:1496:C:H2'	53:A:1497:G:O4'	2.20	0.40
54:01:179:C:O2'	54:01:180:G:H5'	2.21	0.40
54:01:310:A:O2'	54:01:311:A:H2'	2.21	0.40
54:01:468:G:H2'	54:01:469:G:O4'	2.21	0.40
54:01:818:G:H5'	54:01:839:U:OP1	2.21	0.40
54:01:1285:A:H2'	54:01:1286:A:H5'	2.03	0.40
54:01:1414:C:H2'	54:01:1415:U:O4'	2.20	0.40
54:01:1447:C:H2'	54:01:1448:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1571:A:H2'	54:01:1572:A:C8	2.57	0.40
54:01:2619:C:O2'	54:01:2620:C:H5'	2.22	0.40
59:Z:86:ASP:OD2	59:Z:87:TYR:CE2	2.74	0.40
59:Z:211:LEU:HD13	59:Z:298:ILE:HD12	2.03	0.40
2:05:49:GLN:HE22	2:05:79:LEU:HD13	1.86	0.40
2:05:61:THR:HB	2:05:63:PRO:HD2	2.03	0.40
9:12:95:ARG:HG3	9:12:95:ARG:HH11	1.86	0.40
10:13:87:LEU:HD23	10:13:94:PRO:HA	2.04	0.40
14:17:30:ARG:HH11	14:17:102:ARG:HH11	1.69	0.40
16:19:97:ILE:HD13	17:20:40:MET:HE1	2.03	0.40
18:21:107:VAL:O	18:21:107:VAL:HG13	2.22	0.40
19:22:44:LYS:HG3	19:22:55:VAL:HB	2.02	0.40
32:B:16:GLY:HA2	32:B:40:ILE:H	1.85	0.40
32:B:80:LYS:HG3	32:B:90:PHE:CZ	2.56	0.40
34:D:80:ARG:HH21	53:A:613:C:P	2.45	0.40
36:F:88:MET:HE2	36:F:90:MET:HE2	2.03	0.40
37:G:69:ARG:CG	37:G:95:ARG:HG2	2.52	0.40
38:H:45:ILE:HD13	38:H:60:LEU:HD13	2.03	0.40
38:H:76:ARG:NH1	38:H:125:ILE:HG23	2.36	0.40
42:L:3:VAL:O	42:L:7:VAL:HG23	2.21	0.40
43:M:10:ASP:O	43:M:11:HIS:HB2	2.22	0.40
44:N:20:PHE:HD2	44:N:54:SER:O	2.03	0.40
52:03:183:ASP:O	52:03:186:LYS:HB3	2.20	0.40
53:A:300:A:H1'	53:A:565:U:O2	2.22	0.40
53:A:591:U:H2'	53:A:592:G:C8	2.56	0.40
54:01:1112:G:O2'	54:01:1113:U:H5'	2.22	0.40
54:01:2108:A:H2'	54:01:2109:U:H5'	2.03	0.40
59:Z:125:VAL:CG1	59:Z:127:VAL:HG23	2.51	0.40
59:Z:137:CYS:HB2	59:Z:184:TRP:HZ3	1.86	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%)	24 (9%)	4 (2%)	8	37
2	05	207/209 (99%)	191 (92%)	15 (7%)	1 (0%)	24	59
3	06	199/201 (99%)	179 (90%)	19 (10%)	1 (0%)	24	59
4	07	175/177 (99%)	156 (89%)	18 (10%)	1 (1%)	21	56
5	08	174/176 (99%)	155 (89%)	15 (9%)	4 (2%)	5	29
6	09	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	9	39
7	10	129/131 (98%)	90 (70%)	32 (25%)	7 (5%)	1	12
8	11	139/141 (99%)	113 (81%)	19 (14%)	7 (5%)	1	13
9	12	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
10	13	120/122 (98%)	99 (82%)	19 (16%)	2 (2%)	7	35
11	14	141/143 (99%)	120 (85%)	14 (10%)	7 (5%)	1	13
12	15	134/136 (98%)	118 (88%)	13 (10%)	3 (2%)	5	29
13	16	118/120 (98%)	104 (88%)	12 (10%)	2 (2%)	7	35
14	17	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
15	18	112/114 (98%)	103 (92%)	8 (7%)	1 (1%)	14	47
16	19	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
17	20	101/103 (98%)	87 (86%)	13 (13%)	1 (1%)	12	45
18	21	108/110 (98%)	97 (90%)	8 (7%)	3 (3%)	4	25
19	22	91/93 (98%)	76 (84%)	15 (16%)	0	100	100
20	23	100/102 (98%)	79 (79%)	17 (17%)	4 (4%)	2	17
21	24	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	25	73/75 (97%)	62 (85%)	11 (15%)	0	100	100
23	26	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	27	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	36
25	28	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
26	29	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
27	30	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	31	48/50 (96%)	43 (90%)	3 (6%)	2 (4%)	2	16
29	32	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
30	33	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	36
31	34	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	25
32	B	216/218 (99%)	181 (84%)	30 (14%)	5 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	C	204/206 (99%)	188 (92%)	15 (7%)	1 (0%)	24	59
34	D	203/205 (99%)	172 (85%)	26 (13%)	5 (2%)	4	27
35	E	155/157 (99%)	122 (79%)	26 (17%)	7 (4%)	2	15
36	F	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	3	22
37	G	149/151 (99%)	131 (88%)	18 (12%)	0	100	100
38	H	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	16	50
39	I	125/127 (98%)	102 (82%)	17 (14%)	6 (5%)	2	14
40	J	96/98 (98%)	76 (79%)	14 (15%)	6 (6%)	1	8
41	K	114/116 (98%)	94 (82%)	16 (14%)	4 (4%)	3	20
42	L	121/123 (98%)	98 (81%)	18 (15%)	5 (4%)	2	17
43	M	112/114 (98%)	97 (87%)	12 (11%)	3 (3%)	4	25
44	N	98/100 (98%)	78 (80%)	18 (18%)	2 (2%)	6	31
45	O	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	42
46	P	80/82 (98%)	67 (84%)	9 (11%)	4 (5%)	1	13
47	Q	78/80 (98%)	63 (81%)	11 (14%)	4 (5%)	1	13
48	R	63/65 (97%)	54 (86%)	7 (11%)	2 (3%)	3	21
49	S	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	4	26
50	T	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	42
51	U	63/65 (97%)	43 (68%)	17 (27%)	3 (5%)	2	14
52	03	130/223 (58%)	114 (88%)	14 (11%)	2 (2%)	8	37
59	Z	390/392 (100%)	328 (84%)	54 (14%)	8 (2%)	5	31
All	All	6366/6563 (97%)	5507 (86%)	729 (12%)	130 (2%)	8	31

All (130) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	04	232	GLY
3	06	83	VAL
5	08	45	ALA
5	08	119	GLY
7	10	81	LEU
7	10	108	VAL
7	10	118	ILE
8	11	13	ALA
10	13	92	GLU

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Mol	Chain	Res	Type
12	15	58	LYS
17	20	54	VAL
18	21	63	GLY
20	23	6	ARG
24	27	24	GLU
28	31	45	HIS
31	34	37	GLN
32	B	13	VAL
34	D	152	SER
36	F	40	GLU
36	F	53	LYS
36	F	99	ALA
38	H	47	ASP
39	I	57	VAL
40	J	34	ALA
40	J	58	ASN
41	K	125	LYS
42	L	101	LEU
43	M	65	GLU
45	O	46	LYS
46	P	79	ASN
47	Q	49	ASN
48	R	13	THR
59	Z	85	ALA
59	Z	161	ASP
59	Z	317	GLY
1	04	240	GLY
5	08	175	LYS
6	09	41	LYS
7	10	55	VAL
7	10	58	THR
7	10	78	GLY
11	14	29	LYS
11	14	31	GLY
11	14	36	LYS
11	14	86	GLU
15	18	113	LEU
18	21	64	ALA
20	23	97	SER
20	23	98	ASN
30	33	31	ILE
32	B	12	GLY

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Mol	Chain	Res	Type
33	C	126	ARG
34	D	29	THR
34	D	191	SER
35	E	122	VAL
39	I	91	GLU
39	I	102	PHE
40	J	42	LEU
41	K	89	GLY
42	L	75	GLU
43	M	4	ALA
44	N	3	GLN
46	P	43	ALA
47	Q	15	LYS
47	Q	17	GLU
48	R	17	VAL
51	U	8	ASN
59	Z	356	ILE
1	04	233	GLY
7	10	119	PRO
8	11	11	GLN
18	21	11	ARG
20	23	88	ASP
34	D	167	PRO
35	E	89	THR
35	E	99	SER
35	E	121	ASN
39	I	90	ASP
40	J	33	GLY
40	J	92	LEU
41	K	13	LYS
42	L	3	VAL
42	L	102	ASP
43	M	7	ASN
46	P	44	SER
49	S	4	LEU
51	U	14	ALA
59	Z	42	ALA
59	Z	270	ALA
2	05	148	GLN
5	08	117	PRO
6	09	89	LYS
8	11	89	SER

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Mol	Chain	Res	Type
11	14	85	VAL
13	16	117	ASP
32	B	19	THR
32	B	150	ILE
35	E	23	THR
35	E	90	GLY
39	I	107	ALA
46	P	8	ARG
47	Q	79	GLU
52	03	34	ALA
1	04	254	LYS
4	07	174	PHE
10	13	93	GLN
11	14	94	THR
12	15	6	ARG
12	15	69	PRO
32	B	73	ARG
39	I	100	ALA
42	L	27	PRO
52	03	210	LYS
59	Z	357	LYS
8	11	22	PRO
50	T	67	HIS
34	D	23	GLY
41	K	88	PRO
49	S	53	GLY
51	U	9	GLU
8	11	92	PRO
28	31	40	PRO
8	11	90	GLY
40	J	43	PRO
59	Z	128	PRO
11	14	16	GLY
13	16	109	PRO
8	11	74	PRO
35	E	50	GLY
44	N	33	VAL

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	04	216/216 (100%)	215 (100%)	1 (0%)	81	85
2	05	164/164 (100%)	164 (100%)	0	100	100
3	06	165/165 (100%)	164 (99%)	1 (1%)	78	84
4	07	148/148 (100%)	146 (99%)	2 (1%)	59	77
5	08	137/137 (100%)	137 (100%)	0	100	100
6	09	114/114 (100%)	114 (100%)	0	100	100
7	10	100/100 (100%)	98 (98%)	2 (2%)	48	72
8	11	109/109 (100%)	109 (100%)	0	100	100
9	12	116/116 (100%)	113 (97%)	3 (3%)	40	69
10	13	103/103 (100%)	103 (100%)	0	100	100
11	14	102/102 (100%)	100 (98%)	2 (2%)	48	72
12	15	109/109 (100%)	108 (99%)	1 (1%)	70	81
13	16	100/100 (100%)	100 (100%)	0	100	100
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	97 (98%)	2 (2%)	48	72
16	19	89/89 (100%)	89 (100%)	0	100	100
17	20	84/84 (100%)	84 (100%)	0	100	100
18	21	93/93 (100%)	92 (99%)	1 (1%)	65	79
19	22	80/80 (100%)	79 (99%)	1 (1%)	61	78
20	23	83/83 (100%)	81 (98%)	2 (2%)	43	70
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%)	55 (100%)	0	100	100
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	57 (97%)	2 (3%)	32	64
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	44 (98%)	1 (2%)	45	71
29	32	38/38 (100%)	37 (97%)	1 (3%)	40	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	32 (94%)	2 (6%)	18	50
32	B	180/180 (100%)	178 (99%)	2 (1%)	65	79
33	C	170/170 (100%)	169 (99%)	1 (1%)	78	84
34	D	172/172 (100%)	169 (98%)	3 (2%)	53	75
35	E	119/119 (100%)	118 (99%)	1 (1%)	73	82
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%)	103 (99%)	1 (1%)	68	80
39	I	105/105 (100%)	104 (99%)	1 (1%)	68	80
40	J	86/86 (100%)	86 (100%)	0	100	100
41	K	89/89 (100%)	87 (98%)	2 (2%)	45	71
42	L	103/103 (100%)	103 (100%)	0	100	100
43	M	92/92 (100%)	91 (99%)	1 (1%)	65	79
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%)	64 (98%)	1 (2%)	57	76
47	Q	74/74 (100%)	73 (99%)	1 (1%)	59	77
48	R	56/56 (100%)	56 (100%)	0	100	100
49	S	70/70 (100%)	69 (99%)	1 (1%)	59	77
50	T	65/65 (100%)	65 (100%)	0	100	100
51	U	55/55 (100%)	54 (98%)	1 (2%)	51	74
52	03	110/174 (63%)	107 (97%)	3 (3%)	39	68
59	Z	324/325 (100%)	305 (94%)	19 (6%)	18	50
All	All	5285/5350 (99%)	5223 (99%)	62 (1%)	61	79

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	04	252	LYS
3	06	7	ASP
4	07	91	ARG
4	07	140	ILE
7	10	118	ILE

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Mol	Chain	Res	Type
7	10	119	PRO
9	12	57	LEU
9	12	81	ILE
9	12	101	ILE
11	14	96	LYS
11	14	111	ILE
12	15	70	ASP
15	18	3	ILE
15	18	50	ARG
18	21	62	ASP
19	22	32	LEU
20	23	4	ILE
20	23	82	VAL
26	29	16	CYS
26	29	40	CYS
28	31	45	HIS
29	32	1	MET
31	34	11	CYS
31	34	15	LYS
32	B	17	HIS
32	B	18	GLN
33	C	78	LYS
34	D	131	ILE
34	D	183	ARG
34	D	191	SER
35	E	133	ILE
38	H	59	GLU
39	I	103	VAL
41	K	12	ARG
41	K	30	ILE
43	M	8	ILE
46	P	67	ILE
47	Q	18	LYS
49	S	17	LYS
51	U	32	ARG
52	03	20	GLN
52	03	24	ASN
52	03	170	ILE
59	Z	20	VAL
59	Z	25	THR
59	Z	44	ARG
59	Z	53	PRO

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Mol	Chain	Res	Type
59	Z	97	GLN
59	Z	134	LEU
59	Z	151	MET
59	Z	156	LEU
59	Z	183	GLU
59	Z	191	LEU
59	Z	236	ILE
59	Z	237	LYS
59	Z	247	ILE
59	Z	263	LYS
59	Z	292	LEU
59	Z	308	VAL
59	Z	328	PRO
59	Z	332	PHE
59	Z	356	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (124) such sidechains are listed below:

Mol	Chain	Res	Type
1	04	20	ASN
1	04	24	HIS
1	04	36	ASN
1	04	44	ASN
1	04	52	HIS
1	04	85	ASN
1	04	116	GLN
1	04	127	ASN
1	04	162	GLN
1	04	196	ASN
1	04	238	ASN
2	05	49	GLN
2	05	67	HIS
2	05	94	GLN
2	05	173	GLN
3	06	90	GLN
3	06	94	GLN
3	06	97	ASN
3	06	163	ASN
3	06	195	GLN
4	07	51	ASN
5	08	21	GLN
5	08	72	ASN

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Mol	Chain	Res	Type
5	08	103	ASN
5	08	138	GLN
6	09	43	ASN
6	09	66	ASN
6	09	73	ASN
6	09	128	HIS
6	09	133	GLN
7	10	103	ASN
7	10	122	GLN
8	11	30	GLN
9	12	40	HIS
9	12	58	ASN
11	14	4	ASN
11	14	38	GLN
12	15	3	GLN
12	15	13	HIS
12	15	22	GLN
12	15	45	GLN
13	16	3	HIS
13	16	62	ASN
13	16	81	ASN
13	16	107	ASN
14	17	38	GLN
15	18	2	ASN
15	18	11	GLN
15	18	51	ASN
15	18	55	HIS
16	19	19	GLN
16	19	43	GLN
17	20	12	HIS
17	20	18	GLN
19	22	15	HIS
19	22	28	ASN
19	22	59	ASN
20	23	65	GLN
20	23	68	ASN
20	23	73	ASN
21	24	24	ASN
21	24	49	ASN
23	26	15	ASN
23	26	16	ASN
24	27	41	HIS

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Mol	Chain	Res	Type
27	30	3	GLN
27	30	5	ASN
30	33	27	ASN
32	B	17	HIS
32	B	35	ASN
32	B	102	ASN
32	B	176	ASN
32	B	202	ASN
33	C	2	GLN
33	C	31	ASN
33	C	40	GLN
33	C	122	GLN
33	C	139	ASN
34	D	73	ASN
34	D	125	ASN
35	E	81	GLN
35	E	134	ASN
36	F	11	HIS
36	F	17	GLN
36	F	55	HIS
37	G	129	ASN
37	G	147	ASN
38	H	66	GLN
40	J	58	ASN
41	K	14	GLN
41	K	118	ASN
42	L	4	ASN
42	L	45	ASN
43	M	7	ASN
44	N	3	GLN
44	N	42	ASN
44	N	59	GLN
44	N	65	GLN
45	O	36	ASN
45	O	41	HIS
45	O	49	HIS
46	P	26	ASN
47	Q	8	GLN
48	R	51	GLN
48	R	53	GLN
49	S	51	HIS
49	S	68	HIS

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Mol	Chain	Res	Type
50	T	20	ASN
50	T	47	GLN
50	T	51	ASN
50	T	69	ASN
50	T	83	ASN
52	03	24	ASN
52	03	58	ASN
52	03	168	ASN
59	Z	22	HIS
59	Z	63	ASN
59	Z	90	ASN
59	Z	114	GLN
59	Z	118	HIS
59	Z	124	GLN
59	Z	301	HIS
59	Z	319	HIS
59	Z	364	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	147 (9%)	8 (0%)
54	01	2902/2903 (99%)	359 (12%)	22 (0%)
55	02	119/120 (99%)	11 (9%)	1 (0%)
56	W	76/77 (98%)	7 (9%)	0
56	X	76/77 (98%)	18 (23%)	0
57	V	17/18 (94%)	2 (11%)	0
58	Y	75/76 (98%)	12 (16%)	1 (1%)
All	All	4803/4810 (99%)	556 (11%)	32 (0%)

All (556) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	9	G
53	A	22	G
53	A	31	G
53	A	32	A
53	A	39	G
53	A	48	C
53	A	51	A

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Mol	Chain	Res	Type
53	A	71	A
53	A	85	U
53	A	87	C
53	A	95	C
53	A	100	G
53	A	144	G
53	A	183	C
53	A	184	G
53	A	197	A
53	A	210	C
53	A	211	G
53	A	226	G
53	A	247	G
53	A	251	G
53	A	266	G
53	A	267	C
53	A	281	G
53	A	289	G
53	A	328	C
53	A	345	C
53	A	352	C
53	A	355	C
53	A	367	U
53	A	372	C
53	A	411	A
53	A	412	A
53	A	413	G
53	A	422	C
53	A	429	U
53	A	439	U
53	A	467	U
53	A	479	U
53	A	484	G
53	A	485	U
53	A	486	U
53	A	496	A
53	A	518	C
53	A	531	U
53	A	533	A
53	A	547	A
53	A	561	U
53	A	564	C

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Mol	Chain	Res	Type
53	A	572	A
53	A	573	A
53	A	575	G
53	A	576	C
53	A	577	G
53	A	633	G
53	A	642	A
53	A	665	A
53	A	688	G
53	A	703	G
53	A	724	G
53	A	755	G
53	A	777	A
53	A	794	A
53	A	815	A
53	A	817	C
53	A	818	G
53	A	819	A
53	A	821	G
53	A	842	U
53	A	843	U
53	A	844	G
53	A	846	G
53	A	871	U
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	1004	A
53	A	1020	G
53	A	1027	C
53	A	1030	U

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Mol	Chain	Res	Type
53	A	1031	C
53	A	1033	G
53	A	1034	G
53	A	1053	G
53	A	1094	G
53	A	1101	A
53	A	1130	A
53	A	1136	C
53	A	1137	C
53	A	1138	G
53	A	1139	G
53	A	1159	U
53	A	1168	U
53	A	1182	G
53	A	1184	G
53	A	1191	A
53	A	1196	A
53	A	1198	G
53	A	1201	A
53	A	1202	U
53	A	1225	A
53	A	1227	A
53	A	1238	A
53	A	1240	U
53	A	1241	G
53	A	1253	G
53	A	1257	A
53	A	1258	G
53	A	1260	G
53	A	1275	A
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	1317	C
53	A	1346	A
53	A	1347	G
53	A	1363	A
53	A	1381	U
53	A	1395	C

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Mol	Chain	Res	Type
53	A	1419	G
53	A	1446	A
53	A	1448	C
53	A	1452	C
53	A	1492	A
53	A	1502	A
53	A	1503	A
53	A	1506	U
53	A	1517	G
53	A	1529	G
53	A	1530	G
53	A	1533	C
53	A	1540	U
54	01	10	A
54	01	12	U
54	01	34	U
54	01	35	G
54	01	46	G
54	01	50	U
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	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	219	A
54	01	221	A
54	01	222	A
54	01	228	C
54	01	229	C
54	01	233	A
54	01	248	G
54	01	249	C

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Mol	Chain	Res	Type
54	01	255	A
54	01	266	G
54	01	276	U
54	01	281	C
54	01	294	A
54	01	301	G
54	01	311	A
54	01	312	G
54	01	323	C
54	01	324	A
54	01	329	G
54	01	330	A
54	01	353	C
54	01	361	G
54	01	371	A
54	01	372	G
54	01	373	U
54	01	386	G
54	01	387	U
54	01	404	A
54	01	406	G
54	01	411	G
54	01	422	A
54	01	424	G
54	01	457	A
54	01	458	G
54	01	481	G
54	01	491	G
54	01	504	A
54	01	505	A
54	01	529	A
54	01	530	G
54	01	531	C
54	01	532	A
54	01	543	G
54	01	545	U
54	01	547	A
54	01	563	A
54	01	573	U
54	01	574	A
54	01	575	A
54	01	588	U

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Mol	Chain	Res	Type
54	01	603	A
54	01	614	A
54	01	616	A
54	01	627	A
54	01	637	A
54	01	645	C
54	01	646	U
54	01	654	A
54	01	655	A
54	01	669	G
54	01	686	U
54	01	687	C
54	01	695	G
54	01	730	A
54	01	747	C
54	01	748	G
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	802	A
54	01	805	G
54	01	812	C
54	01	819	A
54	01	822	G
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	887	U
54	01	888	C
54	01	896	A
54	01	897	C

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Mol	Chain	Res	Type
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	983	A
54	01	990	A
54	01	995	C
54	01	996	A
54	01	1009	A
54	01	1012	U
54	01	1013	C
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	1061	U
54	01	1062	G
54	01	1065	U
54	01	1066	U
54	01	1069	A
54	01	1070	A
54	01	1071	G
54	01	1078	U
54	01	1079	C
54	01	1084	A
54	01	1088	A
54	01	1104	C
54	01	1106	G
54	01	1111	A
54	01	1131	G
54	01	1132	U
54	01	1135	C
54	01	1143	A
54	01	1174	U
54	01	1175	A

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Mol	Chain	Res	Type
54	01	1176	U
54	01	1177	G
54	01	1178	C
54	01	1180	U
54	01	1212	G
54	01	1238	G
54	01	1250	G
54	01	1251	C
54	01	1253	A
54	01	1256	G
54	01	1271	G
54	01	1272	A
54	01	1275	A
54	01	1300	G
54	01	1301	A
54	01	1306	C
54	01	1321	A
54	01	1329	U
54	01	1330	C
54	01	1332	G
54	01	1345	C
54	01	1352	U
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	1454	C
54	01	1461	C
54	01	1476	U
54	01	1482	G
54	01	1490	A
54	01	1491	G
54	01	1498	C
54	01	1504	A
54	01	1515	A
54	01	1524	G
54	01	1533	C
54	01	1535	A

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Mol	Chain	Res	Type
54	01	1536	C
54	01	1555	G
54	01	1559	U
54	01	1560	G
54	01	1569	A
54	01	1578	U
54	01	1581	G
54	01	1584	U
54	01	1585	C
54	01	1608	A
54	01	1611	C
54	01	1647	U
54	01	1648	U
54	01	1654	A
54	01	1674	G
54	01	1715	G
54	01	1729	U
54	01	1730	C
54	01	1731	G
54	01	1738	G
54	01	1758	U
54	01	1764	C
54	01	1773	A
54	01	1780	A
54	01	1800	C
54	01	1801	A
54	01	1808	A
54	01	1816	C
54	01	1829	A
54	01	1833	C
54	01	1847	A
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	1937	A
54	01	1938	A
54	01	1944	U

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Mol	Chain	Res	Type
54	01	1955	U
54	01	1966	A
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	2021	C
54	01	2022	U
54	01	2023	C
54	01	2030	A
54	01	2031	A
54	01	2033	A
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	2096	C
54	01	2110	G
54	01	2111	U
54	01	2112	G
54	01	2113	U
54	01	2118	U
54	01	2119	A
54	01	2132	U
54	01	2133	G
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

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Mol	Chain	Res	Type
54	01	2211	A
54	01	2213	U
54	01	2225	A
54	01	2238	G
54	01	2239	G
54	01	2278	A
54	01	2283	C
54	01	2287	A
54	01	2297	A
54	01	2305	U
54	01	2309	A
54	01	2325	G
54	01	2327	A
54	01	2334	U
54	01	2345	G
54	01	2350	C
54	01	2383	G
54	01	2385	C
54	01	2392	A
54	01	2402	U
54	01	2406	A
54	01	2407	A
54	01	2423	U
54	01	2424	C
54	01	2427	C
54	01	2429	G
54	01	2430	A
54	01	2435	A
54	01	2441	U
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	2529	G
54	01	2547	A
54	01	2554	U
54	01	2566	A
54	01	2567	G
54	01	2572	A

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Mol	Chain	Res	Type
54	01	2573	C
54	01	2582	G
54	01	2602	A
54	01	2609	U
54	01	2613	U
54	01	2646	C
54	01	2655	G
54	01	2682	A
54	01	2689	U
54	01	2690	U
54	01	2714	G
54	01	2716	C
54	01	2744	G
54	01	2748	A
54	01	2757	A
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	2799	A
54	01	2800	A
54	01	2809	A
54	01	2820	A
54	01	2821	A
54	01	2833	U
54	01	2848	G
54	01	2849	U
54	01	2867	G
54	01	2868	A
54	01	2872	A
54	01	2879	A
54	01	2880	C
54	01	2884	U
55	02	4	C
55	02	13	G
55	02	35	C
55	02	40	U
55	02	41	G
55	02	44	G

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Mol	Chain	Res	Type
55	02	67	G
55	02	89	U
55	02	90	C
55	02	108	A
55	02	109	A
56	X	2	G
56	X	3	C
56	X	5	G
56	X	8	U
56	X	9	G
56	X	10	G
56	X	14	A
56	X	19	G
56	X	20	U
56	X	21	A
56	X	22	G
56	X	30	G
56	X	34	C
56	X	46	G
56	X	61	C
56	X	64	G
56	X	70	G
56	X	71	C
57	V	12	A
57	V	13	A
56	W	9	G
56	W	19	G
56	W	20	U
56	W	47	U
56	W	48	C
56	W	61	C
56	W	76	A
58	Y	8	U
58	Y	9	A
58	Y	10	G
58	Y	17	C
58	Y	18	G
58	Y	21	A
58	Y	43	C
58	Y	44	G
58	Y	45	U
58	Y	46	G

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Mol	Chain	Res	Type
58	Y	48	C
58	Y	49	C

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	70	U
53	A	280	C
53	A	421	U
53	A	438	U
53	A	495	A
53	A	960	U
53	A	1190	G
53	A	1201	A
54	01	227	A
54	01	372	G
54	01	421	C
54	01	490	C
54	01	774	G
54	01	858	G
54	01	859	G
54	01	1020	A
54	01	1130	U
54	01	1475	G
54	01	1730	C
54	01	1801	A
54	01	2238	G
54	01	2286	G
54	01	2296	U
54	01	2326	C
54	01	2391	G
54	01	2423	U
54	01	2609	U
54	01	2756	U
54	01	2808	G
54	01	2848	G
55	02	88	C
58	Y	42	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 388 ligands modelled in this entry, 385 are monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
62	FME	W	101	-	8,9,10	0.83	0	8,9,11	1.16	1 (12%)
64	GCP	Z	402	60	32,34,34	2.33	11 (34%)	49,54,54	2.46	14 (28%)
63	PHE	Y	101	58	10,11,12	0.71	0	8,13,15	0.21	0

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
62	FME	W	101	-	-	3/7/9/11	-
64	GCP	Z	402	60	-	9/19/38/38	0/3/3/3
63	PHE	Y	101	58	-	0/5/6/8	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	Z	402	GCP	PA-O3A	-7.55	1.51	1.59
64	Z	402	GCP	PB-O3A	-5.90	1.51	1.58
64	Z	402	GCP	C1'-N9	3.14	1.56	1.47
64	Z	402	GCP	O4'-C1'	2.72	1.48	1.42
64	Z	402	GCP	PB-O2B	-2.66	1.49	1.56
64	Z	402	GCP	C3'-C4'	2.45	1.59	1.53
64	Z	402	GCP	C8-N9	2.39	1.42	1.37
64	Z	402	GCP	C2'-C3'	2.30	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	Z	402	GCP	C2-N2	2.24	1.39	1.34
64	Z	402	GCP	O4'-C4'	2.05	1.49	1.45
64	Z	402	GCP	C2'-C1'	2.04	1.59	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	Z	402	GCP	C1'-N9-C4	7.68	149.17	126.49
64	Z	402	GCP	C1'-N9-C8	-7.57	105.23	126.73
64	Z	402	GCP	O1G-PG-C3B	-7.42	95.20	111.37
64	Z	402	GCP	O5'-PA-O1A	-4.14	92.53	108.94
64	Z	402	GCP	O2A-PA-O3A	-3.86	96.84	107.27
64	Z	402	GCP	O2B-PB-O1B	3.49	121.33	109.95
64	Z	402	GCP	O4'-C1'-C2'	-3.19	99.79	106.62
64	Z	402	GCP	O3'-C3'-C4'	-3.07	102.28	111.08
64	Z	402	GCP	O2G-PG-C3B	2.65	112.84	106.40
64	Z	402	GCP	PB-O3A-PA	2.62	140.90	132.37
64	Z	402	GCP	O2A-PA-O1A	2.38	123.51	112.44
64	Z	402	GCP	O3G-PG-O1G	2.34	118.45	112.39
64	Z	402	GCP	O4'-C4'-C5'	2.26	116.57	109.33
62	W	101	FME	O-C-CA	-2.23	119.04	124.77
64	Z	402	GCP	O3G-PG-C3B	2.06	111.40	106.40

There are no chirality outliers.

All (12) torsion outliers are listed below:

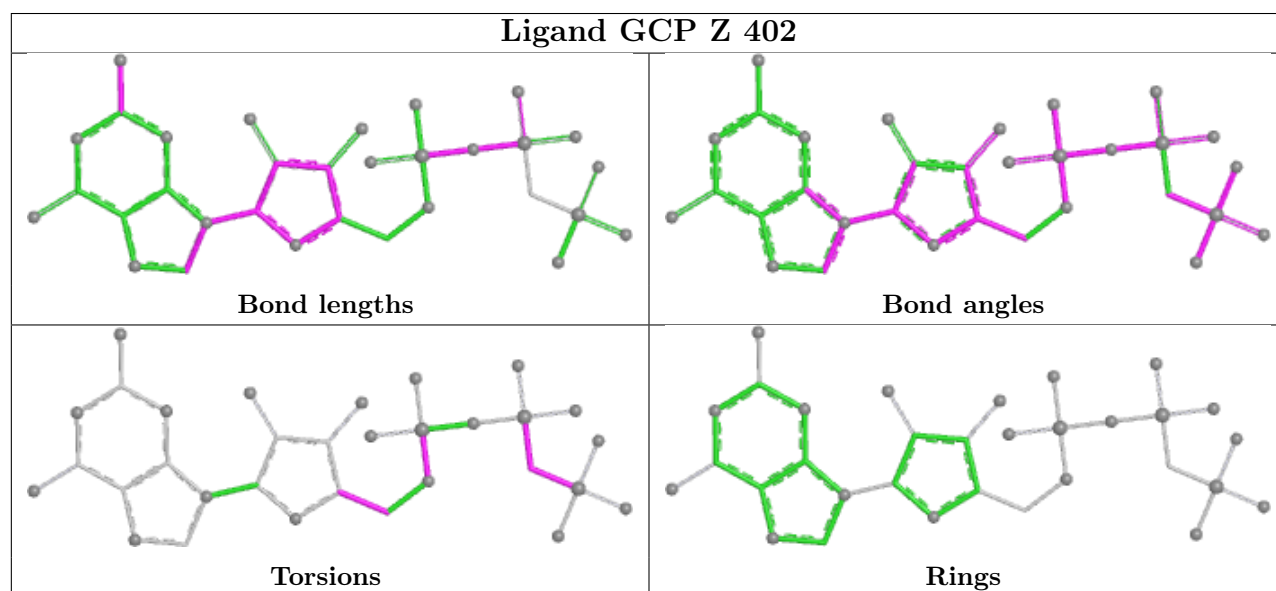
Mol	Chain	Res	Type	Atoms
62	W	101	FME	O1-CN-N-CA
62	W	101	FME	O-C-CA-CB
64	Z	402	GCP	PB-C3B-PG-O1G
64	Z	402	GCP	PB-C3B-PG-O2G
64	Z	402	GCP	PG-C3B-PB-O1B
64	Z	402	GCP	C5'-O5'-PA-O2A
64	Z	402	GCP	O4'-C4'-C5'-O5'
64	Z	402	GCP	PB-C3B-PG-O3G
64	Z	402	GCP	C5'-O5'-PA-O3A
64	Z	402	GCP	C5'-O5'-PA-O1A
62	W	101	FME	C-CA-CB-CG
64	Z	402	GCP	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
64	Z	402	GCP	1	0
63	Y	101	PHE	3	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 than 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.



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.

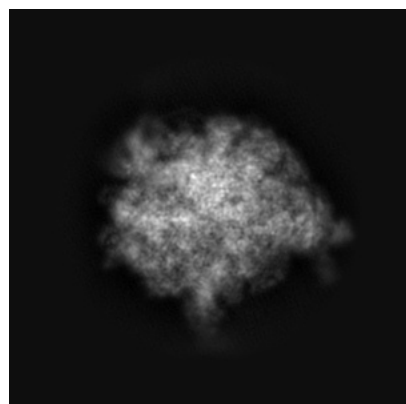
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8617. These allow visual inspection of the internal detail of the map and identification of artifacts.

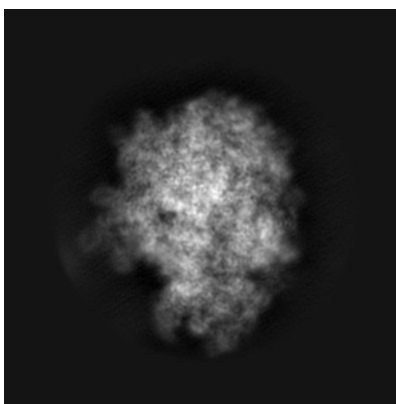
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

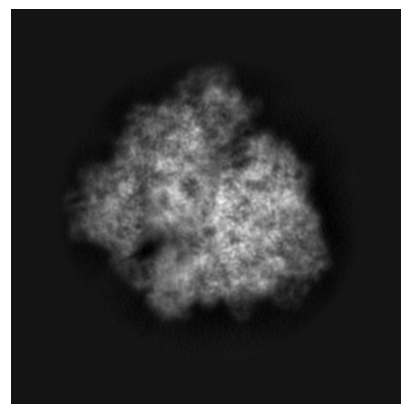
6.1.1 Primary map



X

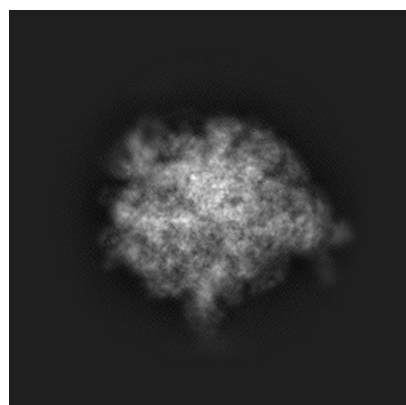


Y

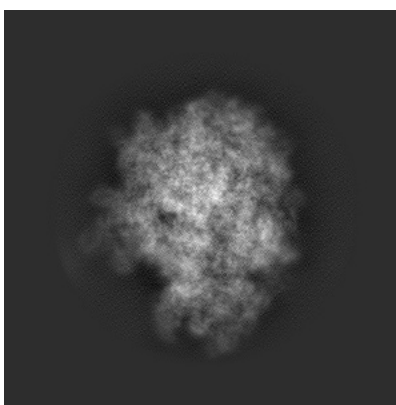


Z

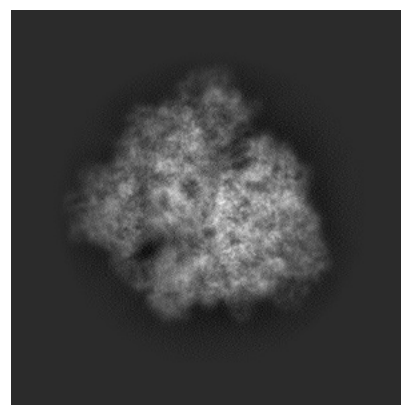
6.1.2 Raw map



X



Y

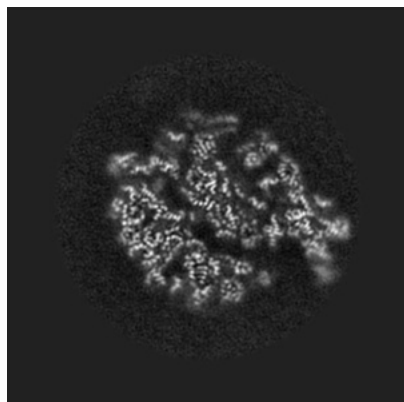


Z

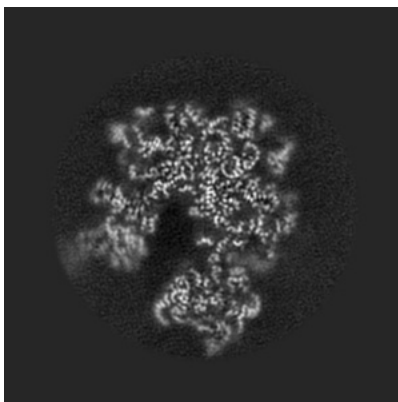
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

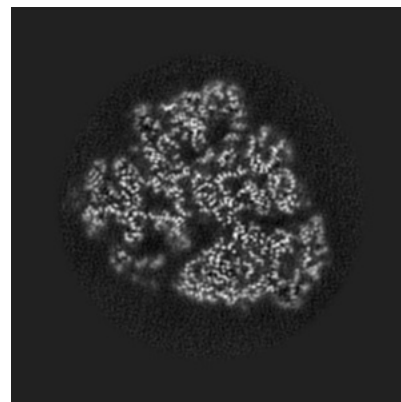
6.2.1 Primary map



X Index: 240

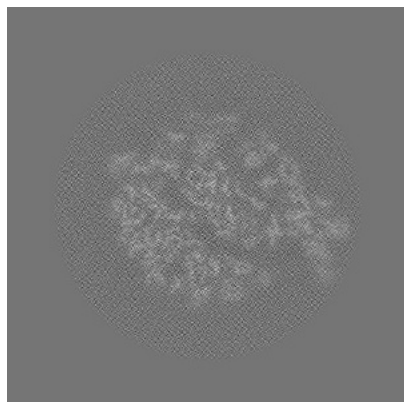


Y Index: 240

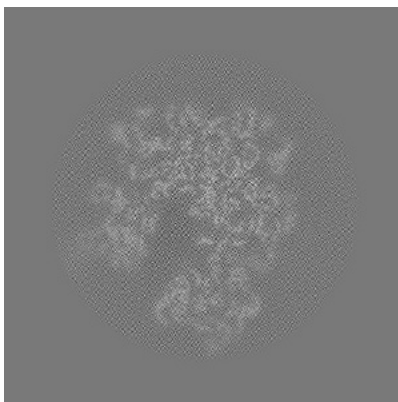


Z Index: 240

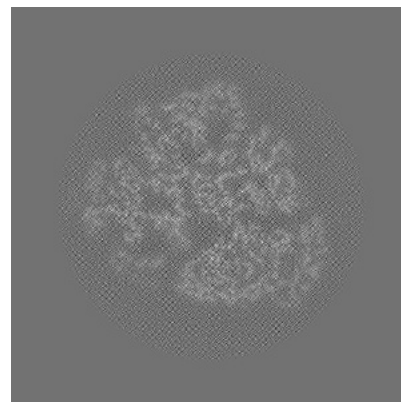
6.2.2 Raw map



X Index: 240



Y Index: 240

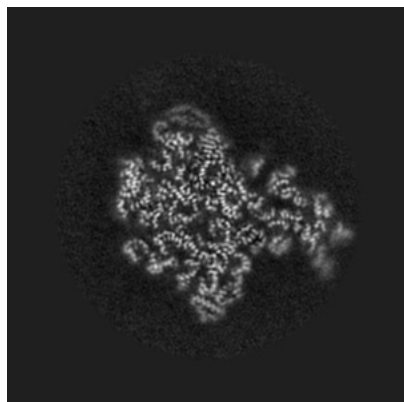


Z Index: 240

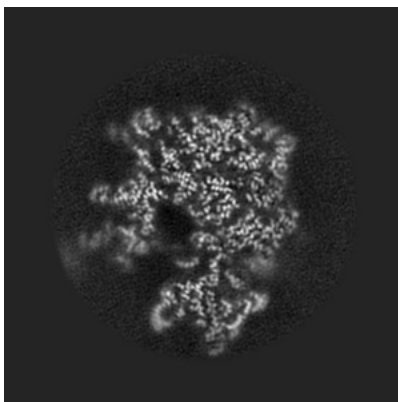
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

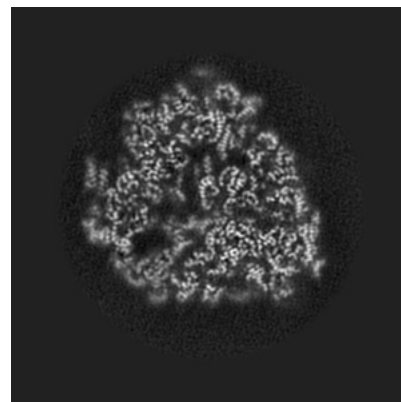
6.3.1 Primary map



X Index: 252

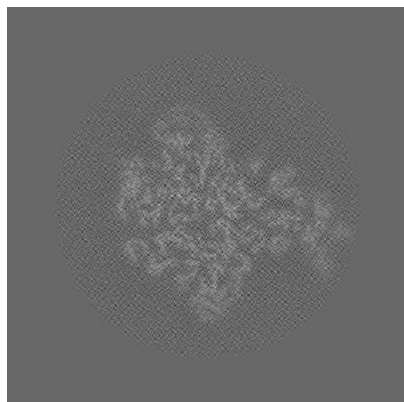


Y Index: 248

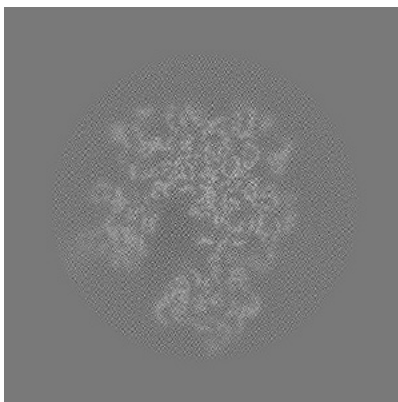


Z Index: 228

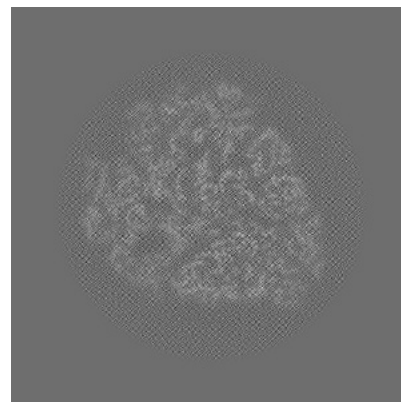
6.3.2 Raw map



X Index: 251



Y Index: 240

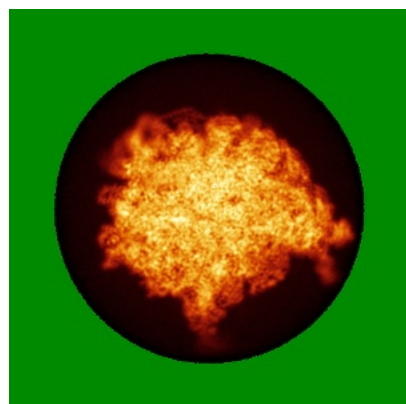


Z Index: 233

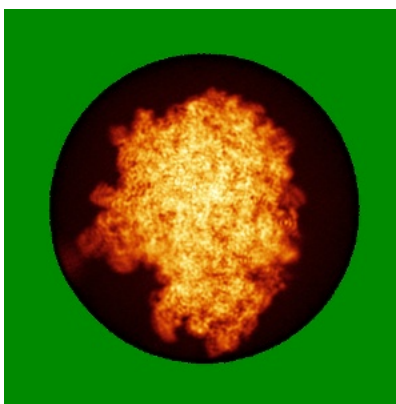
The images above show the largest variance slices of the map in three orthogonal directions.

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

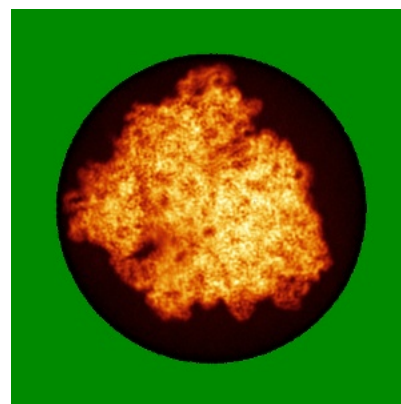
6.4.1 Primary map



X

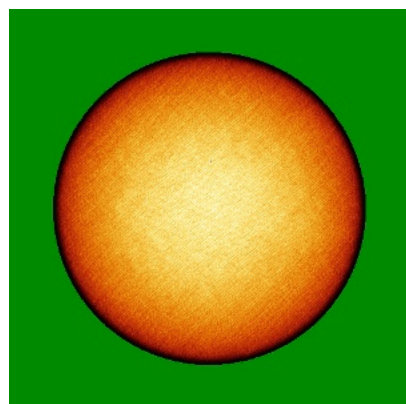


Y

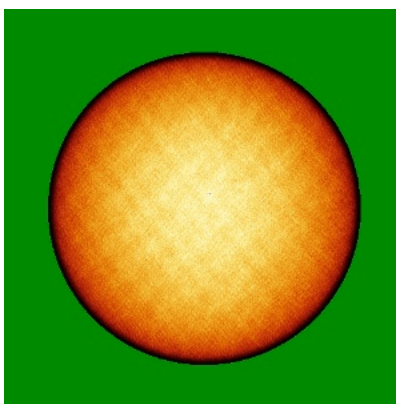


Z

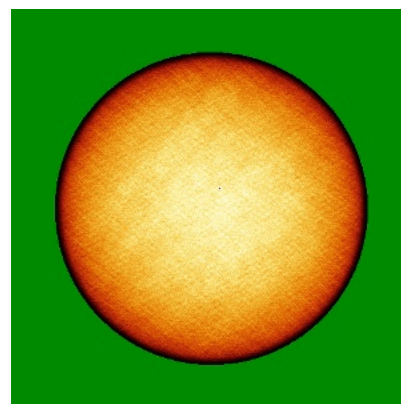
6.4.2 Raw map



X



Y



Z

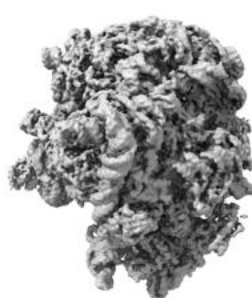
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

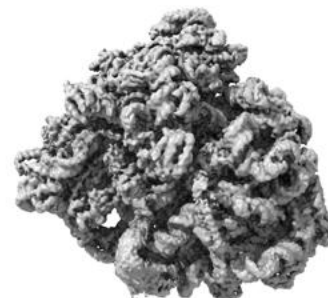
6.5.1 Primary map



X



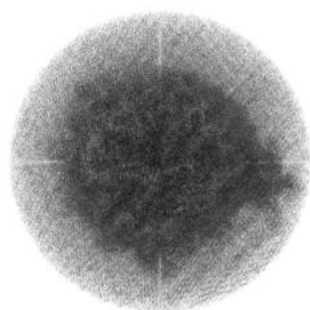
Y



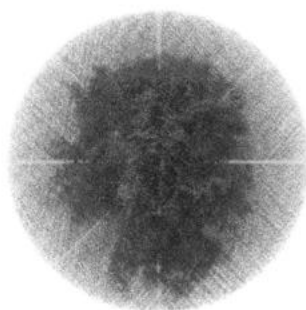
Z

The images above show the 3D surface view of the map at the recommended contour level 3.17. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

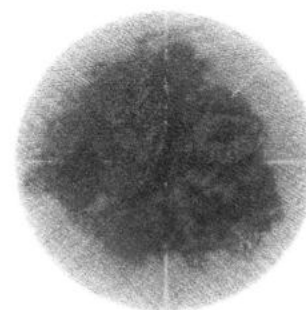
6.5.2 Raw map



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.

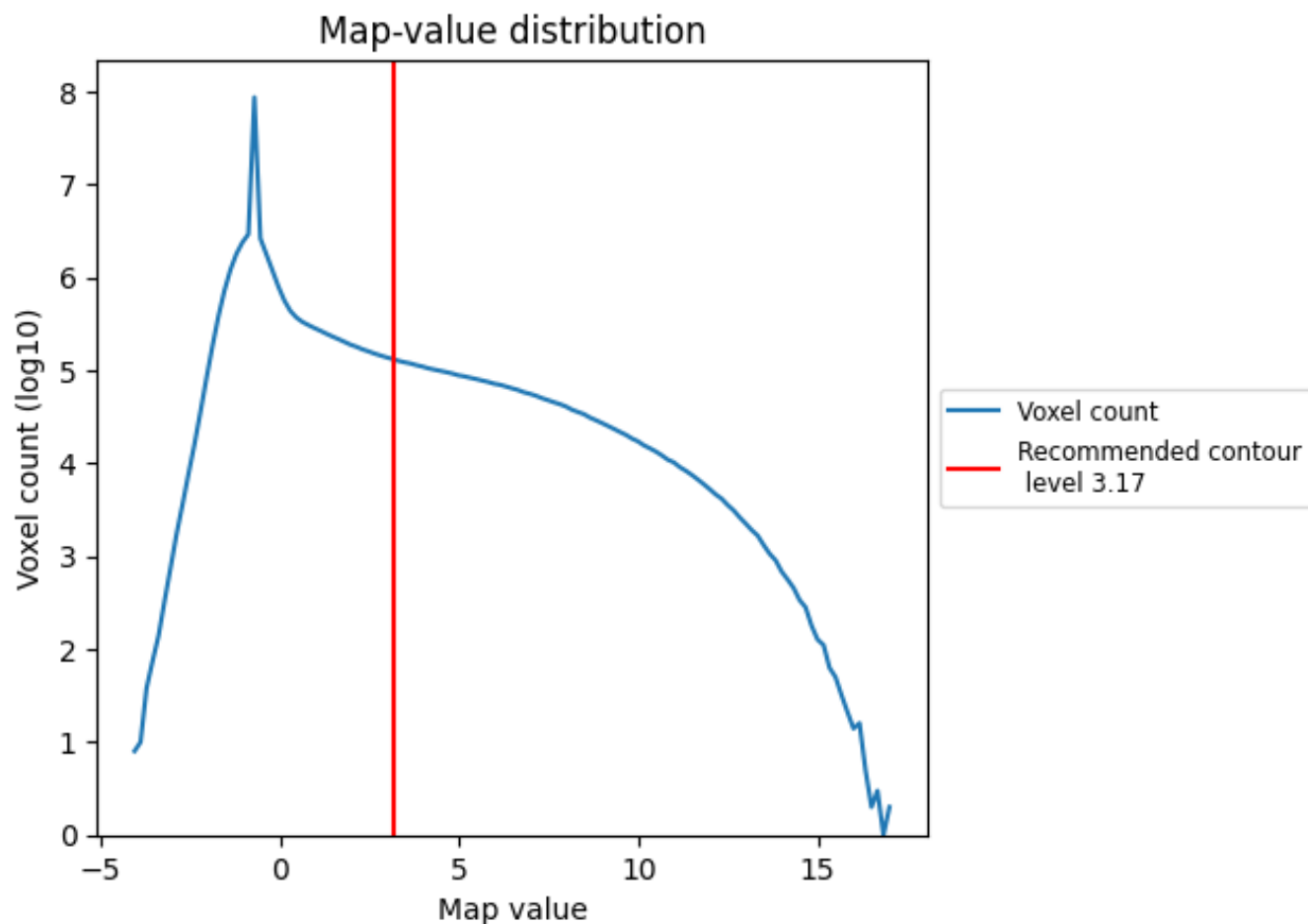
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

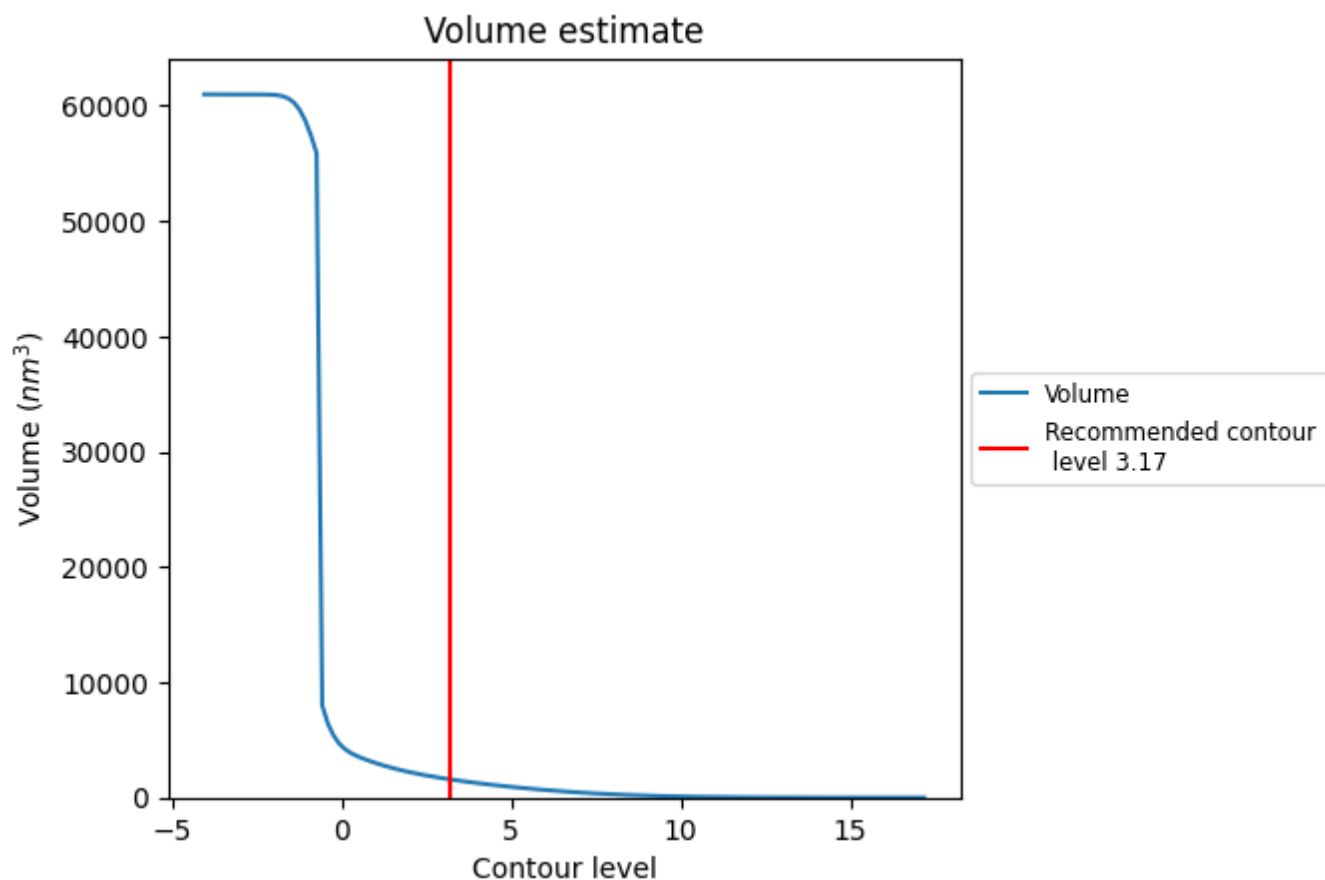
This section contains the results of statistical analysis of the map.

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.

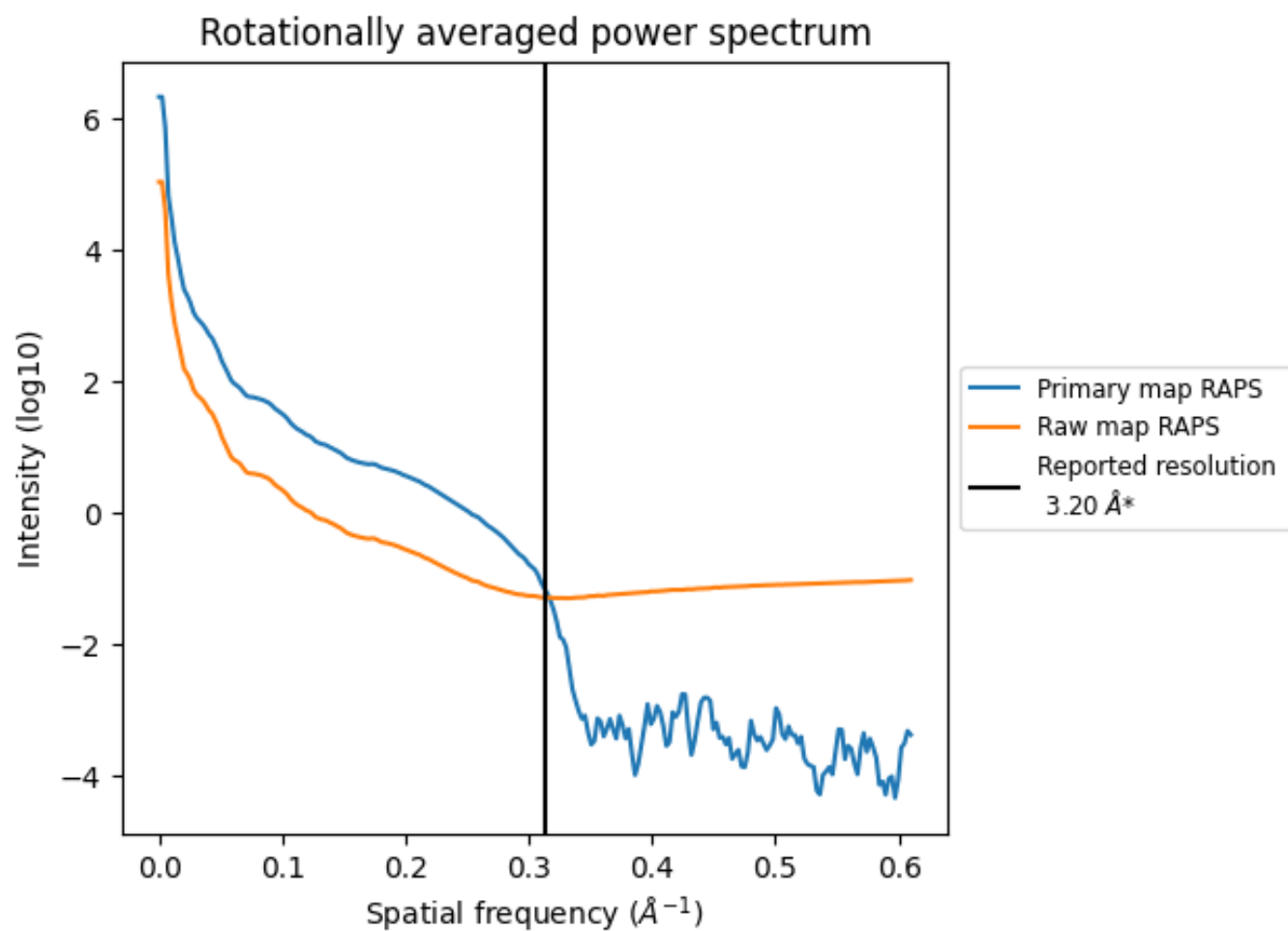
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1587 nm³; this corresponds to an approximate mass of 1433 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

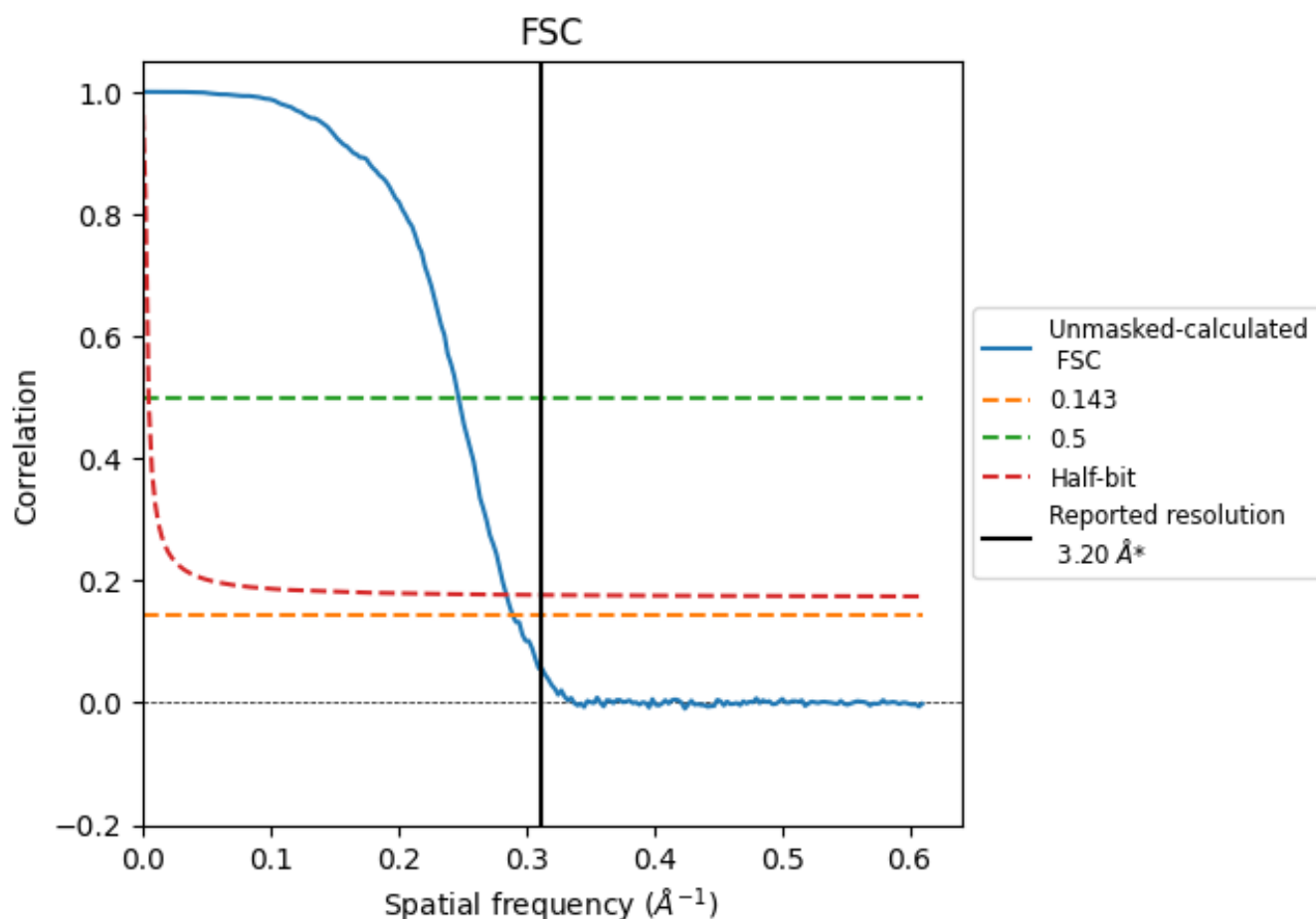


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

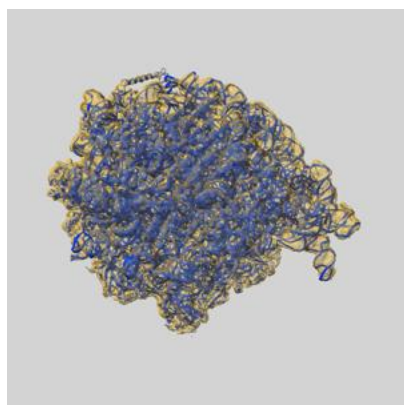
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.45	4.05	3.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

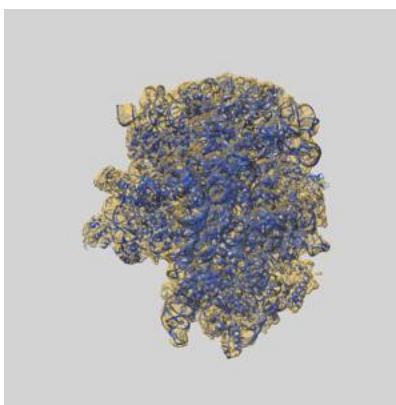
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8617 and PDB model 5UYM. Per-residue inclusion information can be found in section [3](#) on page [17](#).

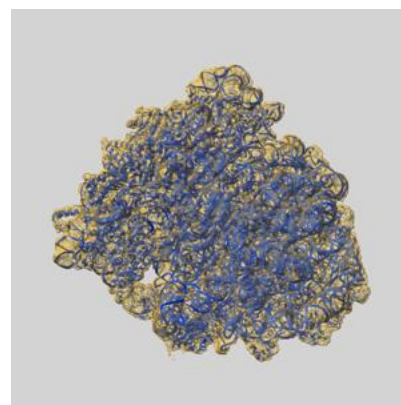
9.1 Map-model overlay [i](#)



X



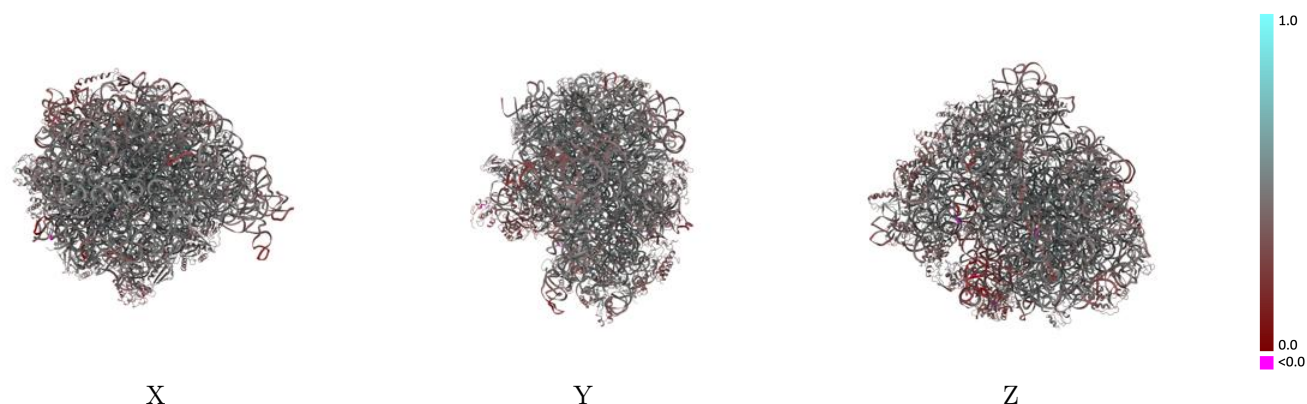
Y



Z

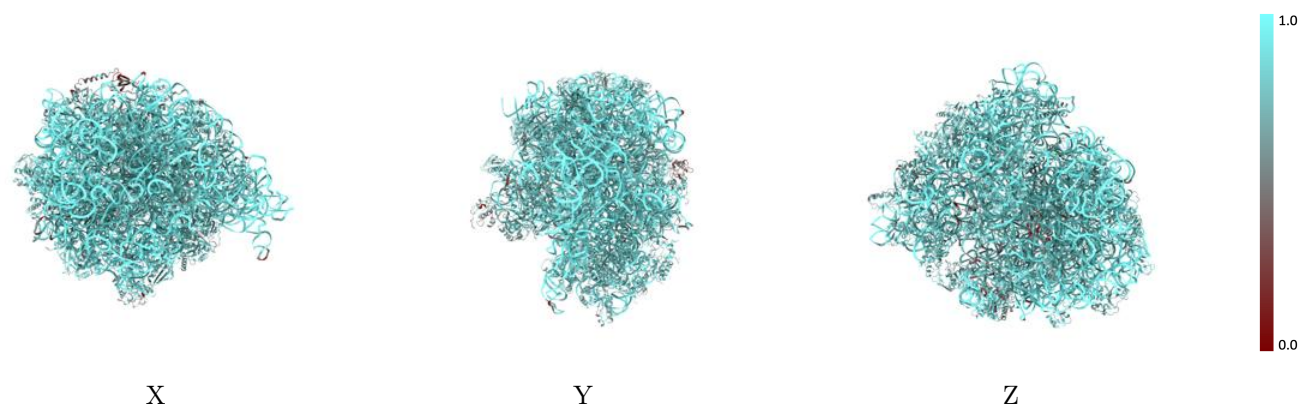
The images above show the 3D surface view of the map at the recommended contour level 3.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



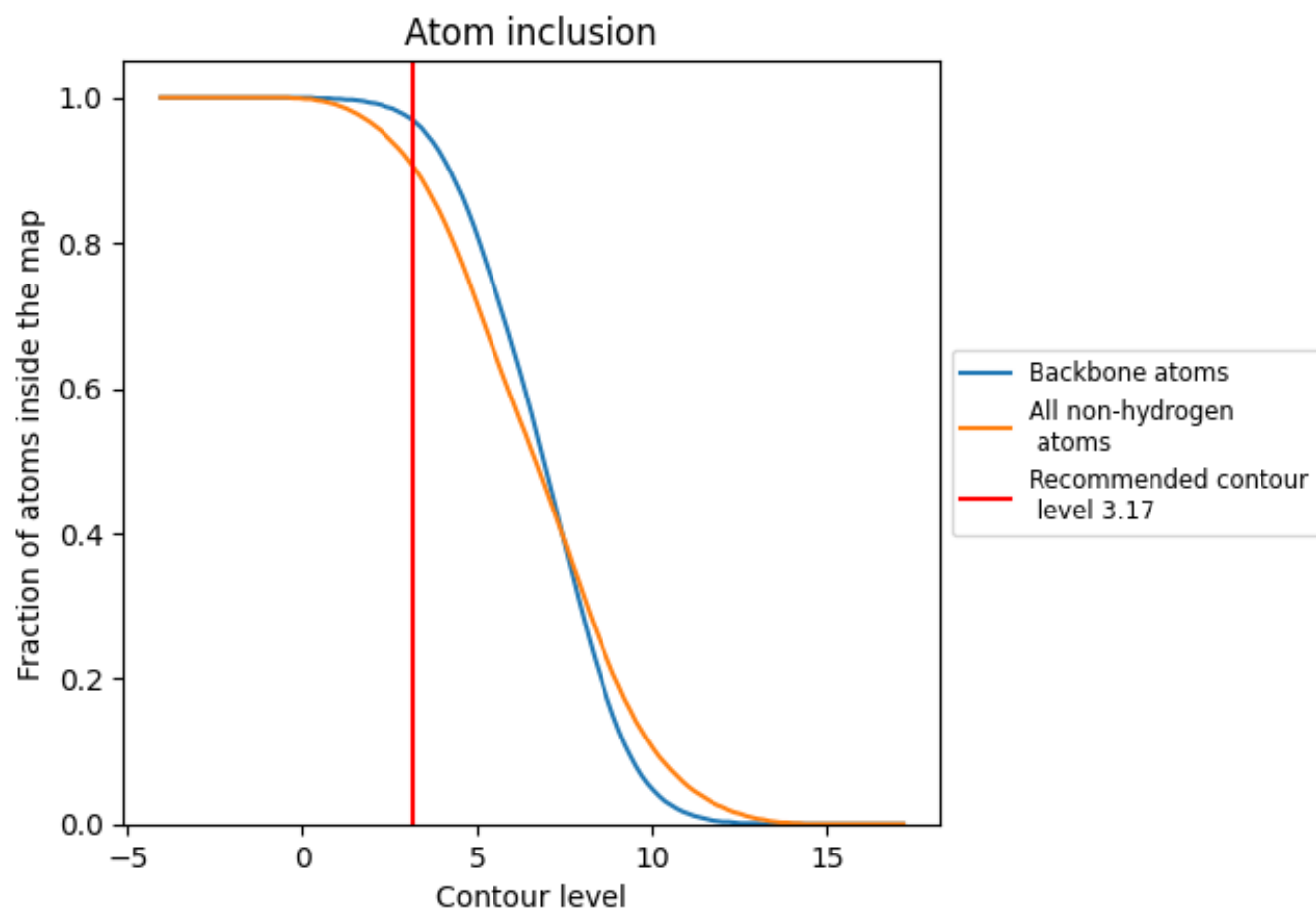
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.17).

9.4 Atom inclusion ⓘ



At the recommended contour level, 97% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (3.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.4440
01	 0.9670	 0.4590
02	 0.9660	 0.4320
03	 0.6340	 0.2870
04	 0.8560	 0.4910
05	 0.8240	 0.4790
06	 0.8040	 0.4450
07	 0.8060	 0.4040
08	 0.8060	 0.4290
09	 0.4960	 0.3490
10	 0.4920	 0.2500
11	 0.6400	 0.2700
12	 0.8130	 0.4530
13	 0.7640	 0.4680
14	 0.8350	 0.4640
15	 0.7730	 0.4700
16	 0.8670	 0.4670
17	 0.8400	 0.4260
18	 0.7900	 0.4550
19	 0.8480	 0.4680
20	 0.8160	 0.4560
21	 0.7830	 0.4570
22	 0.7830	 0.4360
23	 0.8020	 0.4340
24	 0.7990	 0.4440
25	 0.8360	 0.4800
26	 0.8100	 0.4670
27	 0.7730	 0.3830
28	 0.8030	 0.4470
29	 0.7270	 0.3660
30	 0.8130	 0.4570
31	 0.7590	 0.4570
32	 0.8450	 0.4800
33	 0.8680	 0.5030
34	 0.8260	 0.4810



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Chain	Atom inclusion	Q-score
A	 0.9730	 0.4590
B	 0.7480	 0.3790
C	 0.7930	 0.4380
D	 0.7910	 0.4180
E	 0.8110	 0.4510
F	 0.7930	 0.3980
G	 0.7870	 0.4010
H	 0.8150	 0.4450
I	 0.8130	 0.4210
J	 0.7400	 0.4080
K	 0.8180	 0.4400
L	 0.8100	 0.4810
M	 0.8040	 0.4130
N	 0.8220	 0.4340
O	 0.8220	 0.4150
P	 0.8410	 0.4480
Q	 0.8090	 0.4500
R	 0.8140	 0.4280
S	 0.8340	 0.4270
T	 0.8140	 0.4140
U	 0.6580	 0.2960
V	 0.7590	 0.3690
W	 0.9110	 0.4410
X	 0.7250	 0.2460
Y	 0.9080	 0.4100
Z	 0.7900	 0.4140