Full wwPDB EM Validation Report ⓘ

Feb 2, 2022 – 11:20 pm GMT

PDB ID	:	7QEP
EMDB ID	:	EMD-13936
Title	:	Cryo-EM structure of the ribosome from Encephalitozoon cuniculi
Authors	:	Nicholson, D.; Ranson, N.A.; Melnikov, S.V.
Deposited on	:	2021-12-03
Resolution	:	2.70 Å(reported)
Based on initial models	:	6RM3, 4V88

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

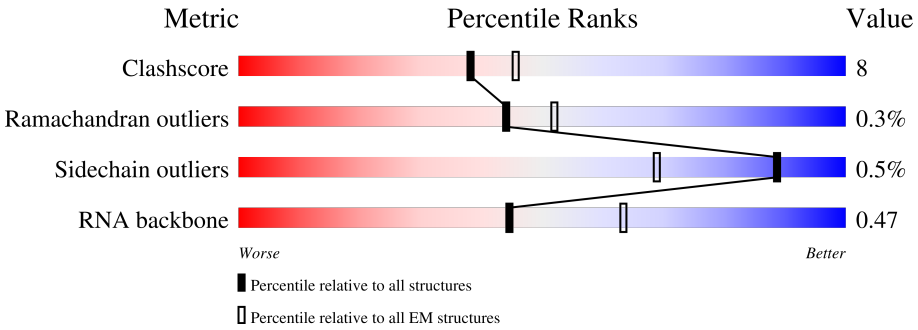
EMDB validation analysis	:	0.0.0.dev97
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	RA	334	97% 55% 43%
2	1	2486	66% 22% 6% 7%
3	2	119	72% 24%
4	3	1300	5% 63% 28% 9%
5	C0	96	72% 60% 24% 16%
6	C1	156	17% 67% 22% 10%
7	C2	134	88% 35% 53% 12%

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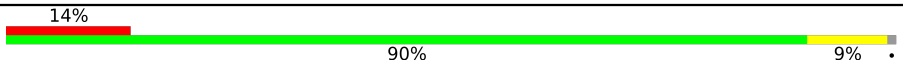
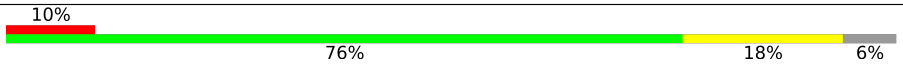
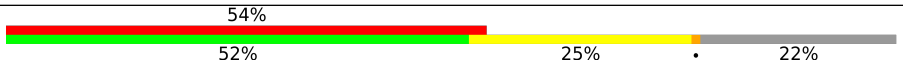
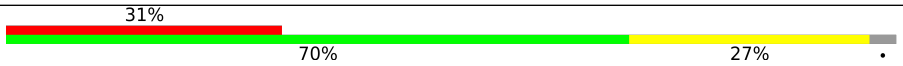
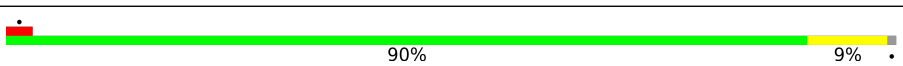
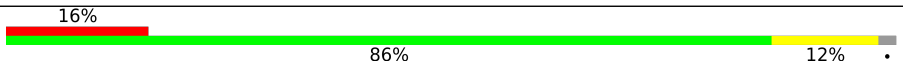
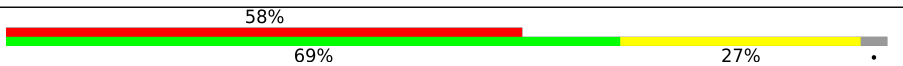
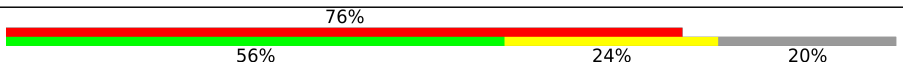
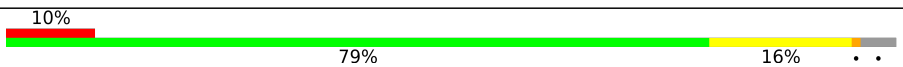
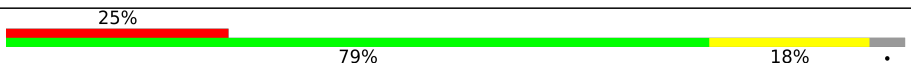
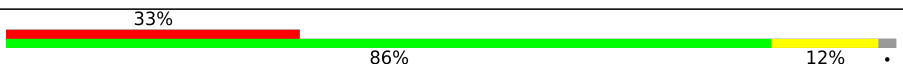
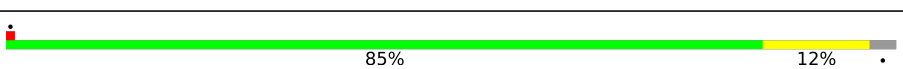
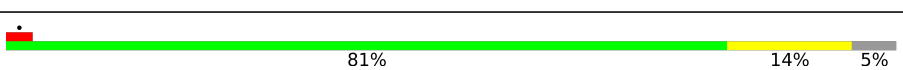
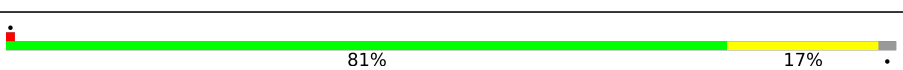
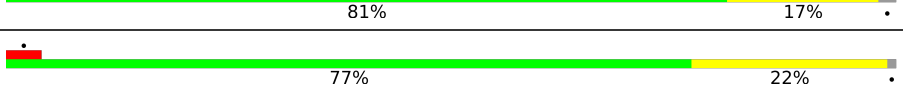
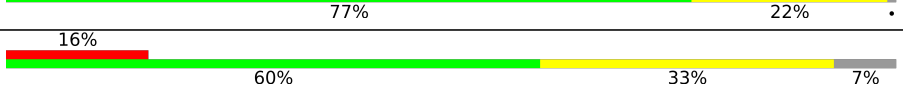
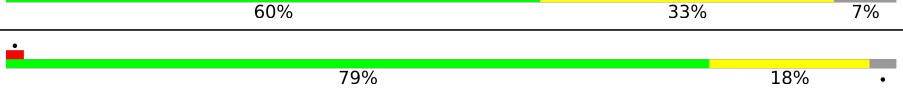
Mol	Chain	Length	Quality of chain
8	C3	148	
9	C4	134	
10	C5	148	
11	C6	145	
12	C7	120	
13	C8	153	
14	C9	137	
15	D0	120	
16	D1	70	
17	D2	128	
18	D3	140	
19	D4	131	
20	D5	109	
21	D6	105	
22	D7	85	
23	D8	65	
24	D9	66	
25	E1	152	
26	L1	219	
27	L2	239	
28	L3	383	
29	L4	335	
30	L5	287	
31	L6	171	
32	L7	239	

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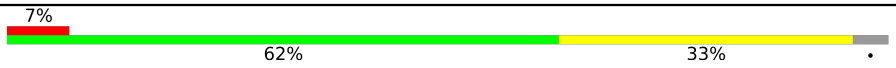
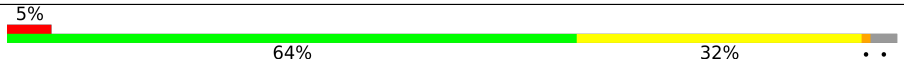
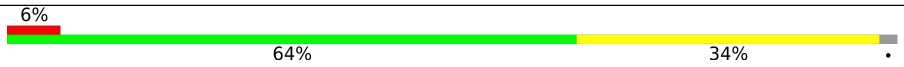
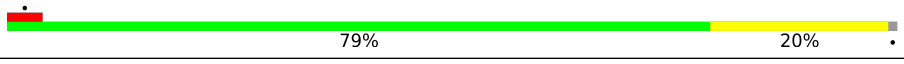
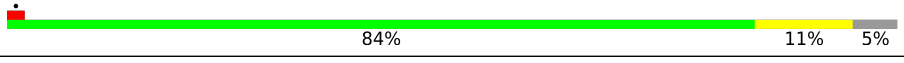
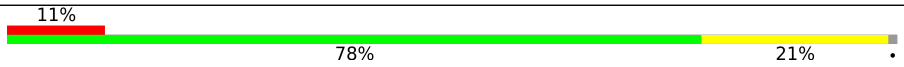
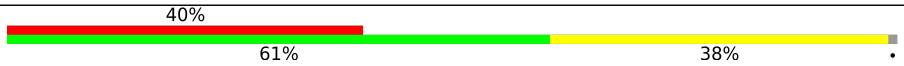
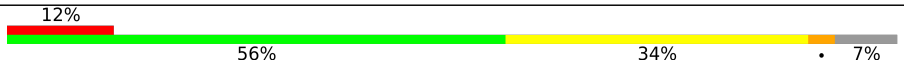
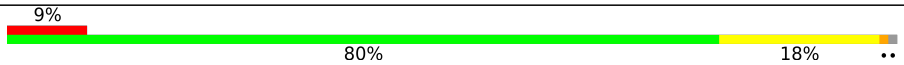
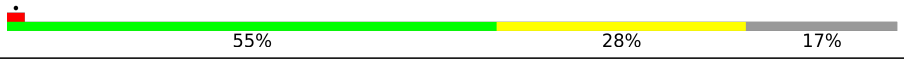
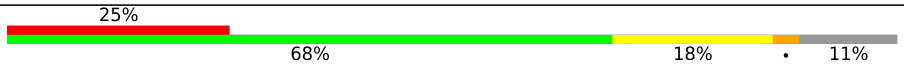
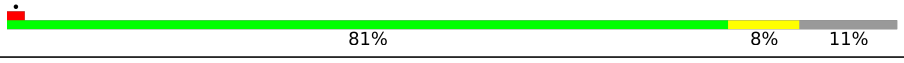
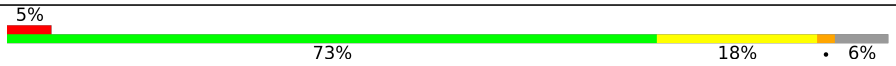
Mol	Chain	Length	Quality of chain
33	L8	206	
34	L9	183	
35	M0	219	
36	M1	173	
37	M3	163	
38	M4	106	
39	M5	204	
40	M6	198	
41	M7	183	
42	M8	200	
43	M9	171	
44	MD	171	
45	MS	73	
46	N0	188	
47	N1	160	
48	N2	112	
49	N3	146	
50	N4	100	
51	N5	105	
52	N6	143	
53	N7	126	
54	N8	147	
55	N9	57	
56	O0	108	
57	O1	111	

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Mol	Chain	Length	Quality of chain
58	O2	139	73% 19% 8%
59	O3	113	84% 12%
60	O4	110	77% 14% 9%
61	O5	122	86% 13%
62	O6	94	77% 23%
63	O7	90	86% 10%
64	O9	52	73% 23%
65	P0	131	30% 8% 63%
66	P2	104	75% 18% 7%
67	P3	89	83% 12%
68	S0	252	36% 54% 26% 19%
69	S1	239	29% 68% 20% 13%
70	S2	242	14% 71% 19% 10%
71	S3	216	58% 74% 24%
72	S4	268	29% 79% 17%
73	S5	189	69% 75% 24%
74	S6	217	40% 54% 38% 6%
75	S7	170	56% 51% 36% 12%
76	S8	173	9% 76% 18% 5%
77	S9	184	34% 65% 28% 7%

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 166143 atoms, of which 31 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 Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	RA	328	2537	1594	427	502	14	0	0

- Molecule 2 is a RNA chain called 5.8S-23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	2319	49833	22195	9045	16274	2319	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 13560063

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	119	2550	1138	469	824	119	0	0

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	3	1295	27838	12399	5052	9092	1295	0	0

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C0	81	686	449	122	112	3	0	0

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C1	141	Total	C	N	O	S	0	0
			1126	718	206	194	8		

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C2	118	Total	C	N	O	S	0	0
			879	548	154	166	11		

- Molecule 8 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C3	146	Total	C	N	O	S	0	0
			1166	736	221	205	4		

- Molecule 9 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C4	126	Total	C	N	O	S	0	0
			942	583	192	163	4		

- Molecule 10 is a protein called RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C5	116	Total	C	N	O	S	0	0
			903	576	167	154	6		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C6	141	Total	C	N	O	S	0	0
			1132	727	202	197	6		

- Molecule 12 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C7	117	Total	C	N	O	S	0	0
			962	611	166	180	5		

- Molecule 13 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C8	141	Total	C	N	O	S	0	0
			1121	692	220	203	6		

- Molecule 14 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C9	135	Total	C	N	O	S	0	0
			1089	690	187	206	6		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D0	93	Total	C	N	O	S	0	0
			779	498	137	140	4		

- Molecule 16 is a protein called ECU11_0225 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	D1	68	Total	C	N	O	S	0	0
			518	323	89	103	3		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S15A (S22 in yeast).

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D2	127	Total	C	N	O	S	0	0
			1012	639	190	176	7		

- Molecule 18 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	D3	137	Total	C	N	O	S	0	0
			1052	669	196	185	2		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	D4	127	Total	C	N	O	S	0	0
			1056	668	199	186	3		

- Molecule 20 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	D5	87	Total	C	N	O	S	0	0
			691	424	141	123	3		

- Molecule 21 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D6	101	Total	C	N	O	S	0	0
			801	494	161	139	7		

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	D7	82	Total	C	N	O	S	0	0
			633	391	117	117	8		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D8	57	Total	C	N	O	S	0	0
			446	278	84	81	3		

- Molecule 24 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	D9	65	Total	C	N	O	S	0	0
			524	334	96	88	6		

- Molecule 25 is a protein called Similarity to monoubiquitin/carboxy-extension protein fusion.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	E1	58	Total	C	N	O	0	0
			276	168	58	50		

- Molecule 26 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	L1	206	Total	C	N	O	0	0
			1016	604	206	206		

- Molecule 27 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L2	232	Total	C	N	O	S	0	0
			1759	1098	328	324	9		

- Molecule 28 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L3	363	Total	C	N	O	S	0	0
			2827	1781	539	491	16		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L4	329	Total	C	N	O	S	0	0
			2596	1621	488	474	13		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L5	283	Total	C	N	O	S	0	0
			2273	1421	425	420	7		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L6	159	Total	C	N	O	S	0	0
			1279	811	220	241	7		

- Molecule 32 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L7	231	Total	C	N	O	S	0	0
			1903	1203	352	337	11		

- Molecule 33 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L8	197	Total	C	N	O	S	0	0
			1573	1015	269	282	7		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L9	182	Total	C	N	O	S	1	0
			1443	909	265	260	9		

- Molecule 35 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M0	211	Total	C	N	O	S	0	0
			1706	1079	329	291	7		

- Molecule 36 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M1	167	Total	C	N	O	S	0	0
			1336	845	247	237	7		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M3	161	Total	C	N	O	S	0	0
			1308	825	253	225	5		

- Molecule 38 is a protein called ECU06_1215 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M4	104	Total	C	N	O	S	0	0
			848	537	150	160	1		

- Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	M5	203	Total	C	N	O	S	0	0
			1657	1031	335	279	12		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L13A (L16).

Mol	Chain	Residues	Atoms					AltConf	Trace
40	M6	196	Total	C	N	O	S	0	0
			1577	1001	291	276	9		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	M7	174	Total	C	N	O	S	0	0
			1363	861	263	234	5		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	M8	186	Total	C	N	O	S	0	0
			1470	929	266	266	9		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M9	170	Total	C	N	O	S	0	0
			1398	864	285	238	11		

- Molecule 44 is a protein called Uncharacterized protein ECU01_0250.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	MD	170	Total	C	N	O	S	0	0
			1349	848	230	260	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MD	59	GLY	SER	variant	UNP Q8SWQ4

- Molecule 45 is a protein called ECU06_1135 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	MS	68	Total	C	N	O	S	0	0
			592	372	121	97	2		

- Molecule 46 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	N0	178	Total	C	N	O	S	0	0
			1438	929	249	254	6		

- Molecule 47 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	N1	159	Total	C	N	O	S	0	0
			1288	812	249	220	7		

- Molecule 48 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	N2	93	Total	C	N	O	S	0	0
			735	477	130	125	3		

- Molecule 49 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	N3	135	Total	C	N	O	S	0	0
			1058	666	206	179	7		

- Molecule 50 is a protein called Similarity to 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	N4	89	Total	C	N	O	S	0	0
			709	443	136	126	4		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	N5	93	Total	C	N	O	S	0	0
			720	460	123	134	3		

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	N6	142	Total	C	N	O	S	0	0
			1171	730	230	208	3		

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	N7	118	Total	C	N	O	S	0	0
			938	617	162	154	5		

- Molecule 54 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	N8	146	Total	C	N	O	S	0	0
			1196	763	232	198	3		

- Molecule 55 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	N9	55	Total	C	N	O	S	0	0
			437	272	90	74	1		

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	O0	90	Total	C	N	O	S	0	0
			692	442	122	124	4		

- Molecule 57 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	O1	108	Total	C	N	O	S	0	0
			879	559	164	153	3		

- Molecule 58 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	O2	128	Total	C	N	O	S	0	0
			1062	674	215	169	4		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L35A (L33).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	O3	109	Total	C	N	O	S	0	0
			861	543	166	149	3		

- Molecule 60 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O4	100	Total	C	N	O	S	0	0
			807	493	177	131	6		

- Molecule 61 is a protein called 60S ribosomal protein L35-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O5	121	Total	C	N	O	S	0	0
			981	609	201	170	1		

- Molecule 62 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	O6	94	Total	C	N	O	S	0	0
			735	461	147	125	2		

- Molecule 63 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	O7	86	Total	C	N	O	S	0	0
			691	416	152	115	8		

- Molecule 64 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	O9	50	Total	C	N	O	S	0	0
			434	271	97	63	3		

- Molecule 65 is a protein called UBIQUITIN/ L40 RIBOSOMAL PROTEIN FUSION.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	P0	49	Total	C	N	O	S	0	0
			381	230	75	68	8		

- Molecule 66 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	P2	97	Total	C	N	O	S	0	0
			788	492	167	125	4		

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L37A (L43).

Mol	Chain	Residues	Atoms					AltConf	Trace
67	P3	86	Total	C	N	O	S	0	0
			664	419	128	111	6		

- Molecule 68 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	S0	203	Total	C	N	O	S	0	0
			1584	1017	272	289	6		

- Molecule 69 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	S1	209	Total	C	N	O	S	0	0
			1670	1058	299	300	13		

- Molecule 70 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	S2	217	Total	C	N	O	S	0	0
			1636	1037	293	300	6		

- Molecule 71 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	S3	210	Total	C	N	O	S	0	0
			1658	1057	295	298	8		

- Molecule 72 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	S4	259	Total	C	N	O	S	0	0
			2045	1301	361	374	9		

- Molecule 73 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	S5	188	Total	C	N	O	S	0	0
			1461	905	282	269	5		

- Molecule 74 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	S6	204	Total	C	N	O	S	0	0
			1680	1049	321	301	9		

- Molecule 75 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	S7	149	Total	C	N	O	S	0	0
			1173	745	212	208	8		

- Molecule 76 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S8	164	Total	C	N	O	S	0	0
			1300	812	255	230	3		

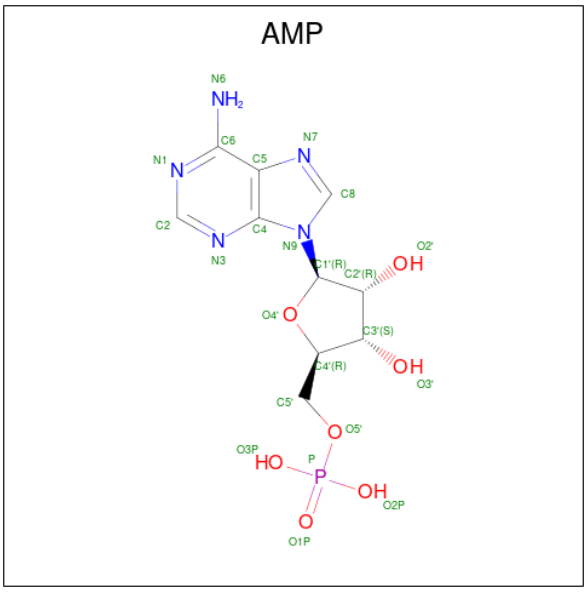
- Molecule 77 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	S9	171	Total	C	N	O	S	0	0
			1374	873	255	241	5		

- Molecule 78 is ZINC ION (three-letter code: ZN) (formula: Zn).

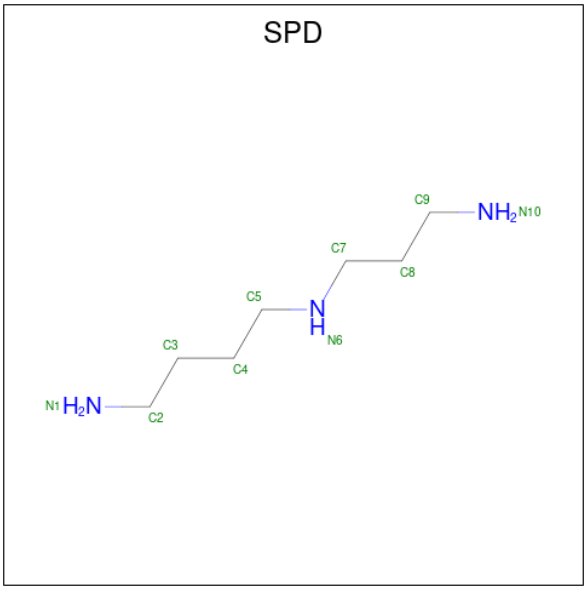
Mol	Chain	Residues	Atoms		AltConf
78	D6	1	Total	Zn	0
			1	1	
78	D7	1	Total	Zn	0
			1	1	
78	D9	1	Total	Zn	0
			1	1	
78	E1	1	Total	Zn	0
			1	1	
78	O7	1	Total	Zn	0
			1	1	
78	P0	1	Total	Zn	0
			1	1	
78	P2	1	Total	Zn	0
			1	1	
78	P3	1	Total	Zn	0
			1	1	

- Molecule 79 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
79	L9	1	Total	C	H	N	O	P	0
			35	10	12	5	7	1	

- Molecule 80 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



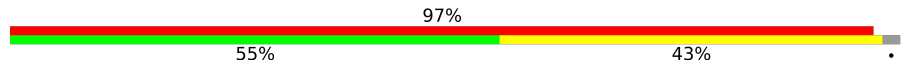
Mol	Chain	Residues	Atoms				AltConf
80	N8	1	Total	C	H	N	0
			29	7	19	3	

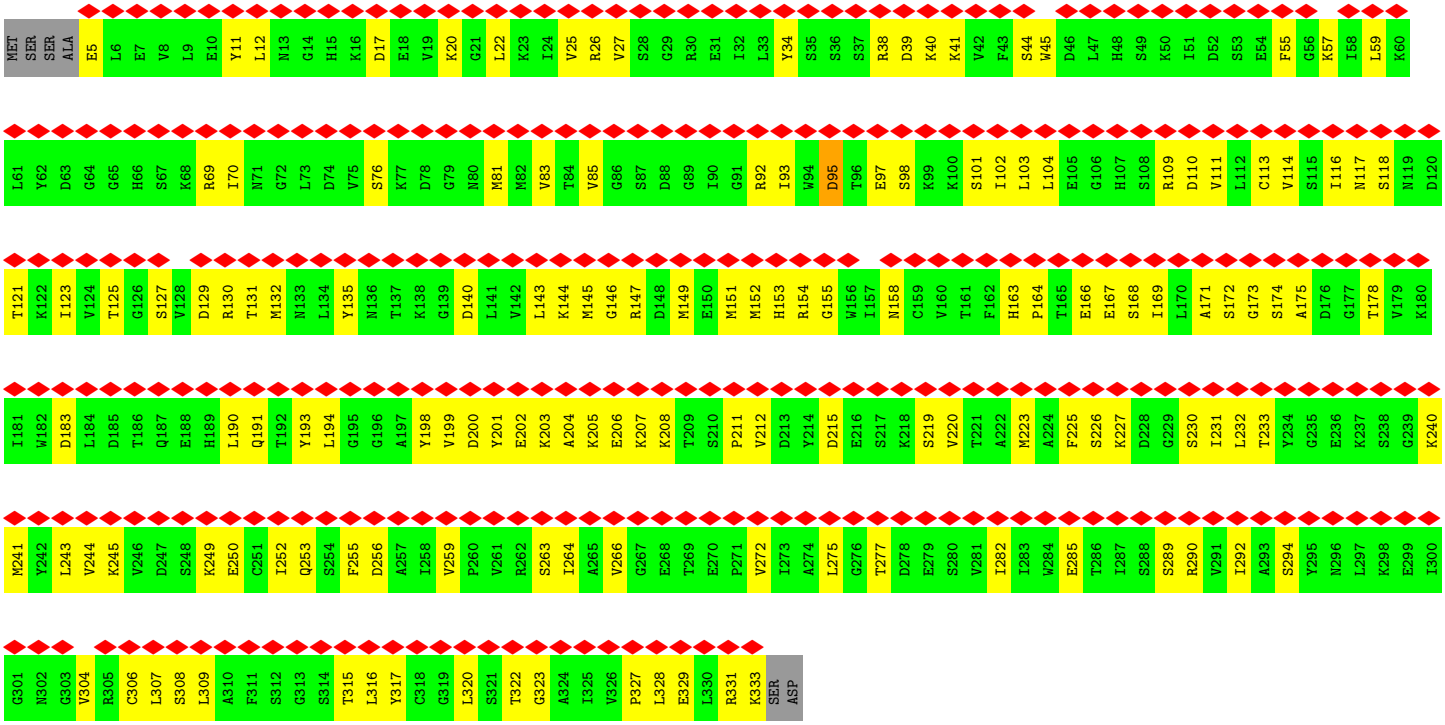
3 Residue-property plots (i)

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

• Molecule 1: Guanine nucleotide binding protein beta subunit

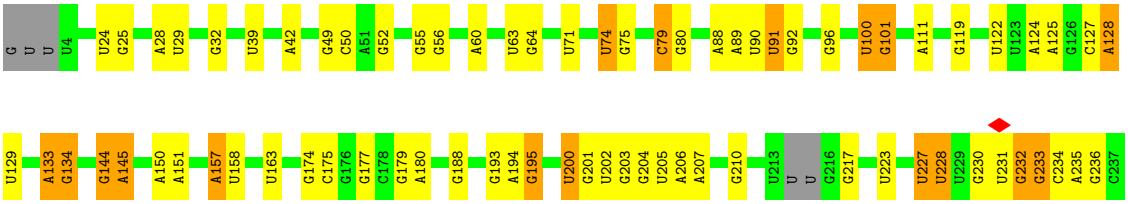
Chain RA:

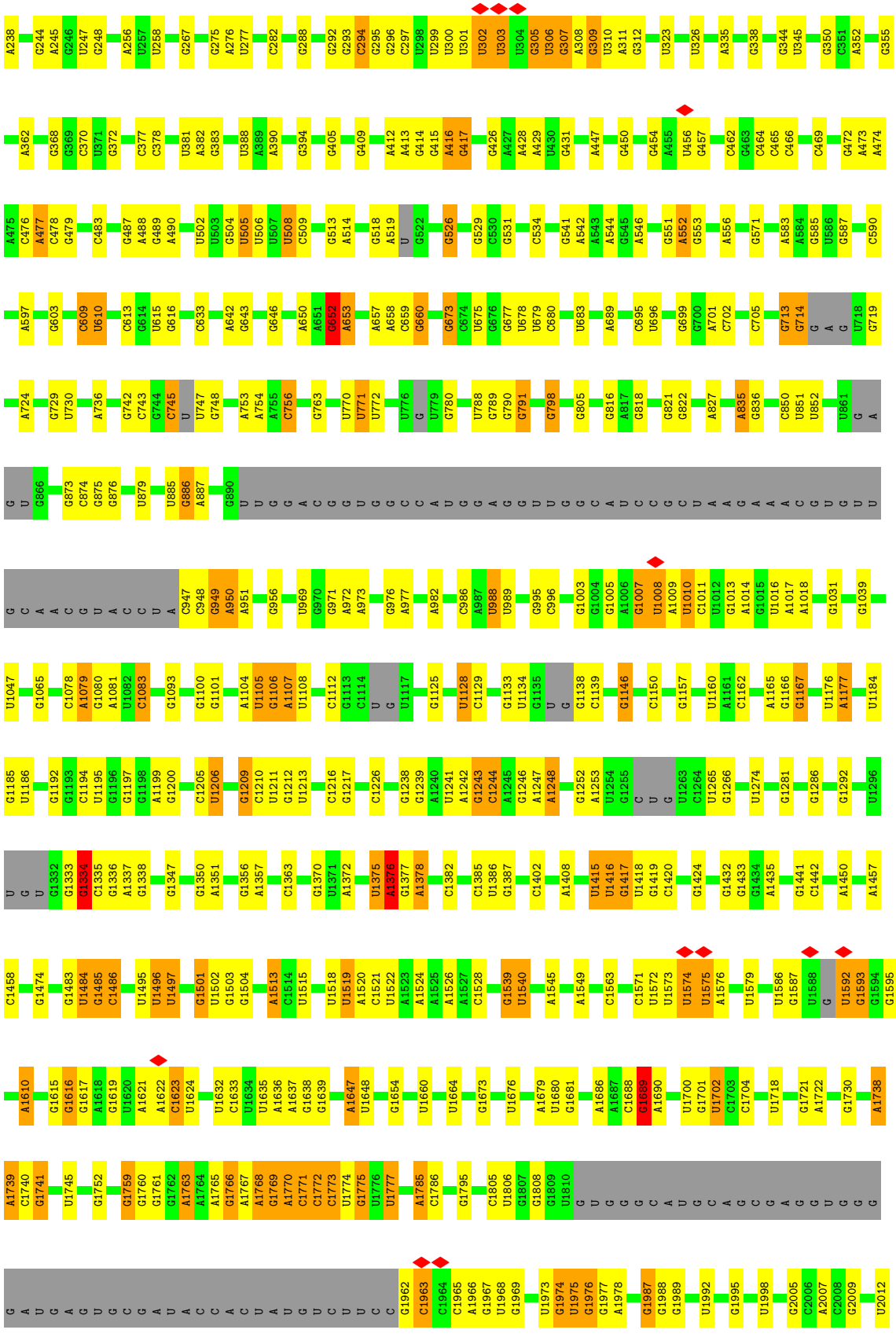


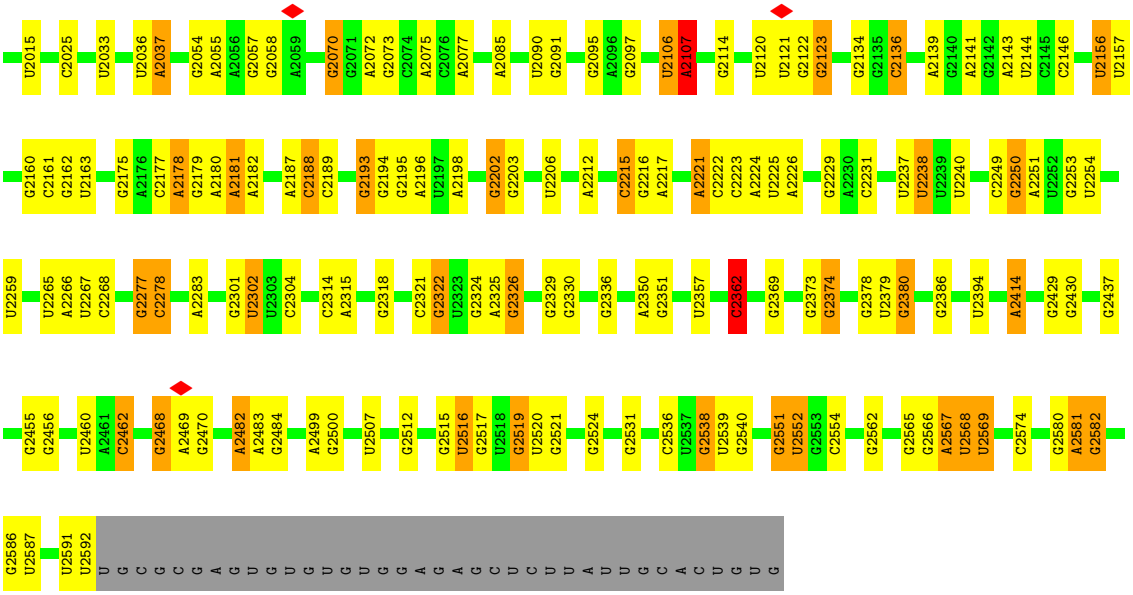


• Molecule 2: 5.8S-23S ribosomal RNA

Chain 1:

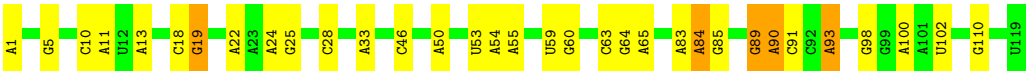






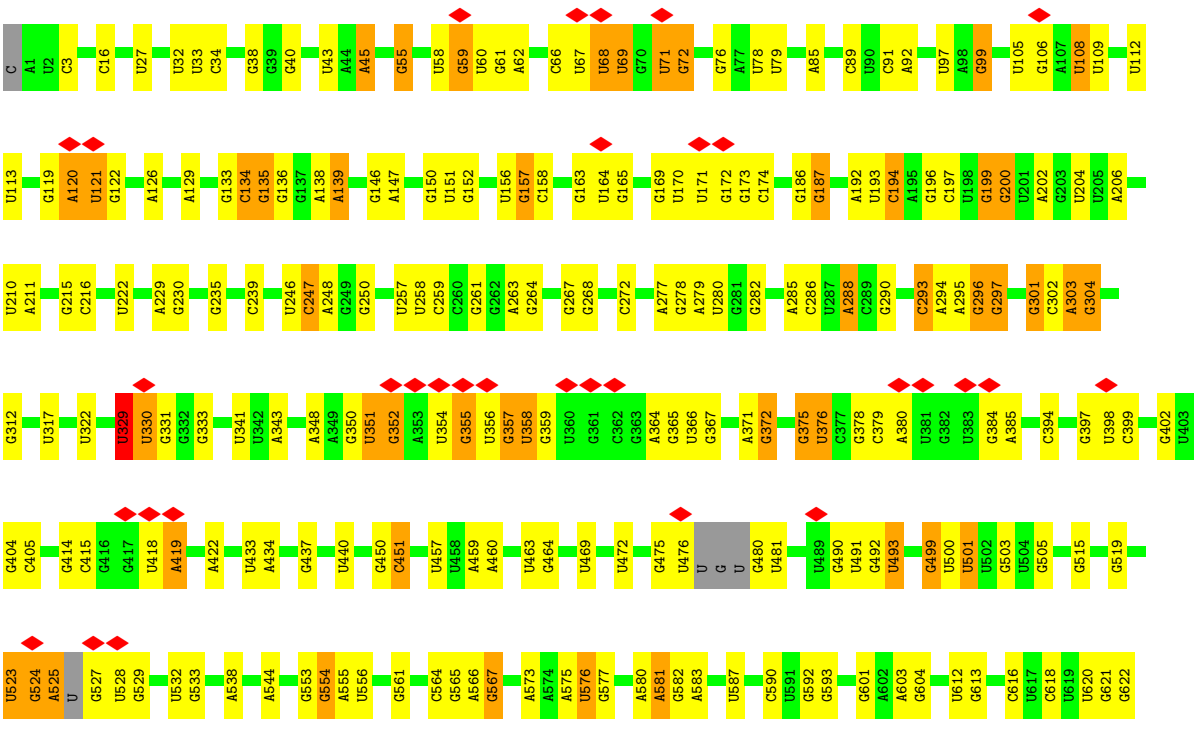
• Molecule 3: 5S ribosomal RNA

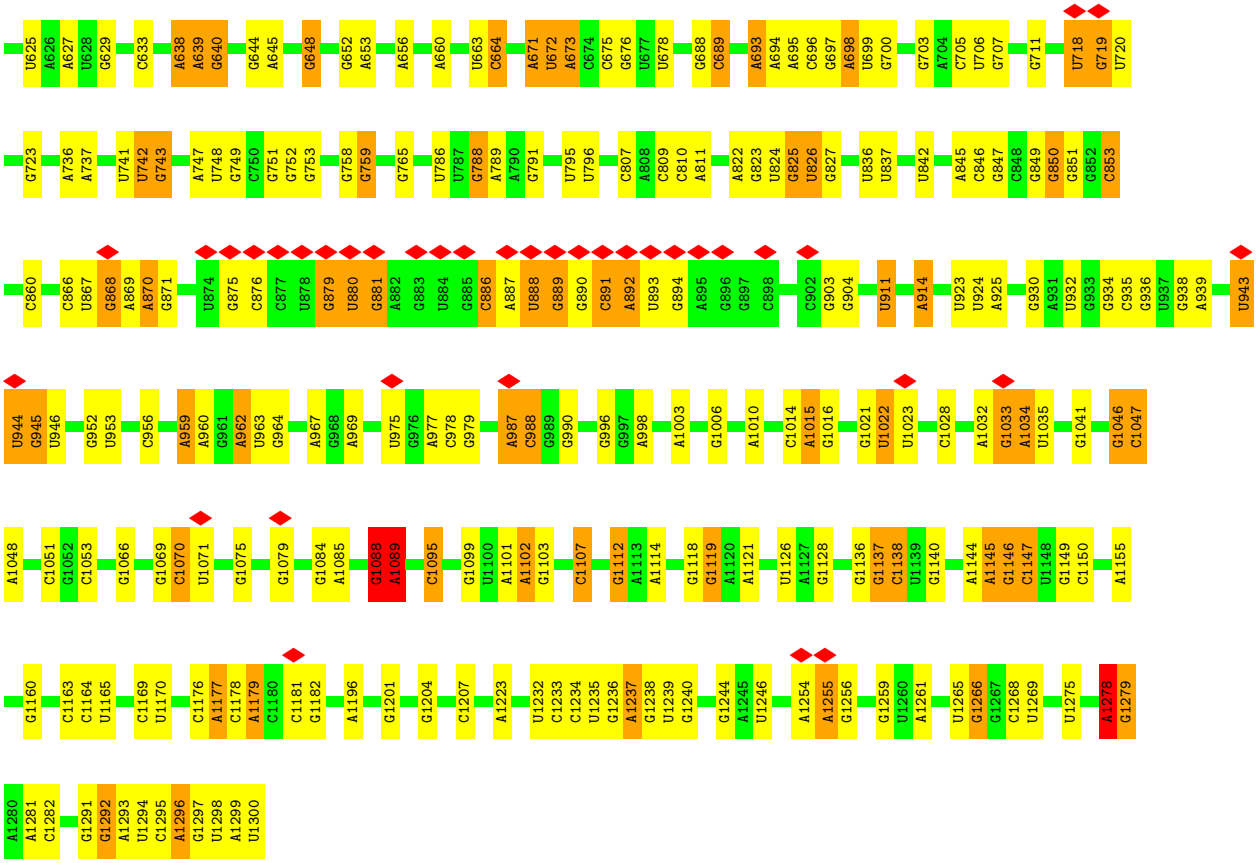
Chain 2:



• Molecule 4: 18S ribosomal RNA

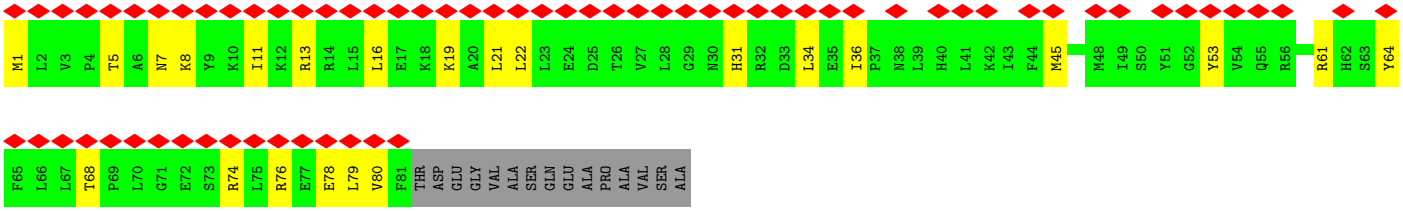
Chain 3:





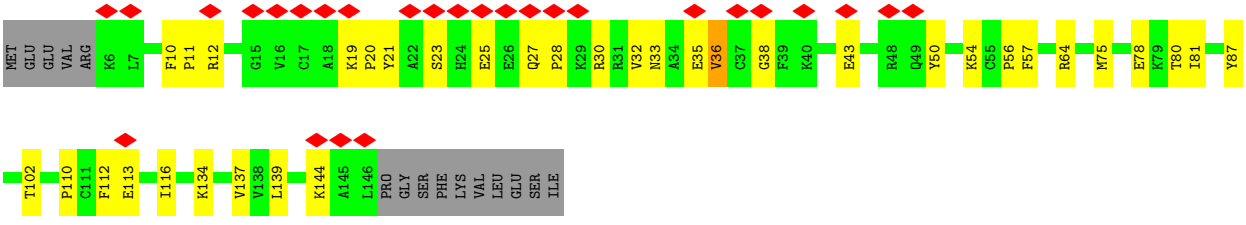
• Molecule 5: 40S RIBOSOMAL PROTEIN S10

Chain C0:



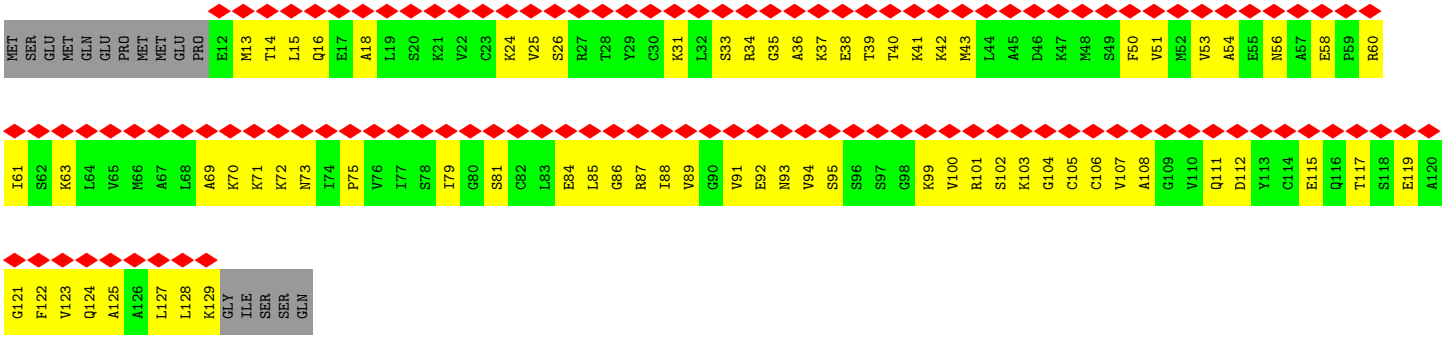
• Molecule 6: 40S RIBOSOMAL PROTEIN S11

Chain C1:



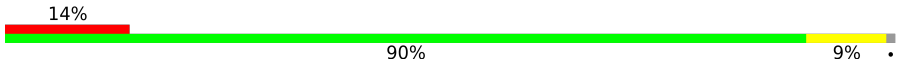
• Molecule 7: 40S RIBOSOMAL PROTEIN S12

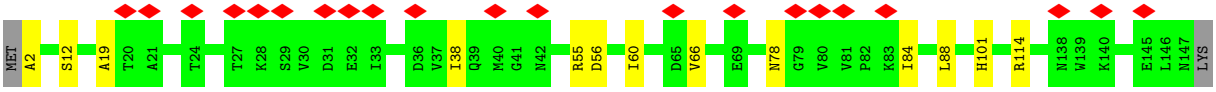
Chain C2:



• Molecule 8: 40S ribosomal protein S13

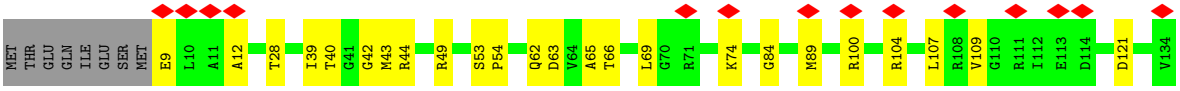
Chain C3:





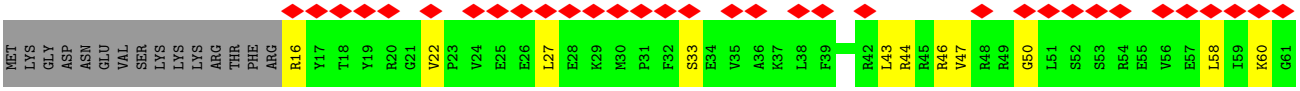
• Molecule 9: 40S ribosomal protein S14

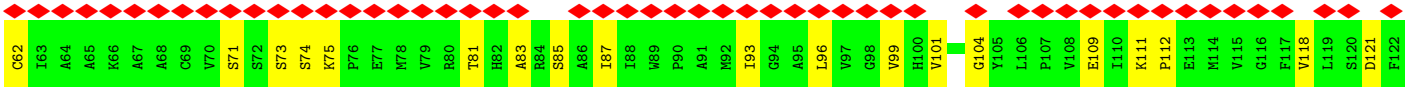
Chain C4:

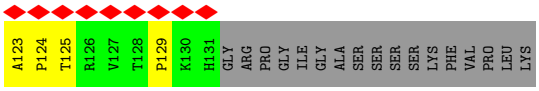


• Molecule 10: RIBOSOMAL PROTEIN S15

Chain C5:

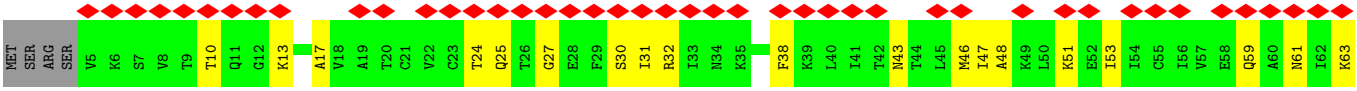


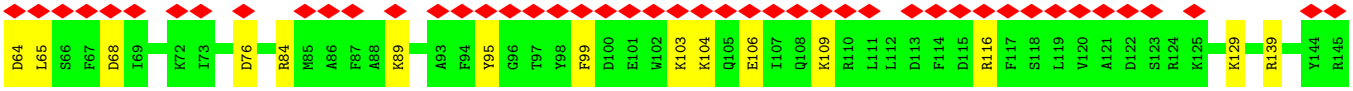




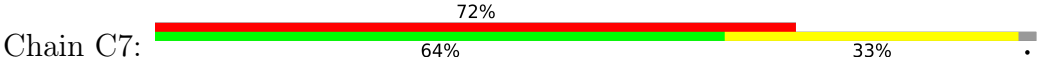
• Molecule 11: 40S RIBOSOMAL PROTEIN S16

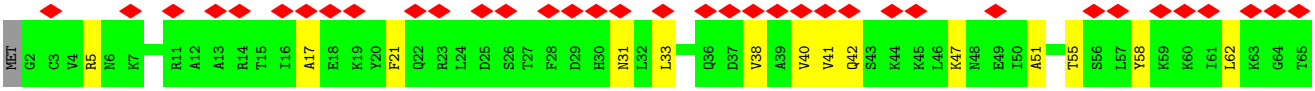
Chain C6:

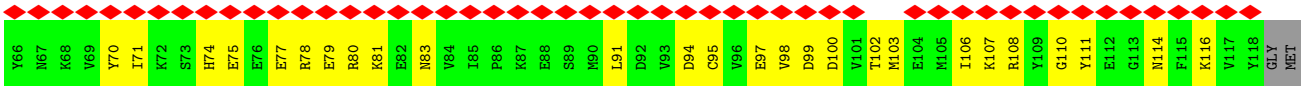




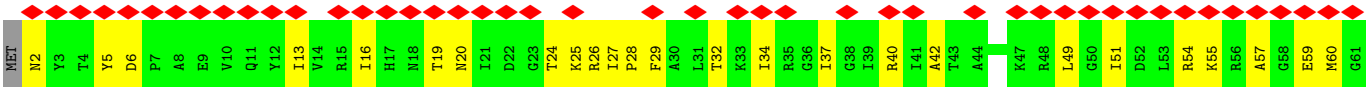
• Molecule 12: 40S ribosomal protein S17

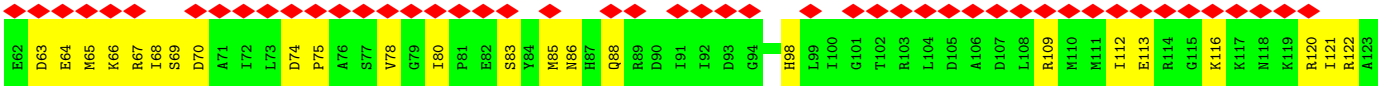


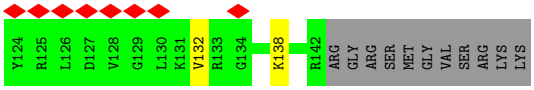




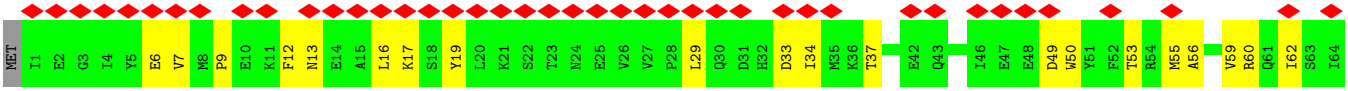
• Molecule 13: 40S ribosomal protein S18

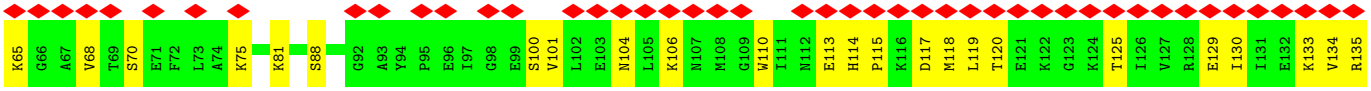




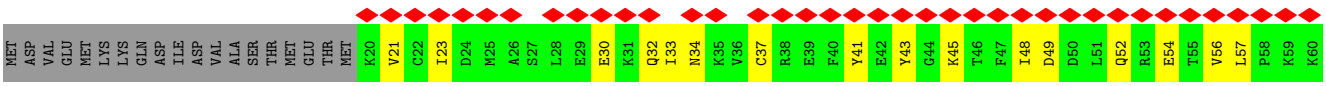


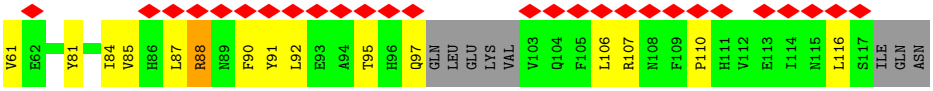
• Molecule 14: 40S ribosomal protein S19





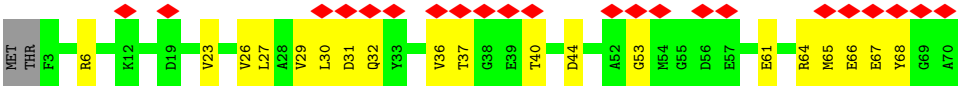
• Molecule 15: 40S RIBOSOMAL PROTEIN S20





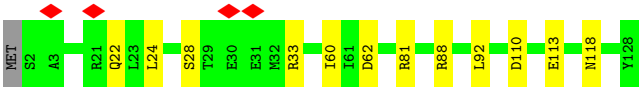
• Molecule 16: ECU11_0225 protein

Chain D1:



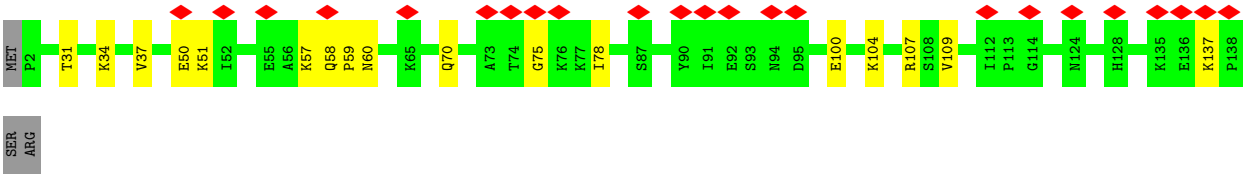
• Molecule 17: 40S RIBOSOMAL PROTEIN S15A (S22 in yeast)

Chain D2:



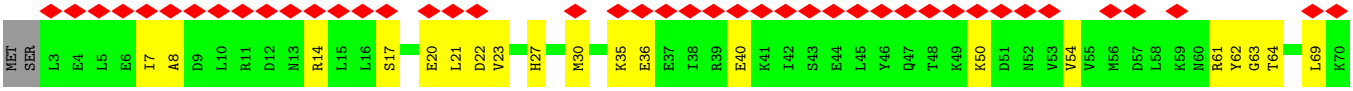
• Molecule 18: 40S ribosomal protein S23

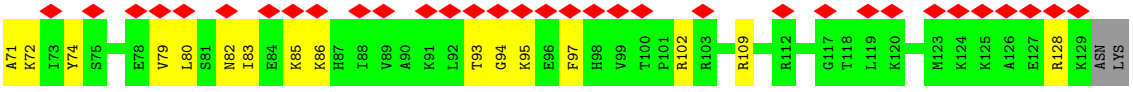
Chain D3:



• Molecule 19: 40S RIBOSOMAL PROTEIN S24

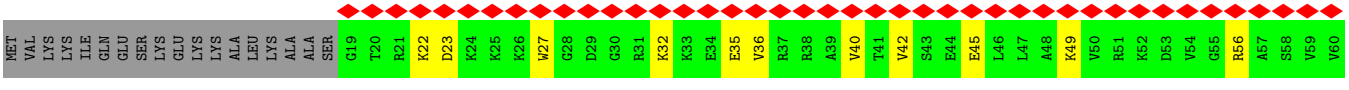
Chain D4:

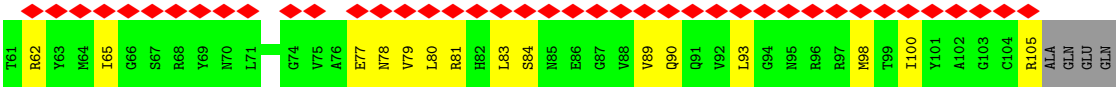




• Molecule 20: 40S ribosomal protein S25

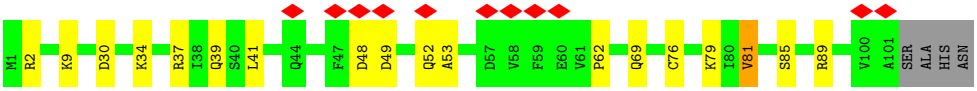
Chain D5:





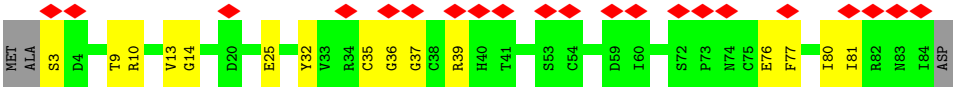
• Molecule 21: 40S ribosomal protein S26

Chain D6:



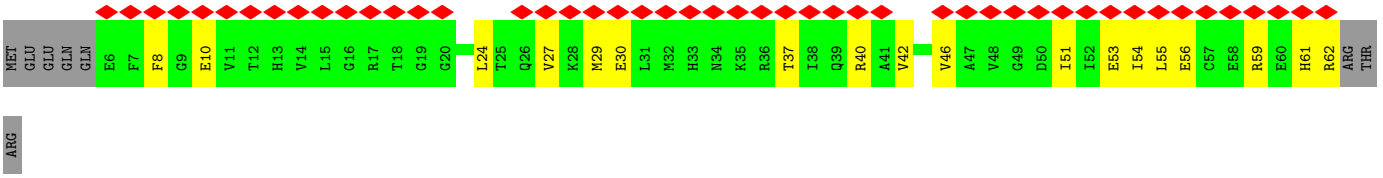
• Molecule 22: 40S RIBOSOMAL PROTEIN S27

Chain D7:



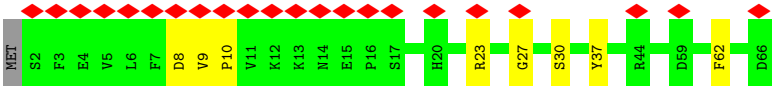
• Molecule 23: 40S RIBOSOMAL PROTEIN S28

Chain D8:



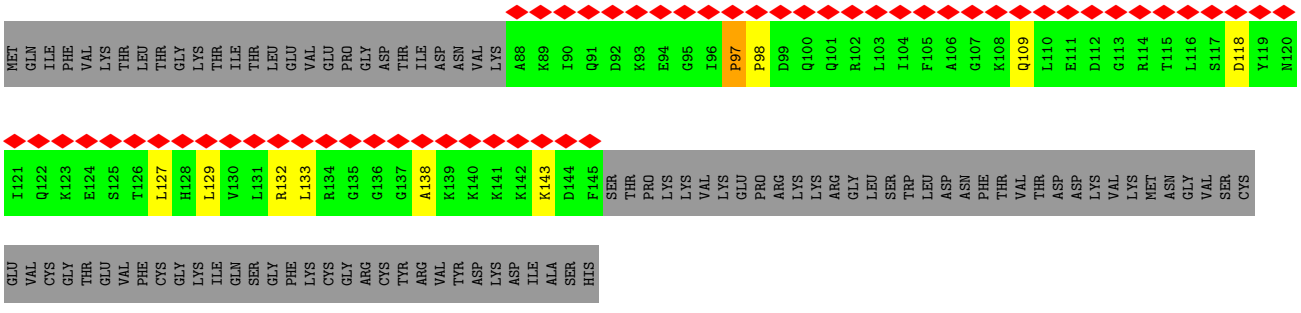
• Molecule 24: 40S ribosomal protein S29

Chain D9:



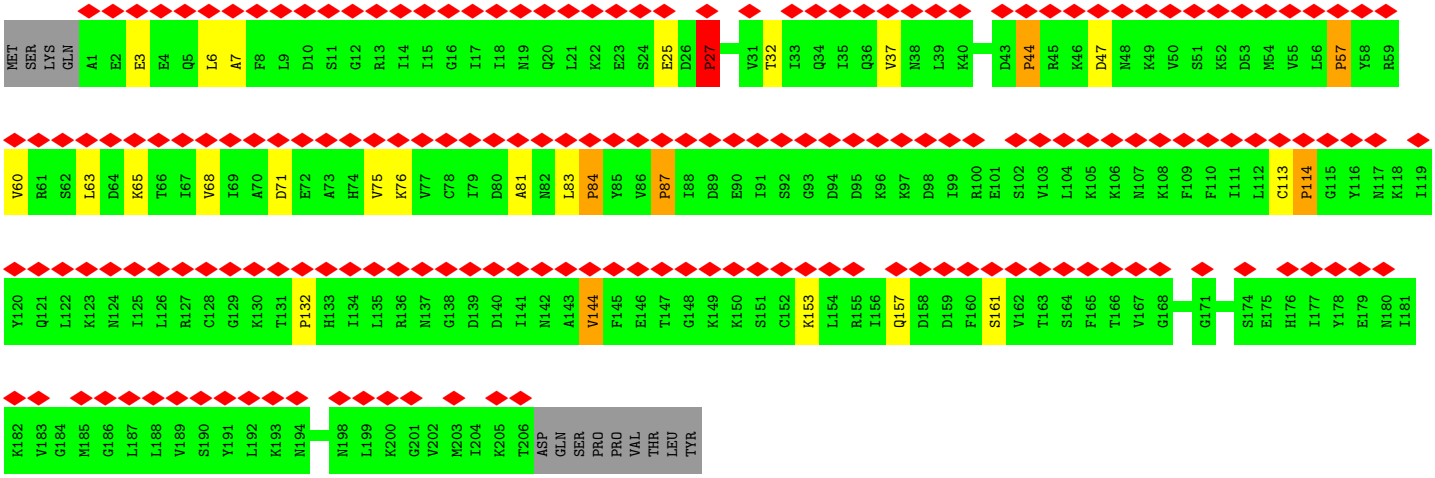
• Molecule 25: Similarity to monoubiquitin/carboxy-extension protein fusion

Chain E1:



• Molecule 26: 60S ribosomal protein L1

Chain L1:

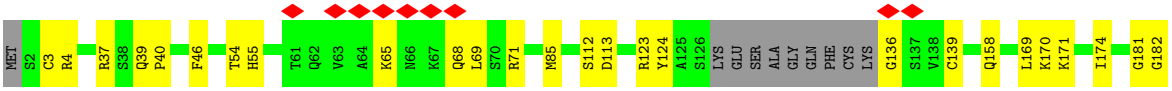


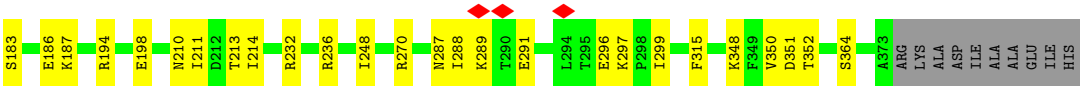
• Molecule 27: 60S ribosomal protein L8

Chain L2:

• Molecule 28: 60S ribosomal protein L3

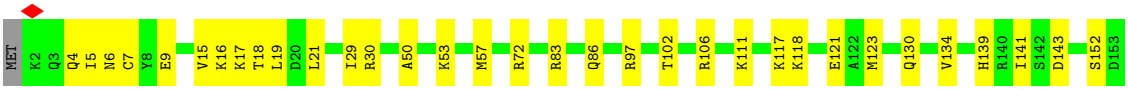
Chain L3:

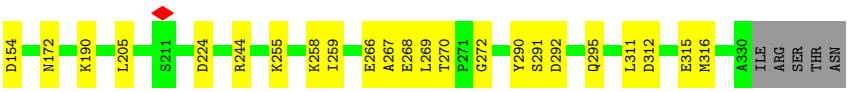




• Molecule 29: 60S RIBOSOMAL PROTEIN L4

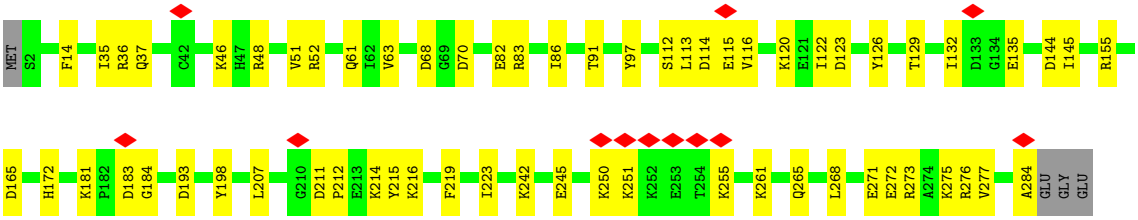
Chain L4:





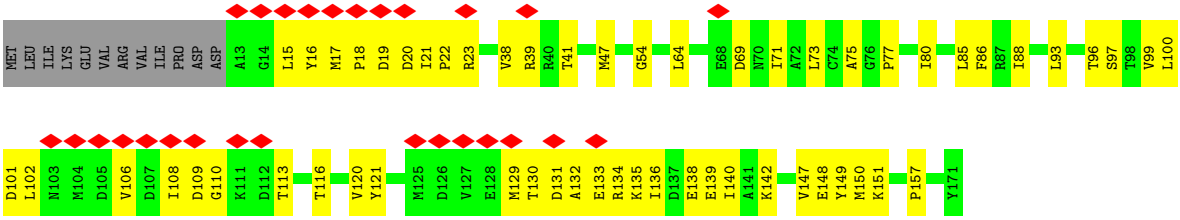
• Molecule 30: 60S RIBOSOMAL PROTEIN L5

Chain L5:



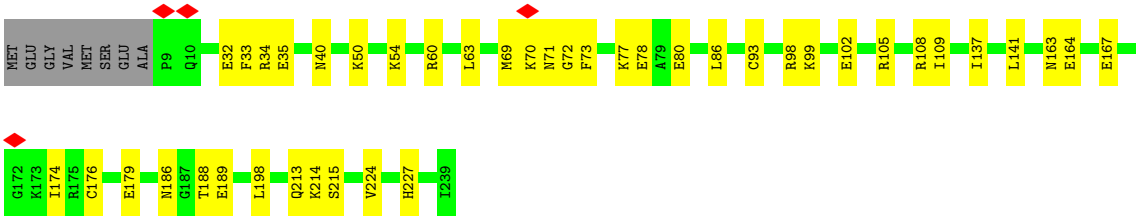
• Molecule 31: 60S RIBOSOMAL PROTEIN L6

Chain L6:



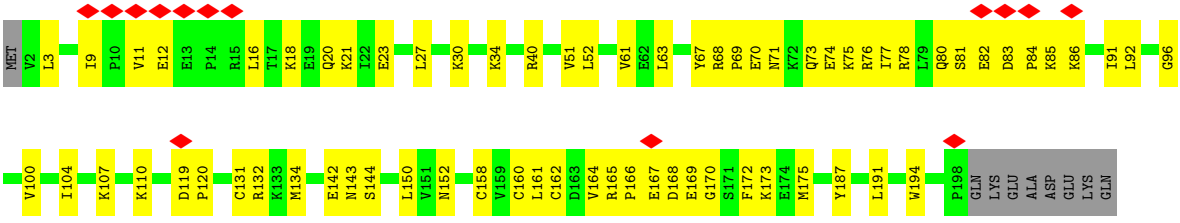
• Molecule 32: 60S ribosomal protein L7

Chain L7:



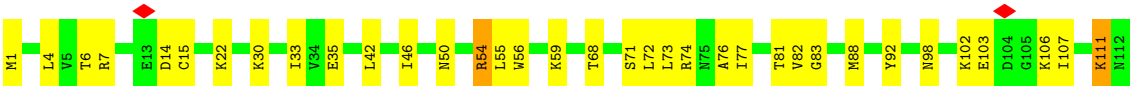
• Molecule 33: 60S ribosomal protein L7a

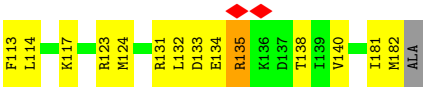
Chain L8:



• Molecule 34: 60S RIBOSOMAL PROTEIN L9

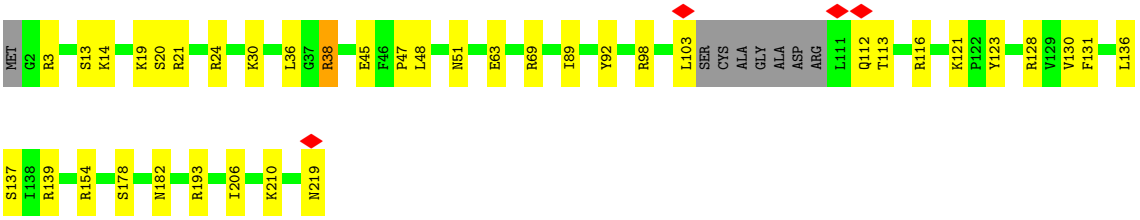
Chain L9:





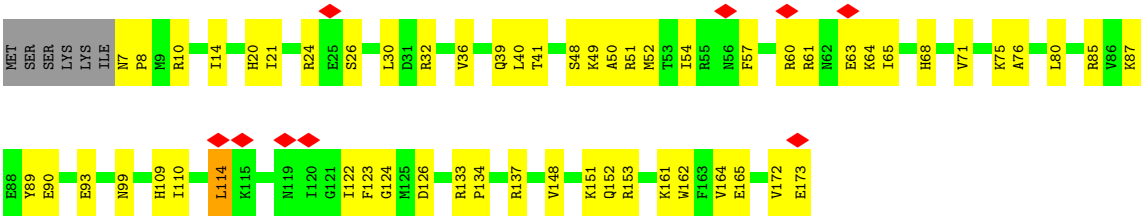
• Molecule 35: 60S ribosomal protein L10

Chain M0:



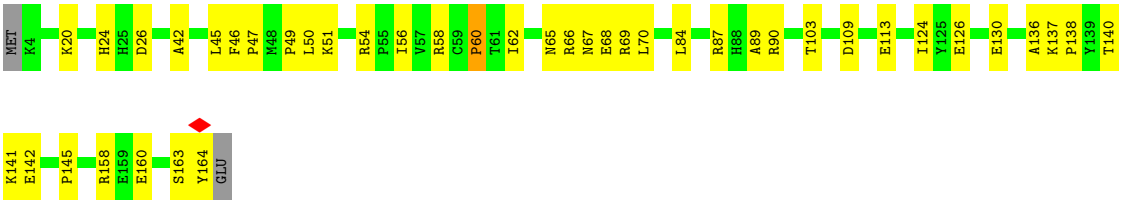
• Molecule 36: 60S ribosomal protein L11

Chain M1:



• Molecule 37: 60S RIBOSOMAL PROTEIN L13

Chain M3:

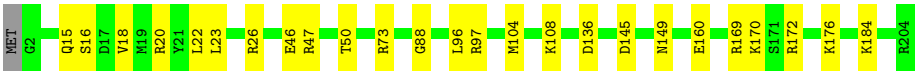


• Molecule 38: ECU06_1215 protein

Chain M4:

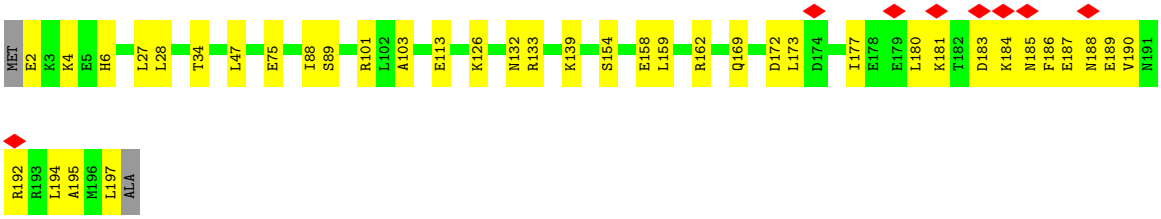
• Molecule 39: Ribosomal protein L15

Chain M5:



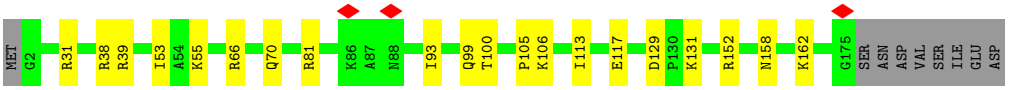
• Molecule 40: 60S RIBOSOMAL PROTEIN L13A (L16)

Chain M6:



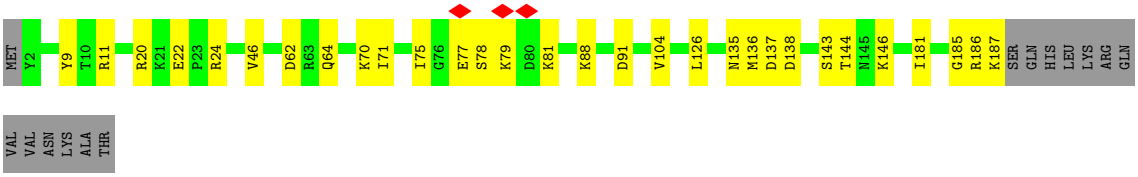
• Molecule 41: 60S RIBOSOMAL PROTEIN L17

Chain M7:



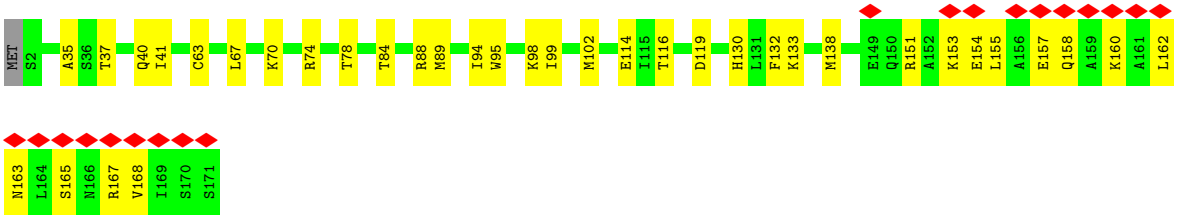
• Molecule 42: 60S RIBOSOMAL PROTEIN L18

Chain M8:



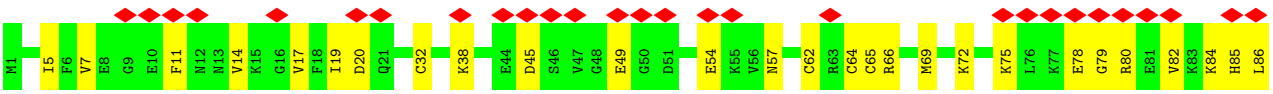
• Molecule 43: 60S RIBOSOMAL PROTEIN L19

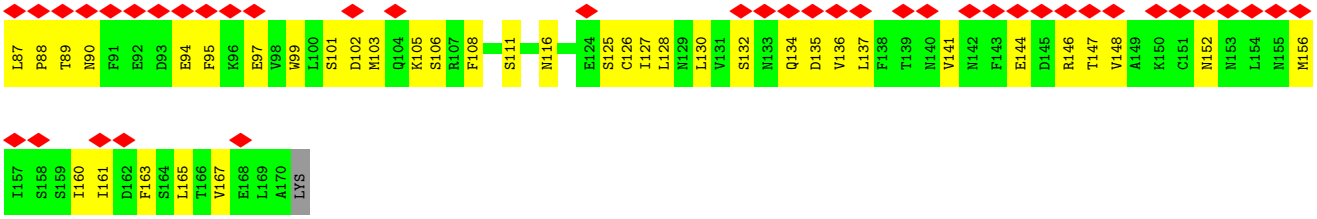
Chain M9:



• Molecule 44: Uncharacterized protein ECU01_0250

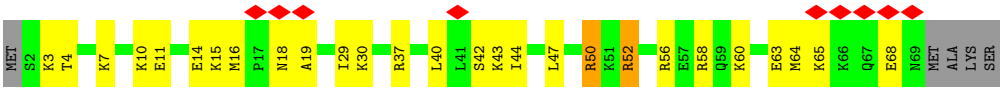
Chain MD:





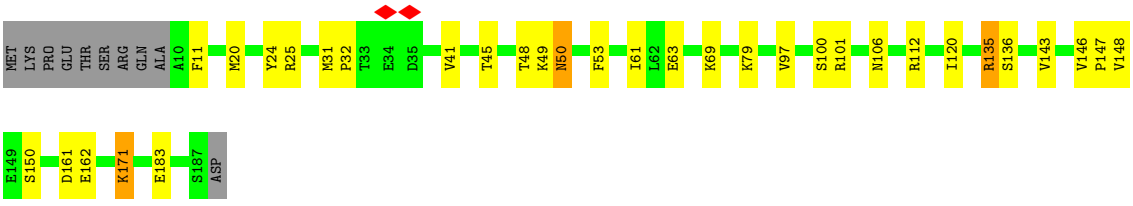
• Molecule 45: ECU06_1135 protein

Chain MS:



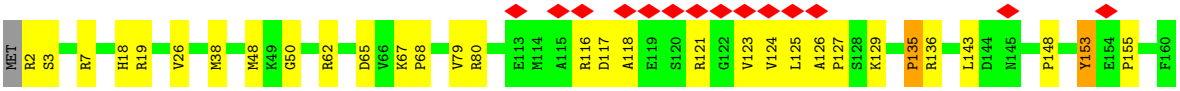
• Molecule 46: 60S ribosomal protein L20

Chain N0:



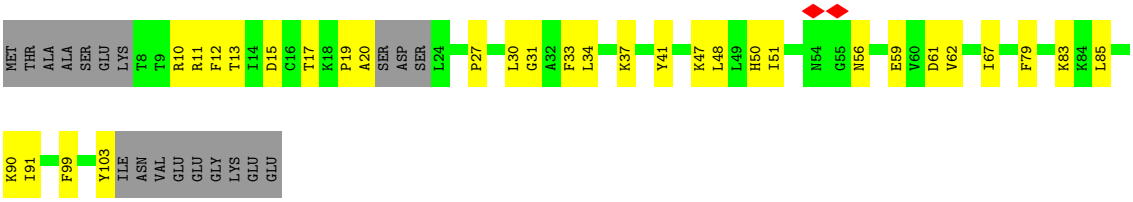
• Molecule 47: 60S ribosomal protein L21

Chain N1:



• Molecule 48: 60S ribosomal protein L22

Chain N2:

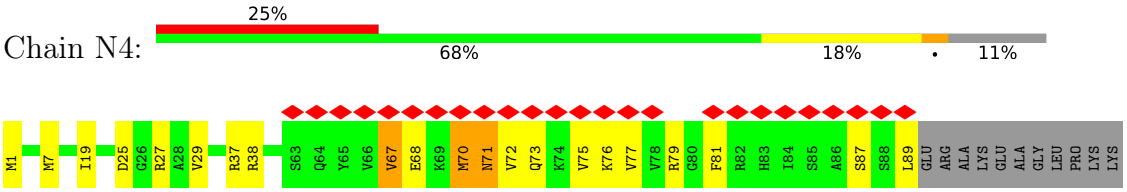


• Molecule 49: 60S ribosomal protein L23

Chain N3:

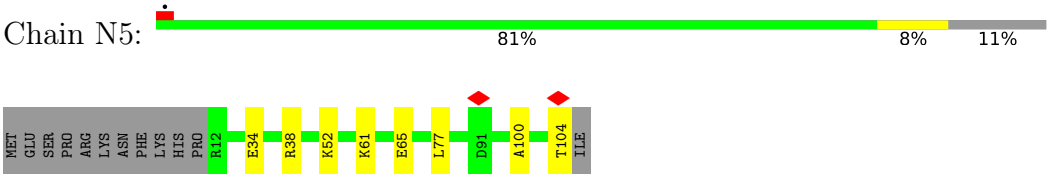
• Molecule 50: Similarity to 60S RIBOSOMAL PROTEIN L24

Chain N4:



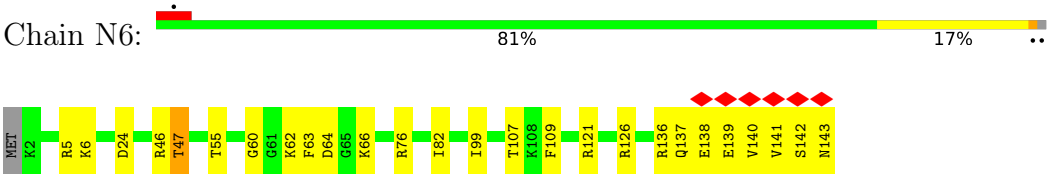
• Molecule 51: 60S RIBOSOMAL PROTEIN L23A

Chain N5:



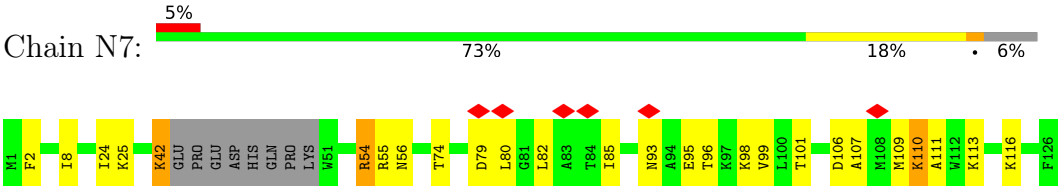
• Molecule 52: 60S RIBOSOMAL PROTEIN L26

Chain N6:



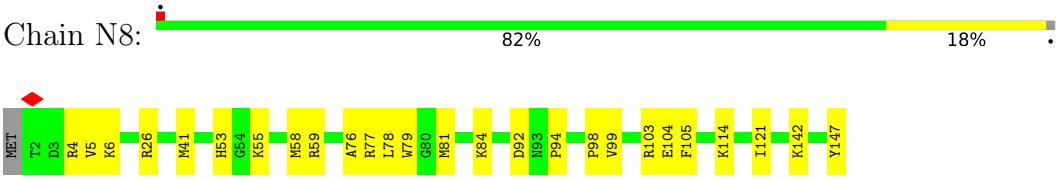
• Molecule 53: 60S RIBOSOMAL PROTEIN L27

Chain N7:



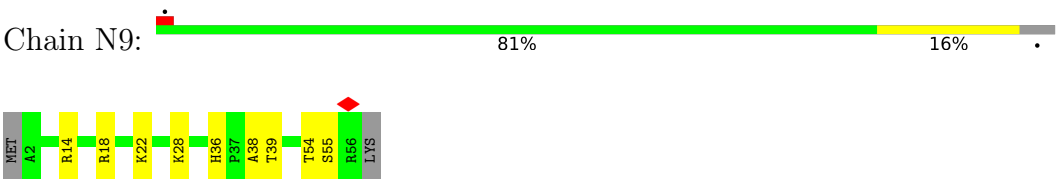
• Molecule 54: 60S ribosomal protein L27a

Chain N8:



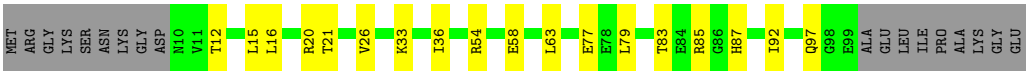
• Molecule 55: 60S ribosomal protein L29

Chain N9:



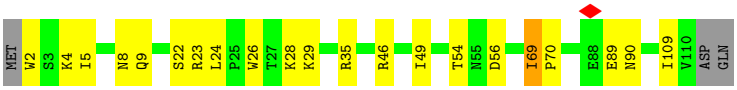
• Molecule 56: 60S RIBOSOMAL PROTEIN L30

Chain O0:



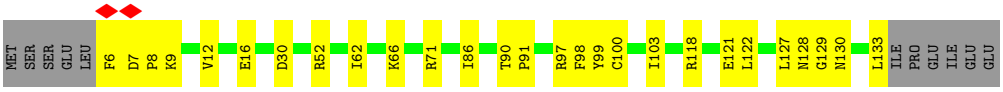
• Molecule 57: 60S ribosomal protein L31

Chain O1:



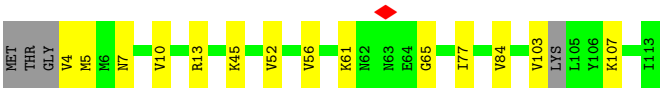
• Molecule 58: 60S ribosomal protein L32

Chain O2:



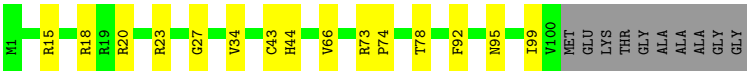
• Molecule 59: 60S RIBOSOMAL PROTEIN L35A (L33)

Chain O3:



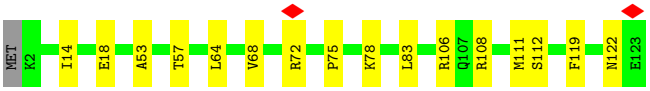
• Molecule 60: 60S ribosomal protein L34

Chain O4:



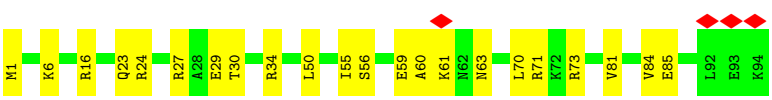
• Molecule 61: 60S ribosomal protein L35-1

Chain O5:



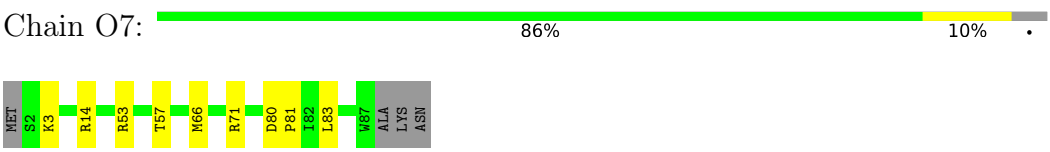
• Molecule 62: 60S ribosomal protein L36

Chain O6:



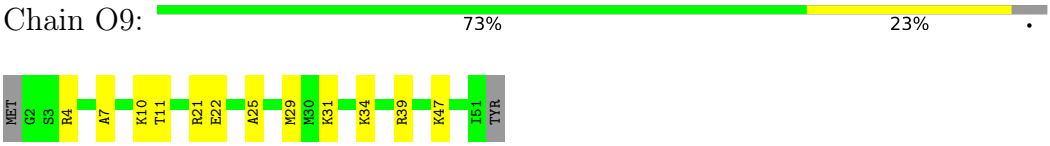
• Molecule 63: 60S ribosomal protein L37

Chain O7:



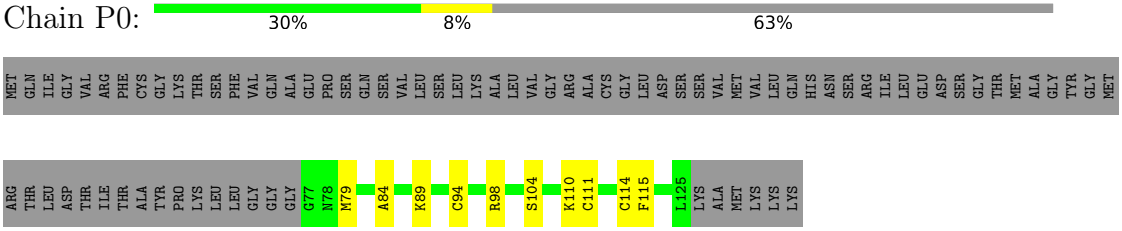
• Molecule 64: 60S ribosomal protein L39

Chain O9:



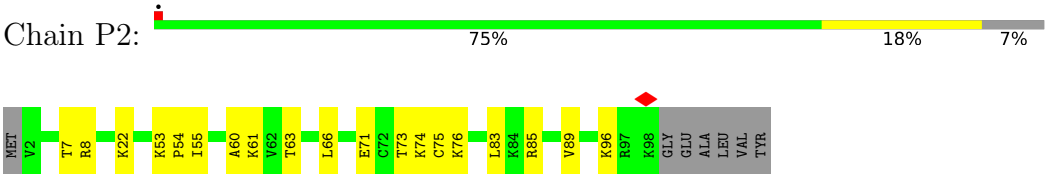
• Molecule 65: UBIQUITIN/ L40 RIBOSOMAL PROTEIN FUSION

Chain P0:



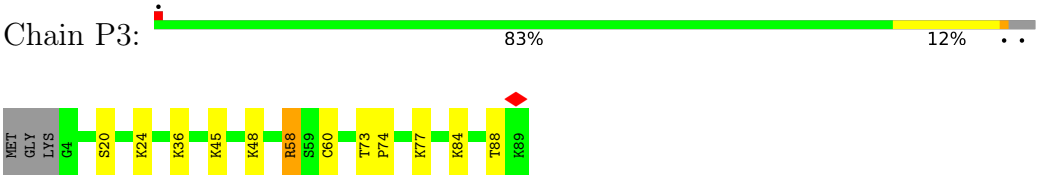
• Molecule 66: 60S ribosomal protein L44

Chain P2:



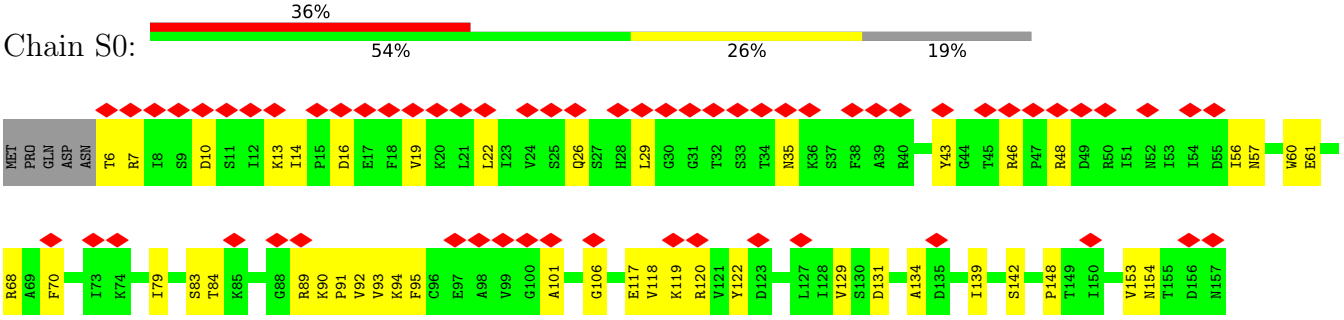
• Molecule 67: 60S RIBOSOMAL PROTEIN L37A (L43)

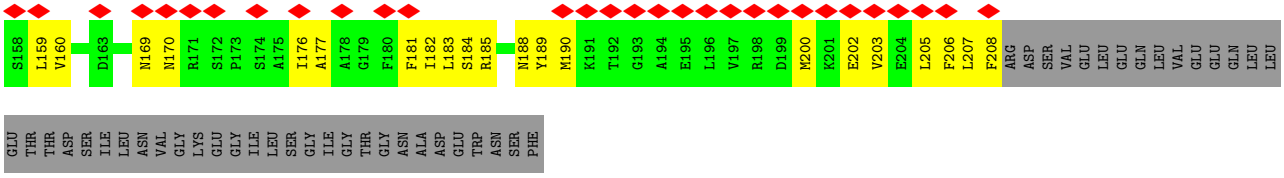
Chain P3:



• Molecule 68: 40S ribosomal protein S0

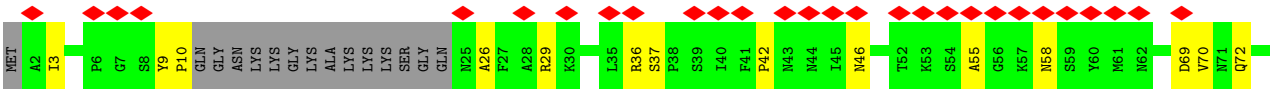
Chain S0:

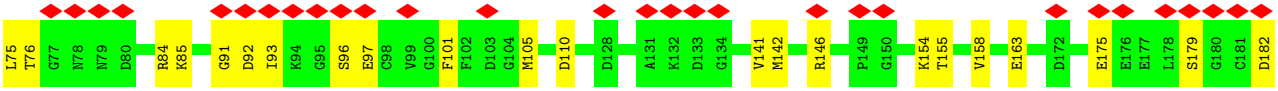




• Molecule 69: 40S ribosomal protein S1

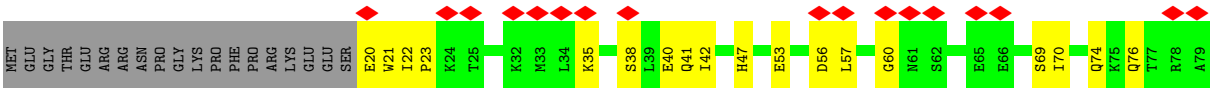
Chain S1:

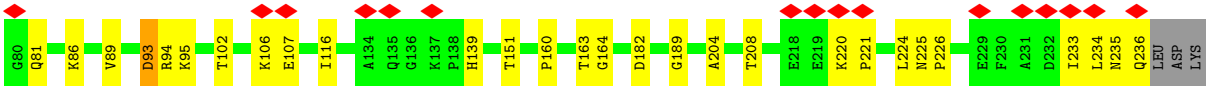




• Molecule 70: 40S RIBOSOMAL PROTEIN S2

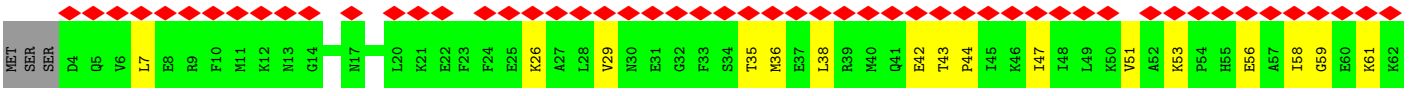
Chain S2:

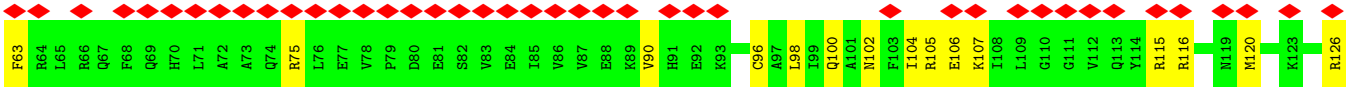




• Molecule 71: 40S ribosomal protein S3

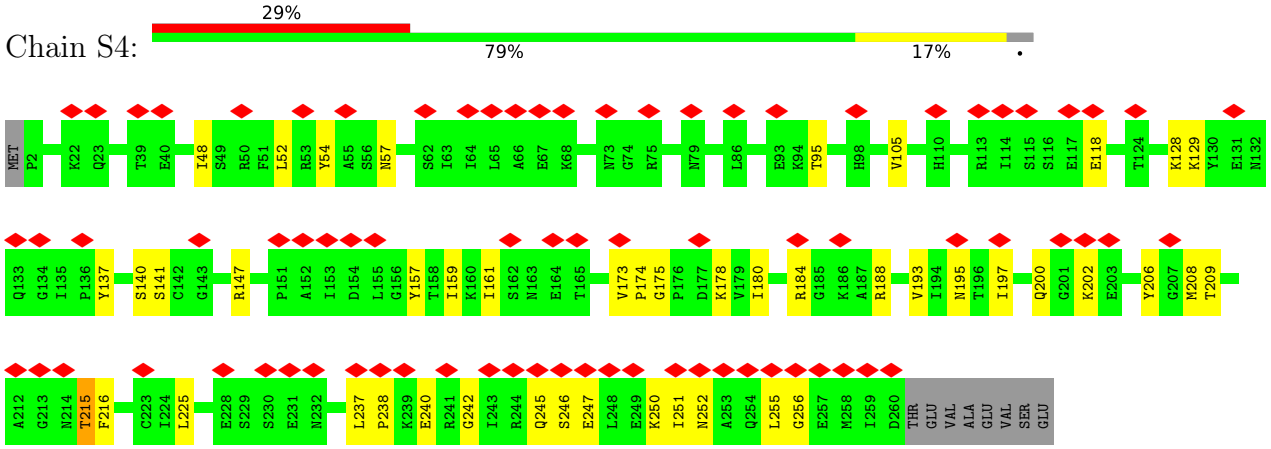
Chain S3:





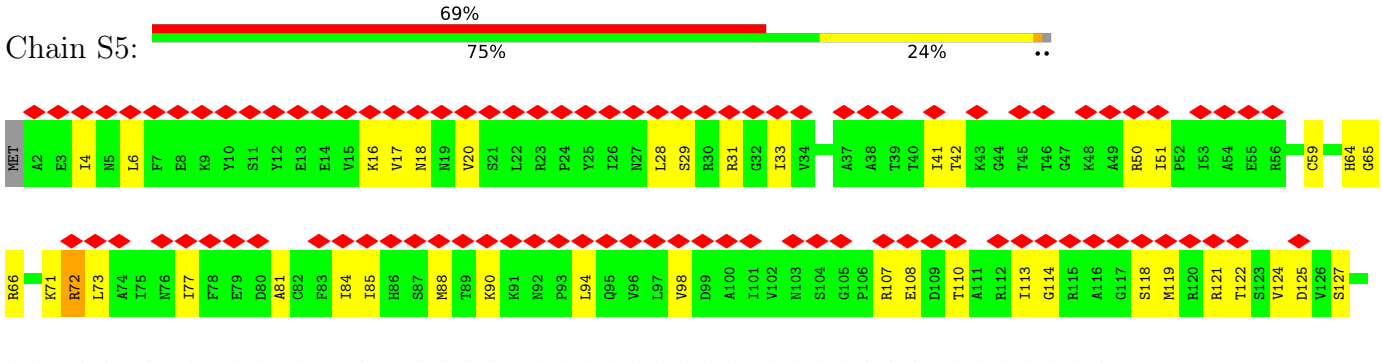
• Molecule 72: 40S ribosomal protein S4

Chain S4:



• Molecule 73: 40S ribosomal protein S5

Chain S5:

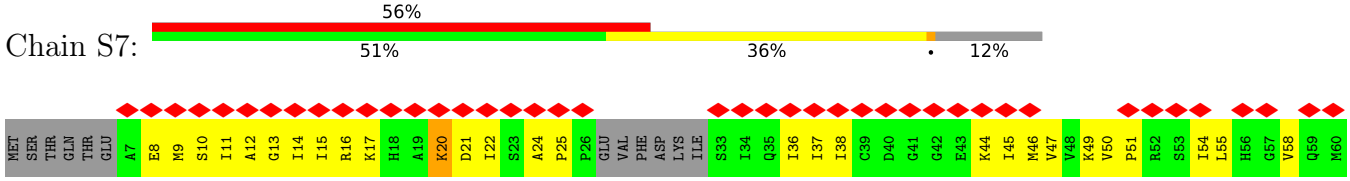


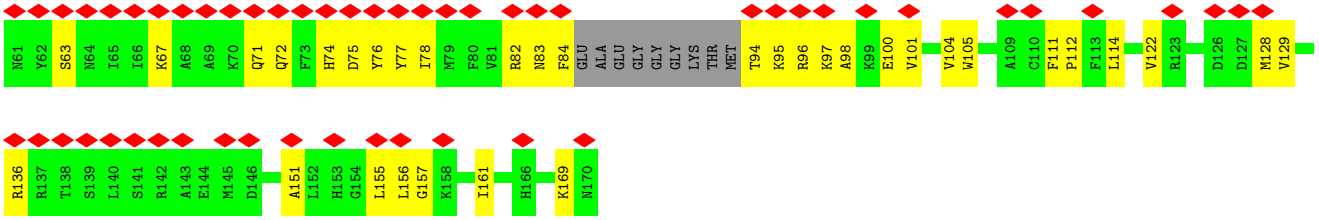
• Molecule 74: 40S ribosomal protein S6

Chain S6:

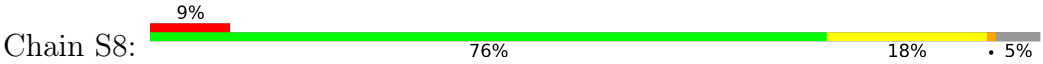
• Molecule 75: 40S ribosomal protein S7

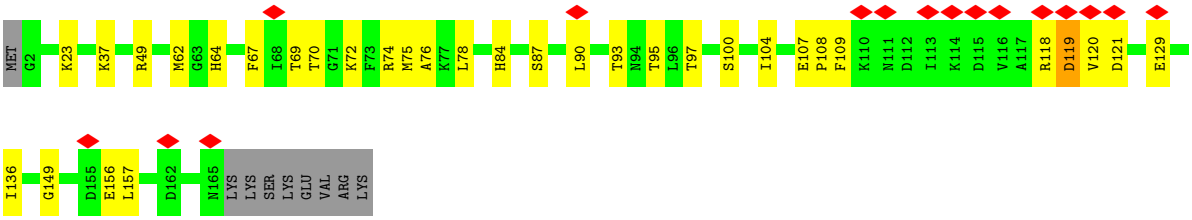
Chain S7:



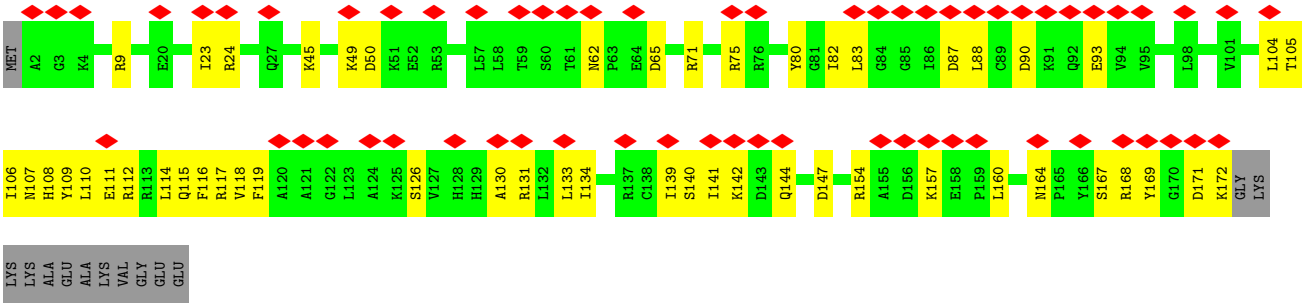


• Molecule 76: 40S ribosomal protein S8





• Molecule 77: 40S ribosomal protein S9



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	108005	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.928	Depositor
Minimum map value	-0.411	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	440.832, 440.832, 440.832	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.861, 0.861, 0.861	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, AMP, 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	RA	0.39	0/2576	0.58	0/3470
2	1	1.09	25/55780 (0.0%)	1.14	190/87016 (0.2%)
3	2	0.91	0/2854	0.86	3/4449 (0.1%)
4	3	1.14	6/31169 (0.0%)	1.03	51/48638 (0.1%)
5	C0	0.40	0/701	0.55	0/943
6	C1	0.50	0/1150	0.57	0/1543
7	C2	0.30	0/884	0.50	0/1180
8	C3	0.49	0/1190	0.56	0/1601
9	C4	0.44	0/952	0.60	0/1276
10	C5	0.41	0/923	0.53	0/1246
11	C6	0.48	0/1150	0.55	0/1538
12	C7	0.42	0/975	0.52	0/1306
13	C8	0.42	0/1133	0.62	0/1516
14	C9	0.44	0/1109	0.55	0/1490
15	D0	0.41	0/794	0.65	2/1066 (0.2%)
16	D1	0.40	0/522	0.49	0/701
17	D2	0.49	0/1029	0.60	0/1375
18	D3	0.47	0/1068	0.60	0/1430
19	D4	0.37	0/1070	0.51	0/1426
20	D5	0.37	0/696	0.57	0/928
21	D6	0.47	0/813	0.57	0/1082
22	D7	0.48	0/645	0.53	0/865
23	D8	0.39	0/451	0.63	0/603
24	D9	0.55	0/538	0.66	1/718 (0.1%)
25	E1	0.26	0/275	0.65	2/375 (0.5%)
26	L1	0.27	0/1015	0.64	7/1411 (0.5%)
27	L2	0.42	0/1788	0.58	0/2408
28	L3	0.42	0/2876	0.59	0/3854
29	L4	0.40	0/2634	0.58	1/3533 (0.0%)
30	L5	0.36	0/2315	0.47	0/3097
31	L6	0.33	0/1299	0.48	0/1753
32	L7	0.39	0/1936	0.51	0/2580

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	L8	0.33	0/1600	0.49	1/2156 (0.0%)
34	L9	0.36	0/1462	0.53	0/1961
35	M0	0.40	0/1738	0.55	0/2319
36	M1	0.32	0/1357	0.50	0/1813
37	M3	0.41	0/1333	0.54	0/1785
38	M4	0.33	0/857	0.48	0/1150
39	M5	0.49	0/1684	0.58	0/2244
40	M6	0.40	0/1602	0.50	0/2142
41	M7	0.42	0/1389	0.56	0/1865
42	M8	0.38	0/1494	0.51	0/2003
43	M9	0.36	0/1413	0.48	0/1866
44	MD	0.28	0/1368	0.51	0/1842
45	MS	0.38	0/597	0.51	0/782
46	N0	0.41	0/1470	0.52	0/1980
47	N1	0.45	0/1313	0.62	1/1759 (0.1%)
48	N2	0.29	0/748	0.49	0/1001
49	N3	0.38	0/1074	0.60	0/1438
50	N4	0.36	0/719	0.52	0/959
51	N5	0.40	0/730	0.56	0/983
52	N6	0.38	0/1187	0.52	0/1576
53	N7	0.33	0/954	0.46	0/1279
54	N8	0.48	0/1230	0.69	0/1648
55	N9	0.39	0/447	0.58	0/597
56	O0	0.34	0/701	0.49	0/939
57	O1	0.37	0/889	0.51	0/1194
58	O2	0.43	0/1084	0.60	0/1448
59	O3	0.40	0/876	0.58	0/1180
60	O4	0.42	0/817	0.53	0/1085
61	O5	0.36	0/988	0.47	0/1314
62	O6	0.33	0/742	0.46	0/988
63	O7	0.45	0/702	0.65	0/927
64	O9	0.38	0/441	0.56	0/580
65	P0	0.37	0/383	0.51	0/503
66	P2	0.39	0/800	0.58	0/1056
67	P3	0.40	0/673	0.52	0/893
68	S0	0.36	0/1615	0.49	0/2189
69	S1	0.44	0/1701	0.55	0/2275
70	S2	0.43	0/1660	0.55	0/2238
71	S3	0.41	0/1684	0.54	0/2263
72	S4	0.43	0/2087	0.55	0/2810
73	S5	0.39	0/1478	0.57	0/1989
74	S6	0.40	0/1700	0.56	0/2259
75	S7	0.36	0/1191	0.49	0/1602

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	S8	0.47	0/1323	0.59	1/1769 (0.1%)
77	S9	0.38	0/1397	0.52	0/1874
All	All	0.84	31/177008 (0.0%)	0.89	260/256940 (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
1	RA	0	1
6	C1	0	1
7	C2	0	1
14	C9	0	1
32	L7	0	1
34	L9	0	2
37	M3	0	1
43	M9	0	1
50	N4	0	2
62	O6	0	1
70	S2	0	1
72	S4	0	1
74	S6	0	1
All	All	0	15

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	2193	G	C8-N7	-6.47	1.27	1.30
2	1	816	G	C8-N7	-6.07	1.27	1.30
2	1	472	G	C8-N7	-5.88	1.27	1.30
2	1	2322	G	C8-N7	-5.55	1.27	1.30
2	1	1017	A	C8-N7	-5.54	1.27	1.31
2	1	689	A	C8-N7	-5.46	1.27	1.31
2	1	2455	G	C8-N7	-5.41	1.27	1.30
2	1	798	G	C6-N1	-5.40	1.35	1.39
2	1	816	G	C6-N1	-5.39	1.35	1.39
2	1	477	A	N7-C5	-5.35	1.36	1.39
2	1	119	G	N7-C5	-5.33	1.36	1.39
2	1	489	G	C8-N7	-5.31	1.27	1.30
2	1	2336	G	C8-N7	-5.28	1.27	1.30
2	1	2250	G	N7-C5	-5.24	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	3	472	U	C2-N3	-5.23	1.34	1.37
2	1	124	A	C8-N7	-5.23	1.27	1.31
4	3	644	G	C8-N7	-5.23	1.27	1.30
2	1	473	A	N7-C5	-5.23	1.36	1.39
2	1	1761	G	C8-N7	-5.20	1.27	1.30
2	1	1766	G	C8-N7	-5.18	1.27	1.30
2	1	2322	G	C6-O6	-5.17	1.19	1.24
4	3	645	A	N7-C5	-5.14	1.36	1.39
2	1	791	G	C8-N7	-5.13	1.27	1.30
4	3	451	C	N3-C4	-5.12	1.30	1.33
2	1	519	A	C1'-N9	-5.10	1.39	1.46
2	1	1387	G	C8-N7	-5.07	1.27	1.30
4	3	644	G	N7-C5	-5.06	1.36	1.39
2	1	1018	A	N7-C5	-5.06	1.36	1.39
4	3	469	U	C2-N3	-5.05	1.34	1.37
2	1	1125	G	C8-N7	-5.02	1.27	1.30
2	1	1760	G	N7-C5	-5.01	1.36	1.39

All (260) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	3	451	C	N3-C2-O2	-11.03	114.18	121.90
2	1	2249	C	C6-N1-C2	-10.79	115.99	120.30
2	1	431	G	O4'-C1'-N9	9.04	115.43	108.20
4	3	451	C	N1-C2-O2	8.44	123.96	118.90
2	1	129	U	N3-C2-O2	-8.09	116.54	122.20
2	1	2156	U	C2-N1-C1'	8.08	127.40	117.70
2	1	1521	C	C6-N1-C2	-7.95	117.12	120.30
2	1	1083	C	C6-N1-C2	-7.93	117.13	120.30
2	1	2107	A	O4'-C1'-N9	7.91	114.53	108.20
2	1	128	A	N1-C6-N6	-7.91	113.86	118.60
2	1	487	G	N3-C4-C5	-7.91	124.65	128.60
4	3	853	C	N1-C2-O2	7.85	123.61	118.90
4	3	853	C	N3-C2-O2	-7.59	116.59	121.90
2	1	1998	U	N3-C2-O2	-7.42	117.01	122.20
4	3	91	C	C6-N1-C2	-7.30	117.38	120.30
2	1	1769	G	O5'-P-OP2	-7.27	99.16	105.70
4	3	451	C	C6-N1-C2	-7.27	117.39	120.30
2	1	609	C	C6-N1-C2	-7.25	117.40	120.30
2	1	1176	U	N3-C2-O2	-7.25	117.13	122.20
2	1	1647	A	O4'-C1'-N9	7.21	113.97	108.20
4	3	257	U	N3-C2-O2	-7.17	117.18	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	L1	27	PRO	N-CA-CB	7.03	111.74	103.30
2	1	200	U	C2-N1-C1'	7.02	126.12	117.70
2	1	2250	G	O5'-P-OP2	-7.00	99.40	105.70
2	1	2025	C	C6-N1-C2	-6.97	117.51	120.30
2	1	2362	C	C2-N1-C1'	6.97	126.46	118.80
2	1	127	C	C6-N1-C2	-6.94	117.52	120.30
24	D9	23	ARG	C-N-CA	6.92	139.01	121.70
4	3	1292	G	N1-C6-O6	-6.90	115.76	119.90
3	2	102	U	N3-C2-O2	-6.78	117.46	122.20
2	1	660	G	C8-N9-C4	-6.68	103.73	106.40
4	3	45	A	C8-N9-C4	-6.66	103.14	105.80
2	1	2194	G	N1-C6-O6	-6.64	115.91	119.90
26	L1	57	PRO	N-CA-CB	6.60	111.22	103.30
2	1	1211	U	N3-C2-O2	-6.56	117.61	122.20
26	L1	114	PRO	N-CA-CB	6.53	111.14	103.30
4	3	375	G	O4'-C1'-N9	6.53	113.42	108.20
2	1	1176	U	C2-N1-C1'	6.52	125.53	117.70
2	1	659	C	C6-N1-C2	-6.50	117.70	120.30
2	1	2324	G	N1-C6-O6	-6.50	116.00	119.90
2	1	1079	A	C8-N9-C4	-6.49	103.20	105.80
26	L1	44	PRO	N-CA-CB	6.49	111.08	103.30
2	1	673	G	C8-N9-C4	-6.47	103.81	106.40
15	D0	43	TYR	CB-CG-CD2	-6.45	117.13	121.00
2	1	790	G	C8-N9-C4	-6.44	103.83	106.40
2	1	2362	C	C6-N1-C2	-6.39	117.74	120.30
47	N1	50	GLY	C-N-CA	-6.39	105.73	121.70
2	1	1128	U	C5-C6-N1	-6.38	119.51	122.70
2	1	976	G	C4-N9-C1'	6.38	134.80	126.50
2	1	1081	A	C8-N9-C4	-6.37	103.25	105.80
2	1	200	U	N3-C2-O2	-6.35	117.75	122.20
3	2	102	U	N1-C2-O2	6.34	127.24	122.80
2	1	2253	G	C8-N9-C4	-6.34	103.86	106.40
2	1	134	G	O4'-C1'-N9	6.34	113.27	108.20
2	1	551	G	C2-N3-C4	6.34	115.07	111.90
4	3	277	A	C8-N9-C4	-6.32	103.27	105.80
2	1	473	A	C8-N9-C4	-6.32	103.27	105.80
4	3	469	U	C2-N3-C4	6.31	130.79	127.00
2	1	2206	U	C5-C6-N1	-6.30	119.55	122.70
2	1	1777	U	N3-C2-O2	-6.28	117.80	122.20
2	1	134	G	O5'-P-OP1	6.28	118.23	110.70
2	1	200	U	N1-C2-O2	6.28	127.19	122.80
4	3	853	C	C2-N1-C1'	6.27	125.69	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	3	451	C	C2-N1-C1'	6.24	125.66	118.80
2	1	2554	C	N3-C2-O2	-6.23	117.54	121.90
2	1	465	C	C6-N1-C2	-6.22	117.81	120.30
26	L1	87	PRO	N-CA-CB	6.22	110.76	103.30
4	3	978	C	C2-N1-C1'	6.20	125.62	118.80
76	S8	119	ASP	CB-CG-OD1	-6.19	112.73	118.30
4	3	450	G	C4-N9-C1'	6.17	134.53	126.50
2	1	2177	C	C6-N1-C2	-6.16	117.84	120.30
4	3	695	A	C2-N3-C4	6.16	113.68	110.60
2	1	1484	U	N3-C2-O2	-6.15	117.89	122.20
2	1	552	A	C8-N9-C4	-6.11	103.36	105.80
2	1	613	C	C5-C4-N4	6.09	124.47	120.20
2	1	2329	G	O4'-C1'-N9	6.08	113.07	108.20
2	1	1987	G	C8-N9-C4	-6.08	103.97	106.40
4	3	1128	G	O4'-C1'-N9	6.08	113.06	108.20
2	1	2249	C	C6-N1-C1'	6.05	128.06	120.80
2	1	2202	G	C8-N9-C4	-6.05	103.98	106.40
2	1	702	C	C6-N1-C2	-6.04	117.88	120.30
2	1	381	U	N3-C2-O2	-6.00	118.00	122.20
2	1	2362	C	N3-C2-O2	-5.99	117.70	121.90
2	1	551	G	N3-C4-C5	-5.98	125.61	128.60
2	1	323	U	N3-C2-O2	-5.98	118.02	122.20
2	1	1775	G	C8-N9-C4	-5.95	104.02	106.40
2	1	1176	U	N1-C2-O2	5.94	126.96	122.80
25	E1	98	PRO	N-CA-CB	5.94	110.42	103.30
4	3	288	A	O4'-C1'-N9	5.90	112.92	108.20
26	L1	132	PRO	N-CA-CB	5.90	110.38	103.30
2	1	571	G	O4'-C1'-N9	5.90	112.92	108.20
2	1	2324	G	O4'-C1'-N9	5.90	112.92	108.20
2	1	1519	U	C4-C5-C6	5.88	123.23	119.70
2	1	1424	G	N3-C4-C5	-5.88	125.66	128.60
4	3	671	A	O4'-C1'-N9	5.87	112.89	108.20
2	1	1519	U	C5-C6-N1	-5.86	119.77	122.70
2	1	476	C	N3-C2-O2	-5.84	117.81	121.90
2	1	382	A	N1-C6-N6	-5.83	115.10	118.60
2	1	128	A	N9-C4-C5	5.83	108.13	105.80
2	1	1016	U	N1-C2-O2	5.82	126.88	122.80
2	1	660	G	N3-C4-C5	-5.82	125.69	128.60
2	1	534	C	C6-N1-C2	-5.82	117.97	120.30
2	1	988	U	C2-N1-C1'	5.82	124.68	117.70
2	1	469	C	N3-C4-N4	-5.81	113.94	118.00
2	1	556	A	C8-N9-C4	-5.80	103.48	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	3	1278	A	O4'-C1'-N9	5.80	112.84	108.20
2	1	2156	U	C6-N1-C1'	-5.78	113.11	121.20
2	1	652	G	P-O3'-C3'	5.77	126.62	119.70
4	3	329	U	N1-C2-O2	5.75	126.83	122.80
2	1	134	G	OP1-P-OP2	-5.75	110.98	119.60
4	3	329	U	N3-C2-O2	-5.73	118.19	122.20
2	1	133	A	P-O3'-C3'	5.73	126.58	119.70
2	1	466	C	C6-N1-C2	-5.71	118.02	120.30
2	1	2202	G	N1-C6-O6	-5.70	116.48	119.90
26	L1	84	PRO	N-CA-CB	5.69	110.13	103.30
2	1	1772	C	C6-N1-C2	-5.69	118.03	120.30
2	1	487	G	N1-C6-O6	-5.68	116.49	119.90
2	1	1777	U	N1-C2-O2	5.68	126.78	122.80
2	1	1528	C	C6-N1-C2	-5.68	118.03	120.30
2	1	790	G	N3-C4-C5	-5.67	125.76	128.60
2	1	1741	G	O4'-C1'-N9	5.67	112.74	108.20
2	1	699	G	C8-N9-C4	-5.66	104.14	106.40
2	1	2554	C	N1-C2-O2	5.65	122.29	118.90
2	1	478	C	C5-C4-N4	5.65	124.16	120.20
4	3	303	A	N1-C6-N6	-5.64	115.21	118.60
2	1	789	G	N7-C8-N9	5.63	115.91	113.10
2	1	474	A	O5'-P-OP1	-5.61	100.65	105.70
2	1	788	U	N3-C2-O2	-5.61	118.28	122.20
2	1	2225	U	N3-C2-O2	-5.60	118.28	122.20
2	1	1206	U	N3-C2-O2	-5.58	118.29	122.20
2	1	2362	C	C4-C5-C6	5.58	120.19	117.40
3	2	98	G	N1-C6-O6	-5.58	116.55	119.90
25	E1	97	PRO	N-CA-CB	5.57	109.99	103.30
4	3	648	G	N1-C6-O6	-5.57	116.56	119.90
2	1	1083	C	N3-C4-C5	-5.57	119.67	121.90
15	D0	43	TYR	CB-CG-CD1	5.56	124.34	121.00
2	1	2322	G	N3-C4-N9	5.51	129.31	126.00
2	1	2249	C	C5-C4-N4	5.51	124.05	120.20
4	3	698	A	C8-N9-C4	-5.50	103.60	105.80
2	1	2178	A	C8-N9-C4	-5.50	103.60	105.80
4	3	91	C	N3-C2-O2	-5.50	118.05	121.90
2	1	2097	G	O4'-C1'-N9	5.49	112.59	108.20
4	3	693	A	N1-C6-N6	-5.49	115.30	118.60
4	3	695	A	N1-C2-N3	-5.49	126.55	129.30
4	3	1088	G	P-O3'-C3'	5.49	126.29	119.70
4	3	475	G	C4-N9-C1'	5.49	133.64	126.50
2	1	531	G	O4'-C1'-N9	5.49	112.59	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	1	677	G	C8-N9-C4	-5.48	104.21	106.40
2	1	2554	C	C2-N1-C1'	5.47	124.82	118.80
2	1	546	A	O5'-P-OP2	-5.47	100.77	105.70
2	1	976	G	N3-C4-C5	-5.47	125.86	128.60
2	1	1701	G	N1-C6-O6	-5.47	116.62	119.90
2	1	609	C	P-O3'-C3'	5.47	126.26	119.70
2	1	483	C	N3-C4-N4	-5.46	114.18	118.00
2	1	2362	C	O4'-C1'-N1	5.46	112.56	108.20
2	1	383	G	C2-N3-C4	5.45	114.63	111.90
2	1	2322	G	C5-C6-N1	5.45	114.23	111.50
2	1	678	U	C5-C4-O4	5.44	129.17	125.90
2	1	323	U	C2-N1-C1'	5.43	124.21	117.70
2	1	472	G	C2-N3-C4	5.43	114.61	111.90
2	1	128	A	C8-N9-C4	-5.42	103.63	105.80
4	3	723	G	O4'-C1'-N9	5.41	112.53	108.20
2	1	1206	U	C2-N1-C1'	5.40	124.17	117.70
2	1	1432	G	N1-C6-O6	-5.39	116.66	119.90
4	3	457	U	C2-N1-C1'	5.39	124.16	117.70
2	1	1177	A	O4'-C1'-N9	5.38	112.50	108.20
4	3	272	C	C6-N1-C2	-5.38	118.15	120.30
4	3	689	C	C6-N1-C2	-5.38	118.15	120.30
2	1	551	G	C5-C6-N1	5.37	114.19	111.50
2	1	2531	G	C8-N9-C4	-5.37	104.25	106.40
2	1	1745	U	N3-C2-O2	-5.36	118.44	122.20
2	1	616	G	O4'-C1'-N9	5.36	112.49	108.20
2	1	616	G	N1-C6-O6	-5.35	116.69	119.90
2	1	1081	A	N1-C6-N6	-5.35	115.39	118.60
2	1	679	U	N3-C2-O2	-5.35	118.46	122.20
2	1	2225	U	C2-N1-C1'	5.35	124.12	117.70
2	1	1484	U	N1-C2-O2	5.35	126.54	122.80
2	1	1741	G	O5'-P-OP2	-5.34	100.89	105.70
2	1	790	G	N1-C6-O6	-5.34	116.70	119.90
2	1	1211	U	N1-C2-O2	5.32	126.52	122.80
2	1	472	G	N1-C6-O6	-5.31	116.72	119.90
4	3	112	U	C2-N1-C1'	5.31	124.07	117.70
2	1	378	C	C6-N1-C2	-5.30	118.18	120.30
2	1	1162	C	C6-N1-C2	-5.30	118.18	120.30
2	1	2215	C	N3-C2-O2	-5.30	118.19	121.90
2	1	462	C	C6-N1-C2	-5.29	118.18	120.30
2	1	1485	G	C4-N9-C1'	-5.29	119.62	126.50
2	1	469	C	O4'-C1'-N1	5.29	112.43	108.20
2	1	2462	C	C6-N1-C2	-5.29	118.19	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	3	1089	A	N7-C8-N9	5.29	116.44	113.80
4	3	394	C	C6-N1-C2	-5.28	118.19	120.30
2	1	1998	U	C5-C4-O4	5.28	129.06	125.90
4	3	450	G	C8-N9-C1'	-5.27	120.15	127.00
2	1	1513	A	N9-C1'-C2'	-5.26	106.21	112.00
2	1	1992	U	N3-C2-O2	-5.26	118.52	122.20
4	3	723	G	C4-N9-C1'	5.26	133.34	126.50
2	1	2322	G	N3-C4-C5	-5.26	125.97	128.60
4	3	753	G	N1-C6-O6	-5.25	116.75	119.90
2	1	2322	G	N1-C6-O6	-5.25	116.75	119.90
2	1	2249	C	N3-C2-O2	-5.24	118.23	121.90
2	1	1738	A	P-O3'-C3'	5.24	125.99	119.70
2	1	2253	G	N9-C4-C5	5.24	107.50	105.40
2	1	551	G	C6-N1-C2	-5.23	121.96	125.10
2	1	1773	C	C6-N1-C2	-5.22	118.21	120.30
2	1	2215	C	C2-N1-C1'	5.22	124.54	118.80
2	1	1777	U	C5-C4-O4	5.22	129.03	125.90
2	1	1763	A	OP1-P-O3'	5.21	116.67	105.20
2	1	976	G	O4'-C1'-N9	5.21	112.37	108.20
2	1	1079	A	N9-C4-C5	5.21	107.88	105.80
2	1	1702	U	N3-C2-O2	-5.21	118.56	122.20
2	1	1484	U	C2-N1-C1'	5.20	123.94	117.70
2	1	2520	U	N3-C2-O2	-5.20	118.56	122.20
2	1	487	G	N3-C4-N9	5.19	129.11	126.00
4	3	210	U	N3-C2-O2	-5.18	118.57	122.20
2	1	2156	U	N1-C2-O2	5.18	126.42	122.80
2	1	2206	U	C2-N3-C4	-5.17	123.90	127.00
2	1	642	A	C2-N3-C4	5.16	113.18	110.60
2	1	1515	U	N3-C2-O2	-5.16	118.59	122.20
2	1	1334	G	O4'-C1'-N9	5.16	112.32	108.20
2	1	541	G	C2-N3-C4	5.15	114.48	111.90
4	3	633	C	C2-N1-C1'	5.14	124.46	118.80
2	1	1768	A	C8-N9-C4	-5.14	103.75	105.80
2	1	2250	G	C5-C6-O6	5.13	131.68	128.60
2	1	464	C	C6-N1-C2	-5.13	118.25	120.30
2	1	613	C	N3-C4-N4	-5.13	114.41	118.00
2	1	851	U	N3-C2-O2	-5.12	118.61	122.20
2	1	175	C	C6-N1-C2	-5.12	118.25	120.30
2	1	1376	A	C8-N9-C4	-5.12	103.75	105.80
4	3	759	G	C8-N9-C4	-5.11	104.35	106.40
4	3	765	G	O4'-C1'-N9	5.11	112.29	108.20
2	1	1730	G	N1-C6-O6	-5.10	116.84	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	1	122	U	C6-N1-C2	-5.10	117.94	121.00
2	1	1081	A	C2-N3-C4	5.10	113.15	110.60
29	L4	72	ARG	CA-C-N	5.09	128.41	117.20
2	1	821	G	C2-N3-C4	5.09	114.45	111.90
2	1	2278	C	N3-C2-O2	-5.09	118.34	121.90
2	1	323	U	N1-C2-O2	5.09	126.36	122.80
2	1	2265	U	N3-C2-O2	-5.09	118.64	122.20
4	3	257	U	N1-C2-O2	5.08	126.36	122.80
2	1	2139	A	O4'-C1'-N9	5.08	112.27	108.20
4	3	267	G	N1-C6-O6	-5.08	116.85	119.90
2	1	2202	G	N9-C4-C5	5.07	107.43	105.40
2	1	129	U	C5-C4-O4	5.06	128.94	125.90
2	1	534	C	N3-C4-C5	-5.06	119.88	121.90
2	1	479	G	N3-C4-C5	-5.05	126.08	128.60
2	1	1998	U	N1-C2-N3	5.05	117.93	114.90
2	1	128	A	C5-C6-N6	5.05	127.74	123.70
2	1	1689	G	C8-N9-C4	-5.04	104.38	106.40
4	3	633	C	C6-N1-C2	-5.04	118.28	120.30
4	3	1112	G	O4'-C1'-N9	5.04	112.23	108.20
2	1	472	G	C5-C6-N1	5.04	114.02	111.50
33	L8	3	LEU	CA-CB-CG	5.03	126.88	115.30
2	1	646	G	N1-C6-O6	-5.03	116.88	119.90
2	1	705	C	C6-N1-C2	-5.03	118.29	120.30
2	1	2554	C	C6-N1-C2	-5.02	118.29	120.30
2	1	1435	A	C8-N9-C4	-5.02	103.79	105.80
2	1	673	G	N7-C8-N9	5.01	115.61	113.10
4	3	450	G	N3-C4-N9	5.01	129.01	126.00
4	3	450	G	N3-C4-C5	-5.01	126.09	128.60
2	1	1424	G	N1-C6-O6	-5.00	116.90	119.90

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C1	36	VAL	Peptide
7	C2	104	GLY	Peptide
14	C9	113	GLU	Peptide
32	L7	227	HIS	Peptide
34	L9	111	LYS	Peptide
34	L9	135	ARG	Peptide
37	M3	45	LEU	Peptide
43	M9	130	HIS	Peptide

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Mol	Chain	Res	Type	Group
50	N4	67	VAL	Peptide
50	N4	70	MET	Peptide
62	O6	60	ALA	Peptide
1	RA	95	ASP	Peptide
70	S2	93	ASP	Peptide
72	S4	215	THR	Peptide
74	S6	34	GLN	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RA	2537	0	2550	139	0
2	1	49833	0	24957	253	0
3	2	2550	0	1288	11	0
4	3	27838	0	13926	194	0
5	C0	686	0	730	21	0
6	C1	1126	0	1172	33	0
7	C2	879	0	937	76	0
8	C3	1166	0	1210	11	0
9	C4	942	0	1005	18	0
10	C5	903	0	945	31	0
11	C6	1132	0	1193	26	0
12	C7	962	0	987	39	0
13	C8	1121	0	1170	42	0
14	C9	1089	0	1103	38	0
15	D0	779	0	787	32	0
16	D1	518	0	526	17	0
17	D2	1012	0	1033	9	0
18	D3	1052	0	1126	12	0
19	D4	1056	0	1135	31	0
20	D5	691	0	727	22	0
21	D6	801	0	820	13	0
22	D7	633	0	621	15	0
23	D8	446	0	457	23	0
24	D9	524	0	517	7	0
25	E1	276	0	128	6	0
26	L1	1016	0	439	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	L2	1759	0	1817	21	0
28	L3	2827	0	2945	49	0
29	L4	2596	0	2669	42	0
30	L5	2273	0	2281	42	0
31	L6	1279	0	1302	63	0
32	L7	1903	0	1962	32	0
33	L8	1573	0	1682	57	0
34	L9	1443	0	1504	37	0
35	M0	1706	0	1750	29	0
36	M1	1336	0	1378	47	0
37	M3	1308	0	1374	34	0
38	M4	848	0	881	35	0
39	M5	1657	0	1719	19	0
40	M6	1577	0	1659	45	0
41	M7	1363	0	1399	14	0
42	M8	1470	0	1551	26	0
43	M9	1398	0	1483	27	0
44	MD	1349	0	1346	64	0
45	MS	592	0	661	23	0
46	N0	1438	0	1490	26	0
47	N1	1288	0	1331	32	0
48	N2	735	0	757	21	0
49	N3	1058	0	1138	22	0
50	N4	709	0	738	31	0
51	N5	720	0	757	6	0
52	N6	1171	0	1219	20	0
53	N7	938	0	1008	28	0
54	N8	1196	0	1207	26	0
55	N9	437	0	442	9	0
56	O0	692	0	736	12	0
57	O1	879	0	946	19	0
58	O2	1062	0	1135	19	0
59	O3	861	0	879	12	0
60	O4	807	0	868	12	0
61	O5	981	0	1075	14	0
62	O6	735	0	796	14	0
63	O7	691	0	715	9	0
64	O9	434	0	478	8	0
65	P0	381	0	394	10	0
66	P2	788	0	860	12	0
67	P3	664	0	708	10	0
68	S0	1584	0	1630	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	S1	1670	0	1705	32	0
70	S2	1636	0	1731	31	0
71	S3	1658	0	1728	37	0
72	S4	2045	0	2092	37	0
73	S5	1461	0	1523	40	0
74	S6	1680	0	1756	87	0
75	S7	1173	0	1206	66	0
76	S8	1300	0	1344	25	0
77	S9	1374	0	1435	46	0
78	D6	1	0	0	0	0
78	D7	1	0	0	0	0
78	D9	1	0	0	0	0
78	E1	1	0	0	0	0
78	O7	1	0	0	0	0
78	P0	1	0	0	0	0
78	P2	1	0	0	0	0
78	P3	1	0	0	0	0
79	L9	23	12	12	0	0
80	N8	10	19	19	0	0
All	All	166112	31	128710	2343	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (2343) 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)
4:3:573:A:H5”	9:C4:49:ARG:HD3	1.39	1.03
75:S7:49:LYS:HB3	75:S7:83:ASN:HB3	1.44	0.99
50:N4:73:GLN:HE22	74:S6:114:ARG:HB2	1.31	0.95
2:1:2538:G:H2’	2:1:2539:U:H5”	1.48	0.95
73:S5:6:LEU:HD23	73:S5:94:LEU:HD22	1.49	0.95
33:L8:69:PRO:HA	33:L8:92:LEU:HD23	1.49	0.94
71:S3:105:ARG:HG3	71:S3:174:VAL:HG22	1.49	0.93
1:RA:194:LEU:HD22	1:RA:212:VAL:HG23	1.52	0.92
2:1:850:C:H4’	40:M6:88:ILE:HD12	1.54	0.90
45:MS:4:THR:H	45:MS:7:LYS:HE2	1.34	0.90
48:N2:27:PRO:HG2	48:N2:56:ASN:HA	1.49	0.90
4:3:527:G:H1	75:S7:96:ARG:HD2	1.34	0.89
38:M4:59:ILE:HA	38:M4:62:LEU:HD13	1.56	0.88
7:C2:39:THR:HA	7:C2:42:LYS:HE2	1.53	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:199:VAL:HG11	1:RA:212:VAL:HG22	1.52	0.88
31:L6:151:LYS:HE2	40:M6:197:LEU:HD12	1.56	0.87
1:RA:163:HIS:HB2	1:RA:169:ILE:HB	1.57	0.87
4:3:987:A:H5'	4:3:988:C:H5	1.41	0.86
7:C2:79:ILE:HD11	7:C2:85:LEU:HG	1.53	0.86
13:C8:13:ILE:HD11	13:C8:20:ASN:HB3	1.58	0.85
14:C9:12:PHE:HB3	14:C9:60:ARG:HH21	1.42	0.85
57:O1:5:ILE:HD13	57:O1:109:ILE:HD11	1.56	0.85
7:C2:16:GLN:HB3	7:C2:87:ARG:HH22	1.39	0.84
1:RA:76:SER:HB3	1:RA:81:MET:HB3	1.59	0.84
2:1:2567:A:H2'	2:1:2568:U:H4'	1.60	0.83
2:1:1485:G:O2'	2:1:1486:C:O4'	1.96	0.83
31:L6:88:ILE:HG22	31:L6:116:THR:HB	1.60	0.83
44:MD:89:THR:HG21	44:MD:94:GLU:HB2	1.58	0.83
38:M4:17:ARG:HH12	46:N0:11:PHE:HB2	1.44	0.83
48:N2:83:LYS:HB2	48:N2:85:LEU:HD22	1.59	0.83
31:L6:16:TYR:HB2	31:L6:18:PRO:HD3	1.60	0.82
7:C2:53:VAL:HA	7:C2:107:VAL:HG12	1.61	0.82
12:C7:91:LEU:HG	68:S0:200:MET:HB3	1.60	0.82
32:L7:186:ASN:HB2	32:L7:188:THR:HG23	1.62	0.82
42:M8:181:ILE:HG22	42:M8:187:LYS:HB2	1.61	0.82
50:N4:73:GLN:HE21	74:S6:113:LEU:HB3	1.45	0.82
1:RA:253:GLN:HE22	1:RA:289:SER:HB2	1.42	0.81
68:S0:46:ARG:HD2	68:S0:48:ARG:HD3	1.62	0.81
1:RA:203:LYS:HA	1:RA:206:GLU:HB2	1.60	0.80
29:L4:312:ASP:HB3	29:L4:315:GLU:HG3	1.62	0.80
4:3:1089:A:N6	4:3:1112:G:O2'	2.14	0.80
4:3:553:G:N2	9:C4:121:ASP:OD2	2.14	0.80
23:D8:42:VAL:HG21	23:D8:46:VAL:HG21	1.63	0.80
33:L8:91:ILE:HD12	33:L8:165:ARG:HG3	1.64	0.80
3:2:19:G:H1	3:2:59:U:H3	1.27	0.80
20:D5:93:LEU:HD21	20:D5:100:ILE:HD12	1.63	0.80
29:L4:17:LYS:HE3	29:L4:19:LEU:HD21	1.64	0.79
2:1:2322:G:N7	28:L3:4:ARG:NH2	2.31	0.79
33:L8:119:ASP:HB3	33:L8:120:PRO:HD3	1.65	0.79
4:3:135:G:H5'	19:D4:128:ARG:HH12	1.48	0.79
1:RA:20:LYS:O	1:RA:308:SER:OG	2.02	0.78
2:1:886:G:HO2'	2:1:949:G:H1	1.22	0.78
73:S5:77:ILE:HG21	73:S5:154:LEU:HD22	1.65	0.78
4:3:371:A:H2'	4:3:372:G:H5"	1.64	0.78
40:M6:126:LYS:HD2	46:N0:171:LYS:HD2	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1965:C:H2'	2:1:1966:A:H8	1.47	0.78
1:RA:285:GLU:HB2	1:RA:292:ILE:HD11	1.66	0.78
2:1:1197:G:H3'	53:N7:54:ARG:HH12	1.47	0.78
77:S9:82:ILE:HG22	77:S9:83:LEU:HD12	1.66	0.78
77:S9:104:LEU:HD22	77:S9:108:HIS:HD2	1.50	0.77
4:3:376:U:OP1	19:D4:63:GLY:N	2.17	0.77
10:C5:43:LEU:HD13	10:C5:87:ILE:HD11	1.67	0.77
22:D7:10:ARG:HD2	75:S7:136:ARG:HH22	1.49	0.77
74:S6:69:LYS:HE3	74:S6:102:SER:HB3	1.67	0.76
7:C2:26:SER:HA	7:C2:31:LYS:HE2	1.66	0.76
4:3:1021:G:O2'	4:3:1022:U:O2	2.03	0.76
7:C2:127:LEU:HG	7:C2:128:LEU:HD22	1.68	0.76
9:C4:69:LEU:HD13	9:C4:107:LEU:HD21	1.67	0.76
28:L3:65:LYS:HD2	28:L3:69:LEU:HD21	1.68	0.76
1:RA:92:ARG:HD2	1:RA:101:SER:HB3	1.68	0.76
9:C4:44:ARG:NH2	9:C4:63:ASP:OD2	2.18	0.76
59:O3:7:ASN:HB3	59:O3:10:VAL:HG12	1.66	0.75
1:RA:173:GLY:HA3	1:RA:220:VAL:HG21	1.68	0.75
35:M0:103:LEU:N	35:M0:112:GLN:OE1	2.19	0.75
1:RA:117:ASN:ND2	1:RA:121:THR:OG1	2.19	0.75
14:C9:17:LYS:NZ	14:C9:49:ASP:OD1	2.17	0.75
68:S0:170:ASN:HA	68:S0:176:ILE:HD11	1.69	0.75
6:C1:35:GLU:HG3	6:C1:36:VAL:H	1.52	0.75
74:S6:34:GLN:CB	74:S6:50:GLU:HA	2.16	0.75
66:P2:22:LYS:HE3	66:P2:73:THR:HG22	1.69	0.75
2:1:2037:A:H4'	66:P2:96:LYS:HE3	1.68	0.75
29:L4:118:LYS:NZ	29:L4:270:THR:OG1	2.20	0.75
31:L6:97:SER:OG	38:M4:82:ASN:ND2	2.19	0.74
33:L8:70:GLU:O	33:L8:152:ASN:ND2	2.20	0.74
2:1:1704:C:OP1	28:L3:232:ARG:NH2	2.18	0.74
19:D4:62:TYR:O	77:S9:144:GLN:NE2	2.20	0.74
53:N7:8:ILE:O	53:N7:74:THR:OG1	2.04	0.74
68:S0:184:SER:O	68:S0:188:ASN:ND2	2.20	0.74
4:3:1254:A:H2'	4:3:1255:A:H2'	1.69	0.74
30:L5:91:THR:O	30:L5:155:ARG:NH1	2.20	0.74
10:C5:33:SER:HB3	24:D9:8:ASP:HB2	1.68	0.74
18:D3:58:GLN:HA	18:D3:60:ASN:H	1.53	0.74
29:L4:117:LYS:NZ	29:L4:121:GLU:OE2	2.19	0.74
34:L9:123:ARG:NH1	34:L9:124:MET:O	2.21	0.74
2:1:2226:A:OP2	65:P0:98:ARG:NH1	2.20	0.74
28:L3:288:ILE:HG21	28:L3:299:ILE:HB	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L4:6:ASN:HB3	29:L4:15:VAL:HG13	1.70	0.74
29:L4:258:LYS:HE3	29:L4:269:LEU:HD11	1.69	0.74
9:C4:9:GLU:HG2	9:C4:74:LYS:HD2	1.69	0.73
14:C9:56:ALA:HA	14:C9:59:VAL:HG12	1.69	0.73
39:M5:15:GLN:HA	39:M5:20:ARG:HG3	1.71	0.73
69:S1:37:SER:OG	69:S1:46:ASN:ND2	2.21	0.73
68:S0:185:ARG:NH2	68:S0:202:GLU:OE2	2.22	0.73
2:1:1722:A:H61	2:1:2362:C:H5	1.37	0.73
2:1:1975:U:H2'	2:1:1976:G:H5"	1.71	0.73
29:L4:224:ASP:OD2	29:L4:244:ARG:NH2	2.22	0.73
4:3:527:G:H22	75:S7:96:ARG:HB2	1.53	0.73
16:D1:6:ARG:NH2	16:D1:44:ASP:OD1	2.21	0.73
37:M3:66:ARG:NH1	54:N8:104:GLU:OE2	2.22	0.73
4:3:1070:C:O2'	14:C9:65:LYS:NZ	2.21	0.73
1:RA:309:LEU:HD12	1:RA:316:LEU:HD12	1.69	0.73
74:S6:30:LYS:HE3	74:S6:67:LEU:HD21	1.70	0.72
1:RA:191:GLN:NE2	1:RA:200:ASP:OD2	2.21	0.72
1:RA:202:GLU:O	1:RA:206:GLU:N	2.22	0.72
2:1:303:U:O4	61:O5:106:ARG:NH1	2.19	0.72
11:C6:53:ILE:HD11	11:C6:84:ARG:HD3	1.72	0.72
14:C9:7:VAL:HG21	14:C9:134:VAL:HG23	1.71	0.72
33:L8:83:ASP:HA	33:L8:86:LYS:HD3	1.70	0.72
27:L2:55:PHE:O	45:MS:58:ARG:NH1	2.14	0.72
34:L9:35:GLU:HG2	34:L9:73:LEU:HD23	1.71	0.72
38:M4:105:LEU:HB3	40:M6:177:ILE:HG22	1.70	0.72
1:RA:178:THR:HG22	1:RA:194:LEU:HD11	1.72	0.72
8:C3:60:ILE:HD12	8:C3:66:VAL:HG21	1.72	0.72
75:S7:45:ILE:HD12	75:S7:151:ALA:HB2	1.71	0.72
48:N2:31:GLY:HA2	48:N2:51:ILE:HD11	1.72	0.72
39:M5:73:ARG:NH1	39:M5:88:GLY:O	2.23	0.71
2:1:1197:G:O2'	53:N7:55:ARG:NH1	2.23	0.71
4:3:147:A:H4'	74:S6:130:VAL:HG13	1.72	0.71
1:RA:38:ARG:HG3	1:RA:69:ARG:HB3	1.72	0.71
4:3:573:A:O2'	44:MD:116:ASN:ND2	2.24	0.71
74:S6:34:GLN:HB3	74:S6:50:GLU:HA	1.72	0.71
21:D6:48:ASP:O	21:D6:52:GLN:NE2	2.23	0.71
44:MD:57:ASN:HD22	44:MD:72:LYS:HA	1.55	0.71
2:1:2226:A:H5"	65:P0:98:ARG:HH12	1.55	0.71
4:3:357:G:H5'	77:S9:168:ARG:HH22	1.55	0.71
29:L4:152:SER:OG	29:L4:154:ASP:OD1	2.07	0.71
53:N7:96:THR:HA	53:N7:99:VAL:HG12	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:S4:245:GLN:HE21	72:S4:250:LYS:HG2	1.56	0.71
2:1:188:G:OP1	37:M3:69:ARG:NH2	2.24	0.71
2:1:300:U:H3	61:O5:111:MET:HE3	1.55	0.71
40:M6:6:HIS:HE1	40:M6:34:THR:HG23	1.56	0.70
40:M6:47:LEU:HD22	40:M6:139:LYS:HE3	1.73	0.70
42:M8:135:ASN:ND2	42:M8:137:ASP:OD1	2.23	0.70
18:D3:104:LYS:HE2	18:D3:109:VAL:HG12	1.72	0.70
30:L5:126:TYR:OH	30:L5:172:HIS:O	2.08	0.70
74:S6:44:PHE:O	74:S6:47:THR:OG1	2.09	0.70
46:N0:183:GLU:OE1	46:N0:183:GLU:N	2.23	0.70
58:O2:7:ASP:HB2	58:O2:8:PRO:HD3	1.71	0.70
31:L6:19:ASP:HA	31:L6:22:PRO:HD2	1.73	0.70
11:C6:61:ASN:O	11:C6:95:TYR:OH	2.10	0.70
15:D0:23:ILE:HB	15:D0:90:PHE:HB2	1.71	0.70
33:L8:82:GLU:O	33:L8:86:LYS:NZ	2.24	0.70
2:1:1974:G:H3'	2:1:1975:U:H5"	1.73	0.70
69:S1:70:VAL:HG21	69:S1:75:LEU:HD21	1.73	0.70
69:S1:175:GLU:O	69:S1:179:SER:OG	2.10	0.70
74:S6:11:GLY:O	74:S6:128:ASN:ND2	2.23	0.70
1:RA:282:ILE:HA	1:RA:294:SER:HB3	1.72	0.70
22:D7:36:GLY:O	22:D7:39:ARG:NH1	2.23	0.70
62:O6:61:LYS:O	62:O6:63:ASN:ND2	2.24	0.70
6:C1:12:ARG:NH1	76:S8:156:GLU:OE2	2.24	0.70
7:C2:94:VAL:HG22	7:C2:100:VAL:HG22	1.73	0.70
26:L1:71:ASP:O	26:L1:76:LYS:N	2.25	0.70
44:MD:5:ILE:HD13	44:MD:111:SER:HB3	1.74	0.70
10:C5:93:ILE:HD11	10:C5:112:PRO:HA	1.74	0.69
14:C9:16:LEU:HD11	14:C9:59:VAL:HG11	1.73	0.69
31:L6:64:LEU:HD23	31:L6:106:VAL:HG11	1.72	0.69
36:M1:30:LEU:HD11	36:M1:64:LYS:HB2	1.72	0.69
70:S2:160:PRO:O	70:S2:163:THR:OG1	2.06	0.69
10:C5:16:ARG:HH21	36:M1:85:ARG:HH21	1.40	0.69
42:M8:181:ILE:HA	42:M8:187:LYS:HB3	1.75	0.69
49:N3:26:ILE:HG13	49:N3:87:LEU:HD11	1.73	0.69
62:O6:27:ARG:NH1	62:O6:29:GLU:OE2	2.25	0.69
1:RA:114:VAL:HG23	1:RA:125:THR:HG22	1.74	0.69
17:D2:28:SER:OG	17:D2:33:ARG:NH1	2.26	0.69
50:N4:68:GLU:OE2	50:N4:71:ASN:HB2	1.93	0.69
56:O0:79:LEU:O	56:O0:83:THR:OG1	2.08	0.69
8:C3:84:ILE:HG23	8:C3:88:LEU:HD23	1.75	0.69
46:N0:25:ARG:HH21	46:N0:45:THR:HG23	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:N6:139:GLU:O	52:N6:142:SER:OG	2.09	0.69
73:S5:6:LEU:CD2	73:S5:94:LEU:HD22	2.21	0.69
32:L7:213:GLN:NE2	32:L7:215:SER:OG	2.26	0.69
68:S0:10:ASP:OD2	68:S0:57:ASN:ND2	2.26	0.69
31:L6:131:ASP:HA	31:L6:134:ARG:HB2	1.75	0.69
20:D5:98:MET:HE1	73:S5:155:ALA:HB3	1.74	0.68
22:D7:35:CYS:SG	22:D7:36:GLY:N	2.66	0.68
29:L4:5:ILE:HD11	29:L4:21:LEU:HD13	1.74	0.68
44:MD:88:PRO:HD3	44:MD:135:ASP:HB2	1.75	0.68
50:N4:87:SER:HB3	50:N4:89:LEU:HD23	1.75	0.68
53:N7:111:ALA:HB1	53:N7:116:LYS:HB3	1.74	0.68
5:C0:53:TYR:O	5:C0:68:THR:OG1	2.08	0.68
2:1:2322:G:O6	28:L3:4:ARG:HD2	1.93	0.68
4:3:703:G:OP1	8:C3:2:ALA:HB2	1.93	0.68
4:3:796:U:O2'	70:S2:76:GLN:O	2.12	0.68
77:S9:90:ASP:OD2	77:S9:93:GLU:N	2.24	0.68
12:C7:31:ASN:HD22	12:C7:55:THR:HG22	1.59	0.68
1:RA:127:SER:OG	1:RA:129:ASP:OD1	2.10	0.68
31:L6:75:ALA:HB2	31:L6:85:LEU:HG	1.74	0.68
4:3:880:U:OP2	7:C2:36:ALA:N	2.23	0.68
75:S7:129:VAL:HG13	75:S7:161:ILE:HD13	1.75	0.68
23:D8:10:GLU:HB3	23:D8:51:ILE:HG22	1.76	0.68
23:D8:54:ILE:HG22	23:D8:56:GLU:H	1.59	0.68
28:L3:68:GLN:HG2	28:L3:71:ARG:HD2	1.76	0.68
2:1:2394:U:O2'	34:L9:117:LYS:NZ	2.27	0.67
4:3:164:U:OP1	76:S8:72:LYS:NZ	2.27	0.67
4:3:348:A:OP1	77:S9:9:ARG:NH1	2.25	0.67
2:1:1105:U:O2'	2:1:1106:G:OP1	2.09	0.67
12:C7:106:ILE:HG23	12:C7:111:TYR:HB2	1.76	0.67
32:L7:174:ILE:HG23	32:L7:179:GLU:HB2	1.75	0.67
28:L3:183:SER:O	28:L3:186:GLU:N	2.27	0.67
71:S3:166:TYR:OH	71:S3:201:TYR:O	2.10	0.67
76:S8:37:LYS:HE2	76:S8:93:THR:HG22	1.76	0.67
10:C5:81:THR:HG22	10:C5:83:ALA:H	1.59	0.67
14:C9:68:VAL:H	14:C9:118:MET:HE1	1.58	0.67
28:L3:288:ILE:HG12	28:L3:297:LYS:O	1.94	0.67
44:MD:89:THR:HG21	44:MD:95:PHE:H	1.59	0.67
1:RA:116:ILE:HG13	1:RA:123:ILE:HD11	1.77	0.67
12:C7:71:ILE:O	12:C7:75:GLU:HG2	1.95	0.67
27:L2:43:GLU:HG3	45:MS:47:LEU:HD21	1.77	0.67
60:O4:23:ARG:NH1	60:O4:27:GLY:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:175:ALA:HA	1:RA:219:SER:OG	1.95	0.67
5:C0:78:GLU:HB2	5:C0:79:LEU:HD12	1.77	0.67
31:L6:18:PRO:HD2	31:L6:20:ASP:HB2	1.77	0.67
12:C7:95:CYS:HA	12:C7:116:LYS:HZ1	1.60	0.67
13:C8:66:LYS:NZ	13:C8:70:ASP:OD2	2.25	0.67
32:L7:78:GLU:HG3	47:N1:136:ARG:HB3	1.77	0.67
1:RA:202:GLU:O	1:RA:206:GLU:HG2	1.95	0.66
2:1:1592:U:O2'	2:1:1593:G:O5'	2.13	0.66
40:M6:185:ASN:HA	40:M6:188:ASN:HD21	1.60	0.66
71:S3:126:ARG:NH2	71:S3:130:ALA:O	2.28	0.66
76:S8:84:HIS:HE2	76:S8:97:THR:HG1	1.42	0.66
4:3:888:U:O2'	4:3:889:G:O4'	2.12	0.66
74:S6:84:ARG:HE	74:S6:86:ARG:HH12	1.44	0.66
2:1:1107:A:H5'	2:1:1108:U:H5	1.59	0.66
27:L2:54:SER:OG	45:MS:58:ARG:NH2	2.28	0.66
30:L5:37:GLN:HB3	30:L5:46:LYS:HD2	1.75	0.66
2:1:302:U:H2'	2:1:303:U:H4'	1.78	0.66
4:3:1278:A:H5"	4:3:1279:G:OP2	1.96	0.66
33:L8:16:LEU:HD12	33:L8:20:GLN:HB2	1.76	0.66
50:N4:68:GLU:O	50:N4:71:ASN:ND2	2.28	0.66
69:S1:146:ARG:NH2	69:S1:209:LEU:O	2.29	0.66
57:O1:24:LEU:O	57:O1:29:LYS:NZ	2.29	0.66
73:S5:41:ILE:O	73:S5:50:ARG:NH1	2.29	0.66
2:1:1660:U:OP2	49:N3:80:LYS:NZ	2.29	0.66
6:C1:19:LYS:HG2	6:C1:20:PRO:HD2	1.78	0.66
36:M1:52:MET:HA	36:M1:61:ARG:HG3	1.78	0.66
52:N6:140:VAL:HA	52:N6:143:ASN:HB2	1.77	0.66
4:3:879:G:H4'	4:3:880:U:H5"	1.77	0.66
1:RA:163:HIS:HB3	1:RA:166:GLU:O	1.96	0.66
4:3:121:U:OP2	74:S6:188:ARG:NH1	2.29	0.66
68:S0:181:PHE:O	68:S0:184:SER:OG	2.14	0.66
7:C2:42:LYS:HD2	7:C2:111:GLN:HE21	1.60	0.65
32:L7:40:ASN:ND2	32:L7:164:GLU:OE2	2.25	0.65
2:1:2374:G:N1	2:1:2516:U:O2'	2.26	0.65
6:C1:27:GLN:HB2	6:C1:28:PRO:HD2	1.77	0.65
31:L6:38:VAL:HG23	31:L6:39:ARG:H	1.60	0.65
49:N3:12:LYS:HD3	49:N3:13:LYS:H	1.62	0.65
2:1:2538:G:C2'	2:1:2539:U:H5"	2.26	0.65
44:MD:89:THR:CG2	44:MD:94:GLU:HB2	2.26	0.65
7:C2:39:THR:HA	7:C2:42:LYS:CE	2.26	0.65
43:M9:35:ALA:O	43:M9:40:GLN:NE2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:N1:118:ALA:CB	47:N1:124:VAL:HG12	2.26	0.65
2:1:100:U:O2'	2:1:101:G:O5'	2.12	0.65
4:3:996:G:OP2	11:C6:116:ARG:NH2	2.30	0.65
29:L4:266:GLU:OE2	29:L4:272:GLY:N	2.28	0.65
35:M0:51:ASN:OD1	35:M0:137:SER:OG	2.15	0.65
40:M6:28:LEU:HD11	40:M6:88:ILE:CD1	2.26	0.65
4:3:868:G:OP1	5:C0:1:MET:N	2.29	0.65
4:3:1296:A:N6	21:D6:81:VAL:HG22	2.12	0.65
1:RA:83:VAL:HG12	1:RA:93:ILE:HG13	1.77	0.65
13:C8:2:ASN:ND2	13:C8:6:ASP:OD2	2.28	0.65
74:S6:150:GLU:O	74:S6:152:ASN:N	2.27	0.65
1:RA:191:GLN:HE21	1:RA:249:LYS:HE3	1.60	0.65
2:1:1416:U:O2'	57:O1:35:ARG:NH2	2.28	0.65
1:RA:263:SER:HB2	1:RA:309:LEU:HD23	1.79	0.65
7:C2:34:ARG:HA	7:C2:108:ALA:HB1	1.79	0.65
28:L3:55:HIS:HB2	28:L3:351:ASP:HB3	1.78	0.65
38:M4:81:THR:HB	38:M4:85:ASP:HB2	1.79	0.65
40:M6:187:GLU:N	40:M6:187:GLU:OE1	2.30	0.65
69:S1:188:LYS:O	69:S1:192:ASN:ND2	2.29	0.65
1:RA:123:ILE:HB	1:RA:135:TYR:HB2	1.78	0.64
4:3:1088:G:N2	4:3:1112:G:H2'	2.12	0.64
11:C6:48:ALA:HA	73:S5:33:ILE:HD11	1.79	0.64
50:N4:25:ASP:OD2	50:N4:27:ARG:NH1	2.31	0.64
1:RA:226:SER:HB3	1:RA:266:VAL:HG21	1.80	0.64
4:3:719:G:OP2	4:3:719:G:N2	2.31	0.64
6:C1:32:VAL:HG12	6:C1:33:ASN:H	1.62	0.64
7:C2:94:VAL:HG13	7:C2:100:VAL:HG22	1.78	0.64
14:C9:9:PRO:O	14:C9:60:ARG:NH2	2.30	0.64
31:L6:129:MET:HB2	31:L6:133:GLU:CG	2.27	0.64
2:1:1333:G:H2'	2:1:1334:G:H5'	1.77	0.64
33:L8:16:LEU:HD12	33:L8:20:GLN:CB	2.26	0.64
33:L8:76:ARG:O	33:L8:80:GLN:HG2	1.98	0.64
73:S5:17:VAL:HG22	73:S5:98:VAL:HG11	1.80	0.64
2:1:1333:G:C2'	2:1:1334:G:H5'	2.27	0.64
49:N3:89:ARG:NH2	49:N3:124:ALA:O	2.31	0.64
31:L6:73:LEU:HD11	31:L6:85:LEU:HD21	1.79	0.64
32:L7:77:LYS:NZ	32:L7:80:GLU:OE2	2.29	0.64
2:1:529:G:H4'	54:N8:4:ARG:O	1.98	0.64
4:3:1178:C:O2'	4:3:1179:A:OP1	2.14	0.64
50:N4:79:ARG:HH12	74:S6:11:GLY:HA3	1.61	0.64
52:N6:24:ASP:OD2	52:N6:76:ARG:NH1	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:O2:12:VAL:O	58:O2:16:GLU:HG2	1.97	0.64
77:S9:141:ILE:HD11	77:S9:157:LYS:O	1.98	0.64
34:L9:82:VAL:CG2	34:L9:181:ILE:HD11	2.28	0.64
69:S1:42:PRO:HD2	69:S1:76:THR:HG22	1.79	0.64
74:S6:136:LYS:HA	74:S6:136:LYS:HE2	1.79	0.64
72:S4:184:ARG:HA	72:S4:188:ARG:HD3	1.79	0.64
4:3:499:G:N2	77:S9:157:LYS:HE3	2.13	0.64
4:3:524:G:H2'	4:3:525:A:O4'	1.98	0.63
7:C2:124:GLN:HA	7:C2:127:LEU:HB3	1.80	0.63
16:D1:67:GLU:OE2	68:S0:68:ARG:NH2	2.28	0.63
70:S2:86:LYS:NZ	70:S2:102:THR:OG1	2.31	0.63
2:1:2181:A:C8	66:P2:54:PRO:HB3	2.33	0.63
4:3:419:A:N6	71:S3:143:GLY:O	2.31	0.63
4:3:894:G:O6	7:C2:37:LYS:HE3	1.98	0.63
27:L2:100:ASN:ND2	27:L2:153:GLY:O	2.31	0.63
33:L8:170:GLY:HA2	33:L8:173:LYS:NZ	2.14	0.63
36:M1:50:ALA:HB2	36:M1:65:ILE:HD11	1.80	0.63
71:S3:43:THR:HB	71:S3:44:PRO:HD3	1.80	0.63
1:RA:130:ARG:HE	1:RA:155:GLY:HA2	1.62	0.63
33:L8:170:GLY:HA2	33:L8:173:LYS:HZ1	1.63	0.63
75:S7:15:ILE:HB	75:S7:16:ARG:HH12	1.64	0.63
75:S7:51:PRO:HD2	75:S7:54:ILE:HD11	1.81	0.63
2:1:238:A:N6	2:1:292:G:O6	2.17	0.63
6:C1:35:GLU:HG2	6:C1:139:LEU:HD22	1.81	0.63
59:O3:45:LYS:HG3	59:O3:77:ILE:HD12	1.81	0.63
67:P3:36:LYS:HD3	67:P3:48:LYS:HE3	1.81	0.63
75:S7:8:GLU:OE2	75:S7:11:ILE:N	2.32	0.63
76:S8:69:THR:HG23	76:S8:70:THR:HG23	1.80	0.63
48:N2:83:LYS:HB2	48:N2:85:LEU:CD2	2.28	0.63
52:N6:60:GLY:N	52:N6:64:ASP:OD1	2.29	0.63
75:S7:9:MET:SD	75:S7:10:SER:N	2.72	0.63
75:S7:55:LEU:HD22	75:S7:82:ARG:HB2	1.81	0.63
34:L9:82:VAL:HB	34:L9:181:ILE:HD11	1.81	0.63
40:M6:113:GLU:OE2	40:M6:162:ARG:HD2	1.97	0.63
40:M6:184:LYS:O	40:M6:188:ASN:ND2	2.32	0.63
2:1:2223:C:H5	2:1:2277:G:H22	1.45	0.63
32:L7:93:CYS:SG	32:L7:98:ARG:HG3	2.39	0.63
36:M1:161:LYS:O	36:M1:165:GLU:HG2	1.98	0.63
15:D0:54:GLU:OE1	15:D0:54:GLU:N	2.32	0.63
31:L6:102:LEU:HD21	31:L6:140:ILE:HG12	1.80	0.63
53:N7:93:ASN:OD1	53:N7:96:THR:HG23	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:986:C:OP1	46:N0:135:ARG:HD2	1.98	0.62
11:C6:106:GLU:OE1	11:C6:106:GLU:N	2.28	0.62
30:L5:120:LYS:HE3	30:L5:129:THR:HG22	1.81	0.62
35:M0:178:SER:O	35:M0:182:ASN:ND2	2.32	0.62
43:M9:165:SER:HA	43:M9:168:VAL:HG22	1.81	0.62
2:1:1146:G:H5'	51:N5:77:LEU:HD21	1.81	0.62
54:N8:5:VAL:HG23	54:N8:6:LYS:H	1.64	0.62
64:O9:31:LYS:HZ3	64:O9:34:LYS:HE2	1.64	0.62
7:C2:25:VAL:HG11	7:C2:115:GLU:HB3	1.81	0.62
2:1:504:G:O2'	2:1:506:U:OP1	2.15	0.62
2:1:1975:U:O2'	2:1:1976:G:N2	2.25	0.62
44:MD:134:GLN:HG2	44:MD:135:ASP:H	1.65	0.62
31:L6:97:SER:HG	38:M4:82:ASN:HD22	1.47	0.62
40:M6:27:LEU:O	40:M6:101:ARG:NH1	2.33	0.62
13:C8:37:ILE:HG23	13:C8:42:ALA:HB2	1.80	0.62
15:D0:41:TYR:CE2	15:D0:52:GLN:HB3	2.34	0.62
36:M1:49:LYS:HE3	36:M1:64:LYS:HE3	1.81	0.62
53:N7:93:ASN:OD1	53:N7:95:GLU:HG3	2.00	0.62
1:RA:135:TYR:HA	1:RA:140:ASP:O	2.00	0.62
1:RA:145:MET:HA	1:RA:149:MET:HE1	1.82	0.62
18:D3:70:GLN:HE21	18:D3:75:GLY:HA2	1.64	0.62
43:M9:114:GLU:OE1	43:M9:114:GLU:N	2.32	0.62
11:C6:64:ASP:O	11:C6:65:LEU:HD23	2.00	0.62
33:L8:96:GLY:O	33:L8:100:VAL:HG22	2.00	0.62
68:S0:6:THR:OG1	68:S0:7:ARG:N	2.31	0.62
2:1:355:G:OP2	62:O6:24:ARG:NH1	2.20	0.61
36:M1:164:VAL:HG23	36:M1:165:GLU:OE2	2.00	0.61
71:S3:51:VAL:O	71:S3:90:VAL:HG23	2.00	0.61
4:3:105:U:OP1	6:C1:64:ARG:NE	2.30	0.61
36:M1:10:ARG:NH1	36:M1:151:LYS:O	2.33	0.61
1:RA:11:TYR:O	1:RA:12:LEU:HD23	1.98	0.61
4:3:1107:C:OP1	14:C9:81:LYS:NZ	2.26	0.61
5:C0:13:ARG:HH11	5:C0:79:LEU:HD23	1.65	0.61
10:C5:43:LEU:HD13	10:C5:87:ILE:CD1	2.30	0.61
29:L4:50:ALA:HA	29:L4:102:THR:HG23	1.83	0.61
2:1:2015:U:O4	47:N1:2:ARG:NH1	2.33	0.61
33:L8:107:LYS:NZ	33:L8:134:MET:O	2.25	0.61
69:S1:91:GLY:HA3	69:S1:101:PHE:HE2	1.64	0.61
4:3:1033:G:O2'	4:3:1034:A:OP1	2.15	0.61
7:C2:26:SER:HA	7:C2:31:LYS:CE	2.29	0.61
40:M6:154:SER:O	40:M6:158:GLU:HG2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:N4:79:ARG:HD2	74:S6:128:ASN:O	2.01	0.61
58:O2:86:ILE:HG13	58:O2:118:ARG:HG3	1.83	0.61
1:RA:282:ILE:HA	1:RA:294:SER:CB	2.30	0.61
4:3:987:A:H5'	4:3:988:C:C5	2.28	0.61
10:C5:46:ARG:NH1	10:C5:85:SER:O	2.28	0.61
44:MD:78:GLU:HA	44:MD:82:VAL:CG2	2.30	0.61
69:S1:204:SER:HA	69:S1:207:PHE:O	2.00	0.61
7:C2:42:LYS:HD2	7:C2:111:GLN:NE2	2.15	0.61
12:C7:102:THR:O	12:C7:106:ILE:HG12	2.01	0.61
43:M9:116:THR:HG23	43:M9:119:ASP:H	1.65	0.61
8:C3:55:ARG:NH1	8:C3:56:ASP:OD1	2.34	0.61
21:D6:48:ASP:OD1	21:D6:49:ASP:N	2.32	0.61
35:M0:193:ARG:CZ	35:M0:219:ASN:HB3	2.31	0.61
70:S2:93:ASP:OD1	70:S2:94:ARG:N	2.34	0.61
4:3:330:U:H3	19:D4:86:LYS:HE3	1.64	0.61
5:C0:76:ARG:HH11	5:C0:80:VAL:HG21	1.65	0.61
47:N1:67:LYS:HB3	47:N1:68:PRO:HD2	1.82	0.61
1:RA:12:LEU:HD22	1:RA:57:LYS:HD2	1.81	0.61
7:C2:54:ALA:H	7:C2:107:VAL:HG12	1.66	0.61
68:S0:90:LYS:NZ	68:S0:205:LEU:O	2.30	0.61
1:RA:193:TYR:CE1	1:RA:244:VAL:HG11	2.36	0.60
2:1:416:A:O2'	2:1:417:G:OP1	2.17	0.60
74:S6:20:ARG:HG2	74:S6:23:GLU:OE1	2.01	0.60
75:S7:49:LYS:HD2	75:S7:83:ASN:HB3	1.83	0.60
33:L8:67:TYR:HE1	33:L8:165:ARG:HD3	1.66	0.60
37:M3:109:ASP:O	37:M3:113:GLU:HG2	2.01	0.60
59:O3:4:VAL:HG22	59:O3:5:MET:H	1.66	0.60
72:S4:195:ASN:ND2	72:S4:209:THR:OG1	2.32	0.60
4:3:881:G:N1	7:C2:38:GLU:OE2	2.33	0.60
13:C8:37:ILE:CG2	13:C8:42:ALA:HB2	2.31	0.60
19:D4:61:ARG:HB3	19:D4:64:THR:OG1	2.00	0.60
68:S0:154:ASN:ND2	68:S0:169:ASN:HA	2.17	0.60
72:S4:215:THR:HG22	72:S4:216:PHE:H	1.65	0.60
2:1:1133:G:H2'	2:1:1134:U:O4'	2.01	0.60
2:1:2146:C:OP1	54:N8:55:LYS:HE3	2.01	0.60
5:C0:21:LEU:HD22	5:C0:45:MET:CE	2.32	0.60
13:C8:26:ARG:NH1	13:C8:54:ARG:HG3	2.16	0.60
28:L3:299:ILE:HG21	28:L3:315:PHE:CE2	2.36	0.60
52:N6:137:GLN:O	52:N6:141:VAL:HG23	2.00	0.60
68:S0:10:ASP:HB3	68:S0:61:GLU:HG2	1.84	0.60
33:L8:67:TYR:CE1	33:L8:165:ARG:HD3	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L4:268:GLU:OE2	29:L4:268:GLU:N	2.34	0.60
4:3:156:U:H2'	4:3:157:G:O4'	2.02	0.60
16:D1:64:ARG:HB2	16:D1:65:MET:HE2	1.84	0.60
2:1:719:G:H3'	32:L7:99:LYS:HZ2	1.67	0.60
4:3:527:G:N1	75:S7:96:ARG:HD2	2.12	0.60
26:L1:3:GLU:O	26:L1:7:ALA:N	2.35	0.60
67:P3:20:SER:O	67:P3:24:LYS:HG2	2.02	0.60
76:S8:37:LYS:HE3	76:S8:95:THR:HG22	1.84	0.60
13:C8:86:ASN:H	13:C8:98:HIS:HD2	1.48	0.60
20:D5:35:GLU:HG3	20:D5:36:VAL:O	2.02	0.60
36:M1:110:ILE:HD13	36:M1:114:LEU:O	2.02	0.60
41:M7:53:ILE:HA	41:M7:106:LYS:HG2	1.84	0.60
49:N3:22:MET:CE	49:N3:63:PRO:HD2	2.32	0.60
1:RA:194:LEU:HD23	1:RA:215:ASP:OD2	2.02	0.60
21:D6:85:SER:O	21:D6:89:ARG:HG3	2.01	0.60
22:D7:10:ARG:HD2	75:S7:136:ARG:NH2	2.16	0.60
44:MD:130:LEU:O	44:MD:137:LEU:HD12	2.02	0.60
64:O9:25:ALA:O	64:O9:29:MET:HG2	2.02	0.60
77:S9:45:LYS:O	77:S9:49:LYS:HG3	2.02	0.60
2:1:2144:U:H4'	54:N8:53:HIS:HE1	1.67	0.59
2:1:2226:A:H5"	65:P0:98:ARG:NH1	2.17	0.59
19:D4:36:GLU:OE1	19:D4:36:GLU:N	2.35	0.59
50:N4:73:GLN:HG3	74:S6:113:LEU:HD13	1.82	0.59
2:1:1003:G:H1'	58:O2:62:ILE:HD12	1.83	0.59
4:3:146:G:O2'	50:N4:79:ARG:NH2	2.35	0.59
4:3:876:C:OP2	7:C2:101:ARG:NH2	2.23	0.59
7:C2:70:LYS:NZ	25:E1:109:GLN:O	2.31	0.59
19:D4:20:GLU:HG3	19:D4:72:LYS:HG2	1.84	0.59
28:L3:113:ASP:OD1	28:L3:124:TYR:OH	2.19	0.59
39:M5:22:LEU:O	39:M5:26:ARG:HG2	2.02	0.59
47:N1:38:MET:SD	47:N1:62:ARG:NE	2.75	0.59
38:M4:41:GLU:N	38:M4:41:GLU:OE2	2.35	0.59
74:S6:141:ARG:HH21	74:S6:150:GLU:HG3	1.66	0.59
2:1:1419:G:O2'	57:O1:23:ARG:O	2.20	0.59
75:S7:49:LYS:O	75:S7:83:ASN:ND2	2.35	0.59
1:RA:116:ILE:HG13	1:RA:123:ILE:CD1	2.31	0.59
1:RA:315:THR:HG22	1:RA:329:GLU:HG3	1.84	0.59
2:1:1688:C:H2'	2:1:1689:G:H5'	1.83	0.59
4:3:826:U:O2'	4:3:827:G:OP2	2.18	0.59
2:1:1575:U:O4	69:S1:10:PRO:HG2	2.03	0.59
34:L9:133:ASP:OD2	34:L9:135:ARG:NH2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:MS:63:GLU:OE2	45:MS:64:MET:HG3	2.03	0.59
50:N4:79:ARG:NH1	74:S6:11:GLY:HA3	2.17	0.59
2:1:2318:G:OP2	28:L3:3:CYS:HB3	2.02	0.59
4:3:822:A:H2'	4:3:823:G:C8	2.37	0.59
10:C5:111:LYS:HB2	10:C5:112:PRO:HD2	1.84	0.59
29:L4:9:GLU:OE2	29:L4:16:LYS:HD2	2.02	0.59
30:L5:48:ARG:NH1	30:L5:144:ASP:OD2	2.34	0.59
31:L6:47:MET:HA	31:L6:99:VAL:HA	1.84	0.59
58:O2:100:CYS:SG	58:O2:127:LEU:HB2	2.42	0.59
2:1:2507:U:H5"	28:L3:270:ARG:HG2	1.84	0.59
4:3:499:G:H22	77:S9:157:LYS:HE3	1.66	0.59
29:L4:4:GLN:HB3	29:L4:18:THR:CG2	2.32	0.59
30:L5:52:ARG:NH2	30:L5:145:ILE:O	2.36	0.59
33:L8:11:VAL:HG23	33:L8:12:GLU:H	1.67	0.59
40:M6:2:GLU:O	40:M6:4:LYS:NZ	2.34	0.59
77:S9:142:LYS:HD3	77:S9:160:LEU:HD13	1.85	0.59
33:L8:165:ARG:HB3	33:L8:167:GLU:OE1	2.03	0.59
34:L9:1:MET:HE1	34:L9:59:LYS:HG2	1.85	0.59
20:D5:45:GLU:OE1	20:D5:45:GLU:N	2.33	0.59
2:1:79:C:H3'	63:O7:71:ARG:NH1	2.18	0.58
3:2:55:A:O2'	36:M1:148:VAL:O	2.17	0.58
14:C9:100:SER:O	14:C9:104:ASN:ND2	2.34	0.58
36:M1:30:LEU:HD11	36:M1:64:LYS:CB	2.33	0.58
75:S7:8:GLU:OE2	75:S7:10:SER:OG	2.11	0.58
4:3:187:G:OP1	6:C1:87:TYR:OH	2.16	0.58
70:S2:107:GLU:OE1	70:S2:107:GLU:N	2.34	0.58
1:RA:164:PRO:HG2	1:RA:227:LYS:HB2	1.84	0.58
2:1:1765:A:O2'	2:1:1766:G:H5'	2.03	0.58
2:1:2221:A:OP1	2:1:2223:C:N4	2.35	0.58
7:C2:53:VAL:HG13	7:C2:107:VAL:HG11	1.84	0.58
13:C8:83:SER:HA	13:C8:88:GLN:NE2	2.18	0.58
20:D5:78:ASN:OD1	20:D5:81:ARG:NH1	2.30	0.58
34:L9:98:ASN:HB2	34:L9:111:LYS:HB2	1.84	0.58
75:S7:49:LYS:HB3	75:S7:83:ASN:CB	2.28	0.58
57:O1:26:TRP:HA	57:O1:29:LYS:HD2	1.85	0.58
2:1:1107:A:H5'	2:1:1108:U:C5	2.37	0.58
4:3:119:G:H2'	74:S6:195:ARG:NH1	2.18	0.58
12:C7:31:ASN:ND2	12:C7:55:THR:HG22	2.17	0.58
33:L8:142:GLU:OE1	33:L8:142:GLU:N	2.36	0.58
45:MS:3:LYS:HA	45:MS:7:LYS:HE3	1.85	0.58
76:S8:62:MET:HA	76:S8:76:ALA:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:366:U:OP1	19:D4:35:LYS:HG3	2.04	0.58
30:L5:112:SER:O	30:L5:113:LEU:HD23	2.04	0.58
37:M3:163:SER:HA	54:N8:142:LYS:CE	2.34	0.58
40:M6:28:LEU:HD11	40:M6:88:ILE:HD13	1.86	0.58
43:M9:157:GLU:HA	43:M9:160:LYS:HB2	1.85	0.58
2:1:2057:G:N7	36:M1:24:ARG:NH1	2.46	0.58
35:M0:20:SER:O	35:M0:21:ARG:HG2	2.04	0.58
2:1:675:U:H5	54:N8:26:ARG:HH22	1.52	0.58
12:C7:70:TYR:CE1	12:C7:75:GLU:HG3	2.38	0.58
74:S6:180:ARG:O	74:S6:184:GLU:HG2	2.03	0.58
75:S7:50:VAL:HG22	75:S7:54:ILE:HG13	1.86	0.58
2:1:207:A:OP1	33:L8:75:LYS:NZ	2.29	0.58
45:MS:42:SER:O	45:MS:43:LYS:HD3	2.03	0.58
51:N5:61:LYS:O	51:N5:65:GLU:HG3	2.03	0.58
58:O2:9:LYS:O	58:O2:12:VAL:HG22	2.04	0.58
10:C5:33:SER:CB	24:D9:8:ASP:HB2	2.33	0.58
29:L4:259:ILE:O	29:L4:270:THR:HG21	2.04	0.58
38:M4:96:GLU:OE2	40:M6:181:LYS:HE3	2.04	0.58
43:M9:151:ARG:HA	43:M9:154:GLU:OE1	2.03	0.58
44:MD:88:PRO:CD	44:MD:135:ASP:HB2	2.33	0.58
46:N0:48:THR:HG23	46:N0:49:LYS:O	2.04	0.58
46:N0:50:ASN:HB3	46:N0:53:PHE:H	1.69	0.58
48:N2:13:THR:HG22	48:N2:59:GLU:OE1	2.03	0.58
58:O2:8:PRO:O	58:O2:12:VAL:HG13	2.03	0.58
14:C9:114:HIS:ND1	14:C9:115:PRO:HD2	2.19	0.57
50:N4:73:GLN:CB	74:S6:113:LEU:HD13	2.34	0.57
57:O1:2:TRP:HZ3	57:O1:46:ARG:HE	1.49	0.57
69:S1:84:ARG:NH2	69:S1:193:GLU:OE2	2.34	0.57
1:RA:241:MET:HE1	1:RA:255:PHE:HB3	1.86	0.57
2:1:205:U:O2	33:L8:70:GLU:HB2	2.04	0.57
4:3:293:C:O2	4:3:296:G:N2	2.25	0.57
32:L7:70:LYS:HE2	32:L7:70:LYS:HA	1.87	0.57
45:MS:4:THR:N	45:MS:7:LYS:HE2	2.11	0.57
61:O5:14:ILE:O	61:O5:18:GLU:HG3	2.03	0.57
13:C8:65:MET:O	13:C8:69:SER:OG	2.12	0.57
35:M0:112:GLN:HG2	35:M0:113:THR:H	1.69	0.57
44:MD:78:GLU:HA	44:MD:82:VAL:HG22	1.86	0.57
15:D0:34:ASN:HA	15:D0:37:CYS:SG	2.44	0.57
32:L7:188:THR:O	32:L7:189:GLU:HG3	2.05	0.57
38:M4:62:LEU:H	38:M4:62:LEU:HD12	1.69	0.57
52:N6:138:GLU:O	52:N6:141:VAL:HB	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2551:G:O2'	2:1:2552:U:O5'	2.15	0.57
4:3:150:G:H2'	4:3:151:U:H5'	1.87	0.57
19:D4:14:ARG:HB2	72:S4:95:THR:CG2	2.33	0.57
40:M6:184:LYS:HE2	40:M6:184:LYS:HA	1.87	0.57
75:S7:122:VAL:HG22	75:S7:128:MET:HG3	1.86	0.57
2:1:2591:U:H2'	2:1:2592:U:C6	2.39	0.57
4:3:134:C:H3'	4:3:135:G:H5"	1.86	0.57
15:D0:45:LYS:HE2	15:D0:52:GLN:HG3	1.85	0.57
36:M1:32:ARG:O	36:M1:36:VAL:HG23	2.05	0.57
68:S0:83:SER:HB3	68:S0:92:VAL:HG21	1.87	0.57
4:3:592:G:H2'	4:3:593:G:C8	2.39	0.57
5:C0:22:LEU:HD11	71:S3:75:ARG:NH2	2.18	0.57
9:C4:109:VAL:HG23	21:D6:53:ALA:HB1	1.84	0.57
13:C8:24:THR:HG23	20:D5:40:VAL:HG11	1.87	0.57
17:D2:81:ARG:HD3	17:D2:118:ASN:HA	1.87	0.57
31:L6:21:ILE:HB	31:L6:22:PRO:HD3	1.85	0.57
43:M9:37:THR:OG1	43:M9:40:GLN:HG3	2.05	0.57
48:N2:17:THR:HG22	48:N2:56:ASN:HB3	1.85	0.57
70:S2:139:HIS:ND1	70:S2:182:ASP:OD2	2.29	0.57
71:S3:137:VAL:HG12	71:S3:141:LEU:HD21	1.86	0.57
77:S9:62:ASN:HB2	77:S9:65:ASP:OD2	2.05	0.57
1:RA:199:VAL:HG11	1:RA:212:VAL:CG2	2.31	0.57
2:1:1967:G:H2'	2:1:1968:U:O4'	2.04	0.57
13:C8:29:PHE:O	13:C8:32:THR:OG1	2.21	0.57
17:D2:81:ARG:NE	17:D2:118:ASN:OD1	2.37	0.57
2:1:309:G:OP1	39:M5:47:ARG:NE	2.38	0.57
2:1:1574:U:H3	4:3:581:A:HO2'	1.51	0.57
2:1:2468:G:O2'	2:1:2469:A:H4'	2.05	0.57
4:3:962:A:OP1	68:S0:119:LYS:NZ	2.20	0.57
4:3:1095:C:OP1	10:C5:44:ARG:NH2	2.38	0.57
10:C5:58:LEU:O	10:C5:62:CYS:HB2	2.05	0.57
44:MD:11:PHE:HB3	44:MD:14:VAL:CG1	2.35	0.57
44:MD:84:LYS:HB2	44:MD:99:TRP:CZ3	2.40	0.57
47:N1:118:ALA:HB1	47:N1:123:VAL:O	2.04	0.57
77:S9:164:ASN:HB3	77:S9:167:SER:OG	2.05	0.57
1:RA:44:SER:O	1:RA:59:LEU:HB2	2.05	0.57
2:1:2565:G:H21	2:1:2567:A:H62	1.51	0.57
4:3:61:G:O2'	4:3:76:G:N2	2.29	0.57
17:D2:81:ARG:CD	17:D2:118:ASN:HA	2.34	0.57
28:L3:181:GLY:O	28:L3:187:LYS:NZ	2.21	0.57
53:N7:85:ILE:H	53:N7:85:ILE:HD12	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:N7:107:ALA:O	53:N7:110:LYS:HG3	2.04	0.57
75:S7:17:LYS:HE3	75:S7:72:GLN:HE21	1.70	0.57
7:C2:99:LYS:HD3	7:C2:101:ARG:HH21	1.70	0.56
29:L4:4:GLN:HB3	29:L4:18:THR:HG21	1.86	0.56
36:M1:87:LYS:O	36:M1:90:GLU:HG3	2.05	0.56
43:M9:155:LEU:HA	43:M9:158:GLN:HG2	1.87	0.56
2:1:193:G:O6	37:M3:54:ARG:NH1	2.38	0.56
2:1:1375:U:H4'	2:1:1376:A:OP1	2.04	0.56
7:C2:75:PRO:HB2	7:C2:127:LEU:HD11	1.87	0.56
8:C3:38:ILE:HD11	8:C3:78:ASN:HB3	1.86	0.56
37:M3:56:ILE:HD13	37:M3:70:LEU:HD23	1.86	0.56
58:O2:86:ILE:CG1	58:O2:118:ARG:HG3	2.35	0.56
70:S2:225:ASN:HB2	70:S2:226:PRO:HD2	1.87	0.56
77:S9:50:ASP:OD2	77:S9:109:TYR:OH	2.20	0.56
2:1:1415:U:H5"	2:1:1416:U:OP1	2.06	0.56
4:3:1088:G:H22	4:3:1112:G:H2'	1.70	0.56
8:C3:19:ALA:O	75:S7:114:LEU:HD22	2.06	0.56
13:C8:49:LEU:HG	13:C8:68:ILE:HG22	1.86	0.56
29:L4:5:ILE:CD1	29:L4:21:LEU:HD13	2.35	0.56
32:L7:174:ILE:HG23	32:L7:179:GLU:CB	2.35	0.56
66:P2:66:LEU:HD23	66:P2:83:LEU:HD12	1.87	0.56
70:S2:93:ASP:OD1	70:S2:95:LYS:N	2.28	0.56
75:S7:24:ALA:HB1	75:S7:25:PRO:HD2	1.85	0.56
6:C1:10:PHE:CD1	6:C1:11:PRO:HD2	2.40	0.56
66:P2:60:ALA:O	66:P2:61:LYS:HG3	2.05	0.56
76:S8:78:LEU:HD23	76:S8:104:ILE:HD11	1.88	0.56
77:S9:71:ARG:O	77:S9:75:ARG:HG3	2.05	0.56
1:RA:12:LEU:HB3	1:RA:45:TRP:CZ3	2.40	0.56
2:1:1785:A:H2'	2:1:1786:C:C6	2.41	0.56
31:L6:39:ARG:HB3	31:L6:41:THR:HG23	1.87	0.56
45:MS:11:GLU:O	45:MS:15:LYS:NZ	2.27	0.56
46:N0:135:ARG:NH1	46:N0:136:SER:HB3	2.20	0.56
2:1:822:G:H21	3:2:84:A:H61	1.53	0.56
2:1:1610:A:O2'	27:L2:209:THR:HG22	2.05	0.56
31:L6:130:THR:OG1	31:L6:131:ASP:N	2.38	0.56
45:MS:3:LYS:HA	45:MS:7:LYS:CE	2.36	0.56
62:O6:56:SER:HA	62:O6:59:GLU:HB2	1.87	0.56
65:P0:79:MET:HG2	65:P0:84:ALA:HB2	1.86	0.56
68:S0:154:ASN:HB2	68:S0:170:ASN:ND2	2.21	0.56
1:RA:203:LYS:O	1:RA:207:LYS:HG2	2.06	0.56
50:N4:7:MET:SD	50:N4:29:VAL:HG23	2.46	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S0:26:GLN:HB3	68:S0:29:LEU:HD12	1.88	0.56
74:S6:43:GLU:HA	74:S6:118:LYS:NZ	2.21	0.56
2:1:2160:G:H2'	2:1:2161:C:H5'	1.87	0.56
15:D0:85:VAL:HG21	71:S3:7:LEU:HD21	1.88	0.56
2:1:1419:G:O6	57:O1:28:LYS:HE2	2.04	0.56
31:L6:16:TYR:HB2	31:L6:18:PRO:CD	2.35	0.56
37:M3:136:ALA:O	37:M3:137:LYS:HD2	2.06	0.56
2:1:701:A:H4'	54:N8:41:MET:HE1	1.87	0.56
4:3:121:U:C2	74:S6:188:ARG:HD2	2.41	0.56
4:3:135:G:H4'	74:S6:15:MET:CE	2.36	0.56
14:C9:12:PHE:HB3	14:C9:60:ARG:NH2	2.16	0.56
15:D0:45:LYS:HG2	15:D0:52:GLN:HG3	1.88	0.56
29:L4:312:ASP:HB3	29:L4:315:GLU:CG	2.35	0.56
74:S6:5:ILE:HD12	74:S6:16:PHE:CD2	2.41	0.56
44:MD:85:HIS:O	44:MD:86:LEU:HD12	2.06	0.55
57:O1:54:THR:HG22	57:O1:56:ASP:H	1.71	0.55
1:RA:275:LEU:HD11	1:RA:282:ILE:HD11	1.87	0.55
2:1:745:C:H1'	2:1:747:U:O4	2.07	0.55
13:C8:25:LYS:HD3	13:C8:29:PHE:CD1	2.40	0.55
19:D4:14:ARG:NE	72:S4:95:THR:HG22	2.21	0.55
34:L9:131:ARG:HG2	34:L9:132:LEU:H	1.71	0.55
70:S2:164:GLY:O	70:S2:182:ASP:HA	2.06	0.55
1:RA:130:ARG:HG2	1:RA:155:GLY:O	2.06	0.55
2:1:179:G:H2'	2:1:180:A:C8	2.42	0.55
4:3:1088:G:O2'	4:3:1089:A:H8	1.90	0.55
48:N2:47:LYS:O	48:N2:48:LEU:HD23	2.06	0.55
4:3:108:U:H2'	4:3:109:U:C6	2.42	0.55
4:3:892:A:H2'	4:3:893:U:C6	2.41	0.55
32:L7:176:CYS:SG	32:L7:179:GLU:HG3	2.47	0.55
1:RA:92:ARG:HH11	1:RA:101:SER:HB3	1.71	0.55
1:RA:103:LEU:O	1:RA:104:LEU:HD23	2.06	0.55
1:RA:306:CYS:O	1:RA:307:LEU:HD23	2.06	0.55
6:C1:112:PHE:HB3	6:C1:116:ILE:CD1	2.37	0.55
10:C5:71:SER:O	10:C5:74:SER:OG	2.13	0.55
33:L8:68:ARG:HG3	33:L8:150:LEU:O	2.07	0.55
43:M9:95:TRP:CH2	43:M9:99:ILE:HG21	2.42	0.55
44:MD:84:LYS:HG3	44:MD:97:GLU:OE2	2.06	0.55
72:S4:255:LEU:HD11	77:S9:88:LEU:HD13	1.88	0.55
38:M4:97:GLU:O	38:M4:101:LYS:HG3	2.07	0.55
49:N3:12:LYS:HD3	49:N3:13:LYS:N	2.21	0.55
75:S7:8:GLU:HG3	75:S7:11:ILE:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:C7:78:ARG:HA	12:C7:81:LYS:NZ	2.21	0.55
23:D8:27:VAL:HG12	23:D8:40:ARG:O	2.06	0.55
27:L2:116:ASN:OD1	27:L2:157:GLY:HA3	2.07	0.55
31:L6:88:ILE:CG2	31:L6:116:THR:HB	2.33	0.55
43:M9:37:THR:O	43:M9:41:ILE:HG12	2.06	0.55
44:MD:79:GLY:O	44:MD:80:ARG:NH1	2.40	0.55
56:O0:12:THR:O	56:O0:16:LEU:HG	2.07	0.55
58:O2:90:THR:HB	58:O2:91:PRO:HD3	1.88	0.55
75:S7:37:ILE:HD12	75:S7:49:LYS:NZ	2.21	0.55
2:1:2551:G:HO2'	2:1:2552:U:P	2.30	0.55
37:M3:163:SER:OG	54:N8:142:LYS:HE3	2.06	0.55
61:O5:83:LEU:HD22	63:O7:83:LEU:HD11	1.87	0.55
69:S1:91:GLY:HA3	69:S1:101:PHE:CE2	2.42	0.55
77:S9:133:LEU:CD1	77:S9:139:ILE:HD11	2.36	0.55
1:RA:5:GLU:OE1	1:RA:331:ARG:HB2	2.06	0.55
2:1:1962:G:H2'	2:1:1963:C:H6	1.72	0.55
4:3:371:A:C2'	4:3:372:G:H5"	2.35	0.55
7:C2:14:THR:HB	7:C2:16:GLN:OE1	2.06	0.55
34:L9:46:ILE:HA	34:L9:50:ASN:O	2.06	0.55
37:M3:84:LEU:HD23	37:M3:89:ALA:HB2	1.87	0.55
38:M4:95:VAL:HG21	40:M6:194:LEU:CD2	2.37	0.55
44:MD:88:PRO:HG3	44:MD:135:ASP:HB2	1.88	0.55
53:N7:80:LEU:HD11	53:N7:111:ALA:CB	2.37	0.55
1:RA:166:GLU:HG3	1:RA:168:SER:H	1.71	0.55
4:3:33:U:H2'	4:3:34:C:C6	2.42	0.55
9:C4:62:GLN:O	9:C4:66:THR:HG23	2.06	0.55
23:D8:8:PHE:CE1	23:D8:53:GLU:HG2	2.42	0.55
38:M4:103:LYS:HE2	40:M6:180:LEU:HD13	1.89	0.55
44:MD:32:CYS:SG	44:MD:65:CYS:N	2.80	0.55
77:S9:133:LEU:HD12	77:S9:139:ILE:HD11	1.88	0.55
1:RA:233:THR:HG22	1:RA:243:LEU:CB	2.37	0.54
2:1:282:C:H5"	52:N6:47:THR:HG21	1.88	0.54
5:C0:53:TYR:OH	5:C0:74:ARG:HG2	2.07	0.54
10:C5:101:VAL:O	10:C5:125:THR:HG22	2.06	0.54
35:M0:38:ARG:NH1	35:M0:45:GLU:OE2	2.31	0.54
41:M7:113:ILE:O	41:M7:117:GLU:HG2	2.07	0.54
68:S0:95:PHE:HE1	68:S0:184:SER:HA	1.70	0.54
19:D4:17:SER:OG	19:D4:79:VAL:HG11	2.08	0.54
19:D4:93:THR:OG1	19:D4:95:LYS:HE3	2.07	0.54
33:L8:100:VAL:HG21	33:L8:158:CYS:SG	2.47	0.54
44:MD:87:LEU:HB3	44:MD:88:PRO:HD2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:MD:89:THR:OG1	44:MD:90:ASN:N	2.39	0.54
49:N3:27:GLN:O	49:N3:30:THR:HG23	2.06	0.54
66:P2:63:THR:HG21	66:P2:85:ARG:HB3	1.88	0.54
75:S7:151:ALA:O	75:S7:155:LEU:HB2	2.07	0.54
77:S9:105:THR:HB	77:S9:107:ASN:HD22	1.70	0.54
1:RA:130:ARG:HD2	1:RA:147:ARG:HH21	1.73	0.54
7:C2:95:SER:OG	7:C2:99:LYS:HB3	2.08	0.54
13:C8:63:ASP:O	13:C8:67:ARG:HG3	2.07	0.54
20:D5:45:GLU:O	20:D5:49:LYS:HG2	2.07	0.54
50:N4:19:ILE:HD12	50:N4:37:ARG:NH2	2.21	0.54
61:O5:75:PRO:HG2	61:O5:78:LYS:HD3	1.89	0.54
74:S6:2:LYS:HG3	74:S6:107:VAL:HG22	1.89	0.54
23:D8:30:GLU:OE1	23:D8:37:THR:HG22	2.07	0.54
56:O0:54:ARG:NH1	56:O0:58:GLU:OE2	2.39	0.54
76:S8:74:ARG:HB2	76:S8:109:PHE:CE1	2.43	0.54
1:RA:163:HIS:HD2	1:RA:166:GLU:H	1.54	0.54
30:L5:115:GLU:OE1	30:L5:116:VAL:HG23	2.07	0.54
44:MD:144:GLU:HG2	44:MD:148:VAL:O	2.08	0.54
49:N3:75:LYS:HB3	49:N3:77:GLU:OE1	2.07	0.54
2:1:1721:G:OP1	41:M7:162:LYS:HG2	2.07	0.54
5:C0:76:ARG:O	5:C0:80:VAL:HB	2.07	0.54
16:D1:26:VAL:HG11	70:S2:224:LEU:HD21	1.89	0.54
16:D1:36:VAL:HG13	68:S0:190:MET:O	2.08	0.54
31:L6:129:MET:HB2	31:L6:133:GLU:HG3	1.89	0.54
44:MD:11:PHE:HB3	44:MD:14:VAL:HG12	1.90	0.54
44:MD:105:LYS:HD2	44:MD:105:LYS:O	2.07	0.54
49:N3:17:LYS:NZ	49:N3:133:ASP:O	2.31	0.54
2:1:450:G:H4'	58:O2:30:ASP:OD2	2.07	0.54
11:C6:59:GLN:O	11:C6:63:LYS:HE3	2.08	0.54
13:C8:16:ILE:HD11	13:C8:65:MET:SD	2.48	0.54
31:L6:149:TYR:CD1	40:M6:197:LEU:HD22	2.43	0.54
42:M8:185:GLY:O	42:M8:186:ARG:HG3	2.08	0.54
53:N7:109:MET:O	53:N7:113:LYS:HG2	2.07	0.54
59:O3:7:ASN:HB3	59:O3:10:VAL:CG1	2.35	0.54
74:S6:150:GLU:OE2	74:S6:153:VAL:HB	2.07	0.54
3:2:1:A:P	30:L5:261:LYS:HD2	2.48	0.54
44:MD:62:CYS:HB2	44:MD:69:MET:SD	2.48	0.54
47:N1:125:LEU:HG	47:N1:127:PRO:HD2	1.89	0.54
12:C7:51:ALA:O	12:C7:55:THR:HG23	2.08	0.54
24:D9:27:GLY:O	24:D9:30:SER:OG	2.19	0.54
38:M4:80:THR:O	38:M4:81:THR:OG1	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:N1:62:ARG:NH1	55:N9:54:THR:HG22	2.23	0.54
75:S7:129:VAL:CG1	75:S7:161:ILE:HD13	2.37	0.54
77:S9:80:TYR:O	77:S9:112:ARG:NE	2.27	0.54
10:C5:99:VAL:HG21	10:C5:123:ALA:HB2	1.89	0.53
27:L2:195:HIS:HD2	27:L2:197:HIS:H	1.54	0.53
30:L5:63:VAL:CG1	30:L5:70:ASP:HB3	2.39	0.53
44:MD:103:MET:HB2	44:MD:108:PHE:CE1	2.43	0.53
45:MS:40:LEU:HD12	45:MS:40:LEU:O	2.08	0.53
1:RA:198:TYR:OH	1:RA:250:GLU:HA	2.08	0.53
2:1:1376:A:O2'	2:1:1378:A:OP1	2.22	0.53
6:C1:19:LYS:CG	6:C1:20:PRO:HD2	2.38	0.53
13:C8:2:ASN:OD1	13:C8:5:TYR:HB2	2.09	0.53
15:D0:49:ASP:CG	15:D0:92:LEU:HB3	2.28	0.53
27:L2:174:LYS:HE2	27:L2:180:HIS:HE1	1.73	0.53
29:L4:205:LEU:HD12	29:L4:224:ASP:HB2	1.90	0.53
30:L5:122:ILE:HG22	30:L5:123:ASP:OD1	2.07	0.53
46:N0:120:ILE:HD11	46:N0:143:VAL:HG21	1.89	0.53
53:N7:2:PHE:HZ	56:O0:63:LEU:HB2	1.74	0.53
71:S3:35:THR:HG22	71:S3:36:MET:H	1.72	0.53
1:RA:168:SER:O	1:RA:169:ILE:HD13	2.08	0.53
1:RA:168:SER:O	1:RA:183:ASP:HA	2.08	0.53
2:1:747:U:O2'	2:1:748:G:O4'	2.26	0.53
19:D4:7:ILE:HD11	19:D4:21:LEU:HD22	1.91	0.53
48:N2:19:PRO:HA	48:N2:103:TYR:OH	2.07	0.53
75:S7:63:SER:O	75:S7:67:LYS:HG3	2.09	0.53
1:RA:285:GLU:CB	1:RA:292:ILE:HD11	2.38	0.53
36:M1:14:ILE:HD11	36:M1:162:TRP:CH2	2.43	0.53
38:M4:99:LEU:O	38:M4:102:GLU:HG3	2.09	0.53
42:M8:75:ILE:HG13	42:M8:81:LYS:HB2	1.91	0.53
46:N0:20:MET:CE	46:N0:49:LYS:HD3	2.39	0.53
53:N7:106:ASP:OD1	53:N7:107:ALA:N	2.42	0.53
61:O5:68:VAL:O	61:O5:72:ARG:HD2	2.08	0.53
2:1:1212:G:H5"	60:O4:78:THR:CG2	2.38	0.53
2:1:1485:G:O2'	2:1:1486:C:O5'	2.26	0.53
2:1:2259:U:H5"	28:L3:232:ARG:HD3	1.90	0.53
4:3:186:G:OP1	6:C1:102:THR:OG1	2.17	0.53
4:3:788:G:N7	18:D3:107:ARG:NH2	2.54	0.53
42:M8:181:ILE:CA	42:M8:187:LYS:HE3	2.39	0.53
47:N1:118:ALA:HB3	47:N1:124:VAL:HG12	1.90	0.53
2:1:163:U:OP1	39:M5:176:LYS:NZ	2.42	0.53
4:3:62:A:N6	4:3:76:G:H1'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:L7:86:LEU:HD23	32:L7:108:ARG:O	2.09	0.53
57:O1:4:LYS:HD2	57:O1:46:ARG:HB2	1.91	0.53
61:O5:53:ALA:O	61:O5:57:THR:HG23	2.08	0.53
71:S3:105:ARG:HG3	71:S3:174:VAL:CG2	2.31	0.53
2:1:1501:G:H2'	2:1:1502:U:C5	2.43	0.53
10:C5:50:GLY:HA2	24:D9:10:PRO:O	2.09	0.53
39:M5:104:MET:SD	39:M5:160:GLU:HG2	2.48	0.53
40:M6:28:LEU:HD11	40:M6:88:ILE:HD11	1.90	0.53
1:RA:26:ARG:NH1	1:RA:26:ARG:O	2.41	0.53
2:1:873:G:O2'	2:1:874:C:H5'	2.08	0.53
7:C2:53:VAL:HA	7:C2:107:VAL:CG1	2.37	0.53
13:C8:122:ARG:HG3	13:C8:132:VAL:HG11	1.90	0.53
29:L4:143:ASP:O	29:L4:172:ASN:ND2	2.41	0.53
68:S0:90:LYS:HB3	68:S0:91:PRO:HD3	1.90	0.53
77:S9:115:GLN:NE2	77:S9:131:ARG:HB2	2.24	0.53
2:1:1965:C:H2'	2:1:1966:A:C8	2.36	0.53
3:2:83:A:H61	3:2:93:A:H61	1.55	0.53
26:L1:3:GLU:HA	26:L1:6:LEU:CB	2.38	0.53
40:M6:187:GLU:HA	40:M6:190:VAL:HG12	1.91	0.53
42:M8:75:ILE:HD11	42:M8:81:LYS:O	2.08	0.53
64:O9:7:ALA:O	64:O9:11:THR:HG23	2.09	0.53
72:S4:208:MET:HB2	72:S4:216:PHE:HB3	1.91	0.53
74:S6:69:LYS:HE3	74:S6:102:SER:CB	2.38	0.53
9:C4:84:GLY:HA2	9:C4:89:MET:HB3	1.91	0.53
15:D0:41:TYR:HA	15:D0:52:GLN:NE2	2.23	0.53
31:L6:39:ARG:HB3	31:L6:41:THR:CG2	2.39	0.53
58:O2:66:LYS:HB2	58:O2:71:ARG:HG3	1.90	0.53
68:S0:129:VAL:HG12	68:S0:131:ASP:H	1.74	0.53
70:S2:89:VAL:HG11	70:S2:116:ILE:HG12	1.91	0.53
77:S9:119:PHE:CE1	77:S9:126:SER:HA	2.44	0.53
4:3:296:G:O2'	4:3:297:G:O4'	2.24	0.52
4:3:499:G:O6	77:S9:154:ARG:HG3	2.09	0.52
7:C2:16:GLN:HB3	7:C2:87:ARG:NH2	2.18	0.52
22:D7:76:GLU:OE1	22:D7:76:GLU:N	2.42	0.52
44:MD:146:ARG:HG3	44:MD:148:VAL:HG22	1.91	0.52
70:S2:40:GLU:OE1	70:S2:40:GLU:N	2.42	0.52
74:S6:150:GLU:C	74:S6:151:LYS:HG3	2.30	0.52
1:RA:264:ILE:HD12	1:RA:275:LEU:HB3	1.91	0.52
2:1:1197:G:H2'	53:N7:54:ARG:HH22	1.74	0.52
4:3:891:C:O2'	4:3:892:A:OP1	2.27	0.52
15:D0:23:ILE:HG13	15:D0:116:LEU:HD12	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:L8:84:PRO:HD2	33:L8:86:LYS:HZ2	1.73	0.52
34:L9:35:GLU:HG2	34:L9:73:LEU:CD2	2.37	0.52
44:MD:84:LYS:HB2	44:MD:99:TRP:CH2	2.44	0.52
70:S2:20:GLU:O	70:S2:22:ILE:HD12	2.08	0.52
74:S6:17:GLU:OE1	74:S6:18:ILE:N	2.40	0.52
75:S7:51:PRO:HD2	75:S7:54:ILE:CG1	2.39	0.52
75:S7:84:PHE:CD2	75:S7:101:VAL:HG22	2.45	0.52
2:1:293:G:O2'	2:1:294:C:H5'	2.08	0.52
7:C2:34:ARG:HA	7:C2:108:ALA:CB	2.39	0.52
14:C9:114:HIS:HB3	14:C9:117:ASP:O	2.09	0.52
36:M1:21:ILE:HG23	36:M1:124:GLY:O	2.09	0.52
37:M3:163:SER:HA	54:N8:142:LYS:NZ	2.24	0.52
44:MD:103:MET:HE2	44:MD:106:SER:HA	1.91	0.52
73:S5:64:HIS:O	73:S5:66:ARG:N	2.43	0.52
74:S6:43:GLU:HA	74:S6:118:LYS:CE	2.39	0.52
2:1:1105:U:H3'	2:1:1106:G:H5"	1.91	0.52
4:3:944:U:H3'	4:3:945:G:H5"	1.90	0.52
31:L6:73:LEU:HD11	31:L6:85:LEU:CD2	2.38	0.52
44:MD:148:VAL:HG12	44:MD:161:ILE:HA	1.91	0.52
48:N2:79:PHE:CZ	48:N2:83:LYS:HD2	2.45	0.52
68:S0:46:ARG:HD2	68:S0:48:ARG:HH11	1.74	0.52
72:S4:240:GLU:HG2	72:S4:242:GLY:H	1.75	0.52
74:S6:64:SER:HA	74:S6:99:SER:OG	2.09	0.52
74:S6:207:LYS:O	74:S6:211:GLU:HG3	2.09	0.52
2:1:1433:G:O2'	49:N3:30:THR:HG22	2.09	0.52
2:1:1688:C:C2'	2:1:1689:G:H5'	2.40	0.52
2:1:2054:G:O2'	36:M1:126:ASP:OD1	2.16	0.52
4:3:358:U:O4	77:S9:131:ARG:HG2	2.10	0.52
4:3:1046:G:H2'	4:3:1046:G:N3	2.23	0.52
5:C0:19:LYS:HD2	71:S3:63:PHE:HE2	1.75	0.52
13:C8:138:LYS:O	13:C8:138:LYS:HG2	2.10	0.52
32:L7:163:ASN:O	32:L7:167:GLU:HG3	2.10	0.52
34:L9:134:GLU:OE1	34:L9:134:GLU:N	2.42	0.52
42:M8:181:ILE:HA	42:M8:187:LYS:HE3	1.92	0.52
45:MS:10:LYS:O	45:MS:14:GLU:HG3	2.09	0.52
60:O4:43:CYS:O	60:O4:44:HIS:HB2	2.10	0.52
73:S5:42:THR:HB	73:S5:51:ILE:CD1	2.39	0.52
74:S6:43:GLU:HA	74:S6:118:LYS:HE3	1.90	0.52
1:RA:174:SER:OG	1:RA:175:ALA:N	2.42	0.52
4:3:554:G:H2'	4:3:555:A:C8	2.44	0.52
12:C7:77:GLU:O	12:C7:81:LYS:NZ	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:D4:85:LYS:HE3	72:S4:57:ASN:HD21	1.73	0.52
36:M1:54:ILE:HG22	36:M1:57:PHE:H	1.74	0.52
54:N8:77:ARG:O	54:N8:79:TRP:N	2.43	0.52
74:S6:27:TYR:CZ	74:S6:103:GLU:HG3	2.45	0.52
75:S7:46:MET:SD	75:S7:78:ILE:HG23	2.50	0.52
4:3:138:A:H2'	4:3:139:A:O4'	2.09	0.52
8:C3:84:ILE:CG2	8:C3:88:LEU:HD23	2.39	0.52
14:C9:130:ILE:O	14:C9:134:VAL:HG22	2.10	0.52
28:L3:289:LYS:HD3	28:L3:291:GLU:H	1.74	0.52
30:L5:277:VAL:HG13	35:M0:206:ILE:HD11	1.91	0.52
72:S4:251:ILE:O	72:S4:255:LEU:N	2.42	0.52
2:1:1093:G:OP1	41:M7:66:ARG:HB2	2.08	0.52
2:1:2325:A:H5"	2:1:2326:G:H5'	1.92	0.52
30:L5:251:LYS:O	30:L5:251:LYS:HD3	2.10	0.52
54:N8:98:PRO:HD2	54:N8:121:ILE:HG22	1.91	0.52
72:S4:255:LEU:HD13	77:S9:75:ARG:HD3	1.92	0.52
74:S6:26:LEU:O	74:S6:29:LYS:HG3	2.10	0.52
74:S6:42:GLU:O	74:S6:45:GLU:HG3	2.10	0.52
77:S9:82:ILE:HG22	77:S9:83:LEU:CD1	2.37	0.52
2:1:300:U:H1'	61:O5:108:ARG:HB2	1.92	0.52
2:1:1805:C:H2'	2:1:1806:U:C6	2.45	0.52
2:1:1975:U:OP1	2:1:1975:U:H4'	2.10	0.52
7:C2:86:GLY:HA2	7:C2:105:CYS:SG	2.50	0.52
20:D5:65:ILE:HD11	20:D5:80:LEU:HD21	1.91	0.52
26:L1:63:LEU:O	26:L1:81:ALA:HB2	2.10	0.52
33:L8:23:GLU:O	33:L8:27:LEU:HD13	2.10	0.52
37:M3:58:ARG:HD2	37:M3:65:ASN:O	2.09	0.52
72:S4:246:SER:O	72:S4:250:LYS:HG3	2.10	0.52
4:3:671:A:H2'	4:3:673:A:N7	2.25	0.52
7:C2:119:GLU:O	7:C2:123:VAL:HG23	2.09	0.52
12:C7:80:ARG:HA	12:C7:83:ASN:HD21	1.74	0.52
44:MD:101:SER:OG	44:MD:102:ASP:N	2.43	0.52
53:N7:24:ILE:HG22	53:N7:25:LYS:HG3	1.92	0.52
54:N8:76:ALA:HA	54:N8:114:LYS:O	2.10	0.52
73:S5:114:GLY:HA3	73:S5:118:SER:O	2.10	0.52
2:1:232:G:H2'	2:1:233:G:O4'	2.09	0.51
4:3:1254:A:H2'	4:3:1255:A:C2'	2.40	0.51
13:C8:80:ILE:HD11	13:C8:85:MET:SD	2.50	0.51
29:L4:7:CYS:HB3	29:L4:16:LYS:O	2.10	0.51
34:L9:4:LEU:HD11	34:L9:54:ARG:HG2	1.90	0.51
44:MD:125:SER:OG	44:MD:126:CYS:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:N1:7:ARG:O	47:N1:7:ARG:HD3	2.10	0.51
49:N3:112:ILE:HG22	49:N3:113:ASN:O	2.10	0.51
7:C2:35:GLY:O	7:C2:39:THR:HG23	2.11	0.51
34:L9:82:VAL:CB	34:L9:181:ILE:HD11	2.39	0.51
42:M8:71:ILE:O	42:M8:75:ILE:HG22	2.10	0.51
44:MD:103:MET:CE	44:MD:106:SER:HA	2.40	0.51
69:S1:92:ASP:OD1	69:S1:93:ILE:N	2.43	0.51
2:1:244:G:H5"	2:1:245:A:OP1	2.11	0.51
3:2:89:G:H2'	3:2:90:A:C8	2.45	0.51
4:3:890:G:O2'	4:3:891:C:O4'	2.20	0.51
4:3:932:U:H1'	68:S0:117:GLU:OE1	2.10	0.51
36:M1:49:LYS:CE	36:M1:64:LYS:HE3	2.39	0.51
36:M1:114:LEU:H	36:M1:114:LEU:HD22	1.76	0.51
68:S0:154:ASN:HD22	68:S0:169:ASN:HA	1.74	0.51
73:S5:28:LEU:HD23	73:S5:28:LEU:H	1.74	0.51
74:S6:122:GLY:O	74:S6:123:LEU:HD23	2.10	0.51
1:RA:191:GLN:NE2	1:RA:249:LYS:HE3	2.25	0.51
2:1:1772:C:H2'	2:1:1773:C:C6	2.45	0.51
4:3:135:G:H5'	19:D4:128:ARG:NH1	2.21	0.51
27:L2:89:LYS:HE3	27:L2:91:LYS:HG2	1.92	0.51
33:L8:84:PRO:HD2	33:L8:86:LYS:NZ	2.25	0.51
40:M6:6:HIS:CE1	40:M6:34:THR:HG23	2.43	0.51
40:M6:183:ASP:HB3	40:M6:186:PHE:HB3	1.92	0.51
52:N6:55:THR:HB	52:N6:107:THR:O	2.10	0.51
72:S4:157:TYR:CE1	72:S4:173:VAL:HG12	2.44	0.51
72:S4:174:PRO:HA	72:S4:225:LEU:HD21	1.91	0.51
2:1:1416:U:H5'	2:1:1417:G:OP2	2.10	0.51
10:C5:22:VAL:HG21	10:C5:27:LEU:HD11	1.91	0.51
12:C7:79:GLU:OE1	12:C7:79:GLU:N	2.42	0.51
27:L2:123:VAL:HG22	27:L2:133:VAL:O	2.10	0.51
31:L6:100:LEU:HG	31:L6:101:ASP:H	1.74	0.51
34:L9:132:LEU:HD23	34:L9:133:ASP:O	2.10	0.51
65:P0:110:LYS:HE2	65:P0:115:PHE:HD2	1.75	0.51
72:S4:128:LYS:HG2	72:S4:129:LYS:H	1.75	0.51
77:S9:87:ASP:HB3	77:S9:93:GLU:OE1	2.10	0.51
32:L7:105:ARG:NH2	32:L7:198:LEU:O	2.40	0.51
48:N2:15:ASP:OD1	48:N2:17:THR:HG23	2.10	0.51
60:O4:95:ASN:O	60:O4:99:ILE:HG23	2.11	0.51
74:S6:20:ARG:HA	74:S6:23:GLU:HB3	1.93	0.51
77:S9:171:ASP:OD1	77:S9:172:LYS:HG3	2.11	0.51
2:1:2519:G:N7	28:L3:123:ARG:HG3	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2591:U:H2'	2:1:2592:U:H6	1.75	0.51
11:C6:47:ILE:O	11:C6:51:LYS:HG2	2.10	0.51
13:C8:27:ILE:HG12	13:C8:55:LYS:O	2.11	0.51
43:M9:84:THR:O	43:M9:88:ARG:HG2	2.11	0.51
48:N2:50:HIS:HB2	48:N2:61:ASP:OD1	2.11	0.51
50:N4:73:GLN:HB2	74:S6:113:LEU:HD13	1.93	0.51
65:P0:111:CYS:HB3	65:P0:114:CYS:O	2.10	0.51
68:S0:22:LEU:HD21	68:S0:182:ILE:HD12	1.91	0.51
75:S7:10:SER:O	75:S7:14:ILE:HG12	2.10	0.51
2:1:1765:A:C2'	2:1:1766:G:H5'	2.41	0.51
2:1:2536:C:OP1	28:L3:171:LYS:HB2	2.11	0.51
11:C6:63:LYS:HA	11:C6:63:LYS:HE2	1.92	0.51
14:C9:110:TRP:O	14:C9:120:THR:HG23	2.10	0.51
15:D0:85:VAL:CG2	71:S3:7:LEU:HD21	2.41	0.51
16:D1:31:ASP:OD1	16:D1:32:GLN:N	2.43	0.51
30:L5:193:ASP:O	30:L5:198:TYR:HB2	2.10	0.51
33:L8:40:ARG:HG2	33:L8:194:TRP:HE3	1.76	0.51
34:L9:98:ASN:O	34:L9:111:LYS:HG2	2.11	0.51
48:N2:27:PRO:CG	48:N2:56:ASN:HA	2.32	0.51
49:N3:22:MET:HE1	49:N3:63:PRO:HD2	1.93	0.51
2:1:1573:U:H5'	2:1:1574:U:O5'	2.10	0.51
3:2:28:C:OP1	36:M1:137:ARG:NH1	2.44	0.51
4:3:68:U:H1'	4:3:69:U:O5'	2.11	0.51
9:C4:100:ARG:HD2	9:C4:104:ARG:HH12	1.76	0.51
14:C9:68:VAL:N	14:C9:118:MET:HE1	2.25	0.51
33:L8:172:PHE:HA	33:L8:175:MET:HG2	1.93	0.51
37:M3:126:GLU:HB2	37:M3:130:GLU:OE2	2.10	0.51
45:MS:29:ILE:HG13	45:MS:30:LYS:N	2.25	0.51
58:O2:103:ILE:O	58:O2:128:ASN:ND2	2.44	0.51
68:S0:79:ILE:O	68:S0:101:ALA:HB1	2.11	0.51
75:S7:51:PRO:HD2	75:S7:54:ILE:CD1	2.39	0.51
1:RA:178:THR:HA	1:RA:193:TYR:O	2.11	0.51
2:1:835:A:H5'	58:O2:52:ARG:HH22	1.76	0.51
2:1:2551:G:H1'	2:1:2581:A:N6	2.26	0.51
7:C2:15:LEU:HA	7:C2:18:ALA:HB3	1.93	0.51
18:D3:37:VAL:HG21	18:D3:78:ILE:CG2	2.41	0.51
22:D7:32:TYR:O	22:D7:77:PHE:HA	2.10	0.51
43:M9:155:LEU:O	43:M9:158:GLN:HG3	2.10	0.51
53:N7:42:LYS:HB3	53:N7:56:ASN:OD1	2.11	0.51
62:O6:70:LEU:HD12	62:O6:84:VAL:HG13	1.93	0.51
74:S6:184:GLU:OE1	74:S6:187:ARG:NH1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:S7:45:ILE:HG22	75:S7:77:TYR:HB3	1.93	0.51
1:RA:130:ARG:HB2	1:RA:147:ARG:HE	1.76	0.50
10:C5:93:ILE:HD11	10:C5:112:PRO:CA	2.39	0.50
15:D0:87:LEU:HD12	15:D0:87:LEU:O	2.11	0.50
33:L8:71:ASN:HB3	33:L8:74:GLU:HG3	1.92	0.50
34:L9:98:ASN:HB2	34:L9:111:LYS:CG	2.40	0.50
34:L9:102:LYS:HB2	34:L9:107:ILE:HB	1.93	0.50
44:MD:49:GLU:HA	44:MD:54:GLU:O	2.11	0.50
52:N6:137:GLN:O	52:N6:141:VAL:N	2.44	0.50
53:N7:74:THR:HG22	60:O4:92:PHE:CZ	2.46	0.50
69:S1:69:ASP:OD2	69:S1:85:LYS:HD2	2.12	0.50
2:1:244:G:OP1	52:N6:126:ARG:NH1	2.44	0.50
2:1:1247:A:H5"	2:1:1248:A:O5'	2.11	0.50
2:1:2414:A:H5"	49:N3:21:LYS:HG2	1.93	0.50
11:C6:27:GLY:HA2	11:C6:64:ASP:HB2	1.93	0.50
23:D8:46:VAL:HG22	73:S5:127:SER:CB	2.41	0.50
30:L5:36:ARG:O	30:L5:46:LYS:NZ	2.42	0.50
41:M7:129:ASP:OD2	41:M7:131:LYS:HE3	2.12	0.50
50:N4:68:GLU:OE1	50:N4:70:MET:N	2.38	0.50
2:1:652:G:H5'	2:1:653:A:OP1	2.11	0.50
2:1:1252:G:O2'	2:1:1253:A:H5'	2.10	0.50
7:C2:26:SER:HA	7:C2:31:LYS:NZ	2.26	0.50
11:C6:32:ARG:NH2	11:C6:68:ASP:OD1	2.45	0.50
22:D7:25:GLU:OE2	75:S7:169:LYS:HB3	2.11	0.50
34:L9:6:THR:O	34:L9:7:ARG:HD3	2.11	0.50
66:P2:7:THR:O	66:P2:8:ARG:HG3	2.11	0.50
2:1:2217:A:N6	2:1:2229:G:H1'	2.26	0.50
2:1:2519:G:C8	28:L3:123:ARG:HG3	2.47	0.50
4:3:89:C:H1'	4:3:304:G:H5'	1.93	0.50
7:C2:121:GLY:HA2	7:C2:124:GLN:OE1	2.11	0.50
13:C8:85:MET:HG3	13:C8:98:HIS:HB2	1.92	0.50
15:D0:23:ILE:HG13	15:D0:116:LEU:CD1	2.40	0.50
23:D8:56:GLU:HG2	73:S5:189:ARG:NH2	2.26	0.50
30:L5:211:ASP:OD1	30:L5:211:ASP:N	2.44	0.50
30:L5:273:ARG:O	30:L5:277:VAL:HG23	2.12	0.50
50:N4:73:GLN:NE2	74:S6:114:ARG:HB2	2.12	0.50
69:S1:55:ALA:O	69:S1:58:ASN:HB2	2.10	0.50
70:S2:93:ASP:O	70:S2:94:ARG:HG2	2.11	0.50
2:1:1457:A:H2'	2:1:1458:C:O4'	2.12	0.50
4:3:1233:C:H2'	4:3:1234:C:O4'	2.11	0.50
11:C6:95:TYR:HA	11:C6:99:PHE:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L4:290:TYR:O	29:L4:295:GLN:HG2	2.11	0.50
33:L8:30:LYS:O	33:L8:34:LYS:HG3	2.12	0.50
41:M7:152:ARG:HG3	41:M7:158:ASN:ND2	2.26	0.50
51:N5:34:GLU:O	51:N5:38:ARG:HG3	2.11	0.50
72:S4:237:LEU:HD22	72:S4:238:PRO:HD2	1.92	0.50
75:S7:71:GLN:O	75:S7:74:HIS:NE2	2.45	0.50
22:D7:14:GLY:HA2	75:S7:169:LYS:HE3	1.92	0.50
31:L6:16:TYR:CB	31:L6:18:PRO:HD3	2.36	0.50
68:S0:170:ASN:O	68:S0:176:ILE:HD11	2.12	0.50
2:1:1518:U:H2'	2:1:1524:A:N6	2.26	0.50
6:C1:80:THR:HG23	6:C1:134:LYS:HD3	1.94	0.50
7:C2:86:GLY:HA3	7:C2:92:GLU:OE2	2.11	0.50
12:C7:95:CYS:HA	12:C7:116:LYS:NZ	2.25	0.50
13:C8:19:THR:HG21	13:C8:34:ILE:HG12	1.92	0.50
20:D5:90:GLN:HG3	20:D5:90:GLN:O	2.10	0.50
28:L3:299:ILE:HG23	28:L3:299:ILE:O	2.11	0.50
35:M0:36:LEU:HD11	35:M0:69:ARG:HD2	1.93	0.50
47:N1:126:ALA:HB3	47:N1:127:PRO:HD3	1.93	0.50
56:O0:20:ARG:HG3	56:O0:21:THR:HG23	1.92	0.50
69:S1:26:ALA:HA	69:S1:29:ARG:CZ	2.42	0.50
75:S7:15:ILE:HB	75:S7:16:ARG:NH1	2.25	0.50
2:1:798:G:OP1	35:M0:14:LYS:HE2	2.11	0.50
2:1:947:C:H2'	2:1:948:C:C6	2.47	0.50
2:1:2469:A:H3'	2:1:2469:A:N3	2.27	0.50
4:3:71:U:O2'	4:3:72:G:OP1	2.26	0.50
4:3:1103:G:O6	13:C8:120:ARG:NH2	2.45	0.50
13:C8:85:MET:CG	13:C8:98:HIS:HB2	2.41	0.50
31:L6:139:GLU:OE1	31:L6:139:GLU:N	2.44	0.50
42:M8:62:ASP:OD1	42:M8:146:LYS:HE2	2.12	0.50
46:N0:97:VAL:HG12	46:N0:106:ASN:HD22	1.77	0.50
69:S1:182:ASP:OD1	69:S1:183:VAL:N	2.45	0.50
74:S6:71:ARG:HG2	74:S6:96:VAL:O	2.12	0.50
1:RA:93:ILE:HD11	1:RA:104:LEU:HD11	1.92	0.50
1:RA:227:LYS:O	1:RA:227:LYS:HD3	2.12	0.50
7:C2:33:SER:OG	7:C2:42:LYS:NZ	2.34	0.50
22:D7:80:ILE:O	22:D7:81:ILE:HD13	2.11	0.50
36:M1:39:GLN:HG2	36:M1:114:LEU:HD11	1.94	0.50
36:M1:60:ARG:N	36:M1:63:GLU:OE2	2.39	0.50
36:M1:85:ARG:HD3	36:M1:89:TYR:HE2	1.77	0.50
39:M5:15:GLN:HA	39:M5:20:ARG:CG	2.39	0.50
42:M8:22:GLU:OE1	42:M8:22:GLU:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:N2:33:PHE:CE1	48:N2:37:LYS:HG3	2.47	0.50
58:O2:121:GLU:O	58:O2:122:LEU:HD12	2.12	0.50
74:S6:50:GLU:O	74:S6:110:LEU:HA	2.12	0.50
1:RA:110:ASP:O	1:RA:127:SER:HB2	2.11	0.49
1:RA:173:GLY:CA	1:RA:220:VAL:HG21	2.41	0.49
2:1:302:U:H2'	2:1:303:U:C4'	2.41	0.49
5:C0:21:LEU:HD22	5:C0:45:MET:HE2	1.94	0.49
7:C2:50:PHE:CZ	7:C2:127:LEU:HD13	2.46	0.49
21:D6:9:LYS:HB2	21:D6:30:ASP:OD1	2.11	0.49
28:L3:297:LYS:NZ	28:L3:350:VAL:O	2.25	0.49
40:M6:185:ASN:HA	40:M6:188:ASN:ND2	2.26	0.49
68:S0:207:LEU:HD23	68:S0:208:PHE:N	2.27	0.49
70:S2:21:TRP:O	70:S2:23:PRO:HD3	2.11	0.49
75:S7:38:ILE:HD13	75:S7:46:MET:HB3	1.94	0.49
4:3:886:C:O2'	25:E1:138:ALA:O	2.30	0.49
6:C1:30:ARG:NH2	6:C1:50:TYR:O	2.45	0.49
8:C3:38:ILE:HD12	8:C3:78:ASN:OD1	2.12	0.49
19:D4:82:ASN:O	19:D4:83:ILE:HD13	2.13	0.49
20:D5:22:LYS:HD3	44:MD:45:ASP:HB2	1.94	0.49
28:L3:289:LYS:HE2	28:L3:289:LYS:HA	1.94	0.49
30:L5:207:LEU:HD12	30:L5:214:LYS:HG3	1.93	0.49
31:L6:19:ASP:CA	31:L6:22:PRO:HD2	2.40	0.49
32:L7:186:ASN:HB2	32:L7:188:THR:CG2	2.39	0.49
43:M9:89:MET:HG3	43:M9:94:ILE:HD11	1.95	0.49
45:MS:60:LYS:O	45:MS:63:GLU:HG3	2.12	0.49
68:S0:22:LEU:HD12	68:S0:56:ILE:HD11	1.93	0.49
5:C0:21:LEU:HD22	5:C0:45:MET:HE1	1.93	0.49
5:C0:61:ARG:HA	24:D9:37:TYR:OH	2.12	0.49
15:D0:61:VAL:HG22	15:D0:84:ILE:HD13	1.94	0.49
23:D8:46:VAL:HG22	73:S5:127:SER:HB3	1.93	0.49
46:N0:100:SER:OG	46:N0:101:ARG:N	2.45	0.49
2:1:1243:G:H2'	2:1:1244:C:C6	2.47	0.49
6:C1:110:PRO:O	6:C1:113:GLU:HG3	2.12	0.49
30:L5:242:LYS:O	30:L5:245:GLU:HG2	2.12	0.49
37:M3:163:SER:HA	54:N8:142:LYS:HZ1	1.78	0.49
53:N7:80:LEU:O	53:N7:82:LEU:HG	2.13	0.49
64:O9:21:ARG:NH1	64:O9:22:GLU:O	2.45	0.49
71:S3:38:LEU:HD12	71:S3:47:ILE:HG12	1.93	0.49
74:S6:197:GLU:O	74:S6:201:ILE:HG12	2.11	0.49
4:3:250:G:O2'	4:3:451:C:H5	1.95	0.49
20:D5:98:MET:CE	73:S5:155:ALA:HB3	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:L5:271:GLU:OE1	30:L5:271:GLU:N	2.46	0.49
39:M5:104:MET:O	39:M5:108:LYS:HG2	2.12	0.49
50:N4:70:MET:O	50:N4:72:VAL:HG13	2.12	0.49
68:S0:170:ASN:CA	68:S0:176:ILE:HD11	2.41	0.49
74:S6:120:ILE:HD12	74:S6:120:ILE:H	1.77	0.49
77:S9:168:ARG:HG2	77:S9:169:TYR:CD2	2.47	0.49
2:1:1370:G:H5"	64:O9:10:LYS:HD3	1.94	0.49
30:L5:212:PRO:O	30:L5:216:LYS:NZ	2.43	0.49
38:M4:73:GLU:N	38:M4:73:GLU:OE2	2.45	0.49
40:M6:189:GLU:HG2	40:M6:192:ARG:NH1	2.27	0.49
64:O9:31:LYS:NZ	64:O9:34:LYS:HE2	2.26	0.49
1:RA:233:THR:HG22	1:RA:243:LEU:HB2	1.93	0.49
2:1:305:G:O2'	2:1:306:U:O2	2.31	0.49
4:3:357:G:H5'	77:S9:168:ARG:NH2	2.27	0.49
15:D0:21:VAL:HB	15:D0:92:LEU:O	2.12	0.49
19:D4:23:VAL:HB	19:D4:69:LEU:CD1	2.43	0.49
22:D7:9:THR:O	22:D7:13:VAL:HG23	2.12	0.49
29:L4:267:ALA:HB3	29:L4:270:THR:HG23	1.92	0.49
30:L5:14:PHE:O	47:N1:19:ARG:HD3	2.12	0.49
31:L6:133:GLU:HA	31:L6:136:ILE:HB	1.95	0.49
37:M3:142:GLU:OE2	37:M3:145:PRO:HB3	2.13	0.49
38:M4:90:LYS:O	38:M4:94:ARG:HG3	2.13	0.49
53:N7:2:PHE:HB2	56:O0:36:ILE:O	2.13	0.49
68:S0:6:THR:OG1	68:S0:7:ARG:HG3	2.12	0.49
70:S2:57:LEU:O	70:S2:57:LEU:HD23	2.12	0.49
75:S7:44:LYS:HE3	75:S7:75:ASP:O	2.13	0.49
4:3:866:C:O2'	4:3:867:U:H5'	2.13	0.49
4:3:943:U:C2'	4:3:944:U:H5'	2.43	0.49
23:D8:53:GLU:OE1	73:S5:107:ARG:HD3	2.12	0.49
29:L4:290:TYR:O	29:L4:292:ASP:N	2.45	0.49
38:M4:16:GLU:O	38:M4:17:ARG:HG2	2.13	0.49
40:M6:173:LEU:O	40:M6:177:ILE:HG12	2.12	0.49
46:N0:162:GLU:OE1	46:N0:162:GLU:N	2.37	0.49
60:O4:20:ARG:HG2	60:O4:34:VAL:HG21	1.94	0.49
74:S6:117:GLU:OE1	74:S6:117:GLU:N	2.34	0.49
4:3:147:A:H4'	74:S6:130:VAL:CG1	2.42	0.49
4:3:879:G:C4'	4:3:880:U:H5"	2.43	0.49
7:C2:38:GLU:HA	7:C2:41:LYS:HE2	1.94	0.49
12:C7:58:TYR:CE2	12:C7:62:LEU:HD13	2.48	0.49
12:C7:95:CYS:HA	12:C7:116:LYS:CE	2.43	0.49
21:D6:62:PRO:HB3	69:S1:110:ASP:OD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L4:141:ILE:HG13	29:L4:141:ILE:O	2.13	0.49
46:N0:20:MET:HE3	46:N0:49:LYS:HD3	1.95	0.49
52:N6:140:VAL:HG13	52:N6:143:ASN:HB2	1.93	0.49
68:S0:131:ASP:HB3	68:S0:134:ALA:HB3	1.94	0.49
1:RA:191:GLN:HG3	1:RA:249:LYS:HE3	1.93	0.49
2:1:202:U:C2'	2:1:203:G:H5'	2.43	0.49
2:1:701:A:H4'	54:N8:41:MET:CE	2.42	0.49
16:D1:29:VAL:O	16:D1:37:THR:HG22	2.13	0.49
47:N1:116:ARG:HB3	47:N1:116:ARG:NH1	2.27	0.49
73:S5:59:CYS:SG	73:S5:71:LYS:HE3	2.53	0.49
1:RA:17:ASP:OD2	1:RA:38:ARG:HB3	2.12	0.48
1:RA:198:TYR:CD2	1:RA:249:LYS:HE2	2.48	0.48
2:1:780:G:OP1	55:N9:22:LYS:HE2	2.14	0.48
19:D4:23:VAL:HB	19:D4:69:LEU:HD11	1.94	0.48
38:M4:27:ILE:O	46:N0:112:ARG:NH1	2.45	0.48
48:N2:10:ARG:HD3	48:N2:12:PHE:CZ	2.48	0.48
50:N4:77:VAL:HB	74:S6:9:THR:CG2	2.43	0.48
76:S8:87:SER:HB3	76:S8:90:LEU:HG	1.95	0.48
1:RA:231:ILE:HG21	1:RA:243:LEU:HD13	1.94	0.48
2:1:2012:U:OP2	47:N1:3:SER:OG	2.31	0.48
4:3:718:U:H4'	4:3:719:G:OP1	2.13	0.48
10:C5:75:LYS:HD3	10:C5:75:LYS:HA	1.71	0.48
31:L6:19:ASP:C	31:L6:22:PRO:HD2	2.34	0.48
31:L6:73:LEU:HD12	31:L6:86:PHE:O	2.13	0.48
33:L8:83:ASP:OD2	33:L8:86:LYS:HB2	2.13	0.48
37:M3:42:ALA:HB2	37:M3:140:THR:HG22	1.95	0.48
39:M5:169:ARG:NH1	39:M5:170:LYS:HA	2.28	0.48
40:M6:189:GLU:HA	40:M6:192:ARG:CZ	2.43	0.48
62:O6:50:LEU:HD13	62:O6:73:ARG:NE	2.28	0.48
71:S3:116:ARG:O	71:S3:120:MET:HG3	2.13	0.48
77:S9:111:GLU:HG2	77:S9:116:PHE:CE1	2.48	0.48
2:1:526:G:O2'	29:L4:111:LYS:O	2.29	0.48
2:1:1519:U:H5	2:1:1524:A:N7	2.12	0.48
6:C1:23:SER:HB2	6:C1:25:GLU:OE1	2.12	0.48
14:C9:55:MET:HG3	14:C9:101:VAL:CG1	2.43	0.48
27:L2:61:MET:SD	45:MS:47:LEU:HD12	2.53	0.48
29:L4:134:VAL:O	29:L4:139:HIS:HB2	2.14	0.48
30:L5:120:LYS:CE	30:L5:129:THR:HG22	2.42	0.48
31:L6:106:VAL:HB	31:L6:136:ILE:CD1	2.42	0.48
36:M1:134:PRO:O	36:M1:152:GLN:NE2	2.46	0.48
38:M4:11:THR:CG2	38:M4:12:PRO:HD2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:S3:61:LYS:NZ	71:S3:63:PHE:HB2	2.27	0.48
75:S7:111:PHE:HB3	75:S7:112:PRO:HD3	1.94	0.48
1:RA:199:VAL:HG12	1:RA:211:PRO:HB2	1.96	0.48
2:1:247:U:O2'	2:1:248:G:OP2	2.22	0.48
2:1:1739:A:H2'	2:1:1739:A:OP2	2.13	0.48
2:1:2070:G:H2'	2:1:2070:G:N3	2.28	0.48
4:3:1237:A:C2'	4:3:1238:G:H5'	2.44	0.48
7:C2:124:GLN:HA	7:C2:127:LEU:CB	2.43	0.48
31:L6:15:LEU:N	58:O2:99:TYR:OH	2.46	0.48
34:L9:113:PHE:O	34:L9:114:LEU:HB2	2.13	0.48
55:N9:36:HIS:CD2	55:N9:38:ALA:H	2.31	0.48
58:O2:6:PHE:CE2	58:O2:97:ARG:HD3	2.49	0.48
70:S2:151:THR:O	70:S2:189:GLY:HA3	2.14	0.48
1:RA:22:LEU:HD12	1:RA:34:TYR:O	2.14	0.48
29:L4:258:LYS:HE3	29:L4:269:LEU:CD1	2.40	0.48
33:L8:167:GLU:HG2	33:L8:168:ASP:N	2.29	0.48
42:M8:104:VAL:HG12	42:M8:126:LEU:HD23	1.95	0.48
44:MD:89:THR:CG2	44:MD:95:PHE:H	2.26	0.48
44:MD:89:THR:CB	44:MD:94:GLU:HB2	2.43	0.48
50:N4:73:GLN:CG	74:S6:113:LEU:HD13	2.42	0.48
52:N6:82:ILE:HD12	52:N6:99:ILE:HD12	1.94	0.48
53:N7:55:ARG:HG2	53:N7:56:ASN:N	2.29	0.48
68:S0:183:LEU:HD23	68:S0:183:LEU:O	2.12	0.48
76:S8:107:GLU:HB2	76:S8:108:PRO:HD3	1.95	0.48
1:RA:118:SER:OG	1:RA:164:PRO:O	2.25	0.48
1:RA:193:TYR:C	1:RA:194:LEU:HD12	2.33	0.48
1:RA:198:TYR:HH	1:RA:250:GLU:HA	1.78	0.48
7:C2:56:ASN:HD21	7:C2:81:SER:HB2	1.78	0.48
32:L7:137:ILE:HD12	32:L7:141:LEU:HD23	1.96	0.48
36:M1:40:LEU:HA	36:M1:114:LEU:HD21	1.96	0.48
43:M9:162:LEU:O	43:M9:165:SER:OG	2.16	0.48
53:N7:80:LEU:HD11	53:N7:111:ALA:HB3	1.94	0.48
57:O1:8:ASN:O	57:O1:9:GLN:HG3	2.14	0.48
66:P2:66:LEU:HD13	66:P2:89:VAL:HG21	1.96	0.48
77:S9:140:SER:HA	77:S9:144:GLN:O	2.14	0.48
2:1:1238:G:O2'	2:1:1239:G:H5'	2.14	0.48
4:3:120:A:H4'	4:3:121:U:OP1	2.14	0.48
4:3:567:G:H5'	9:C4:43:MET:HB3	1.93	0.48
4:3:825:G:C2'	4:3:826:U:H5'	2.44	0.48
4:3:959:A:H4'	4:3:960:A:O5'	2.13	0.48
10:C5:81:THR:CG2	10:C5:83:ALA:H	2.23	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C9:55:MET:HG3	14:C9:101:VAL:HG13	1.95	0.48
30:L5:97:TYR:OH	30:L5:165:ASP:OD2	2.27	0.48
46:N0:97:VAL:HG12	46:N0:106:ASN:ND2	2.28	0.48
50:N4:75:VAL:HG13	74:S6:9:THR:OG1	2.13	0.48
71:S3:53:LYS:HB3	71:S3:56:GLU:OE1	2.13	0.48
2:1:42:A:H5'	63:O7:66:MET:SD	2.54	0.48
2:1:2374:G:H1	2:1:2516:U:HO2'	1.60	0.48
4:3:697:G:O2'	4:3:698:A:H5'	2.14	0.48
4:3:888:U:O2'	4:3:889:G:O5'	2.31	0.48
4:3:1102:A:OP1	10:C5:46:ARG:HD2	2.14	0.48
4:3:1119:G:H5"	44:MD:38:LYS:HE2	1.96	0.48
7:C2:119:GLU:HA	7:C2:122:PHE:CD2	2.49	0.48
12:C7:99:ASP:O	12:C7:103:MET:HB2	2.13	0.48
15:D0:23:ILE:HB	15:D0:90:PHE:CB	2.43	0.48
26:L1:32:THR:H	26:L1:153:LYS:CB	2.26	0.48
31:L6:138:GLU:O	31:L6:142:LYS:HG2	2.14	0.48
33:L8:160:CYS:SG	33:L8:161:LEU:N	2.86	0.48
70:S2:204:ALA:O	70:S2:208:THR:HG23	2.13	0.48
1:RA:164:PRO:CG	1:RA:227:LYS:HB2	2.43	0.48
1:RA:167:GLU:OE1	1:RA:167:GLU:N	2.47	0.48
4:3:889:G:H2'	4:3:889:G:N3	2.28	0.48
13:C8:59:GLU:HG3	13:C8:59:GLU:O	2.13	0.48
13:C8:83:SER:HA	13:C8:88:GLN:HE22	1.77	0.48
17:D2:22:GLN:HG2	17:D2:62:ASP:OD1	2.14	0.48
28:L3:136:GLY:O	28:L3:139:CYS:HB3	2.13	0.48
32:L7:77:LYS:HG3	47:N1:136:ARG:O	2.14	0.48
33:L8:16:LEU:HD12	33:L8:20:GLN:HB3	1.96	0.48
74:S6:34:GLN:HB2	74:S6:49:MET:O	2.14	0.48
2:1:2195:G:N2	2:1:2198:A:OP2	2.47	0.48
4:3:121:U:O4	74:S6:185:GLN:HA	2.14	0.48
16:D1:68:TYR:OH	68:S0:68:ARG:NH1	2.47	0.48
31:L6:16:TYR:CD2	31:L6:18:PRO:HD3	2.49	0.48
32:L7:78:GLU:OE2	47:N1:136:ARG:HB2	2.14	0.48
34:L9:68:THR:O	34:L9:72:LEU:HG	2.14	0.48
59:O3:45:LYS:O	59:O3:45:LYS:HG2	2.12	0.48
2:1:415:G:C2'	2:1:416:A:H5'	2.44	0.47
4:3:135:G:H4'	74:S6:15:MET:HE1	1.96	0.47
7:C2:75:PRO:CB	7:C2:127:LEU:HD11	2.43	0.47
9:C4:100:ARG:HD3	9:C4:104:ARG:HH22	1.79	0.47
19:D4:40:GLU:HG3	19:D4:50:LYS:HD3	1.96	0.47
22:D7:39:ARG:NE	22:D7:39:ARG:HA	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:D8:51:ILE:HD11	73:S5:20:VAL:O	2.14	0.47
25:E1:132:ARG:HA	25:E1:143:LYS:C	2.34	0.47
34:L9:82:VAL:O	34:L9:182:MET:HB2	2.14	0.47
35:M0:3:ARG:HA	35:M0:123:TYR:OH	2.14	0.47
37:M3:158:ARG:NH1	37:M3:160:GLU:OE2	2.47	0.47
75:S7:45:ILE:HG22	75:S7:77:TYR:CB	2.43	0.47
75:S7:97:LYS:O	75:S7:101:VAL:HG23	2.14	0.47
1:RA:272:VAL:HG12	1:RA:285:GLU:OE1	2.13	0.47
2:1:413:A:H5'	2:1:414:G:OP2	2.14	0.47
2:1:885:U:H3'	2:1:886:G:H5"	1.95	0.47
4:3:163:G:H2'	4:3:164:U:H5"	1.96	0.47
29:L4:4:GLN:HA	29:L4:19:LEU:O	2.13	0.47
32:L7:73:PHE:HE2	47:N1:143:LEU:HD11	1.80	0.47
35:M0:113:THR:HG23	35:M0:116:ARG:HD2	1.95	0.47
36:M1:39:GLN:NE2	36:M1:114:LEU:HD12	2.28	0.47
45:MS:52:ARG:O	45:MS:56:ARG:HB2	2.15	0.47
47:N1:117:ASP:O	47:N1:121:ARG:NH1	2.47	0.47
68:S0:13:LYS:HE3	68:S0:189:TYR:HE2	1.79	0.47
2:1:232:G:O2'	2:1:233:G:OP1	2.30	0.47
2:1:2187:A:H4'	2:1:2188:C:H5"	1.95	0.47
4:3:121:U:C6	74:S6:188:ARG:HD2	2.49	0.47
4:3:742:U:H4'	4:3:743:G:O5'	2.13	0.47
4:3:1146:G:H2'	4:3:1147:C:C6	2.49	0.47
7:C2:36:ALA:O	7:C2:40:THR:HG23	2.13	0.47
11:C6:31:ILE:HB	11:C6:38:PHE:HB2	1.95	0.47
13:C8:25:LYS:HD3	13:C8:29:PHE:HD1	1.79	0.47
29:L4:130:GLN:O	29:L4:134:VAL:HG23	2.14	0.47
31:L6:17:MET:HG2	58:O2:98:PHE:CD1	2.48	0.47
31:L6:120:VAL:HG23	31:L6:121:TYR:H	1.78	0.47
33:L8:77:ILE:O	33:L8:81:SER:OG	2.26	0.47
38:M4:11:THR:HG22	38:M4:12:PRO:HD2	1.96	0.47
43:M9:63:CYS:O	43:M9:67:LEU:HG	2.14	0.47
1:RA:164:PRO:CB	1:RA:227:LYS:HB2	2.44	0.47
1:RA:316:LEU:O	1:RA:328:LEU:HD23	2.14	0.47
2:1:227:U:N3	39:M5:145:ASP:HB3	2.29	0.47
4:3:1237:A:H2'	4:3:1238:G:H5'	1.95	0.47
14:C9:16:LEU:HD11	14:C9:59:VAL:CG1	2.43	0.47
20:D5:98:MET:HE1	73:S5:155:ALA:CB	2.44	0.47
31:L6:19:ASP:O	31:L6:23:ARG:HG3	2.15	0.47
31:L6:157:PRO:HB2	59:O3:13:ARG:HH21	1.79	0.47
36:M1:71:VAL:HG23	36:M1:76:ALA:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:O6:55:ILE:O	62:O6:59:GLU:HB2	2.13	0.47
67:P3:84:LYS:O	67:P3:88:THR:HG23	2.14	0.47
68:S0:120:ARG:HD3	68:S0:122:TYR:OH	2.13	0.47
68:S0:181:PHE:CG	68:S0:203:VAL:HG12	2.48	0.47
69:S1:36:ARG:HB2	69:S1:97:GLU:OE2	2.14	0.47
77:S9:130:ALA:O	77:S9:134:ILE:HG13	2.15	0.47
4:3:580:A:OP2	69:S1:9:TYR:OH	2.32	0.47
4:3:625:U:H5	8:C3:12:SER:HB3	1.79	0.47
4:3:1066:G:OP1	14:C9:37:THR:OG1	2.30	0.47
23:D8:40:ARG:HD3	23:D8:59:ARG:NH1	2.29	0.47
29:L4:29:ILE:HA	29:L4:123:MET:SD	2.55	0.47
33:L8:166:PRO:HA	33:L8:169:GLU:HB2	1.97	0.47
38:M4:105:LEU:HD12	40:M6:177:ILE:CG2	2.44	0.47
40:M6:183:ASP:HB3	40:M6:186:PHE:CB	2.45	0.47
44:MD:134:GLN:HG2	44:MD:135:ASP:N	2.29	0.47
61:O5:64:LEU:O	61:O5:68:VAL:HG23	2.14	0.47
68:S0:10:ASP:HB2	68:S0:60:TRP:HD1	1.79	0.47
72:S4:180:ILE:HB	72:S4:208:MET:HE3	1.95	0.47
1:RA:26:ARG:HB3	1:RA:26:ARG:CZ	2.44	0.47
1:RA:193:TYR:O	1:RA:194:LEU:HD12	2.14	0.47
2:1:610:U:OP2	2:1:1442:C:O2'	2.31	0.47
4:3:55:G:H5'	19:D4:109:ARG:HE	1.79	0.47
4:3:1238:G:H2'	4:3:1239:U:C6	2.49	0.47
14:C9:62:ILE:HD12	14:C9:68:VAL:HG23	1.96	0.47
15:D0:48:ILE:HD12	15:D0:97:GLN:CG	2.44	0.47
33:L8:63:LEU:HD13	33:L8:175:MET:CE	2.45	0.47
49:N3:31:LEU:HD23	49:N3:44:ARG:HG3	1.97	0.47
52:N6:5:ARG:NH1	52:N6:6:LYS:HE3	2.30	0.47
69:S1:85:LYS:O	69:S1:105:MET:HG2	2.14	0.47
69:S1:96:SER:O	69:S1:96:SER:OG	2.29	0.47
74:S6:34:GLN:HB2	74:S6:50:GLU:HA	1.93	0.47
1:RA:205:LYS:NZ	1:RA:208:LYS:HG3	2.29	0.47
1:RA:317:TYR:CE1	1:RA:327:PRO:HB3	2.48	0.47
2:1:1549:A:OP1	27:L2:14:LYS:NZ	2.48	0.47
2:1:2414:A:H5"	49:N3:21:LYS:CG	2.45	0.47
2:1:2569:U:O2'	48:N2:41:TYR:HB2	2.15	0.47
4:3:576:U:H5'	4:3:577:G:OP2	2.14	0.47
4:3:890:G:H2'	4:3:891:C:C6	2.49	0.47
4:3:911:U:O2'	4:3:914:A:OP2	2.18	0.47
17:D2:110:ASP:OD1	17:D2:113:GLU:HG3	2.14	0.47
27:L2:195:HIS:HB3	27:L2:197:HIS:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:L3:289:LYS:HA	28:L3:289:LYS:CE	2.44	0.47
32:L7:60:ARG:HA	32:L7:63:LEU:HD12	1.95	0.47
42:M8:78:SER:O	42:M8:79:LYS:HE2	2.15	0.47
58:O2:129:GLY:O	58:O2:130:ASN:HB2	2.15	0.47
73:S5:81:ALA:O	73:S5:85:ILE:HG13	2.15	0.47
74:S6:121:ASP:O	74:S6:125:ASN:ND2	2.47	0.47
75:S7:14:ILE:HA	75:S7:17:LYS:NZ	2.29	0.47
77:S9:119:PHE:HE1	77:S9:126:SER:HA	1.80	0.47
1:RA:164:PRO:HB2	1:RA:227:LYS:HG2	1.97	0.47
1:RA:171:ALA:HB1	1:RA:223:MET:HE1	1.97	0.47
15:D0:57:LEU:HB2	15:D0:87:LEU:CD1	2.44	0.47
45:MS:37:ARG:HD2	45:MS:44:ILE:HD11	1.97	0.47
74:S6:50:GLU:HB3	74:S6:111:ILE:HB	1.96	0.47
75:S7:12:ALA:O	75:S7:16:ARG:HG2	2.15	0.47
75:S7:84:PHE:CE2	75:S7:101:VAL:HG22	2.49	0.47
30:L5:35:ILE:HD11	47:N1:26:VAL:HG13	1.97	0.47
68:S0:118:VAL:HG22	68:S0:119:LYS:H	1.79	0.47
69:S1:158:VAL:CG2	69:S1:163:GLU:HG2	2.45	0.47
2:1:2036:U:H4'	2:1:2037:A:O5'	2.15	0.47
4:3:880:U:OP1	7:C2:106:CYS:HB2	2.15	0.47
4:3:1254:A:C2'	4:3:1255:A:H2'	2.42	0.47
7:C2:37:LYS:O	7:C2:41:LYS:NZ	2.42	0.47
7:C2:93:ASN:HB2	7:C2:102:SER:HB2	1.96	0.47
7:C2:117:THR:HG23	7:C2:119:GLU:H	1.79	0.47
13:C8:49:LEU:HB3	13:C8:51:ILE:HD12	1.96	0.47
18:D3:58:GLN:HA	18:D3:60:ASN:N	2.26	0.47
35:M0:48:LEU:O	35:M0:139:ARG:HA	2.14	0.47
41:M7:81:ARG:NH1	41:M7:93:ILE:HG12	2.30	0.47
73:S5:42:THR:HB	73:S5:51:ILE:HD11	1.96	0.47
2:1:2123:G:H5"	2:1:2123:G:H8	1.80	0.46
26:L1:25:GLU:HA	26:L1:161:SER:HA	1.97	0.46
37:M3:136:ALA:C	37:M3:137:LYS:HD2	2.35	0.46
37:M3:164:TYR:CD1	54:N8:99:VAL:HG21	2.50	0.46
38:M4:81:THR:CB	38:M4:85:ASP:HB2	2.45	0.46
44:MD:66:ARG:NE	44:MD:66:ARG:HA	2.30	0.46
48:N2:30:LEU:O	48:N2:34:LEU:HD23	2.14	0.46
54:N8:5:VAL:HG23	54:N8:6:LYS:N	2.30	0.46
74:S6:179:LYS:HE2	74:S6:179:LYS:HB2	1.76	0.46
1:RA:110:ASP:OD2	12:C7:33:LEU:HD21	2.15	0.46
1:RA:320:LEU:HD12	1:RA:322:THR:H	1.80	0.46
2:1:1007:G:H2'	2:1:1008:U:C5'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:758:G:O2'	4:3:759:G:H5'	2.16	0.46
6:C1:35:GLU:HG2	6:C1:139:LEU:CD2	2.44	0.46
6:C1:75:MET:HE3	6:C1:116:ILE:HG22	1.97	0.46
7:C2:94:VAL:HA	7:C2:100:VAL:HA	1.96	0.46
12:C7:41:VAL:HG23	12:C7:47:LYS:HE3	1.96	0.46
15:D0:61:VAL:HG22	15:D0:84:ILE:CD1	2.45	0.46
41:M7:105:PRO:O	41:M7:106:LYS:HB2	2.15	0.46
77:S9:114:LEU:O	77:S9:118:VAL:HG23	2.15	0.46
1:RA:117:ASN:OD1	1:RA:167:GLU:HB2	2.15	0.46
1:RA:285:GLU:HB3	1:RA:290:ARG:H	1.80	0.46
4:3:71:U:OP2	4:3:71:U:H4'	2.16	0.46
16:D1:30:LEU:HD12	16:D1:30:LEU:HA	1.64	0.46
16:D1:53:GLY:HA2	68:S0:160:VAL:HA	1.97	0.46
20:D5:62:ARG:NH1	20:D5:77:GLU:OE1	2.48	0.46
36:M1:48:SER:O	36:M1:64:LYS:HA	2.15	0.46
44:MD:148:VAL:HA	44:MD:160:ILE:O	2.15	0.46
46:N0:183:GLU:HG2	46:N0:183:GLU:O	2.14	0.46
71:S3:212:PRO:O	71:S3:213:SER:OG	2.33	0.46
72:S4:157:TYR:CZ	72:S4:173:VAL:HG12	2.51	0.46
72:S4:246:SER:OG	72:S4:247:GLU:N	2.48	0.46
75:S7:14:ILE:HA	75:S7:17:LYS:HZ2	1.80	0.46
75:S7:51:PRO:HD2	75:S7:54:ILE:HG12	1.96	0.46
1:RA:40:LYS:H	1:RA:40:LYS:HD3	1.81	0.46
4:3:329:U:O2	4:3:329:U:H2'	2.15	0.46
29:L4:83:ARG:HH11	29:L4:86:GLN:HE21	1.63	0.46
33:L8:119:ASP:HB3	33:L8:120:PRO:CD	2.39	0.46
43:M9:155:LEU:HA	43:M9:158:GLN:CG	2.45	0.46
52:N6:136:ARG:O	52:N6:140:VAL:HG23	2.15	0.46
56:O0:85:ARG:O	56:O0:87:HIS:N	2.46	0.46
70:S2:69:SER:O	70:S2:70:ILE:HG13	2.15	0.46
74:S6:141:ARG:HH21	74:S6:150:GLU:CG	2.28	0.46
2:1:1571:C:O2'	2:1:1572:U:H5'	2.15	0.46
2:1:2217:A:OP1	35:M0:154:ARG:NH1	2.48	0.46
4:3:355:G:C2	4:3:356:U:H1'	2.50	0.46
4:3:524:G:H2'	4:3:525:A:C4'	2.45	0.46
7:C2:39:THR:O	7:C2:43:MET:HG2	2.16	0.46
13:C8:27:ILE:HB	13:C8:28:PRO:HD3	1.96	0.46
23:D8:59:ARG:NH2	23:D8:61:HIS:HB2	2.31	0.46
28:L3:288:ILE:CG2	28:L3:299:ILE:HB	2.44	0.46
30:L5:284:ALA:HB1	35:M0:210:LYS:CD	2.46	0.46
44:MD:132:SER:OG	44:MD:136:VAL:N	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:MD:152:ASN:HA	44:MD:156:MET:O	2.16	0.46
54:N8:58:MET:O	54:N8:59:ARG:HB2	2.15	0.46
69:S1:154:LYS:HZ2	69:S1:155:THR:HG23	1.80	0.46
76:S8:118:ARG:NH1	76:S8:129:GLU:OE2	2.49	0.46
1:RA:144:LYS:O	1:RA:146:GLY:N	2.48	0.46
1:RA:316:LEU:HD23	1:RA:316:LEU:H	1.80	0.46
2:1:1450:A:H5"	43:M9:84:THR:HG22	1.98	0.46
4:3:375:G:H2'	4:3:375:G:N3	2.30	0.46
4:3:480:G:N3	4:3:480:G:H2'	2.31	0.46
7:C2:24:LYS:HE2	7:C2:24:LYS:HA	1.98	0.46
12:C7:106:ILE:HG22	12:C7:107:LYS:HD2	1.98	0.46
15:D0:41:TYR:CZ	15:D0:52:GLN:HB3	2.50	0.46
23:D8:29:MET:CE	23:D8:54:ILE:HD11	2.46	0.46
25:E1:129:LEU:N	25:E1:133:LEU:O	2.48	0.46
33:L8:187:TYR:CE1	33:L8:191:LEU:HD13	2.51	0.46
36:M1:49:LYS:NZ	36:M1:64:LYS:HE3	2.30	0.46
38:M4:105:LEU:HB3	40:M6:177:ILE:CG2	2.43	0.46
39:M5:46:GLU:O	39:M5:50:THR:HG22	2.14	0.46
68:S0:57:ASN:O	68:S0:61:GLU:HG3	2.16	0.46
69:S1:26:ALA:HA	69:S1:29:ARG:NH1	2.30	0.46
2:1:282:C:H5"	52:N6:47:THR:CG2	2.45	0.46
4:3:199:G:H4'	4:3:200:G:O5'	2.16	0.46
5:C0:76:ARG:HD2	5:C0:80:VAL:HG21	1.98	0.46
12:C7:91:LEU:HG	68:S0:200:MET:CB	2.41	0.46
13:C8:16:ILE:O	13:C8:19:THR:HG22	2.16	0.46
30:L5:114:ASP:OD1	30:L5:114:ASP:N	2.42	0.46
31:L6:132:ALA:O	31:L6:136:ILE:HG12	2.16	0.46
39:M5:23:LEU:CD2	39:M5:26:ARG:HH21	2.29	0.46
43:M9:157:GLU:O	43:M9:160:LYS:HB3	2.16	0.46
52:N6:140:VAL:HA	52:N6:143:ASN:CB	2.44	0.46
62:O6:81:VAL:O	62:O6:85:GLU:HG2	2.15	0.46
68:S0:13:LYS:HE3	68:S0:189:TYR:CE2	2.50	0.46
73:S5:90:LYS:HE2	73:S5:90:LYS:HA	1.97	0.46
76:S8:84:HIS:HD2	76:S8:100:SER:HB3	1.81	0.46
4:3:288:A:H62	4:3:301:G:H1	1.64	0.46
16:D1:26:VAL:O	16:D1:27:LEU:HD23	2.15	0.46
23:D8:30:GLU:OE2	23:D8:37:THR:HG22	2.16	0.46
32:L7:33:PHE:HD2	32:L7:34:ARG:HH12	1.64	0.46
34:L9:4:LEU:HD13	34:L9:56:TRP:CE2	2.51	0.46
37:M3:24:HIS:HD2	37:M3:26:ASP:H	1.63	0.46
43:M9:163:ASN:O	43:M9:167:ARG:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:MD:62:CYS:SG	44:MD:65:CYS:HB2	2.55	0.46
60:O4:15:ARG:HH11	60:O4:18:ARG:HH22	1.63	0.46
72:S4:105:VAL:CG1	72:S4:242:GLY:HA2	2.46	0.46
75:S7:17:LYS:HE3	75:S7:72:GLN:NE2	2.30	0.46
7:C2:58:GLU:OE1	7:C2:61:ILE:N	2.47	0.46
28:L3:169:LEU:O	28:L3:170:LYS:HB2	2.15	0.46
31:L6:108:ILE:O	31:L6:110:GLY:N	2.49	0.46
33:L8:51:VAL:HG21	33:L8:142:GLU:HG3	1.97	0.46
36:M1:20:HIS:CB	36:M1:68:HIS:HB3	2.46	0.46
40:M6:189:GLU:HA	40:M6:192:ARG:NH1	2.31	0.46
47:N1:62:ARG:HG2	47:N1:62:ARG:HH11	1.80	0.46
48:N2:17:THR:O	48:N2:20:ALA:HB2	2.15	0.46
57:O1:69:ILE:HD13	57:O1:69:ILE:HA	1.67	0.46
67:P3:45:LYS:HD2	67:P3:45:LYS:O	2.16	0.46
1:RA:317:TYR:CD1	1:RA:327:PRO:HB3	2.50	0.46
2:1:204:G:N2	33:L8:85:LYS:O	2.49	0.46
2:1:1962:G:H2'	2:1:1963:C:C6	2.51	0.46
4:3:322:U:OP2	19:D4:102:ARG:HD2	2.16	0.46
7:C2:40:THR:O	7:C2:43:MET:HB2	2.15	0.46
11:C6:13:LYS:HG3	11:C6:17:ALA:O	2.15	0.46
18:D3:50:GLU:HG2	18:D3:51:LYS:H	1.80	0.46
28:L3:287:ASN:ND2	28:L3:296:GLU:HB3	2.31	0.46
31:L6:131:ASP:O	31:L6:135:LYS:N	2.49	0.46
37:M3:163:SER:HA	54:N8:142:LYS:HE3	1.97	0.46
44:MD:17:VAL:CG1	44:MD:128:LEU:HD11	2.46	0.46
47:N1:62:ARG:HH12	55:N9:54:THR:HG22	1.81	0.46
49:N3:63:PRO:HA	49:N3:87:LEU:HD22	1.97	0.46
72:S4:252:ASN:HA	72:S4:256:GLY:O	2.16	0.46
1:RA:143:LEU:C	1:RA:144:LYS:HD3	2.36	0.45
2:1:2215:C:H5	2:1:2231:C:H42	1.62	0.45
15:D0:81:TYR:HB3	24:D9:62:PHE:HB3	1.98	0.45
33:L8:164:VAL:HG11	33:L8:169:GLU:OE1	2.16	0.45
37:M3:164:TYR:CD1	54:N8:99:VAL:HG11	2.51	0.45
38:M4:95:VAL:O	38:M4:98:GLU:HG3	2.16	0.45
41:M7:99:GLN:O	41:M7:100:THR:HB	2.15	0.45
47:N1:118:ALA:HB1	47:N1:124:VAL:HG12	1.97	0.45
69:S1:141:VAL:HG22	69:S1:142:MET:H	1.80	0.45
75:S7:55:LEU:O	75:S7:58:VAL:HG22	2.16	0.45
2:1:2237:U:C2'	2:1:2238:U:H5'	2.46	0.45
4:3:367:G:H21	4:3:372:G:N2	2.13	0.45
4:3:501:U:H5	77:S9:147:ASP:HB3	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:1177:A:H2	70:S2:76:GLN:HE22	1.63	0.45
14:C9:33:ASP:O	14:C9:34:ILE:HD13	2.16	0.45
16:D1:65:MET:HB2	16:D1:66:GLU:OE1	2.16	0.45
30:L5:271:GLU:O	30:L5:275:LYS:HG3	2.16	0.45
35:M0:45:GLU:O	35:M0:47:PRO:HD3	2.15	0.45
50:N4:87:SER:HB3	50:N4:89:LEU:CD2	2.45	0.45
66:P2:55:ILE:HG13	66:P2:55:ILE:O	2.15	0.45
74:S6:199:LYS:HB3	74:S6:199:LYS:HE2	1.66	0.45
76:S8:67:PHE:CE2	76:S8:69:THR:HG22	2.52	0.45
77:S9:106:ILE:O	77:S9:110:LEU:HD12	2.16	0.45
4:3:556:U:H3	4:3:592:G:H22	1.63	0.45
15:D0:57:LEU:HB2	15:D0:87:LEU:HD12	1.98	0.45
28:L3:65:LYS:CD	28:L3:69:LEU:HD21	2.44	0.45
36:M1:7:ASN:N	36:M1:8:PRO:HD2	2.31	0.45
36:M1:80:LEU:O	36:M1:80:LEU:HD23	2.16	0.45
42:M8:81:LYS:HD3	42:M8:138:ASP:HA	1.98	0.45
54:N8:103:ARG:NH2	54:N8:147:TYR:O	2.49	0.45
58:O2:133:LEU:HD23	58:O2:133:LEU:H	1.81	0.45
2:1:292:G:C2'	2:1:293:G:H5'	2.47	0.45
2:1:1739:A:N3	2:1:2203:G:O2'	2.46	0.45
2:1:2216:G:H22	2:1:2229:G:H2'	1.81	0.45
2:1:2326:G:H4'	2:1:2326:G:OP2	2.16	0.45
12:C7:97:GLU:HA	12:C7:116:LYS:O	2.16	0.45
21:D6:34:LYS:HG2	21:D6:69:GLN:HG2	1.99	0.45
28:L3:183:SER:HB3	28:L3:186:GLU:OE1	2.17	0.45
31:L6:130:THR:O	31:L6:134:ARG:HD3	2.15	0.45
35:M0:193:ARG:NE	35:M0:219:ASN:HB3	2.32	0.45
43:M9:116:THR:HG22	43:M9:119:ASP:HB2	1.98	0.45
44:MD:88:PRO:CG	44:MD:135:ASP:HB2	2.46	0.45
44:MD:130:LEU:HB2	44:MD:141:VAL:HG21	1.98	0.45
45:MS:16:MET:HE3	45:MS:18:ASN:HA	1.98	0.45
46:N0:63:GLU:HG3	46:N0:69:LYS:HG2	1.98	0.45
50:N4:81:PHE:O	74:S6:129:ASP:HB3	2.16	0.45
69:S1:146:ARG:HG3	69:S1:210:GLN:OE1	2.17	0.45
71:S3:35:THR:HG22	71:S3:36:MET:N	2.32	0.45
1:RA:117:ASN:OD1	1:RA:118:SER:N	2.50	0.45
2:1:71:U:OP2	52:N6:121:ARG:NH2	2.46	0.45
12:C7:106:ILE:O	12:C7:110:GLY:N	2.49	0.45
13:C8:66:LYS:HD2	13:C8:66:LYS:O	2.16	0.45
18:D3:58:GLN:HB2	18:D3:59:PRO:HA	1.99	0.45
67:P3:36:LYS:CD	67:P3:48:LYS:HE3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:S2:74:GLN:HG2	70:S2:81:GLN:HE21	1.81	0.45
73:S5:16:LYS:NZ	73:S5:18:ASN:HA	2.31	0.45
75:S7:17:LYS:O	75:S7:20:LYS:HG3	2.16	0.45
2:1:409:G:H4'	2:1:426:G:H1	1.82	0.45
2:1:1770:A:O2'	2:1:1771:C:O5'	2.35	0.45
4:3:936:G:N2	4:3:939:A:OP2	2.45	0.45
14:C9:118:MET:O	14:C9:119:LEU:HG	2.16	0.45
20:D5:93:LEU:HD23	20:D5:100:ILE:HB	1.99	0.45
34:L9:42:LEU:HD23	34:L9:55:LEU:HD13	1.98	0.45
36:M1:93:GLU:HB2	36:M1:172:VAL:O	2.17	0.45
39:M5:97:ARG:HD2	39:M5:170:LYS:NZ	2.32	0.45
45:MS:65:LYS:HA	45:MS:68:GLU:OE2	2.16	0.45
46:N0:31:MET:SD	46:N0:32:PRO:HD2	2.57	0.45
68:S0:22:LEU:HD21	68:S0:182:ILE:CD1	2.47	0.45
2:1:307:G:H4'	2:1:308:A:OP2	2.16	0.45
2:1:394:G:H5"	64:O9:47:LYS:HD3	1.98	0.45
2:1:1539:G:H4'	2:1:1540:U:O5'	2.17	0.45
2:1:1759:G:H4'	28:L3:248:ILE:HD13	1.97	0.45
2:1:1785:A:H2'	2:1:1786:C:H6	1.82	0.45
3:2:63:C:OP2	30:L5:276:ARG:NH1	2.50	0.45
16:D1:61:GLU:O	16:D1:65:MET:HE2	2.17	0.45
18:D3:31:THR:HG22	18:D3:34:LYS:HD2	1.98	0.45
28:L3:348:LYS:HE3	50:N4:1:MET:HE3	1.99	0.45
31:L6:69:ASP:HB3	31:L6:71:ILE:HG12	1.99	0.45
31:L6:147:VAL:HG23	31:L6:150:MET:HB2	1.99	0.45
34:L9:33:ILE:HG21	34:L9:76:ALA:HB1	1.98	0.45
35:M0:30:LYS:NZ	35:M0:63:GLU:OE2	2.40	0.45
46:N0:24:TYR:HA	46:N0:79:LYS:O	2.16	0.45
54:N8:92:ASP:O	54:N8:94:PRO:HD3	2.17	0.45
76:S8:136:ILE:O	76:S8:149:GLY:HA3	2.17	0.45
1:RA:153:HIS:NE2	1:RA:172:SER:OG	2.43	0.45
2:1:1759:G:H4'	28:L3:248:ILE:CD1	2.47	0.45
4:3:99:G:H5"	4:3:261:G:O2'	2.17	0.45
5:C0:7:ASN:O	5:C0:11:ILE:HG13	2.17	0.45
6:C1:21:TYR:OH	76:S8:121:ASP:OD2	2.25	0.45
21:D6:37:ARG:HD3	21:D6:39:GLN:HE21	1.81	0.45
29:L4:258:LYS:HB2	29:L4:269:LEU:HD12	1.99	0.45
33:L8:16:LEU:HB2	33:L8:21:LYS:HG3	1.99	0.45
35:M0:19:LYS:HE2	35:M0:24:ARG:NH1	2.32	0.45
42:M8:79:LYS:HE2	42:M8:79:LYS:HA	1.99	0.45
44:MD:126:CYS:SG	44:MD:165:LEU:HD11	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:N2:11:ARG:NH1	48:N2:59:GLU:OE2	2.50	0.45
50:N4:73:GLN:HG3	74:S6:113:LEU:CD1	2.46	0.45
72:S4:140:SER:OG	72:S4:141:SER:N	2.50	0.45
77:S9:114:LEU:HD23	77:S9:134:ILE:HD13	1.98	0.45
77:S9:117:ARG:HD3	77:S9:117:ARG:HA	1.76	0.45
77:S9:141:ILE:HD11	77:S9:157:LYS:HG2	1.98	0.45
1:RA:240:LYS:HD2	1:RA:240:LYS:HA	1.82	0.45
7:C2:13:MET:HE2	7:C2:122:PHE:HB3	1.98	0.45
7:C2:58:GLU:OE1	7:C2:61:ILE:HG12	2.17	0.45
10:C5:22:VAL:CG2	10:C5:27:LEU:HD11	2.47	0.45
30:L5:68:ASP:OD1	30:L5:68:ASP:N	2.50	0.45
31:L6:138:GLU:OE1	31:L6:138:GLU:N	2.48	0.45
32:L7:99:LYS:O	32:L7:102:GLU:HG3	2.16	0.45
33:L8:73:GLN:HG3	33:L8:76:ARG:NH1	2.32	0.45
33:L8:143:ASN:O	33:L8:144:SER:HB3	2.17	0.45
36:M1:110:ILE:HG22	36:M1:122:ILE:HD12	1.99	0.45
38:M4:93:LYS:HE2	38:M4:97:GLU:OE2	2.16	0.45
48:N2:62:VAL:HG11	48:N2:67:ILE:HG21	1.99	0.45
68:S0:177:ALA:HB1	68:S0:206:PHE:HB3	1.99	0.45
73:S5:4:ILE:HG23	73:S5:33:ILE:HG22	1.99	0.45
2:1:1616:G:C2'	2:1:1617:G:H5'	2.47	0.45
30:L5:82:GLU:HA	30:L5:86:ILE:O	2.16	0.45
31:L6:16:TYR:HD2	31:L6:18:PRO:HD3	1.80	0.45
34:L9:82:VAL:HG23	34:L9:181:ILE:HD11	1.99	0.45
37:M3:137:LYS:HB3	37:M3:138:PRO:HD2	1.99	0.45
44:MD:147:THR:HB	44:MD:163:PHE:H	1.82	0.45
51:N5:100:ALA:O	51:N5:104:THR:HB	2.17	0.45
60:O4:20:ARG:HG2	60:O4:34:VAL:CG2	2.46	0.45
63:O7:53:ARG:NH2	63:O7:57:THR:HG22	2.32	0.45
75:S7:38:ILE:CD1	75:S7:46:MET:HB3	2.47	0.45
1:RA:92:ARG:HD3	1:RA:102:ILE:O	2.17	0.44
2:1:80:G:OP2	63:O7:71:ARG:NH1	2.50	0.44
7:C2:34:ARG:HD3	7:C2:89:VAL:HG11	1.99	0.44
9:C4:40:THR:O	9:C4:43:MET:HG2	2.17	0.44
11:C6:129:LYS:HB2	11:C6:129:LYS:HE3	1.67	0.44
12:C7:111:TYR:CD2	68:S0:19:VAL:HG11	2.52	0.44
15:D0:91:TYR:O	15:D0:92:LEU:HD23	2.16	0.44
17:D2:24:LEU:HD12	17:D2:60:ILE:HG12	1.98	0.44
30:L5:212:PRO:HA	30:L5:215:TYR:HB3	1.99	0.44
31:L6:64:LEU:HD23	31:L6:106:VAL:CG1	2.45	0.44
40:M6:113:GLU:HG3	40:M6:159:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:MD:19:ILE:HG22	44:MD:20:ASP:H	1.82	0.44
47:N1:65:ASP:OD1	55:N9:39:THR:HG21	2.16	0.44
59:O3:56:VAL:HG12	59:O3:103:VAL:HA	1.98	0.44
74:S6:25:ARG:HD2	74:S6:39:ILE:HG23	2.00	0.44
1:RA:200:ASP:H	1:RA:203:LYS:HB2	1.81	0.44
4:3:66:C:H2'	4:3:67:U:C6	2.53	0.44
4:3:524:G:H2'	4:3:525:A:H5"	1.99	0.44
16:D1:27:LEU:O	16:D1:40:THR:HA	2.16	0.44
28:L3:236:ARG:O	28:L3:236:ARG:HG2	2.17	0.44
36:M1:161:LYS:HA	36:M1:164:VAL:HG22	1.99	0.44
38:M4:59:ILE:HG21	38:M4:67:ILE:HG13	1.99	0.44
73:S5:84:ILE:HG23	73:S5:88:MET:HE3	1.99	0.44
73:S5:154:LEU:O	73:S5:158:ILE:HG13	2.17	0.44
76:S8:93:THR:HB	76:S8:95:THR:HG23	1.98	0.44
1:RA:17:ASP:O	1:RA:323:GLY:HA2	2.18	0.44
1:RA:190:LEU:HD23	1:RA:191:GLN:N	2.33	0.44
2:1:1418:U:OP2	57:O1:35:ARG:NH1	2.50	0.44
7:C2:71:LYS:NZ	7:C2:72:LYS:HG2	2.33	0.44
14:C9:6:GLU:HB2	14:C9:135:ARG:HH22	1.83	0.44
15:D0:95:THR:O	15:D0:97:GLN:NE2	2.48	0.44
22:D7:39:ARG:HA	22:D7:39:ARG:CZ	2.47	0.44
27:L2:32:VAL:HA	27:L2:76:ILE:O	2.16	0.44
27:L2:103:GLU:HB3	27:L2:109:GLY:O	2.18	0.44
30:L5:181:LYS:HA	30:L5:181:LYS:HD3	1.66	0.44
43:M9:70:LYS:HA	43:M9:74:ARG:H	1.83	0.44
69:S1:9:TYR:HA	69:S1:10:PRO:HD3	1.86	0.44
70:S2:234:LEU:HD23	70:S2:234:LEU:HA	1.83	0.44
75:S7:37:ILE:HD12	75:S7:49:LYS:HZ3	1.81	0.44
1:RA:39:ASP:O	1:RA:41:LYS:N	2.48	0.44
2:1:311:A:H2'	2:1:312:G:O4'	2.17	0.44
4:3:1047:C:H5'	10:C5:129:PRO:CD	2.48	0.44
23:D8:29:MET:HE1	23:D8:54:ILE:HD11	2.00	0.44
27:L2:229:ARG:NH1	27:L2:230:THR:O	2.51	0.44
33:L8:63:LEU:HD13	33:L8:175:MET:HE3	1.98	0.44
35:M0:130:VAL:HG12	35:M0:131:PHE:N	2.32	0.44
44:MD:87:LEU:HD22	44:MD:135:ASP:O	2.16	0.44
47:N1:18:HIS:O	47:N1:19:ARG:HB2	2.18	0.44
48:N2:91:ILE:HG23	48:N2:99:PHE:HB3	1.99	0.44
49:N3:12:LYS:HE2	49:N3:12:LYS:HA	1.99	0.44
64:O9:39:ARG:HG2	64:O9:39:ARG:O	2.18	0.44
4:3:1232:U:O2'	4:3:1233:C:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C5:118:VAL:HG22	10:C5:121:ASP:OD1	2.17	0.44
11:C6:43:ASN:HB3	11:C6:46:MET:HB3	2.00	0.44
15:D0:56:VAL:HG23	15:D0:56:VAL:O	2.18	0.44
20:D5:22:LYS:HG3	20:D5:23:ASP:OD1	2.17	0.44
52:N6:140:VAL:CA	52:N6:143:ASN:HB2	2.45	0.44
54:N8:84:LYS:HB2	54:N8:84:LYS:HE2	1.72	0.44
2:1:1586:U:H2'	2:1:1587:G:O4'	2.18	0.44
2:1:1967:G:C2	2:1:1968:U:H1'	2.53	0.44
12:C7:74:HIS:HA	12:C7:77:GLU:OE1	2.18	0.44
35:M0:112:GLN:CG	35:M0:113:THR:H	2.29	0.44
42:M8:20:ARG:NH2	42:M8:24:ARG:HG3	2.33	0.44
45:MS:50:ARG:HH12	60:O4:44:HIS:HA	1.82	0.44
51:N5:52:LYS:O	51:N5:52:LYS:HG3	2.17	0.44
75:S7:95:LYS:O	75:S7:98:ALA:HB3	2.18	0.44
1:RA:245:LYS:HB2	1:RA:252:ILE:HD11	1.99	0.44
1:RA:292:ILE:CG2	1:RA:333:LYS:HE2	2.47	0.44
1:RA:304:VAL:HG11	1:RA:320:LEU:HD22	2.00	0.44
2:1:28:A:H2'	2:1:29:U:C6	2.52	0.44
2:1:96:G:O2'	39:M5:136:ASP:OD2	2.30	0.44
2:1:144:G:H4'	2:1:145:A:OP1	2.17	0.44
2:1:295:G:H2'	2:1:296:G:H8	1.83	0.44
2:1:502:U:OP1	29:L4:30:ARG:NH1	2.44	0.44
2:1:1010:U:H2'	2:1:1011:C:C6	2.52	0.44
2:1:1774:U:O2'	2:1:1775:G:H5'	2.18	0.44
4:3:192:A:C2	4:3:194:C:H2'	2.52	0.44
4:3:934:G:O2'	4:3:935:C:H5'	2.17	0.44
5:C0:5:THR:HA	5:C0:8:LYS:HG3	2.00	0.44
6:C1:43:GLU:OE1	6:C1:43:GLU:N	2.50	0.44
7:C2:31:LYS:HD2	7:C2:112:ASP:O	2.18	0.44
7:C2:58:GLU:OE1	7:C2:60:ARG:N	2.51	0.44
14:C9:16:LEU:HA	14:C9:19:TYR:HB3	1.99	0.44
28:L3:348:LYS:HE3	50:N4:1:MET:CE	2.48	0.44
33:L8:18:LYS:HD3	33:L8:18:LYS:HA	1.60	0.44
44:MD:130:LEU:HD12	44:MD:141:VAL:HG21	1.99	0.44
54:N8:81:MET:HE3	54:N8:105:PHE:HB2	2.00	0.44
59:O3:56:VAL:HG12	59:O3:103:VAL:HG22	2.00	0.44
62:O6:30:THR:OG1	62:O6:34:ARG:NH1	2.51	0.44
71:S3:211:GLU:OE1	71:S3:212:PRO:HD2	2.17	0.44
73:S5:154:LEU:O	73:S5:154:LEU:HD23	2.18	0.44
75:S7:20:LYS:HD2	75:S7:21:ASP:OD1	2.18	0.44
2:1:2160:G:C2'	2:1:2161:C:H5'	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:648:G:H4'	4:3:1275:U:H4'	2.00	0.44
4:3:1163:C:H2'	4:3:1164:C:H6	1.82	0.44
5:C0:31:HIS:HD2	5:C0:34:LEU:HB2	1.83	0.44
7:C2:71:LYS:NZ	7:C2:72:LYS:HE2	2.33	0.44
7:C2:94:VAL:CG2	7:C2:100:VAL:HG22	2.45	0.44
13:C8:27:ILE:HD11	13:C8:57:ALA:HA	1.99	0.44
13:C8:112:ILE:O	13:C8:116:LYS:HG3	2.18	0.44
19:D4:8:ALA:O	19:D4:22:ASP:HB2	2.18	0.44
31:L6:96:THR:HG22	31:L6:97:SER:H	1.81	0.44
34:L9:30:LYS:NZ	34:L9:82:VAL:O	2.46	0.44
36:M1:152:GLN:O	36:M1:153:ARG:HB2	2.17	0.44
44:MD:130:LEU:HD12	44:MD:141:VAL:HG11	1.99	0.44
65:P0:89:LYS:O	65:P0:89:LYS:HD3	2.17	0.44
2:1:2380:G:H5'	40:M6:75:GLU:OE2	2.18	0.44
4:3:246:U:C2'	4:3:247:C:H5'	2.48	0.44
4:3:969:A:C2	71:S3:204:PRO:HG2	2.53	0.44
6:C1:35:GLU:CG	6:C1:36:VAL:H	2.27	0.44
43:M9:99:ILE:HA	43:M9:102:MET:HG2	2.00	0.44
47:N1:79:VAL:O	47:N1:79:VAL:HG13	2.18	0.44
49:N3:112:ILE:HD13	49:N3:118:LEU:HA	2.00	0.44
59:O3:61:LYS:NZ	59:O3:65:GLY:HA2	2.33	0.44
68:S0:170:ASN:HA	68:S0:176:ILE:CD1	2.45	0.44
72:S4:197:ILE:HG23	72:S4:206:TYR:CE1	2.53	0.44
73:S5:16:LYS:CE	73:S5:18:ASN:HA	2.48	0.44
2:1:228:U:OP2	61:O5:108:ARG:NH2	2.50	0.43
2:1:301:U:H5'	61:O5:112:SER:HB2	2.00	0.43
2:1:1209:G:H5"	60:O4:66:VAL:HB	2.00	0.43
2:1:1545:A:H5"	27:L2:115:VAL:CG2	2.48	0.43
2:1:2123:G:H5"	2:1:2123:G:C8	2.53	0.43
5:C0:34:LEU:HB3	5:C0:36:ILE:HD13	2.00	0.43
12:C7:108:ARG:HD3	68:S0:43:TYR:HE1	1.82	0.43
13:C8:75:PRO:O	13:C8:78:VAL:HG12	2.18	0.43
19:D4:27:HIS:HB2	19:D4:30:MET:HB2	2.00	0.43
26:L1:63:LEU:C	26:L1:81:ALA:HB2	2.39	0.43
28:L3:54:THR:OG1	28:L3:55:HIS:N	2.50	0.43
29:L4:57:MET:SD	29:L4:97:ARG:HG2	2.58	0.43
33:L8:78:ARG:HD2	33:L8:78:ARG:O	2.18	0.43
33:L8:165:ARG:O	33:L8:167:GLU:N	2.51	0.43
44:MD:132:SER:OG	44:MD:136:VAL:HG12	2.18	0.43
57:O1:5:ILE:CD1	57:O1:109:ILE:HD11	2.37	0.43
71:S3:100:GLN:O	71:S3:104:ILE:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:S5:121:ARG:HB3	73:S5:188:ASN:ND2	2.33	0.43
2:1:74:U:H6	2:1:74:U:H2'	1.62	0.43
2:1:1194:C:H2'	2:1:1195:U:O4'	2.18	0.43
2:1:1635:U:H2'	2:1:1637:A:OP2	2.18	0.43
2:1:2217:A:H61	2:1:2229:G:H1'	1.82	0.43
2:1:2482:A:H2'	2:1:2483:A:O4'	2.19	0.43
4:3:1014:C:H3'	4:3:1015:A:H5"	2.00	0.43
10:C5:47:VAL:HG13	24:D9:9:VAL:HG13	1.99	0.43
19:D4:95:LYS:HE2	19:D4:95:LYS:HB3	1.73	0.43
21:D6:76:CYS:O	21:D6:79:LYS:NZ	2.50	0.43
30:L5:132:ILE:HB	30:L5:135:GLU:OE2	2.18	0.43
33:L8:104:ILE:HD13	33:L8:131:CYS:SG	2.58	0.43
37:M3:62:ILE:O	37:M3:62:ILE:HG13	2.18	0.43
38:M4:39:ASP:HB2	38:M4:41:GLU:OE2	2.18	0.43
40:M6:183:ASP:O	40:M6:184:LYS:HE2	2.18	0.43
43:M9:132:PHE:CD2	43:M9:138:MET:HG3	2.54	0.43
56:O0:33:LYS:HA	56:O0:36:ILE:HG12	1.99	0.43
1:RA:193:TYR:HE1	1:RA:244:VAL:HG11	1.83	0.43
2:1:1616:G:H2'	2:1:1617:G:H5'	2.01	0.43
3:2:5:G:O2'	30:L5:61:GLN:NE2	2.52	0.43
4:3:719:G:H5"	4:3:719:G:N3	2.33	0.43
12:C7:38:VAL:CG1	71:S3:209:ILE:HG23	2.48	0.43
20:D5:32:LYS:HB2	20:D5:32:LYS:HE2	1.70	0.43
26:L1:65:LYS:HA	26:L1:68:VAL:CB	2.48	0.43
29:L4:111:LYS:HZ3	29:L4:111:LYS:HB2	1.82	0.43
38:M4:5:ARG:HH11	38:M4:56:ALA:HB1	1.83	0.43
43:M9:153:LYS:HE3	43:M9:153:LYS:HB3	1.91	0.43
71:S3:98:LEU:O	71:S3:102:ASN:ND2	2.51	0.43
73:S5:110:THR:CG2	73:S5:185:ALA:HA	2.48	0.43
74:S6:49:MET:HA	74:S6:111:ILE:O	2.18	0.43
1:RA:227:LYS:HE2	1:RA:227:LYS:HA	2.00	0.43
1:RA:253:GLN:NE2	1:RA:289:SER:HB2	2.23	0.43
2:1:1167:G:H1	2:1:1184:U:H3	1.66	0.43
4:3:492:G:H2'	4:3:493:U:O4'	2.18	0.43
4:3:620:U:O3'	8:C3:114:ARG:HD2	2.19	0.43
4:3:621:G:H2'	4:3:622:G:C8	2.53	0.43
6:C1:35:GLU:HB2	6:C1:57:PHE:HE1	1.83	0.43
9:C4:9:GLU:CG	9:C4:74:LYS:HD2	2.43	0.43
12:C7:41:VAL:HG12	71:S3:207:ILE:HG12	2.00	0.43
19:D4:14:ARG:CZ	72:S4:95:THR:HG22	2.49	0.43
19:D4:61:ARG:HG2	19:D4:62:TYR:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:D4:86:LYS:HB2	19:D4:97:PHE:CZ	2.53	0.43
36:M1:133:ARG:HB3	36:M1:134:PRO:HD2	2.00	0.43
42:M8:70:LYS:NZ	42:M8:143:SER:O	2.36	0.43
71:S3:190:PRO:O	71:S3:198:GLY:HA3	2.18	0.43
74:S6:154:VAL:HG12	74:S6:158:ARG:HE	1.82	0.43
1:RA:201:TYR:O	1:RA:204:ALA:HB3	2.18	0.43
2:1:508:U:O2'	2:1:509:C:OP2	2.35	0.43
2:1:2144:U:H4'	54:N8:53:HIS:CE1	2.51	0.43
4:3:849:G:H5'	4:3:850:G:O5'	2.17	0.43
4:3:943:U:O2'	4:3:944:U:H5'	2.18	0.43
11:C6:30:SER:O	11:C6:31:ILE:HD13	2.18	0.43
11:C6:103:LYS:HA	11:C6:106:GLU:OE2	2.19	0.43
17:D2:88:ARG:HG2	17:D2:92:LEU:HD12	2.00	0.43
19:D4:93:THR:OG1	19:D4:94:GLY:N	2.52	0.43
22:D7:3:SER:O	22:D7:3:SER:OG	2.31	0.43
23:D8:61:HIS:O	23:D8:62:ARG:NE	2.45	0.43
30:L5:219:PHE:O	30:L5:223:ILE:HG13	2.18	0.43
31:L6:54:GLY:HA3	31:L6:116:THR:CG2	2.49	0.43
34:L9:71:SER:HA	34:L9:74:ARG:HG2	2.00	0.43
34:L9:103:GLU:HB2	34:L9:106:LYS:HB2	2.00	0.43
74:S6:102:SER:H	74:S6:105:ILE:HD13	1.84	0.43
75:S7:8:GLU:OE1	75:S7:9:MET:HG3	2.18	0.43
75:S7:100:GLU:O	75:S7:104:VAL:HG23	2.19	0.43
1:RA:253:GLN:HE22	1:RA:289:SER:CB	2.22	0.43
2:1:771:U:OP2	47:N1:129:LYS:NZ	2.41	0.43
4:3:1137:G:O2'	4:3:1138:C:H5'	2.17	0.43
12:C7:40:VAL:HG13	12:C7:40:VAL:O	2.19	0.43
14:C9:7:VAL:CG2	14:C9:134:VAL:HG23	2.46	0.43
14:C9:106:LYS:HE3	14:C9:106:LYS:HB2	1.83	0.43
15:D0:107:ARG:HD2	15:D0:107:ARG:O	2.18	0.43
20:D5:84:SER:HA	20:D5:89:VAL:HG23	1.99	0.43
28:L3:68:GLN:OE1	28:L3:68:GLN:HA	2.18	0.43
34:L9:103:GLU:N	34:L9:103:GLU:OE1	2.51	0.43
49:N3:22:MET:HE2	49:N3:62:ALA:HB1	2.01	0.43
65:P0:94:CYS:HB2	65:P0:104:SER:O	2.19	0.43
69:S1:72:GLN:HG2	69:S1:72:GLN:O	2.18	0.43
72:S4:159:ILE:HD12	72:S4:161:ILE:HD11	2.01	0.43
1:RA:109:ARG:HD3	1:RA:129:ASP:HB3	2.00	0.43
4:3:1266:G:OP1	4:3:1269:U:H4'	2.19	0.43
12:C7:42:GLN:HE22	71:S3:202:PRO:HG2	1.84	0.43
28:L3:194:ARG:HG3	28:L3:194:ARG:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L4:316:MET:HG3	29:L4:316:MET:O	2.19	0.43
30:L5:83:ARG:NH1	30:L5:250:LYS:HG2	2.34	0.43
33:L8:11:VAL:HG23	33:L8:12:GLU:N	2.33	0.43
33:L8:110:LYS:HD2	33:L8:162:CYS:O	2.19	0.43
34:L9:98:ASN:HB2	34:L9:111:LYS:CB	2.47	0.43
44:MD:75:LYS:HD2	44:MD:75:LYS:O	2.18	0.43
55:N9:14:ARG:O	55:N9:18:ARG:HG3	2.19	0.43
60:O4:73:ARG:HB2	60:O4:74:PRO:HD2	2.01	0.43
69:S1:185:LYS:O	69:S1:189:LYS:HG2	2.17	0.43
72:S4:200:GLN:O	72:S4:202:LYS:N	2.52	0.43
1:RA:164:PRO:HG2	1:RA:227:LYS:HE2	2.01	0.43
2:1:2221:A:H2'	2:1:2221:A:N3	2.33	0.43
4:3:936:G:N2	4:3:938:G:H3'	2.34	0.43
12:C7:40:VAL:HG12	71:S3:208:THR:O	2.19	0.43
14:C9:75:LYS:O	14:C9:75:LYS:HG2	2.19	0.43
15:D0:30:GLU:HA	15:D0:33:ILE:HG22	1.99	0.43
31:L6:136:ILE:HD13	31:L6:136:ILE:HA	1.86	0.43
33:L8:67:TYR:OH	33:L8:164:VAL:O	2.27	0.43
43:M9:98:LYS:HE3	43:M9:133:LYS:O	2.19	0.43
50:N4:73:GLN:HE22	74:S6:114:ARG:CB	2.16	0.43
56:O0:77:GLU:HA	56:O0:77:GLU:OE2	2.19	0.43
68:S0:153:VAL:HG21	68:S0:159:LEU:CD2	2.49	0.43
1:RA:245:LYS:CB	1:RA:252:ILE:HD11	2.49	0.43
2:1:950:A:H2'	2:1:950:A:OP2	2.18	0.43
2:1:995:G:O2'	32:L7:109:ILE:HD11	2.18	0.43
4:3:58:U:HO2'	4:3:60:U:H5	1.67	0.43
4:3:59:G:H2'	4:3:59:G:N3	2.33	0.43
7:C2:51:VAL:HG12	7:C2:53:VAL:HG23	2.00	0.43
10:C5:93:ILE:HD11	10:C5:112:PRO:HB3	2.00	0.43
14:C9:50:TRP:HA	14:C9:53:THR:HG22	2.00	0.43
35:M0:13:SER:O	35:M0:128:ARG:NH2	2.52	0.43
57:O1:22:SER:O	57:O1:23:ARG:HB2	2.19	0.43
67:P3:48:LYS:HD3	67:P3:58:ARG:CD	2.48	0.43
69:S1:141:VAL:HG21	69:S1:199:ILE:CD1	2.48	0.43
74:S6:133:LEU:HD12	74:S6:134:PRO:HD2	2.01	0.43
1:RA:292:ILE:H	1:RA:292:ILE:HD12	1.84	0.43
2:1:1146:G:H5'	51:N5:77:LEU:CD2	2.46	0.43
2:1:1496:U:O2'	2:1:1497:U:OP2	2.26	0.43
2:1:2301:G:H2'	2:1:2302:U:C4'	2.48	0.43
10:C5:101:VAL:HG22	10:C5:104:GLY:O	2.19	0.43
19:D4:74:TYR:CD2	19:D4:80:LEU:HD12	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:D5:56:ARG:HA	20:D5:105:ARG:HG2	2.01	0.43
33:L8:9:ILE:HG23	33:L8:9:ILE:O	2.19	0.43
35:M0:113:THR:CG2	35:M0:116:ARG:HB3	2.49	0.43
35:M0:113:THR:HG22	35:M0:116:ARG:HB3	2.00	0.43
36:M1:26:SER:HB3	36:M1:64:LYS:O	2.19	0.43
36:M1:109:HIS:HB3	36:M1:123:PHE:H	1.83	0.43
40:M6:132:ASN:C	40:M6:133:ARG:HD2	2.39	0.43
42:M8:9:TYR:CZ	42:M8:11:ARG:HB3	2.54	0.43
45:MS:47:LEU:HD23	45:MS:47:LEU:HA	1.86	0.43
71:S3:182:GLY:O	71:S3:183:ILE:HG13	2.19	0.43
74:S6:197:GLU:HA	74:S6:200:ARG:NH1	2.34	0.43
1:RA:20:LYS:HD2	1:RA:70:ILE:O	2.18	0.42
2:1:1718:U:H4'	41:M7:106:LYS:HE3	2.01	0.42
12:C7:17:ALA:O	12:C7:21:PHE:HB2	2.18	0.42
28:L3:213:THR:C	28:L3:214:ILE:HG13	2.39	0.42
28:L3:297:LYS:HE3	28:L3:352:THR:OG1	2.19	0.42
29:L4:205:LEU:CD1	29:L4:224:ASP:HB2	2.48	0.42
29:L4:255:LYS:HB3	29:L4:255:LYS:HE2	1.62	0.42
36:M1:20:HIS:HB3	36:M1:68:HIS:HB3	2.01	0.42
36:M1:41:THR:O	36:M1:75:LYS:NZ	2.34	0.42
41:M7:55:LYS:HE2	41:M7:55:LYS:HB3	1.78	0.42
46:N0:135:ARG:HD3	46:N0:136:SER:N	2.34	0.42
60:O4:15:ARG:HH11	60:O4:18:ARG:NH2	2.16	0.42
75:S7:9:MET:O	75:S7:13:GLY:N	2.52	0.42
75:S7:50:VAL:CG2	75:S7:54:ILE:HG13	2.49	0.42
1:RA:203:LYS:HA	1:RA:206:GLU:CB	2.42	0.42
1:RA:259:VAL:HG23	1:RA:277:THR:HB	2.01	0.42
2:1:1138:G:H2'	2:1:1139:C:O4'	2.18	0.42
4:3:351:U:H5'	4:3:352:G:O4'	2.19	0.42
7:C2:94:VAL:CG1	7:C2:100:VAL:HG22	2.48	0.42
11:C6:10:THR:HG21	11:C6:89:LYS:O	2.19	0.42
11:C6:46:MET:HG3	11:C6:46:MET:O	2.18	0.42
14:C9:13:ASN:HD21	14:C9:60:ARG:HH12	1.67	0.42
18:D3:137:LYS:HB2	18:D3:137:LYS:HE2	1.75	0.42
23:D8:55:LEU:HD21	73:S5:108:GLU:OE1	2.19	0.42
44:MD:86:LEU:HD23	44:MD:95:PHE:HB3	2.01	0.42
66:P2:76:LYS:N	66:P2:76:LYS:HD2	2.34	0.42
1:RA:25:VAL:HG22	1:RA:27:VAL:HG22	2.00	0.42
2:1:583:A:N1	4:3:640:G:O2'	2.47	0.42
3:2:11:A:O2'	3:2:13:A:OP2	2.38	0.42
4:3:71:U:HO2'	4:3:72:G:P	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C1:78:GLU:HG2	6:C1:78:GLU:O	2.19	0.42
7:C2:38:GLU:HA	7:C2:41:LYS:NZ	2.34	0.42
7:C2:87:ARG:O	7:C2:87:ARG:HD2	2.18	0.42
19:D4:54:VAL:O	19:D4:71:ALA:HA	2.19	0.42
20:D5:93:LEU:CD2	20:D5:100:ILE:HB	2.49	0.42
37:M3:58:ARG:HD3	37:M3:67:ASN:O	2.19	0.42
39:M5:172:ARG:HA	39:M5:172:ARG:HD3	1.79	0.42
74:S6:145:GLY:C	74:S6:147:PRO:HD3	2.40	0.42
76:S8:64:HIS:ND1	76:S8:75:MET:HG2	2.34	0.42
1:RA:225:PHE:CZ	1:RA:230:SER:HA	2.55	0.42
4:3:204:U:OP1	6:C1:54:LYS:NZ	2.52	0.42
4:3:945:G:H2'	4:3:946:U:O4'	2.20	0.42
12:C7:100:ASP:OD1	12:C7:100:ASP:N	2.52	0.42
12:C7:111:TYR:CE1	68:S0:56:ILE:HG21	2.54	0.42
19:D4:74:TYR:HD2	19:D4:80:LEU:HD12	1.84	0.42
30:L5:265:GLN:OE1	30:L5:265:GLN:N	2.51	0.42
32:L7:34:ARG:HA	32:L7:34:ARG:HD3	1.80	0.42
34:L9:133:ASP:HB2	34:L9:140:VAL:HG23	2.01	0.42
37:M3:46:PHE:HB3	37:M3:47:PRO:HD3	2.00	0.42
40:M6:169:GLN:HA	40:M6:172:ASP:OD2	2.18	0.42
44:MD:89:THR:OG1	44:MD:94:GLU:HB2	2.19	0.42
46:N0:25:ARG:HD2	46:N0:45:THR:HG22	2.01	0.42
46:N0:146:VAL:HG13	46:N0:150:SER:HB2	2.01	0.42
46:N0:161:ASP:OD1	46:N0:162:GLU:N	2.53	0.42
53:N7:93:ASN:CG	53:N7:96:THR:HG23	2.39	0.42
65:P0:110:LYS:HD2	65:P0:115:PHE:HB3	2.02	0.42
70:S2:106:LYS:HB3	70:S2:107:GLU:OE1	2.19	0.42
73:S5:125:ASP:OD1	73:S5:125:ASP:N	2.40	0.42
74:S6:26:LEU:HD23	74:S6:108:LEU:CD1	2.49	0.42
74:S6:190:GLN:O	74:S6:193:LYS:HB2	2.19	0.42
1:RA:152:MET:HG2	1:RA:153:HIS:H	1.83	0.42
2:1:2136:C:O2'	47:N1:48:MET:HG3	2.19	0.42
7:C2:56:ASN:ND2	7:C2:81:SER:HB2	2.33	0.42
11:C6:64:ASP:C	11:C6:65:LEU:HD23	2.40	0.42
12:C7:42:GLN:NE2	71:S3:202:PRO:HG2	2.34	0.42
12:C7:94:ASP:OD2	12:C7:114:ASN:ND2	2.36	0.42
15:D0:88:ARG:HD2	15:D0:88:ARG:N	2.34	0.42
18:D3:100:GLU:N	18:D3:100:GLU:OE1	2.52	0.42
22:D7:14:GLY:HA2	75:S7:169:LYS:CE	2.49	0.42
30:L5:120:LYS:NZ	30:L5:129:THR:HG22	2.34	0.42
30:L5:268:LEU:HA	30:L5:272:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:M4:95:VAL:HG21	40:M6:194:LEU:HD21	2.01	0.42
40:M6:113:GLU:HG3	40:M6:159:LEU:CD1	2.50	0.42
46:N0:61:ILE:HD11	47:N1:153:TYR:CD1	2.55	0.42
72:S4:255:LEU:CD2	77:S9:71:ARG:HD2	2.49	0.42
74:S6:103:GLU:OE1	74:S6:103:GLU:N	2.43	0.42
77:S9:23:ILE:HG13	77:S9:24:ARG:N	2.33	0.42
1:RA:232:LEU:O	1:RA:243:LEU:HA	2.18	0.42
2:1:504:G:N7	42:M8:88:LYS:NZ	2.58	0.42
2:1:1563:C:O2'	2:1:1636:A:N3	2.45	0.42
4:3:264:G:H5"	76:S8:23:LYS:HE2	2.02	0.42
4:3:1144:A:H4'	4:3:1145:A:OP1	2.19	0.42
12:C7:98:VAL:HG22	12:C7:102:THR:OG1	2.19	0.42
28:L3:85:MET:O	28:L3:198:GLU:HA	2.19	0.42
31:L6:96:THR:HG22	31:L6:97:SER:N	2.34	0.42
37:M3:62:ILE:HD12	37:M3:65:ASN:HD22	1.85	0.42
40:M6:34:THR:HG22	40:M6:103:ALA:HB3	2.02	0.42
46:N0:41:VAL:O	47:N1:148:PRO:HA	2.19	0.42
71:S3:106:GLU:OE2	71:S3:107:LYS:HE2	2.19	0.42
73:S5:72:ARG:H	73:S5:72:ARG:HG2	1.51	0.42
77:S9:168:ARG:HG2	77:S9:169:TYR:HD2	1.84	0.42
1:RA:190:LEU:HD23	1:RA:191:GLN:CB	2.50	0.42
1:RA:191:GLN:CG	1:RA:249:LYS:HE3	2.49	0.42
4:3:638:A:H2'	4:3:639:A:H5'	2.02	0.42
7:C2:70:LYS:HB3	7:C2:70:LYS:HE3	1.73	0.42
10:C5:96:LEU:HD12	10:C5:109:GLU:HG3	2.02	0.42
16:D1:26:VAL:C	16:D1:27:LEU:HD23	2.39	0.42
23:D8:24:LEU:HD21	73:S5:124:VAL:HG11	2.01	0.42
34:L9:92:TYR:O	65:P0:79:MET:HB2	2.20	0.42
37:M3:58:ARG:HE	37:M3:68:GLU:HG2	1.84	0.42
49:N3:89:ARG:NH2	49:N3:125:GLY:HA3	2.35	0.42
52:N6:63:PHE:O	52:N6:66:LYS:HG2	2.19	0.42
59:O3:45:LYS:HG3	59:O3:77:ILE:CD1	2.48	0.42
68:S0:16:ASP:N	68:S0:16:ASP:OD1	2.52	0.42
74:S6:34:GLN:OE1	74:S6:34:GLN:N	2.53	0.42
74:S6:122:GLY:C	74:S6:123:LEU:HD23	2.40	0.42
76:S8:157:LEU:O	76:S8:157:LEU:HD12	2.19	0.42
2:1:91:U:O2'	45:MS:19:ALA:HB1	2.19	0.42
7:C2:129:LYS:N	7:C2:129:LYS:HD2	2.35	0.42
9:C4:12:ALA:HB1	9:C4:28:THR:O	2.19	0.42
14:C9:62:ILE:HD12	14:C9:68:VAL:CG2	2.50	0.42
14:C9:125:THR:O	14:C9:129:GLU:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:E1:118:ASP:HA	25:E1:127:LEU:HA	2.01	0.42
38:M4:43:GLU:HG2	38:M4:44:ILE:N	2.35	0.42
38:M4:105:LEU:HD12	40:M6:177:ILE:HG22	2.02	0.42
42:M8:77:GLU:HG2	42:M8:78:SER:N	2.35	0.42
47:N1:135:PRO:O	47:N1:136:ARG:HB2	2.20	0.42
67:P3:48:LYS:NZ	67:P3:58:ARG:HD3	2.34	0.42
68:S0:89:ARG:O	68:S0:93:VAL:HG12	2.20	0.42
70:S2:56:ASP:O	70:S2:60:GLY:HA2	2.20	0.42
71:S3:164:LYS:HE2	71:S3:164:LYS:HB3	1.82	0.42
75:S7:94:THR:N	75:S7:97:LYS:HD2	2.34	0.42
76:S8:119:ASP:O	76:S8:121:ASP:N	2.53	0.42
1:RA:95:ASP:OD2	1:RA:98:SER:HB3	2.19	0.42
2:1:2591:U:O2'	2:1:2592:U:H5'	2.19	0.42
9:C4:42:GLY:O	69:S1:3:ILE:HG13	2.20	0.42
28:L3:158:GLN:HB3	28:L3:174:ILE:HG22	2.00	0.42
34:L9:14:ASP:OD1	34:L9:15:CYS:N	2.53	0.42
45:MS:16:MET:CE	45:MS:18:ASN:HA	2.49	0.42
50:N4:38:ARG:HA	50:N4:38:ARG:HD2	1.74	0.42
72:S4:137:TYR:CE1	72:S4:147:ARG:HB3	2.54	0.42
72:S4:255:LEU:HD21	77:S9:71:ARG:HD2	2.02	0.42
74:S6:14:LYS:HD3	74:S6:16:PHE:CZ	2.54	0.42
1:RA:151:MET:HB3	1:RA:201:TYR:OH	2.20	0.42
2:1:1975:U:H1'	2:1:1976:G:N2	2.34	0.42
2:1:2378:G:O2'	2:1:2379:U:H5'	2.19	0.42
4:3:1137:G:HO2'	4:3:1138:C:P	2.43	0.42
15:D0:41:TYR:O	15:D0:45:LYS:HG2	2.20	0.42
23:D8:10:GLU:CB	23:D8:51:ILE:HG22	2.46	0.42
50:N4:76:LYS:HG3	50:N4:76:LYS:O	2.20	0.42
55:N9:28:LYS:HE3	55:N9:28:LYS:HB3	1.70	0.42
56:O0:26:VAL:HG22	56:O0:92:ILE:HD12	2.02	0.42
68:S0:94:LYS:HB3	68:S0:206:PHE:CE1	2.54	0.42
69:S1:70:VAL:CG2	69:S1:75:LEU:HD21	2.46	0.42
70:S2:35:LYS:CE	70:S2:233:ILE:HD13	2.50	0.42
70:S2:38:SER:OG	70:S2:41:GLN:HG3	2.19	0.42
70:S2:220:LYS:HB3	70:S2:221:PRO:HD2	2.02	0.42
75:S7:44:LYS:HD2	75:S7:76:TYR:CZ	2.54	0.42
2:1:996:C:H5'	32:L7:109:ILE:HD11	2.02	0.41
2:1:2379:U:H6	2:1:2379:U:H2'	1.63	0.41
4:3:151:U:O2'	4:3:152:G:H5'	2.20	0.41
4:3:523:U:H4'	4:3:524:G:O5'	2.19	0.41
7:C2:63:LYS:HE2	7:C2:63:LYS:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C9:13:ASN:ND2	14:C9:60:ARG:HH12	2.18	0.41
23:D8:55:LEU:HD11	73:S5:108:GLU:OE2	2.20	0.41
27:L2:105:VAL:O	27:L2:105:VAL:HG12	2.19	0.41
32:L7:54:LYS:HG2	32:L7:54:LYS:O	2.19	0.41
39:M5:96:LEU:HD21	39:M5:172:ARG:HH22	1.85	0.41
53:N7:79:ASP:N	53:N7:79:ASP:OD2	2.51	0.41
53:N7:98:LYS:O	53:N7:101:THR:HG22	2.19	0.41
59:O3:52:VAL:O	59:O3:107:LYS:NZ	2.51	0.41
61:O5:64:LEU:HD13	63:O7:83:LEU:HD21	2.02	0.41
73:S5:16:LYS:HE2	73:S5:18:ASN:HA	2.02	0.41
74:S6:130:VAL:HG12	74:S6:131:SER:N	2.35	0.41
2:1:513:G:H2'	2:1:514:A:C8	2.55	0.41
9:C4:39:ILE:HA	9:C4:43:MET:HE2	2.02	0.41
10:C5:73:SER:O	10:C5:73:SER:OG	2.37	0.41
15:D0:107:ARG:HD3	71:S3:42:GLU:OE1	2.20	0.41
31:L6:85:LEU:CD2	31:L6:113:THR:HG21	2.50	0.41
33:L8:91:ILE:HD12	33:L8:165:ARG:CG	2.43	0.41
36:M1:49:LYS:HA	36:M1:63:GLU:O	2.21	0.41
44:MD:132:SER:HG	44:MD:136:VAL:H	1.66	0.41
53:N7:110:LYS:HD2	53:N7:111:ALA:N	2.34	0.41
68:S0:84:THR:HA	68:S0:106:GLY:O	2.20	0.41
70:S2:235:ASN:HB2	70:S2:236:GLN:NE2	2.34	0.41
74:S6:145:GLY:O	74:S6:147:PRO:HD3	2.20	0.41
77:S9:167:SER:H	77:S9:167:SER:HG	1.65	0.41
1:RA:240:LYS:NZ	1:RA:256:ASP:HB2	2.36	0.41
7:C2:84:GLU:O	7:C2:88:ILE:HG12	2.20	0.41
7:C2:125:ALA:O	7:C2:129:LYS:HD3	2.19	0.41
11:C6:109:LYS:O	11:C6:109:LYS:HG2	2.20	0.41
13:C8:63:ASP:OD1	13:C8:64:GLU:N	2.52	0.41
28:L3:348:LYS:HG3	50:N4:1:MET:HE3	2.02	0.41
31:L6:147:VAL:HG23	31:L6:150:MET:CB	2.50	0.41
38:M4:62:LEU:HD23	38:M4:66:GLU:O	2.20	0.41
44:MD:11:PHE:HB3	44:MD:14:VAL:HG11	2.02	0.41
67:P3:74:PRO:O	67:P3:77:LYS:HG2	2.20	0.41
76:S8:67:PHE:CD2	76:S8:69:THR:HG22	2.55	0.41
2:1:1243:G:H2'	2:1:1244:C:H6	1.84	0.41
2:1:1592:U:H4'	2:1:1593:G:OP1	2.20	0.41
6:C1:35:GLU:HB2	6:C1:57:PHE:CE1	2.55	0.41
6:C1:75:MET:CE	6:C1:116:ILE:HG22	2.50	0.41
7:C2:91:VAL:HG12	7:C2:91:VAL:O	2.21	0.41
26:L1:27:PRO:HA	26:L1:157:GLN:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:L3:39:GLN:HB3	28:L3:40:PRO:HD2	2.02	0.41
29:L4:311:LEU:HD23	29:L4:311:LEU:HA	1.86	0.41
30:L5:183:ASP:OD1	30:L5:184:GLY:N	2.54	0.41
31:L6:17:MET:N	31:L6:18:PRO:HD3	2.35	0.41
31:L6:157:PRO:HB2	59:O3:13:ARG:NH2	2.35	0.41
32:L7:71:ASN:OD1	47:N1:143:LEU:HB2	2.21	0.41
33:L8:40:ARG:HG2	33:L8:194:TRP:CE3	2.54	0.41
37:M3:103:THR:HG22	62:O6:16:ARG:NH1	2.36	0.41
41:M7:70:GLN:HA	41:M7:100:THR:O	2.21	0.41
42:M8:46:VAL:HG21	42:M8:136:MET:HG2	2.01	0.41
57:O1:89:GLU:HG3	57:O1:90:ASN:N	2.35	0.41
62:O6:70:LEU:HD12	62:O6:84:VAL:CG1	2.50	0.41
74:S6:48:ILE:O	74:S6:113:LEU:HB2	2.19	0.41
76:S8:118:ARG:HB2	76:S8:118:ARG:NH2	2.34	0.41
1:RA:85:VAL:CG2	1:RA:111:VAL:HB	2.50	0.41
2:1:157:A:H1'	37:M3:60:PRO:O	2.19	0.41
2:1:2301:G:H2'	2:1:2302:U:H4'	2.03	0.41
4:3:296:G:O2'	4:3:297:G:OP2	2.38	0.41
4:3:1099:G:N2	4:3:1102:A:OP2	2.42	0.41
5:C0:31:HIS:HB3	5:C0:34:LEU:O	2.20	0.41
9:C4:53:SER:HB2	9:C4:54:PRO:HD2	2.03	0.41
16:D1:23:VAL:CG2	68:S0:148:PRO:HG3	2.50	0.41
31:L6:148:GLU:HG2	31:L6:149:TYR:CD2	2.56	0.41
39:M5:184:LYS:HB3	39:M5:184:LYS:HE2	1.94	0.41
53:N7:42:LYS:O	53:N7:42:LYS:HD2	2.21	0.41
53:N7:106:ASP:HA	53:N7:109:MET:HG2	2.03	0.41
66:P2:74:LYS:O	66:P2:75:CYS:HB2	2.21	0.41
72:S4:202:LYS:HE3	72:S4:202:LYS:HB3	1.84	0.41
74:S6:173:LYS:HD2	74:S6:173:LYS:O	2.21	0.41
1:RA:154:ARG:HD3	1:RA:154:ARG:HA	1.77	0.41
1:RA:191:GLN:HE21	1:RA:249:LYS:CE	2.32	0.41
2:1:1975:U:H2'	2:1:1976:G:C5'	2.47	0.41
4:3:736:A:H2'	4:3:737:A:C8	2.55	0.41
4:3:870:A:H2'	4:3:871:G:O4'	2.20	0.41
4:3:879:G:H4'	4:3:880:U:C5'	2.49	0.41
5:C0:22:LEU:HD12	5:C0:64:TYR:CD1	2.56	0.41
14:C9:29:LEU:HA	14:C9:29:LEU:HD23	1.83	0.41
14:C9:70:SER:O	14:C9:70:SER:OG	2.32	0.41
28:L3:55:HIS:HB2	28:L3:351:ASP:CB	2.49	0.41
31:L6:77:PRO:HG2	31:L6:80:ILE:HB	2.03	0.41
35:M0:193:ARG:HA	35:M0:193:ARG:HE	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M3:51:LYS:HG3	37:M3:141:LYS:O	2.21	0.41
43:M9:157:GLU:OE1	43:M9:157:GLU:N	2.54	0.41
72:S4:52:LEU:HD13	72:S4:54:TYR:CE2	2.56	0.41
75:S7:37:ILE:O	75:S7:47:VAL:HG22	2.20	0.41
76:S8:118:ARG:HB2	76:S8:118:ARG:HH21	1.86	0.41
4:3:1178:C:O2'	4:3:1178:C:O2	2.38	0.41
5:C0:16:LEU:HD23	5:C0:16:LEU:HA	1.89	0.41
10:C5:96:LEU:HD23	10:C5:96:LEU:O	2.21	0.41
13:C8:74:ASP:N	13:C8:74:ASP:OD1	2.54	0.41
27:L2:7:ARG:O	27:L2:10:GLU:HG3	2.21	0.41
27:L2:158:GLY:HA2	67:P3:73:THR:HG21	2.02	0.41
29:L4:50:ALA:HA	29:L4:102:THR:CG2	2.50	0.41
29:L4:266:GLU:HG2	29:L4:267:ALA:N	2.35	0.41
30:L5:51:VAL:O	30:L5:52:ARG:NE	2.53	0.41
31:L6:149:TYR:OH	40:M6:194:LEU:HD12	2.21	0.41
40:M6:88:ILE:HG13	40:M6:89:SER:N	2.36	0.41
44:MD:7:VAL:CG2	44:MD:108:PHE:HB2	2.51	0.41
48:N2:90:LYS:HB3	48:N2:90:LYS:HE3	1.87	0.41
74:S6:148:ASP:C	74:S6:150:GLU:H	2.24	0.41
1:RA:198:TYR:CG	1:RA:249:LYS:HE2	2.56	0.41
2:1:195:G:H5'	37:M3:90:ARG:NH2	2.36	0.41
2:1:1199:A:N1	2:1:1206:U:H5	2.18	0.41
2:1:2106:U:H4'	2:1:2107:A:OP1	2.20	0.41
6:C1:27:GLN:HB2	6:C1:28:PRO:CD	2.48	0.41
7:C2:91:VAL:HG11	7:C2:105:CYS:HB3	2.01	0.41
14:C9:7:VAL:HG21	14:C9:134:VAL:CG2	2.47	0.41
14:C9:114:HIS:O	14:C9:118:MET:HG3	2.20	0.41
15:D0:32:GLN:HE22	15:D0:110:PRO:HG2	1.85	0.41
16:D1:26:VAL:HG11	70:S2:224:LEU:CD2	2.49	0.41
17:D2:81:ARG:O	17:D2:81:ARG:HG2	2.20	0.41
21:D6:79:LYS:HD3	21:D6:79:LYS:HA	1.82	0.41
23:D8:54:ILE:HG22	23:D8:55:LEU:N	2.36	0.41
31:L6:88:ILE:HD11	31:L6:93:LEU:HD21	2.02	0.41
38:M4:13:ALA:O	38:M4:18:ARG:NH1	2.47	0.41
52:N6:62:LYS:HE3	52:N6:63:PHE:CE2	2.56	0.41
68:S0:14:ILE:O	68:S0:16:ASP:N	2.54	0.41
76:S8:49:ARG:HH21	76:S8:49:ARG:HD2	1.74	0.41
2:1:412:A:H1'	2:1:413:A:H5"	2.02	0.41
2:1:505:U:H5"	42:M8:91:ASP:O	2.21	0.41
2:1:508:U:O2	2:1:508:U:H2'	2.21	0.41
3:2:24:A:H2'	3:2:25:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:285:A:H2'	4:3:286:C:C6	2.56	0.41
4:3:618:C:O2'	8:C3:101:HIS:HD2	2.03	0.41
4:3:849:G:H5'	4:3:850:G:H4'	2.02	0.41
4:3:944:U:C3'	4:3:945:G:H5"	2.49	0.41
4:3:1294:U:H3'	21:D6:2:ARG:HH11	1.86	0.41
6:C1:36:VAL:O	6:C1:38:GLY:N	2.54	0.41
7:C2:69:ALA:O	7:C2:73:ASN:N	2.54	0.41
9:C4:65:ALA:O	9:C4:69:LEU:HB2	2.21	0.41
11:C6:24:THR:OG1	11:C6:25:GLN:N	2.54	0.41
12:C7:41:VAL:CG1	71:S3:207:ILE:HG12	2.51	0.41
12:C7:62:LEU:O	12:C7:62:LEU:HD23	2.21	0.41
15:D0:106:LEU:HA	15:D0:106:LEU:HD23	1.81	0.41
26:L1:47:ASP:O	26:L1:144:VAL:N	2.45	0.41
27:L2:89:LYS:NZ	27:L2:91:LYS:HD3	2.35	0.41
28:L3:112:SER:OG	28:L3:113:ASP:N	2.54	0.41
28:L3:210:ASN:O	28:L3:211:ILE:HD13	2.21	0.41
34:L9:88:MET:O	34:L9:138:THR:HG23	2.20	0.41
35:M0:89:ILE:HD13	35:M0:136:LEU:HD22	2.03	0.41
36:M1:99:ASN:OD1	36:M1:99:ASN:N	2.53	0.41
37:M3:103:THR:HG22	62:O6:16:ARG:HH12	1.86	0.41
37:M3:124:ILE:HD13	61:O5:119:PHE:HB3	2.03	0.41
39:M5:145:ASP:O	39:M5:149:ASN:HB2	2.21	0.41
40:M6:47:LEU:CD2	40:M6:139:LYS:HE3	2.44	0.41
42:M8:64:GLN:HB2	42:M8:144:THR:HB	2.03	0.41
42:M8:181:ILE:HG22	42:M8:187:LYS:CB	2.42	0.41
44:MD:167:VAL:HG23	44:MD:167:VAL:O	2.21	0.41
49:N3:41:LYS:HB2	49:N3:73:LYS:HB3	2.01	0.41
53:N7:111:ALA:HB1	53:N7:116:LYS:CB	2.49	0.41
55:N9:36:HIS:HD2	55:N9:38:ALA:H	1.69	0.41
55:N9:55:SER:O	55:N9:55:SER:OG	2.37	0.41
62:O6:1:MET:SD	62:O6:6:LYS:HG2	2.61	0.41
62:O6:23:GLN:NE2	62:O6:27:ARG:HG2	2.36	0.41
63:O7:14:ARG:HD3	63:O7:14:ARG:HA	1.90	0.41
68:S0:70:PHE:CE2	68:S0:79:ILE:HG21	2.56	0.41
72:S4:118:GLU:HG3	72:S4:118:GLU:O	2.21	0.41
72:S4:178:LYS:O	72:S4:193:VAL:HG13	2.21	0.41
73:S5:29:SER:O	73:S5:31:ARG:HD2	2.20	0.41
73:S5:113:ILE:HD11	73:S5:122:THR:HG21	2.03	0.41
75:S7:105:TRP:HE3	75:S7:156:LEU:HD21	1.86	0.41
77:S9:164:ASN:O	77:S9:167:SER:OG	2.31	0.41
2:1:1520:A:C4	63:O7:3:LYS:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:1150:C:H41	11:C6:129:LYS:NZ	2.19	0.41
6:C1:144:LYS:HE2	6:C1:144:LYS:HB3	1.72	0.41
7:C2:103:LYS:HE2	7:C2:103:LYS:HB2	1.98	0.41
18:D3:57:LYS:HE3	18:D3:57:LYS:HB3	1.79	0.41
25:E1:132:ARG:HA	25:E1:143:LYS:O	2.21	0.41
28:L3:65:LYS:HD2	28:L3:65:LYS:HA	1.75	0.41
31:L6:77:PRO:HB3	31:L6:140:ILE:HG22	2.03	0.41
32:L7:69:MET:HE2	32:L7:72:GLY:HA3	2.01	0.41
33:L8:61:VAL:HG23	33:L8:150:LEU:HD11	2.02	0.41
34:L9:83:GLY:O	34:L9:181:ILE:HD12	2.21	0.41
35:M0:193:ARG:CD	35:M0:219:ASN:HB3	2.51	0.41
36:M1:60:ARG:HB2	36:M1:63:GLU:OE1	2.21	0.41
36:M1:172:VAL:O	36:M1:173:GLU:HG2	2.21	0.41
42:M8:137:ASP:O	42:M8:138:ASP:HB2	2.21	0.41
49:N3:26:ILE:CG1	49:N3:87:LEU:HD11	2.46	0.41
50:N4:67:VAL:HG13	50:N4:68:GLU:N	2.36	0.41
57:O1:46:ARG:HD3	57:O1:46:ARG:HA	1.48	0.41
70:S2:42:ILE:HG23	70:S2:47:HIS:HB2	2.02	0.41
71:S3:26:LYS:O	71:S3:29:VAL:HG23	2.21	0.41
71:S3:58:ILE:HG22	71:S3:59:GLY:O	2.21	0.41
75:S7:129:VAL:HG13	75:S7:161:ILE:CD1	2.48	0.41
2:1:1128:U:H5	2:1:1372:A:N1	2.18	0.40
2:1:1617:G:N2	2:1:1632:U:H1'	2.37	0.40
2:1:1632:U:H2'	2:1:1633:C:C6	2.55	0.40
2:1:2090:U:H2'	2:1:2091:G:C8	2.56	0.40
4:3:119:G:H2'	74:S6:195:ARG:HH11	1.85	0.40
4:3:169:G:C2'	4:3:170:U:H5'	2.51	0.40
4:3:358:U:O2	4:3:358:U:H2'	2.20	0.40
4:3:944:U:H3'	4:3:945:G:C5'	2.51	0.40
4:3:944:U:OP2	4:3:944:U:H2'	2.21	0.40
6:C1:56:PRO:HD3	6:C1:137:VAL:HG21	2.02	0.40
7:C2:86:GLY:C	7:C2:92:GLU:HG2	2.41	0.40
11:C6:64:ASP:N	11:C6:64:ASP:OD1	2.54	0.40
13:C8:40:ARG:O	13:C8:40:ARG:HG3	2.20	0.40
13:C8:109:ARG:O	13:C8:113:GLU:HG2	2.22	0.40
20:D5:42:VAL:O	20:D5:42:VAL:HG13	2.21	0.40
32:L7:50:LYS:HE2	32:L7:50:LYS:HB3	1.94	0.40
32:L7:174:ILE:H	32:L7:174:ILE:HG13	1.58	0.40
33:L8:51:VAL:HG23	33:L8:52:LEU:O	2.21	0.40
38:M4:95:VAL:HA	38:M4:98:GLU:CG	2.51	0.40
39:M5:16:SER:O	39:M5:18:VAL:N	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:M6:192:ARG:O	40:M6:195:ALA:HB3	2.21	0.40
41:M7:38:ARG:O	41:M7:39:ARG:HB2	2.22	0.40
63:O7:80:ASP:OD1	63:O7:81:PRO:HD2	2.22	0.40
75:S7:22:ILE:HG13	75:S7:24:ALA:H	1.86	0.40
1:RA:113:CYS:HB3	1:RA:158:ASN:O	2.20	0.40
1:RA:199:VAL:HG11	1:RA:212:VAL:H	1.86	0.40
4:3:365:G:H2'	4:3:366:U:O4'	2.20	0.40
4:3:663:U:H2'	4:3:664:C:C6	2.56	0.40
6:C1:25:GLU:OE1	6:C1:25:GLU:N	2.46	0.40
6:C1:32:VAL:HG12	6:C1:33:ASN:N	2.32	0.40
14:C9:81:LYS:O	14:C9:88:SER:HB2	2.20	0.40
28:L3:37:ARG:HB3	28:L3:182:GLY:HA3	2.03	0.40
42:M8:9:TYR:OH	42:M8:11:ARG:HB3	2.20	0.40
66:P2:71:GLU:OE2	66:P2:76:LYS:HA	2.21	0.40
67:P3:36:LYS:HG2	67:P3:48:LYS:HE3	2.02	0.40
68:S0:139:ILE:O	68:S0:142:SER:OG	2.34	0.40
70:S2:53:GLU:OE1	70:S2:53:GLU:N	2.53	0.40
74:S6:182:LYS:O	74:S6:186:GLU:HG3	2.21	0.40
74:S6:199:LYS:HG2	74:S6:203:GLU:OE2	2.20	0.40
75:S7:36:ILE:O	75:S7:36:ILE:HG13	2.22	0.40
1:RA:131:THR:O	1:RA:132:MET:HG3	2.19	0.40
2:1:55:G:H2'	2:1:56:G:O4'	2.22	0.40
2:1:753:A:H2'	2:1:756:C:C5	2.57	0.40
2:1:1418:U:P	57:O1:35:ARG:HH12	2.44	0.40
4:3:698:A:H4'	4:3:699:U:OP2	2.21	0.40
10:C5:124:PRO:HB3	13:C8:121:ILE:CD1	2.51	0.40
13:C8:112:ILE:HG22	13:C8:116:LYS:HE3	2.02	0.40
22:D7:37:GLY:O	22:D7:39:ARG:NH1	2.54	0.40
32:L7:32:GLU:HA	32:L7:35:GLU:OE1	2.21	0.40
36:M1:30:LEU:HD23	36:M1:30:LEU:HA	1.92	0.40
38:M4:23:ILE:HB	38:M4:71:ILE:CD1	2.51	0.40
41:M7:129:ASP:CG	41:M7:131:LYS:HG2	2.41	0.40
47:N1:80:ARG:HG3	47:N1:80:ARG:O	2.21	0.40
56:O0:15:LEU:HD12	56:O0:15:LEU:O	2.22	0.40
57:O1:69:ILE:O	57:O1:69:ILE:HG22	2.21	0.40
72:S4:95:THR:O	72:S4:95:THR:OG1	2.39	0.40
1:RA:95:ASP:O	1:RA:97:GLU:N	2.54	0.40
1:RA:205:LYS:HZ2	1:RA:208:LYS:HG3	1.86	0.40
2:1:200:U:H2'	2:1:200:U:O2	2.21	0.40
2:1:293:G:H2'	2:1:294:C:O4'	2.21	0.40
2:1:713:G:H2'	2:1:714:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:672:U:O2'	4:3:673:A:OP1	2.36	0.40
4:3:875:G:H2'	4:3:876:C:C6	2.56	0.40
6:C1:75:MET:HG2	6:C1:81:ILE:HG22	2.04	0.40
10:C5:60:LYS:HE3	10:C5:60:LYS:HB3	1.92	0.40
13:C8:51:ILE:HD12	13:C8:51:ILE:H	1.86	0.40
20:D5:27:TRP:HH2	44:MD:127:ILE:HG12	1.87	0.40
21:D6:41:LEU:HD22	21:D6:62:PRO:HB2	2.03	0.40
28:L3:46:PHE:HA	28:L3:85:MET:HE1	2.02	0.40
31:L6:101:ASP:C	31:L6:102:LEU:HD12	2.41	0.40
31:L6:150:MET:HG3	31:L6:150:MET:O	2.21	0.40
35:M0:98:ARG:HA	35:M0:121:LYS:O	2.21	0.40
37:M3:49:PRO:O	37:M3:50:LEU:HB3	2.21	0.40
44:MD:64:CYS:O	73:S5:119:MET:HG3	2.22	0.40
56:O0:97:GLN:HG3	56:O0:97:GLN:O	2.21	0.40
57:O1:49:ILE:H	57:O1:49:ILE:HG12	1.70	0.40
61:O5:122:ASN:OD1	61:O5:122:ASN:N	2.54	0.40
72:S4:48:ILE:O	72:S4:48:ILE:HG22	2.21	0.40
73:S5:73:LEU:O	73:S5:77:ILE:HG13	2.21	0.40
74:S6:197:GLU:OE1	74:S6:200:ARG:NH1	2.54	0.40
2:1:529:G:H5"	54:N8:5:VAL:O	2.22	0.40
2:1:1623:C:H2'	2:1:1624:U:C6	2.56	0.40
2:1:2581:A:H2'	2:1:2582:G:C8	2.57	0.40
4:3:1169:C:H2'	4:3:1170:U:C6	2.57	0.40
11:C6:27:GLY:HA2	11:C6:64:ASP:CB	2.51	0.40
13:C8:60:MET:HG3	13:C8:65:MET:HE2	2.03	0.40
20:D5:79:VAL:O	20:D5:83:LEU:HG	2.21	0.40
23:D8:30:GLU:CD	23:D8:37:THR:HG22	2.41	0.40
34:L9:77:ILE:O	34:L9:81:THR:HG23	2.21	0.40
35:M0:210:LYS:HE2	35:M0:210:LYS:HB2	1.82	0.40
43:M9:95:TRP:CZ2	43:M9:99:ILE:HD13	2.56	0.40
44:MD:86:LEU:O	44:MD:87:LEU:HG	2.21	0.40
71:S3:96:CYS:O	71:S3:100:GLN:HG2	2.22	0.40
72:S4:175:GLY:O	72:S4:178:LYS:HG2	2.22	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	RA	326/334 (98%)	264 (81%)	62 (19%)	0	100	100
5	C0	79/96 (82%)	72 (91%)	7 (9%)	0	100	100
6	C1	139/156 (89%)	123 (88%)	16 (12%)	0	100	100
7	C2	116/134 (87%)	102 (88%)	14 (12%)	0	100	100
8	C3	144/148 (97%)	136 (94%)	8 (6%)	0	100	100
9	C4	124/134 (92%)	113 (91%)	11 (9%)	0	100	100
10	C5	114/148 (77%)	107 (94%)	7 (6%)	0	100	100
11	C6	139/145 (96%)	124 (89%)	15 (11%)	0	100	100
12	C7	115/120 (96%)	104 (90%)	11 (10%)	0	100	100
13	C8	139/153 (91%)	126 (91%)	13 (9%)	0	100	100
14	C9	133/137 (97%)	123 (92%)	10 (8%)	0	100	100
15	D0	89/120 (74%)	81 (91%)	8 (9%)	0	100	100
16	D1	66/70 (94%)	65 (98%)	1 (2%)	0	100	100
17	D2	125/128 (98%)	122 (98%)	3 (2%)	0	100	100
18	D3	135/140 (96%)	129 (96%)	6 (4%)	0	100	100
19	D4	125/131 (95%)	113 (90%)	12 (10%)	0	100	100
20	D5	85/109 (78%)	72 (85%)	13 (15%)	0	100	100
21	D6	99/105 (94%)	94 (95%)	5 (5%)	0	100	100
22	D7	80/85 (94%)	68 (85%)	12 (15%)	0	100	100
23	D8	55/65 (85%)	47 (86%)	8 (14%)	0	100	100
24	D9	63/66 (96%)	57 (90%)	6 (10%)	0	100	100
25	E1	56/152 (37%)	47 (84%)	8 (14%)	1 (2%)	8	21
26	L1	204/219 (93%)	151 (74%)	41 (20%)	12 (6%)	1	2
27	L2	230/239 (96%)	204 (89%)	26 (11%)	0	100	100
28	L3	359/383 (94%)	315 (88%)	43 (12%)	1 (0%)	41	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
29	L4	327/335 (98%)	293 (90%)	33 (10%)	1 (0%)	41 66
30	L5	281/287 (98%)	262 (93%)	19 (7%)	0	100 100
31	L6	157/171 (92%)	128 (82%)	28 (18%)	1 (1%)	25 50
32	L7	229/239 (96%)	213 (93%)	16 (7%)	0	100 100
33	L8	195/206 (95%)	163 (84%)	32 (16%)	0	100 100
34	L9	181/183 (99%)	154 (85%)	27 (15%)	0	100 100
35	M0	207/219 (94%)	190 (92%)	16 (8%)	1 (0%)	29 54
36	M1	165/173 (95%)	143 (87%)	21 (13%)	1 (1%)	25 50
37	M3	159/163 (98%)	144 (91%)	14 (9%)	1 (1%)	25 50
38	M4	102/106 (96%)	93 (91%)	9 (9%)	0	100 100
39	M5	201/204 (98%)	190 (94%)	11 (6%)	0	100 100
40	M6	194/198 (98%)	187 (96%)	7 (4%)	0	100 100
41	M7	172/183 (94%)	157 (91%)	15 (9%)	0	100 100
42	M8	184/200 (92%)	172 (94%)	12 (6%)	0	100 100
43	M9	168/171 (98%)	157 (94%)	11 (6%)	0	100 100
44	MD	168/171 (98%)	138 (82%)	30 (18%)	0	100 100
45	MS	66/73 (90%)	63 (96%)	3 (4%)	0	100 100
46	N0	176/188 (94%)	157 (89%)	16 (9%)	3 (2%)	9 23
47	N1	157/160 (98%)	136 (87%)	19 (12%)	2 (1%)	12 30
48	N2	89/112 (80%)	76 (85%)	13 (15%)	0	100 100
49	N3	133/146 (91%)	127 (96%)	6 (4%)	0	100 100
50	N4	87/100 (87%)	74 (85%)	12 (14%)	1 (1%)	14 34
51	N5	91/105 (87%)	83 (91%)	8 (9%)	0	100 100
52	N6	140/143 (98%)	131 (94%)	7 (5%)	2 (1%)	11 28
53	N7	114/126 (90%)	100 (88%)	14 (12%)	0	100 100
54	N8	144/147 (98%)	123 (85%)	20 (14%)	1 (1%)	22 46
55	N9	53/57 (93%)	47 (89%)	6 (11%)	0	100 100
56	O0	88/108 (82%)	83 (94%)	5 (6%)	0	100 100
57	O1	106/111 (96%)	94 (89%)	10 (9%)	2 (2%)	8 20
58	O2	126/139 (91%)	123 (98%)	3 (2%)	0	100 100
59	O3	105/113 (93%)	97 (92%)	8 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	O4	98/110 (89%)	94 (96%)	4 (4%)	0	100	100
61	O5	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
62	O6	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
63	O7	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
64	O9	48/52 (92%)	43 (90%)	5 (10%)	0	100	100
65	P0	47/131 (36%)	42 (89%)	5 (11%)	0	100	100
66	P2	95/104 (91%)	81 (85%)	13 (14%)	1 (1%)	14	34
67	P3	84/89 (94%)	80 (95%)	4 (5%)	0	100	100
68	S0	201/252 (80%)	178 (89%)	23 (11%)	0	100	100
69	S1	205/239 (86%)	184 (90%)	21 (10%)	0	100	100
70	S2	215/242 (89%)	199 (93%)	16 (7%)	0	100	100
71	S3	208/216 (96%)	190 (91%)	18 (9%)	0	100	100
72	S4	257/268 (96%)	228 (89%)	29 (11%)	0	100	100
73	S5	186/189 (98%)	171 (92%)	14 (8%)	1 (0%)	29	54
74	S6	200/217 (92%)	182 (91%)	17 (8%)	1 (0%)	29	54
75	S7	143/170 (84%)	132 (92%)	10 (7%)	1 (1%)	22	46
76	S8	162/173 (94%)	148 (91%)	13 (8%)	1 (1%)	25	50
77	S9	169/184 (92%)	147 (87%)	22 (13%)	0	100	100
All	All	10717/11696 (92%)	9640 (90%)	1042 (10%)	35 (0%)	44	66

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	L1	27	PRO
26	L1	37	VAL
26	L1	44	PRO
26	L1	57	PRO
26	L1	83	LEU
26	L1	87	PRO
26	L1	114	PRO
54	N8	78	LEU
74	S6	151	LYS
28	L3	364	SER
46	N0	147	PRO
73	S5	65	GLY
76	S8	120	VAL

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Mol	Chain	Res	Type
25	E1	97	PRO
26	L1	75	VAL
26	L1	84	PRO
31	L6	109	ASP
47	N1	135	PRO
52	N6	47	THR
26	L1	113	CYS
36	M1	114	LEU
50	N4	71	ASN
35	M0	92	TYR
52	N6	46	ARG
26	L1	60	VAL
29	L4	291	SER
46	N0	50	ASN
57	O1	69	ILE
66	P2	53	LYS
26	L1	144	VAL
46	N0	148	VAL
75	S7	157	GLY
37	M3	60	PRO
57	O1	70	PRO
47	N1	155	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	RA	286/291 (98%)	285 (100%)	1 (0%)	92 98
5	C0	76/86 (88%)	76 (100%)	0	100 100
6	C1	124/138 (90%)	124 (100%)	0	100 100
7	C2	99/114 (87%)	99 (100%)	0	100 100
8	C3	127/129 (98%)	127 (100%)	0	100 100
9	C4	93/101 (92%)	93 (100%)	0	100 100
10	C5	98/125 (78%)	98 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
11	C6	121/125 (97%)	118 (98%)	3 (2%)	47 76
12	C7	107/109 (98%)	106 (99%)	1 (1%)	78 92
13	C8	119/129 (92%)	119 (100%)	0	100 100
14	C9	119/121 (98%)	118 (99%)	1 (1%)	81 93
15	D0	88/114 (77%)	87 (99%)	1 (1%)	73 90
16	D1	55/57 (96%)	55 (100%)	0	100 100
17	D2	107/108 (99%)	107 (100%)	0	100 100
18	D3	111/114 (97%)	111 (100%)	0	100 100
19	D4	117/121 (97%)	117 (100%)	0	100 100
20	D5	73/91 (80%)	73 (100%)	0	100 100
21	D6	86/89 (97%)	85 (99%)	1 (1%)	71 88
22	D7	71/73 (97%)	71 (100%)	0	100 100
23	D8	48/56 (86%)	48 (100%)	0	100 100
24	D9	57/58 (98%)	57 (100%)	0	100 100
27	L2	192/198 (97%)	191 (100%)	1 (0%)	88 96
28	L3	298/313 (95%)	298 (100%)	0	100 100
29	L4	274/280 (98%)	271 (99%)	3 (1%)	73 90
30	L5	235/238 (99%)	234 (100%)	1 (0%)	91 97
31	L6	139/151 (92%)	139 (100%)	0	100 100
32	L7	210/216 (97%)	208 (99%)	2 (1%)	76 91
33	L8	181/190 (95%)	180 (99%)	1 (1%)	86 95
34	L9	157/157 (100%)	155 (99%)	2 (1%)	69 87
35	M0	179/184 (97%)	178 (99%)	1 (1%)	86 95
36	M1	143/149 (96%)	142 (99%)	1 (1%)	84 94
37	M3	139/141 (99%)	137 (99%)	2 (1%)	67 86
38	M4	93/94 (99%)	93 (100%)	0	100 100
39	M5	173/174 (99%)	173 (100%)	0	100 100
40	M6	167/168 (99%)	167 (100%)	0	100 100
41	M7	142/160 (89%)	141 (99%)	1 (1%)	84 94
42	M8	165/178 (93%)	165 (100%)	0	100 100
43	M9	147/148 (99%)	146 (99%)	1 (1%)	84 94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	MD	158/159 (99%)	158 (100%)	0	100	100
45	MS	65/69 (94%)	63 (97%)	2 (3%)	40	69
46	N0	160/169 (95%)	158 (99%)	2 (1%)	69	87
47	N1	137/140 (98%)	136 (99%)	1 (1%)	84	94
48	N2	76/94 (81%)	76 (100%)	0	100	100
49	N3	113/122 (93%)	113 (100%)	0	100	100
50	N4	78/86 (91%)	78 (100%)	0	100	100
51	N5	78/91 (86%)	78 (100%)	0	100	100
52	N6	126/127 (99%)	125 (99%)	1 (1%)	81	93
53	N7	98/110 (89%)	95 (97%)	3 (3%)	40	69
54	N8	124/125 (99%)	124 (100%)	0	100	100
55	N9	44/47 (94%)	44 (100%)	0	100	100
56	O0	77/90 (86%)	77 (100%)	0	100	100
57	O1	101/106 (95%)	101 (100%)	0	100	100
58	O2	114/125 (91%)	114 (100%)	0	100	100
59	O3	93/99 (94%)	92 (99%)	1 (1%)	73	90
60	O4	87/91 (96%)	87 (100%)	0	100	100
61	O5	102/103 (99%)	102 (100%)	0	100	100
62	O6	74/79 (94%)	73 (99%)	1 (1%)	67	86
63	O7	73/76 (96%)	73 (100%)	0	100	100
64	O9	44/46 (96%)	43 (98%)	1 (2%)	50	78
65	P0	41/107 (38%)	41 (100%)	0	100	100
66	P2	84/89 (94%)	84 (100%)	0	100	100
67	P3	67/69 (97%)	65 (97%)	2 (3%)	41	70
68	S0	176/219 (80%)	175 (99%)	1 (1%)	86	95
69	S1	184/206 (89%)	184 (100%)	0	100	100
70	S2	177/200 (88%)	177 (100%)	0	100	100
71	S3	178/184 (97%)	177 (99%)	1 (1%)	86	95
72	S4	228/236 (97%)	228 (100%)	0	100	100
73	S5	159/160 (99%)	158 (99%)	1 (1%)	86	95
74	S6	182/194 (94%)	180 (99%)	2 (1%)	73	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
75	S7	127/144 (88%)	126 (99%)	1 (1%)	81 93
76	S8	140/149 (94%)	140 (100%)	0	100 100
77	S9	147/156 (94%)	147 (100%)	0	100 100
All	All	9128/9755 (94%)	9084 (100%)	44 (0%)	89 96

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	RA	55	PHE
11	C6	76	ASP
11	C6	104	LYS
11	C6	139	ARG
12	C7	5	ARG
14	C9	133	LYS
15	D0	88	ARG
21	D6	81	VAL
27	L2	229	ARG
29	L4	53	LYS
29	L4	106	ARG
29	L4	190	LYS
30	L5	255	LYS
32	L7	214	LYS
32	L7	224	VAL
33	L8	132	ARG
34	L9	22	LYS
34	L9	54	ARG
35	M0	38	ARG
36	M1	51	ARG
37	M3	20	LYS
37	M3	87	ARG
41	M7	31	ARG
43	M9	78	THR
45	MS	50	ARG
45	MS	52	ARG
46	N0	135	ARG
46	N0	171	LYS
47	N1	153	TYR
52	N6	109	PHE
53	N7	42	LYS
53	N7	54	ARG
53	N7	110	LYS

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Mol	Chain	Res	Type
59	O3	84	VAL
62	O6	71	ARG
64	O9	4	ARG
67	P3	58	ARG
67	P3	60	CYS
68	S0	35	ASN
71	S3	115	ARG
73	S5	72	ARG
74	S6	151	LYS
74	S6	173	LYS
75	S7	20	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	RA	15	HIS
1	RA	191	GLN
1	RA	253	GLN
5	C0	31	HIS
5	C0	62	HIS
6	C1	107	HIS
7	C2	111	GLN
8	C3	101	HIS
9	C4	96	GLN
12	C7	6	ASN
12	C7	31	ASN
12	C7	48	ASN
12	C7	67	ASN
12	C7	83	ASN
13	C8	98	HIS
15	D0	32	GLN
15	D0	52	GLN
18	D3	70	GLN
19	D4	27	HIS
19	D4	52	ASN
21	D6	39	GLN
22	D7	47	HIS
27	L2	180	HIS
27	L2	195	HIS
27	L2	201	ASN
27	L2	220	GLN
28	L3	39	GLN

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Mol	Chain	Res	Type
28	L3	234	GLN
28	L3	265	GLN
29	L4	86	GLN
29	L4	100	HIS
30	L5	15	GLN
30	L5	30	HIS
30	L5	33	ASN
30	L5	61	GLN
31	L6	165	ASN
32	L7	92	ASN
32	L7	213	GLN
33	L8	152	ASN
34	L9	19	GLN
34	L9	164	ASN
35	M0	55	ASN
35	M0	133	GLN
36	M1	166	ASN
37	M3	13	HIS
37	M3	24	HIS
37	M3	65	ASN
38	M4	19	HIS
39	M5	5	ASN
39	M5	196	ASN
40	M6	6	HIS
40	M6	14	GLN
41	M7	70	GLN
41	M7	158	ASN
42	M8	135	ASN
43	M9	40	GLN
43	M9	54	GLN
43	M9	134	HIS
44	MD	57	ASN
44	MD	116	ASN
46	N0	106	ASN
47	N1	25	HIS
48	N2	35	GLN
50	N4	34	ASN
50	N4	73	GLN
51	N5	44	ASN
52	N6	15	GLN
53	N7	16	ASN
53	N7	70	HIS

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Mol	Chain	Res	Type
54	N8	28	HIS
54	N8	53	HIS
55	N9	36	HIS
57	O1	90	ASN
58	O2	85	ASN
58	O2	130	ASN
59	O3	27	GLN
62	O6	23	GLN
62	O6	63	ASN
63	O7	25	GLN
63	O7	75	ASN
66	P2	3	ASN
68	S0	137	GLN
68	S0	143	GLN
68	S0	146	ASN
68	S0	170	ASN
68	S0	188	ASN
69	S1	46	ASN
69	S1	148	HIS
69	S1	192	ASN
69	S1	223	HIS
70	S2	76	GLN
70	S2	81	GLN
70	S2	97	HIS
70	S2	225	ASN
71	S3	113	GLN
71	S3	168	ASN
72	S4	8	HIS
72	S4	81	HIS
72	S4	195	ASN
72	S4	245	GLN
72	S4	252	ASN
73	S5	168	ASN
74	S6	22	ASN
74	S6	58	GLN
75	S7	59	GLN
76	S8	94	ASN
76	S8	111	ASN
77	S9	107	ASN
77	S9	108	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	2305/2486 (92%)	405 (17%)	25 (1%)
3	2	118/119 (99%)	20 (16%)	0
4	3	1292/1300 (99%)	335 (25%)	13 (1%)
All	All	3715/3905 (95%)	760 (20%)	38 (1%)

All (760) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	24	U
2	1	25	G
2	1	32	G
2	1	39	U
2	1	49	G
2	1	50	C
2	1	52	G
2	1	60	A
2	1	63	U
2	1	64	G
2	1	74	U
2	1	75	G
2	1	79	C
2	1	88	A
2	1	89	A
2	1	90	U
2	1	91	U
2	1	92	G
2	1	100	U
2	1	101	G
2	1	111	A
2	1	125	A
2	1	128	A
2	1	134	G
2	1	144	G
2	1	145	A
2	1	150	A
2	1	151	A
2	1	157	A
2	1	158	U
2	1	174	G
2	1	177	G
2	1	194	A
2	1	195	G
2	1	201	G

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Mol	Chain	Res	Type
2	1	206	A
2	1	210	G
2	1	217	G
2	1	223	U
2	1	227	U
2	1	228	U
2	1	230	G
2	1	231	U
2	1	232	G
2	1	233	G
2	1	234	C
2	1	235	A
2	1	236	G
2	1	256	A
2	1	258	U
2	1	267	G
2	1	275	G
2	1	276	A
2	1	277	U
2	1	288	G
2	1	294	C
2	1	297	C
2	1	299	U
2	1	302	U
2	1	303	U
2	1	305	G
2	1	306	U
2	1	307	G
2	1	309	G
2	1	310	U
2	1	326	U
2	1	335	A
2	1	338	G
2	1	344	G
2	1	345	U
2	1	350	G
2	1	352	A
2	1	362	A
2	1	368	G
2	1	370	C
2	1	372	G
2	1	377	C

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Mol	Chain	Res	Type
2	1	388	U
2	1	390	A
2	1	405	G
2	1	416	A
2	1	417	G
2	1	428	A
2	1	429	A
2	1	447	A
2	1	454	G
2	1	456	U
2	1	457	G
2	1	477	A
2	1	488	A
2	1	490	A
2	1	505	U
2	1	508	U
2	1	518	G
2	1	526	G
2	1	542	A
2	1	544	A
2	1	553	G
2	1	585	G
2	1	587	G
2	1	590	C
2	1	597	A
2	1	603	G
2	1	610	U
2	1	615	U
2	1	633	C
2	1	643	G
2	1	650	A
2	1	652	G
2	1	653	A
2	1	657	A
2	1	658	A
2	1	660	G
2	1	673	G
2	1	680	C
2	1	683	U
2	1	695	C
2	1	696	U
2	1	713	G

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Mol	Chain	Res	Type
2	1	714	G
2	1	724	A
2	1	729	G
2	1	730	U
2	1	736	A
2	1	742	G
2	1	743	C
2	1	745	C
2	1	754	A
2	1	756	C
2	1	763	G
2	1	770	U
2	1	771	U
2	1	772	U
2	1	791	G
2	1	805	G
2	1	818	G
2	1	827	A
2	1	835	A
2	1	836	G
2	1	852	U
2	1	875	G
2	1	876	G
2	1	879	U
2	1	886	G
2	1	887	A
2	1	949	G
2	1	950	A
2	1	951	A
2	1	956	G
2	1	969	U
2	1	971	G
2	1	972	A
2	1	973	A
2	1	977	A
2	1	982	A
2	1	988	U
2	1	989	U
2	1	1005	G
2	1	1007	G
2	1	1008	U
2	1	1009	A

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Mol	Chain	Res	Type
2	1	1010	U
2	1	1013	G
2	1	1014	A
2	1	1039	G
2	1	1047	U
2	1	1065	G
2	1	1078	C
2	1	1079	A
2	1	1080	G
2	1	1083	C
2	1	1100	G
2	1	1101	G
2	1	1104	A
2	1	1105	U
2	1	1106	G
2	1	1107	A
2	1	1112	C
2	1	1129	C
2	1	1146	G
2	1	1150	C
2	1	1157	G
2	1	1160	U
2	1	1165	A
2	1	1166	G
2	1	1167	G
2	1	1177	A
2	1	1185	G
2	1	1186	U
2	1	1192	G
2	1	1200	G
2	1	1205	C
2	1	1209	G
2	1	1210	C
2	1	1213	U
2	1	1216	C
2	1	1217	G
2	1	1226	C
2	1	1241	U
2	1	1242	A
2	1	1244	C
2	1	1246	G
2	1	1248	A

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Mol	Chain	Res	Type
2	1	1265	U
2	1	1266	G
2	1	1274	U
2	1	1281	G
2	1	1286	G
2	1	1292	G
2	1	1334	G
2	1	1335	C
2	1	1337	A
2	1	1338	G
2	1	1347	G
2	1	1350	G
2	1	1351	A
2	1	1356	G
2	1	1357	A
2	1	1363	C
2	1	1376	A
2	1	1377	G
2	1	1378	A
2	1	1382	C
2	1	1385	C
2	1	1386	U
2	1	1402	C
2	1	1408	A
2	1	1415	U
2	1	1416	U
2	1	1417	G
2	1	1420	C
2	1	1441	G
2	1	1474	G
2	1	1483	G
2	1	1484	U
2	1	1486	C
2	1	1495	U
2	1	1497	U
2	1	1501	G
2	1	1503	G
2	1	1504	G
2	1	1513	A
2	1	1522	U
2	1	1526	A
2	1	1539	G

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Mol	Chain	Res	Type
2	1	1540	U
2	1	1574	U
2	1	1575	U
2	1	1576	A
2	1	1579	U
2	1	1593	G
2	1	1595	G
2	1	1610	A
2	1	1615	G
2	1	1616	G
2	1	1619	G
2	1	1621	A
2	1	1622	A
2	1	1623	C
2	1	1638	G
2	1	1639	G
2	1	1647	A
2	1	1648	U
2	1	1654	G
2	1	1664	U
2	1	1673	G
2	1	1676	U
2	1	1679	A
2	1	1680	U
2	1	1681	G
2	1	1686	A
2	1	1689	G
2	1	1690	A
2	1	1700	U
2	1	1702	U
2	1	1739	A
2	1	1740	C
2	1	1741	G
2	1	1752	G
2	1	1759	G
2	1	1763	A
2	1	1767	A
2	1	1768	A
2	1	1769	G
2	1	1770	A
2	1	1771	C
2	1	1777	U

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Mol	Chain	Res	Type
2	1	1785	A
2	1	1795	G
2	1	1808	G
2	1	1963	C
2	1	1969	G
2	1	1973	U
2	1	1974	G
2	1	1975	U
2	1	1976	G
2	1	1977	G
2	1	1978	A
2	1	1987	G
2	1	1988	G
2	1	1989	G
2	1	1995	G
2	1	2005	G
2	1	2007	A
2	1	2009	G
2	1	2033	U
2	1	2037	A
2	1	2055	A
2	1	2058	G
2	1	2070	G
2	1	2072	A
2	1	2073	G
2	1	2075	A
2	1	2077	A
2	1	2085	A
2	1	2095	G
2	1	2106	U
2	1	2107	A
2	1	2114	G
2	1	2120	U
2	1	2121	U
2	1	2122	G
2	1	2123	G
2	1	2134	G
2	1	2136	C
2	1	2141	A
2	1	2143	A
2	1	2156	U
2	1	2157	U

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Mol	Chain	Res	Type
2	1	2162	G
2	1	2163	U
2	1	2175	G
2	1	2178	A
2	1	2179	G
2	1	2180	A
2	1	2181	A
2	1	2182	A
2	1	2188	C
2	1	2189	C
2	1	2193	G
2	1	2196	A
2	1	2202	G
2	1	2212	A
2	1	2221	A
2	1	2222	C
2	1	2224	A
2	1	2238	U
2	1	2240	U
2	1	2250	G
2	1	2254	U
2	1	2266	A
2	1	2267	U
2	1	2268	C
2	1	2277	G
2	1	2278	C
2	1	2283	A
2	1	2302	U
2	1	2304	C
2	1	2314	C
2	1	2315	A
2	1	2321	C
2	1	2326	G
2	1	2330	G
2	1	2350	A
2	1	2351	G
2	1	2357	U
2	1	2362	C
2	1	2369	G
2	1	2373	G
2	1	2374	G
2	1	2380	G

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Mol	Chain	Res	Type
2	1	2386	G
2	1	2414	A
2	1	2429	G
2	1	2430	G
2	1	2437	G
2	1	2456	G
2	1	2460	U
2	1	2462	C
2	1	2468	G
2	1	2470	G
2	1	2482	A
2	1	2484	G
2	1	2499	A
2	1	2500	G
2	1	2512	G
2	1	2515	G
2	1	2516	U
2	1	2517	G
2	1	2519	G
2	1	2521	G
2	1	2524	G
2	1	2538	G
2	1	2540	G
2	1	2552	U
2	1	2562	G
2	1	2566	G
2	1	2568	U
2	1	2569	U
2	1	2574	C
2	1	2580	G
2	1	2581	A
2	1	2582	G
2	1	2586	G
2	1	2587	U
3	2	10	C
3	2	18	C
3	2	19	G
3	2	22	A
3	2	33	A
3	2	46	C
3	2	50	A
3	2	53	U

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Mol	Chain	Res	Type
3	2	54	A
3	2	60	G
3	2	64	G
3	2	65	A
3	2	84	A
3	2	85	G
3	2	89	G
3	2	90	A
3	2	91	C
3	2	93	A
3	2	100	A
3	2	110	G
4	3	3	C
4	3	16	C
4	3	27	U
4	3	32	U
4	3	38	G
4	3	40	G
4	3	43	U
4	3	45	A
4	3	55	G
4	3	59	G
4	3	68	U
4	3	69	U
4	3	71	U
4	3	72	G
4	3	78	U
4	3	79	U
4	3	85	A
4	3	92	A
4	3	97	U
4	3	99	G
4	3	106	G
4	3	108	U
4	3	113	U
4	3	120	A
4	3	121	U
4	3	122	G
4	3	126	A
4	3	129	A
4	3	134	C
4	3	135	G

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Mol	Chain	Res	Type
4	3	136	G
4	3	139	A
4	3	157	G
4	3	158	C
4	3	165	G
4	3	171	U
4	3	172	G
4	3	173	G
4	3	174	C
4	3	187	G
4	3	193	U
4	3	194	C
4	3	196	G
4	3	197	C
4	3	200	G
4	3	202	A
4	3	206	A
4	3	211	A
4	3	215	G
4	3	216	C
4	3	222	U
4	3	229	A
4	3	230	G
4	3	235	G
4	3	239	C
4	3	247	C
4	3	248	A
4	3	258	U
4	3	259	C
4	3	263	A
4	3	268	G
4	3	278	G
4	3	279	A
4	3	280	U
4	3	282	G
4	3	290	G
4	3	293	C
4	3	294	A
4	3	295	A
4	3	296	G
4	3	297	G
4	3	301	G

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Mol	Chain	Res	Type
4	3	302	C
4	3	303	A
4	3	304	G
4	3	312	G
4	3	317	U
4	3	329	U
4	3	330	U
4	3	331	G
4	3	333	G
4	3	341	U
4	3	343	A
4	3	350	G
4	3	351	U
4	3	352	G
4	3	354	U
4	3	355	G
4	3	357	G
4	3	358	U
4	3	359	G
4	3	364	A
4	3	372	G
4	3	376	U
4	3	378	G
4	3	379	C
4	3	380	A
4	3	384	G
4	3	385	A
4	3	397	G
4	3	398	U
4	3	399	C
4	3	402	G
4	3	404	G
4	3	405	C
4	3	414	G
4	3	415	C
4	3	418	U
4	3	419	A
4	3	422	A
4	3	433	U
4	3	434	A
4	3	437	G
4	3	440	U

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Mol	Chain	Res	Type
4	3	459	A
4	3	460	A
4	3	463	U
4	3	464	G
4	3	476	U
4	3	481	U
4	3	490	G
4	3	491	U
4	3	493	U
4	3	499	G
4	3	500	U
4	3	501	U
4	3	503	G
4	3	505	G
4	3	515	G
4	3	519	G
4	3	523	U
4	3	524	G
4	3	525	A
4	3	528	U
4	3	529	G
4	3	532	U
4	3	533	G
4	3	538	A
4	3	544	A
4	3	554	G
4	3	561	G
4	3	565	G
4	3	566	A
4	3	567	G
4	3	575	A
4	3	576	U
4	3	581	A
4	3	582	G
4	3	583	A
4	3	587	U
4	3	590	C
4	3	601	G
4	3	603	A
4	3	604	G
4	3	612	U
4	3	613	G

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Mol	Chain	Res	Type
4	3	616	C
4	3	627	A
4	3	629	G
4	3	638	A
4	3	639	A
4	3	640	G
4	3	652	G
4	3	653	A
4	3	656	A
4	3	660	A
4	3	664	C
4	3	672	U
4	3	673	A
4	3	675	C
4	3	676	G
4	3	678	U
4	3	688	G
4	3	689	C
4	3	693	A
4	3	694	A
4	3	696	C
4	3	700	G
4	3	705	C
4	3	706	U
4	3	707	G
4	3	711	G
4	3	718	U
4	3	719	G
4	3	720	U
4	3	741	U
4	3	742	U
4	3	743	G
4	3	747	A
4	3	748	U
4	3	749	G
4	3	751	G
4	3	752	G
4	3	786	U
4	3	788	G
4	3	789	A
4	3	791	G
4	3	795	U

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Mol	Chain	Res	Type
4	3	807	C
4	3	809	C
4	3	810	C
4	3	811	A
4	3	824	U
4	3	825	G
4	3	826	U
4	3	836	U
4	3	837	U
4	3	842	U
4	3	845	A
4	3	846	C
4	3	847	G
4	3	850	G
4	3	851	G
4	3	853	C
4	3	860	C
4	3	868	G
4	3	869	A
4	3	870	A
4	3	879	G
4	3	880	U
4	3	881	G
4	3	886	C
4	3	887	A
4	3	888	U
4	3	889	G
4	3	891	C
4	3	892	A
4	3	903	G
4	3	904	G
4	3	911	U
4	3	914	A
4	3	923	U
4	3	924	U
4	3	925	A
4	3	930	G
4	3	943	U
4	3	944	U
4	3	945	G
4	3	952	G
4	3	953	U

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Mol	Chain	Res	Type
4	3	956	C
4	3	959	A
4	3	962	A
4	3	963	U
4	3	964	G
4	3	967	A
4	3	975	U
4	3	977	A
4	3	979	G
4	3	987	A
4	3	988	C
4	3	990	G
4	3	998	A
4	3	1003	A
4	3	1006	G
4	3	1010	A
4	3	1015	A
4	3	1016	G
4	3	1022	U
4	3	1023	U
4	3	1028	C
4	3	1032	A
4	3	1033	G
4	3	1034	A
4	3	1035	U
4	3	1041	G
4	3	1046	G
4	3	1047	C
4	3	1048	A
4	3	1051	C
4	3	1053	C
4	3	1069	G
4	3	1070	C
4	3	1071	U
4	3	1075	G
4	3	1079	G
4	3	1084	G
4	3	1085	A
4	3	1089	A
4	3	1095	C
4	3	1101	A
4	3	1102	A

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Mol	Chain	Res	Type
4	3	1107	C
4	3	1114	A
4	3	1118	G
4	3	1119	G
4	3	1121	A
4	3	1126	U
4	3	1136	G
4	3	1137	G
4	3	1138	C
4	3	1140	G
4	3	1145	A
4	3	1146	G
4	3	1147	C
4	3	1149	G
4	3	1155	A
4	3	1160	G
4	3	1165	U
4	3	1176	C
4	3	1177	A
4	3	1179	A
4	3	1181	C
4	3	1182	G
4	3	1196	A
4	3	1201	G
4	3	1204	G
4	3	1207	C
4	3	1223	A
4	3	1235	U
4	3	1236	G
4	3	1237	A
4	3	1240	G
4	3	1244	G
4	3	1246	U
4	3	1255	A
4	3	1256	G
4	3	1259	G
4	3	1261	A
4	3	1265	U
4	3	1266	G
4	3	1268	C
4	3	1278	A
4	3	1279	G

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Mol	Chain	Res	Type
4	3	1281	A
4	3	1282	C
4	3	1291	G
4	3	1292	G
4	3	1293	A
4	3	1295	C
4	3	1296	A
4	3	1297	G
4	3	1298	U
4	3	1299	A
4	3	1300	U

All (38) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	100	U
2	1	128	A
2	1	133	A
2	1	232	G
2	1	552	A
2	1	609	C
2	1	652	G
2	1	988	U
2	1	1007	G
2	1	1031	G
2	1	1243	G
2	1	1336	G
2	1	1375	U
2	1	1376	A
2	1	1496	U
2	1	1501	G
2	1	1575	U
2	1	1592	U
2	1	1647	A
2	1	1738	A
2	1	2180	A
2	1	2251	A
2	1	2551	G
2	1	2567	A
2	1	2568	U
4	3	68	U
4	3	85	A

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Mol	Chain	Res	Type
4	3	121	U
4	3	133	G
4	3	199	G
4	3	329	U
4	3	330	U
4	3	523	U
4	3	564	C
4	3	888	U
4	3	891	C
4	3	1088	G
4	3	1137	G

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
79	AMP	L9	201	-	22,25,25	0.62	0	25,38,38	0.72	1 (4%)
80	SPD	N8	201	-	9,9,9	0.41	0	8,8,8	1.18	1 (12%)

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
79	AMP	L9	201	-	-	3/6/26/26	0/3/3/3
80	SPD	N8	201	-	-	3/7/7/7	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
80	N8	201	SPD	C4-C5-N6	-2.63	105.03	112.14
79	L9	201	AMP	C5-C6-N6	2.13	123.59	120.35

There are no chirality outliers.

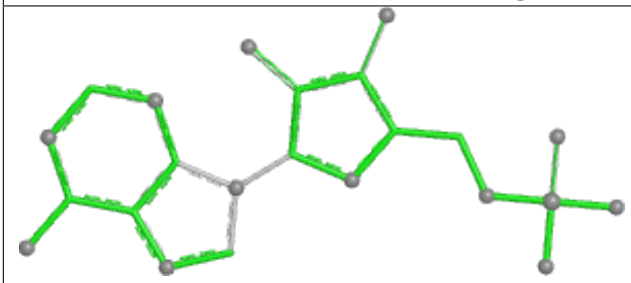
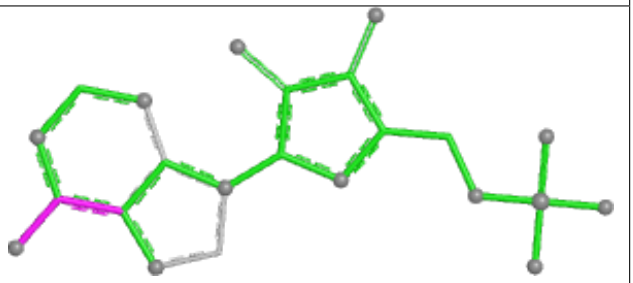
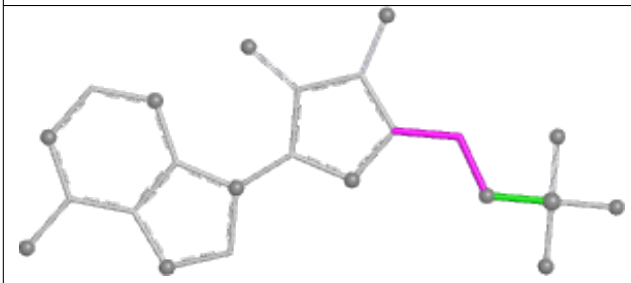
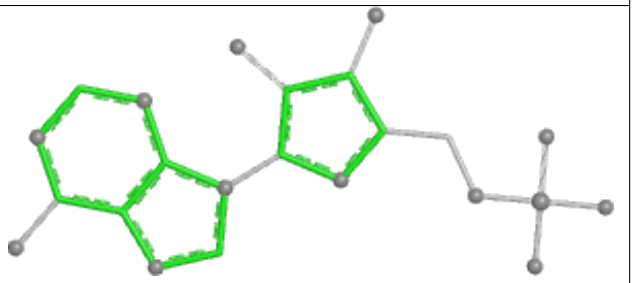
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	L9	201	AMP	O4'-C4'-C5'-O5'
79	L9	201	AMP	C3'-C4'-C5'-O5'
80	N8	201	SPD	N6-C7-C8-C9
80	N8	201	SPD	C4-C5-N6-C7
80	N8	201	SPD	C2-C3-C4-C5
79	L9	201	AMP	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

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

Ligand AMP L9 201	
 Bond lengths	 Bond angles
 Torsions	 Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

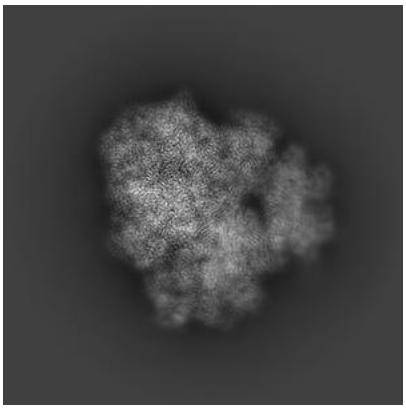
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13936. These allow visual inspection of the internal detail of the map and identification of artifacts.

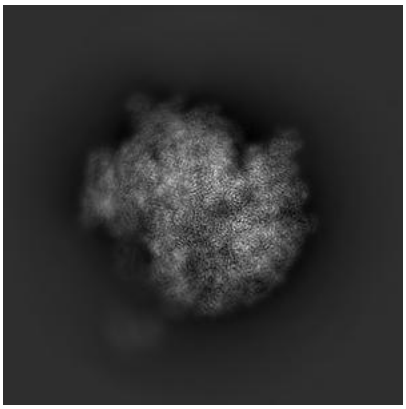
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

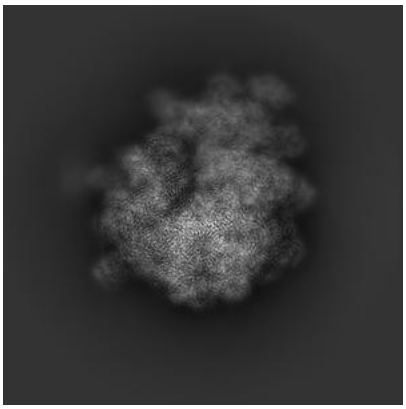
6.1.1 Primary map



X

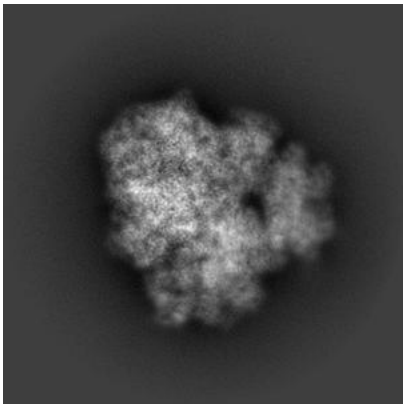


Y

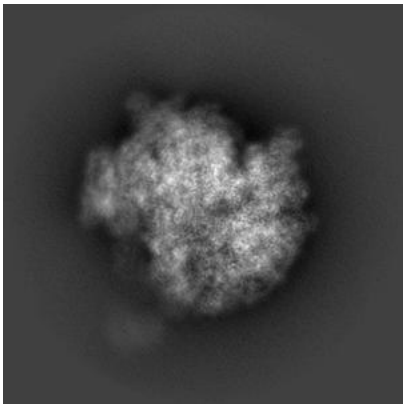


Z

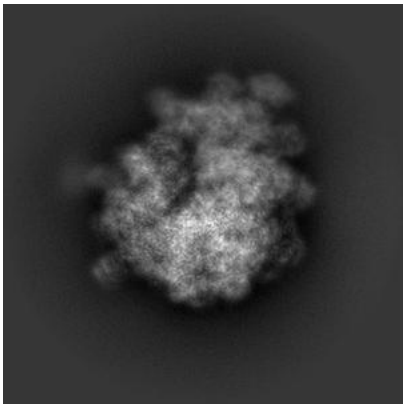
6.1.2 Raw map



X



Y

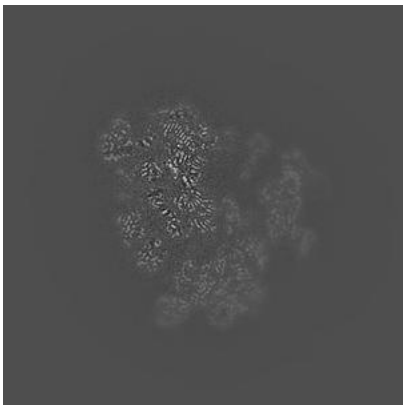


Z

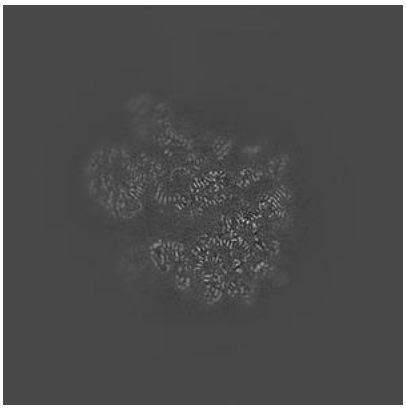
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

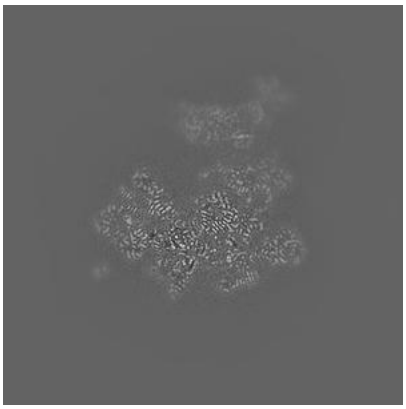
6.2.1 Primary map



X Index: 256

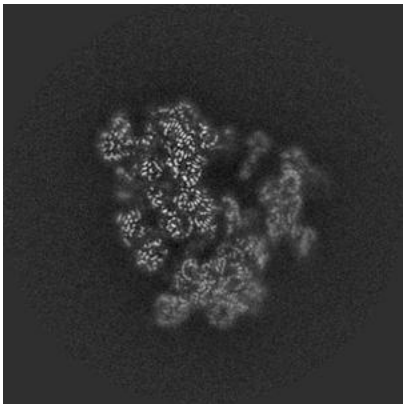


Y Index: 256

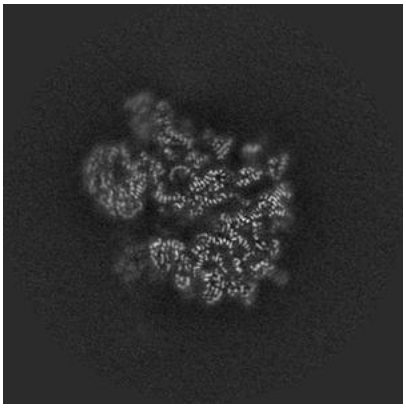


Z Index: 256

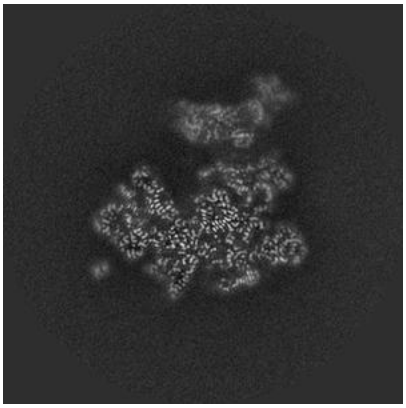
6.2.2 Raw map



X Index: 256



Y Index: 256

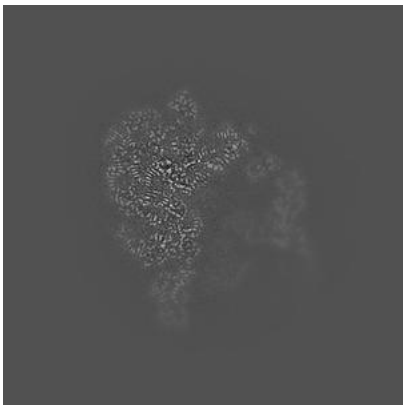


Z Index: 256

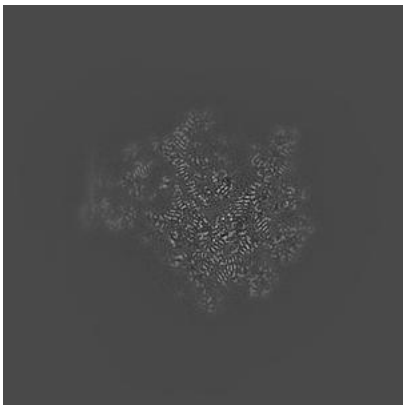
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

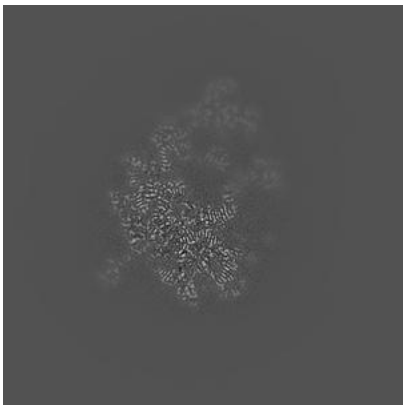
6.3.1 Primary map



X Index: 231

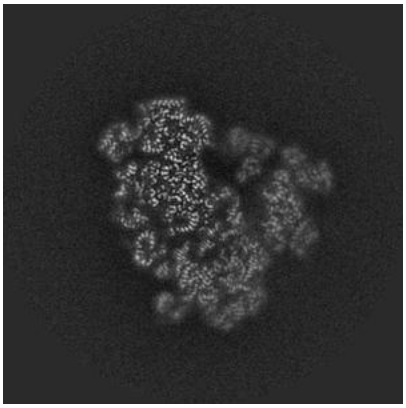


Y Index: 219

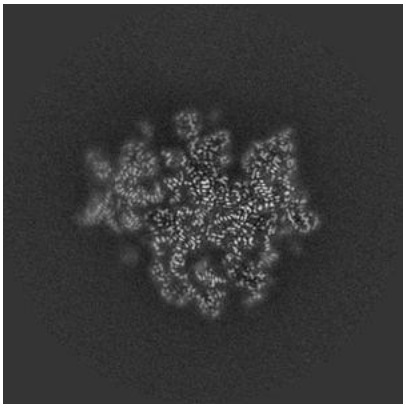


Z Index: 301

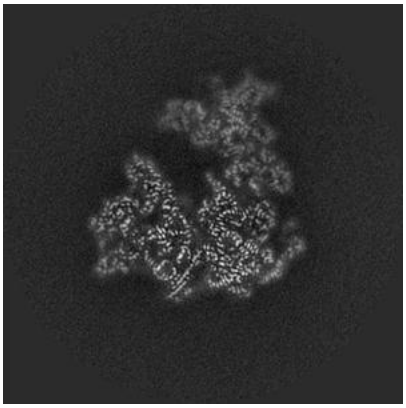
6.3.2 Raw map



X Index: 267



Y Index: 233

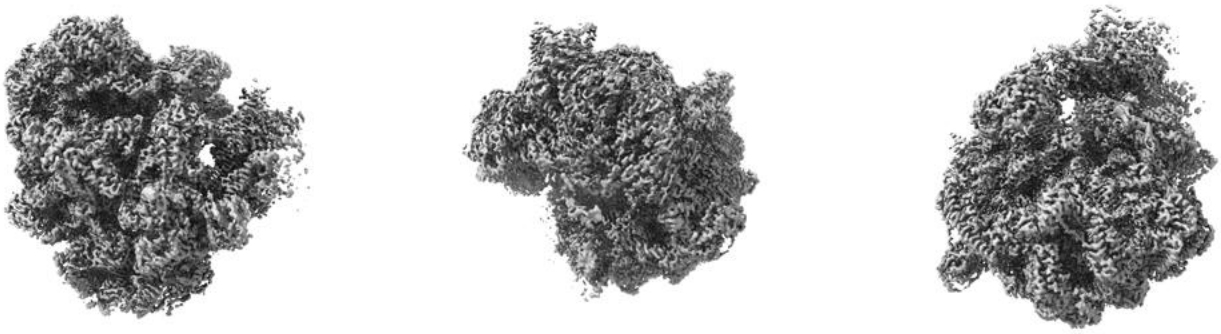


Z Index: 272

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

6.4 Orthogonal surface views (i)

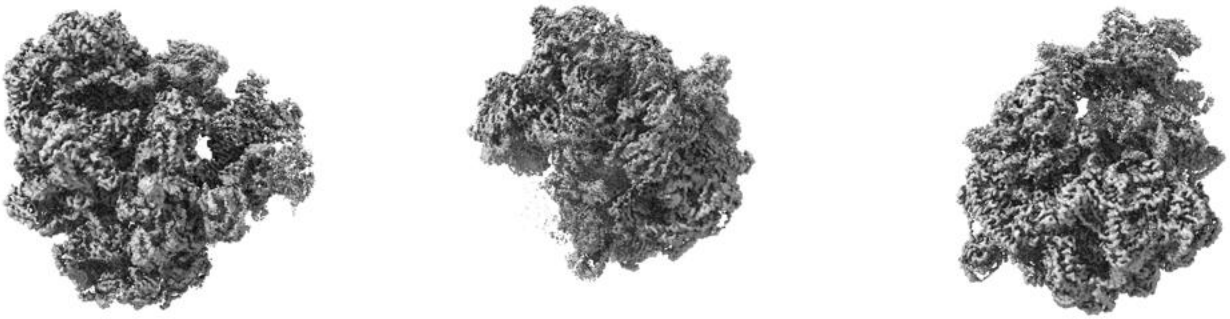
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

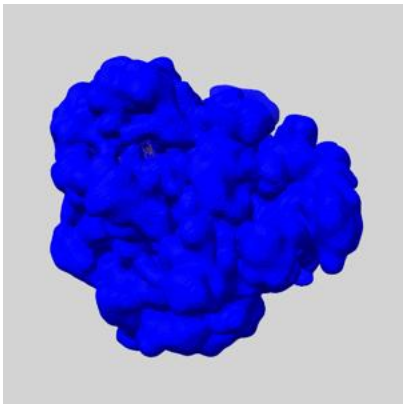
6.5 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

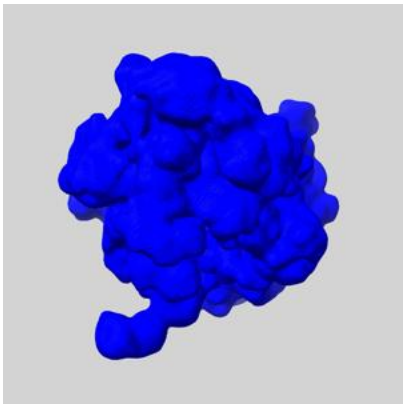
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

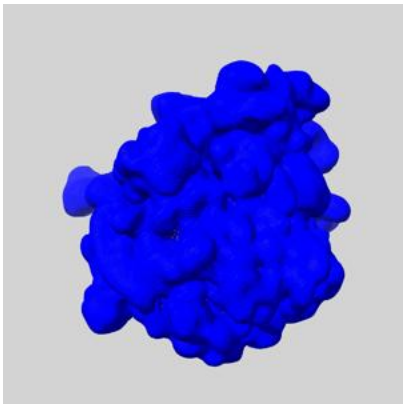
6.5.1 emd_13936_msk_1.map (i)



X



Y

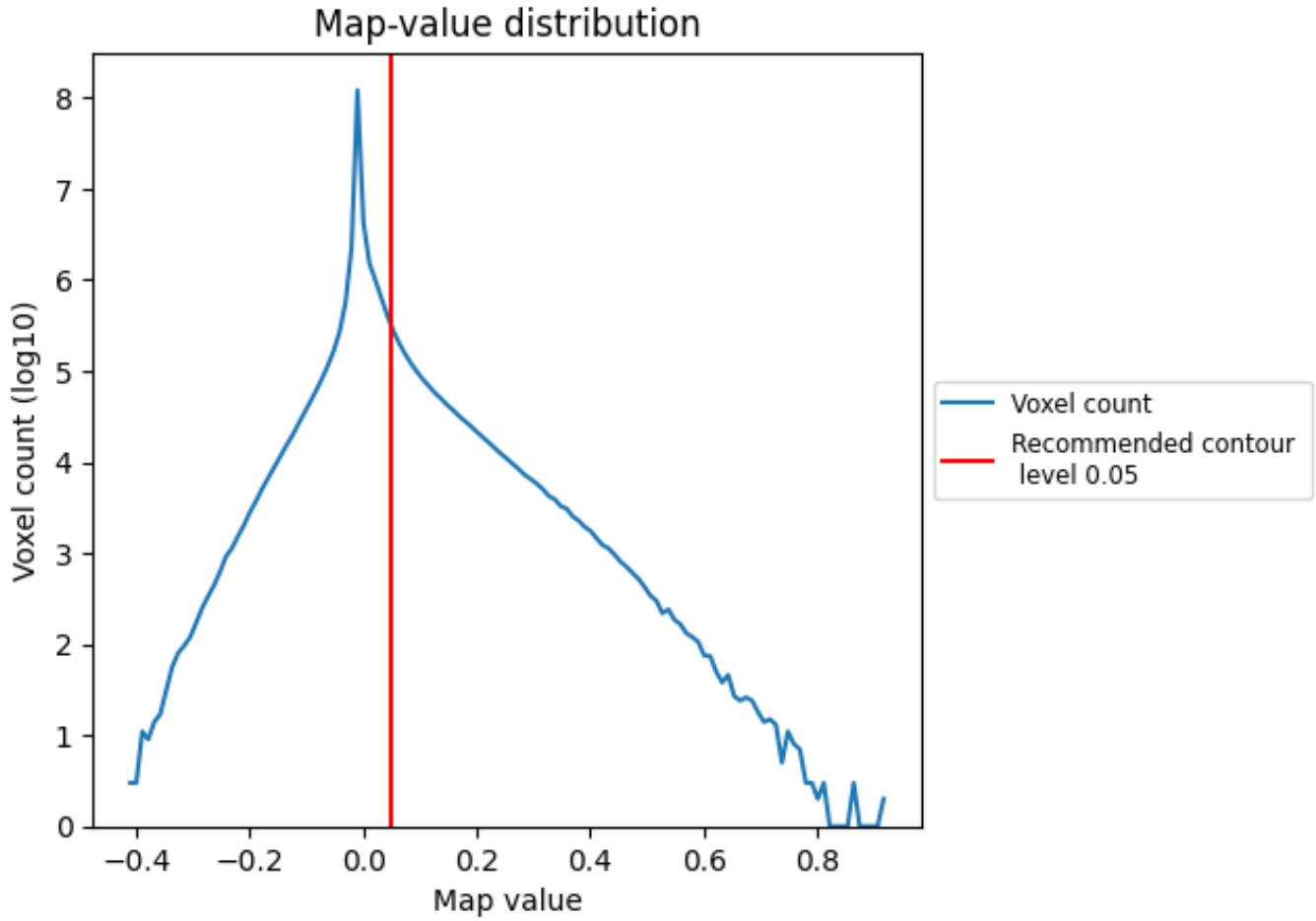


Z

7 Map analysis

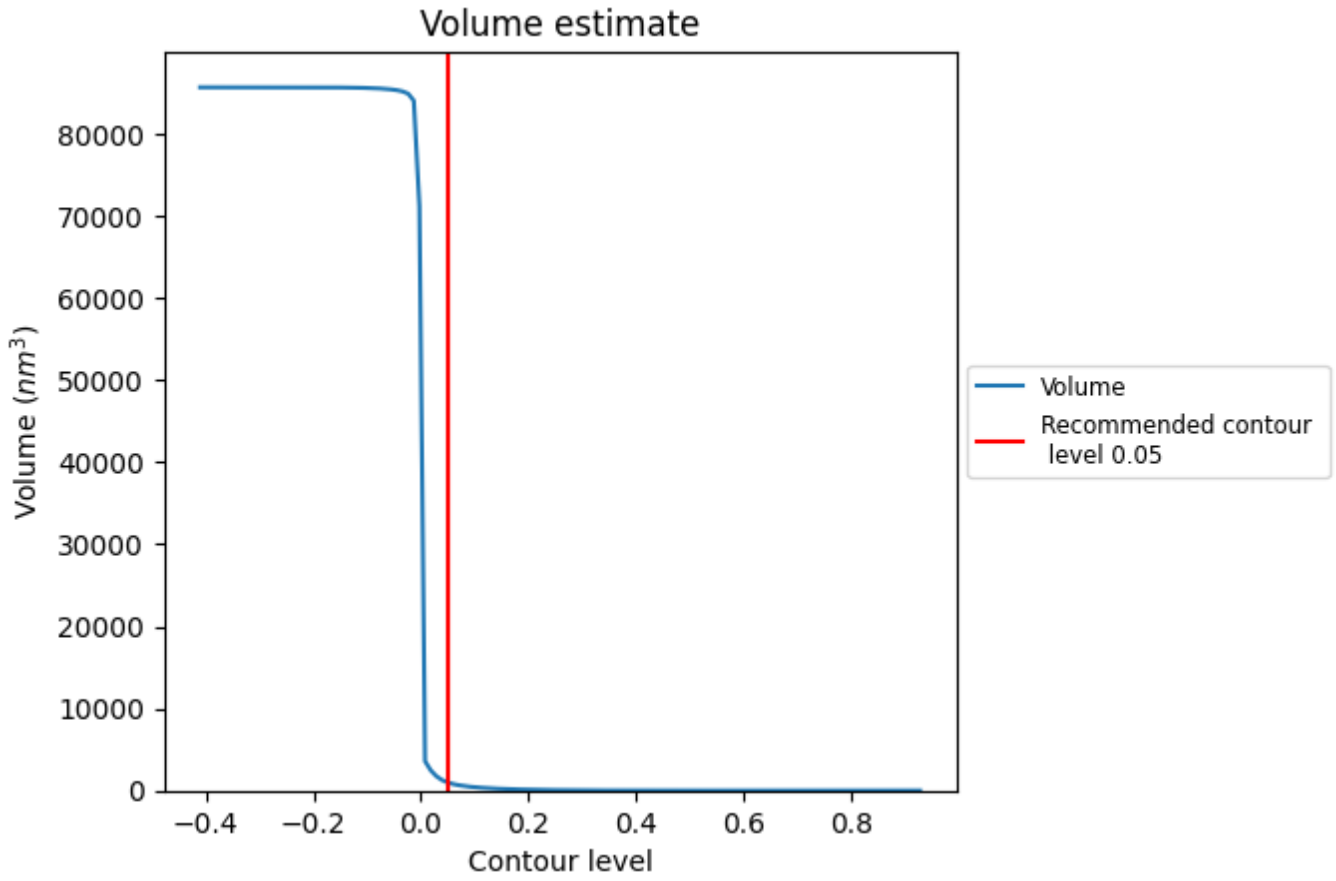
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

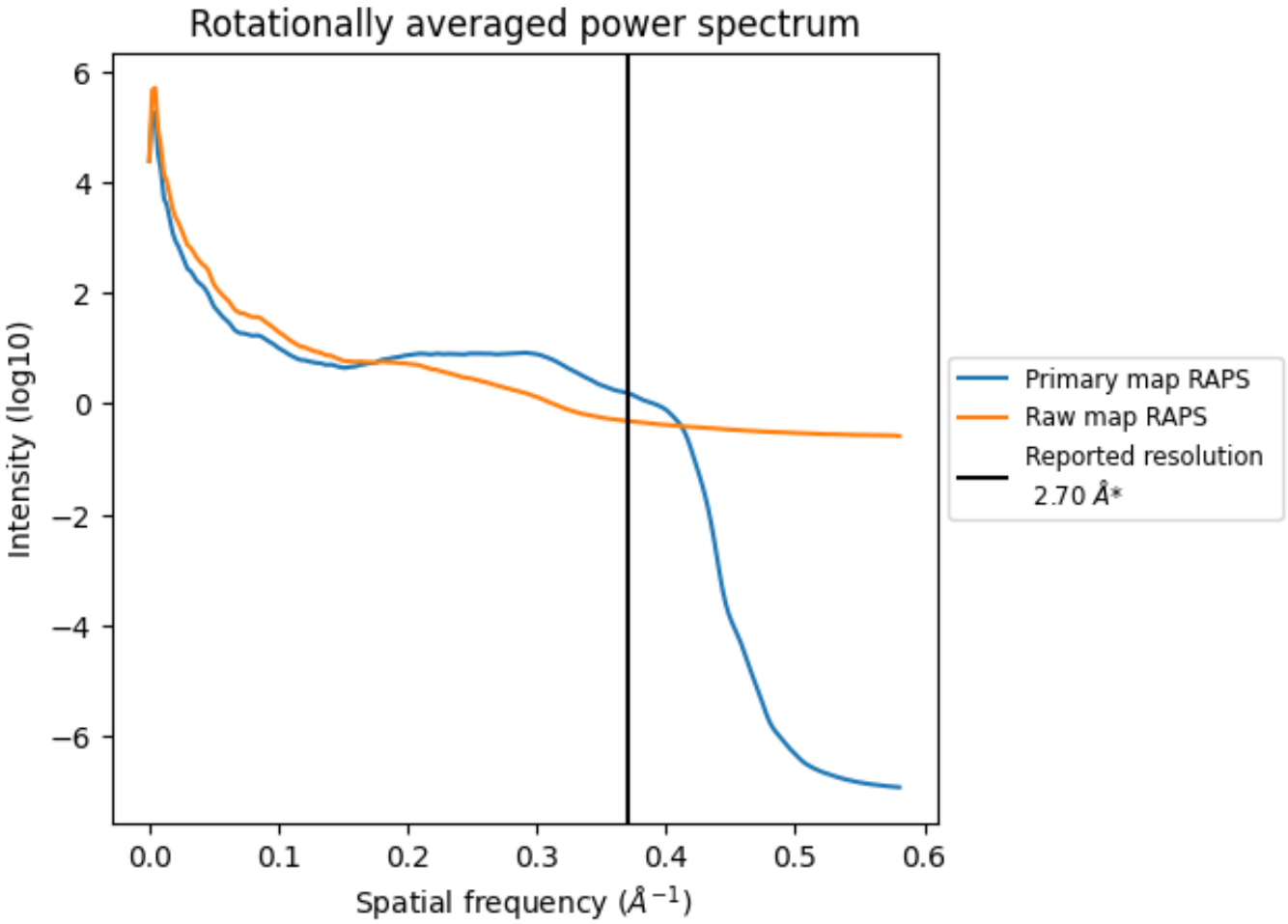
7.2 Volume estimate



The volume at the recommended contour level is 982 nm^3; this corresponds to an approximate mass of 887 kDa.

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

7.3 Rotationally averaged power spectrum (i)

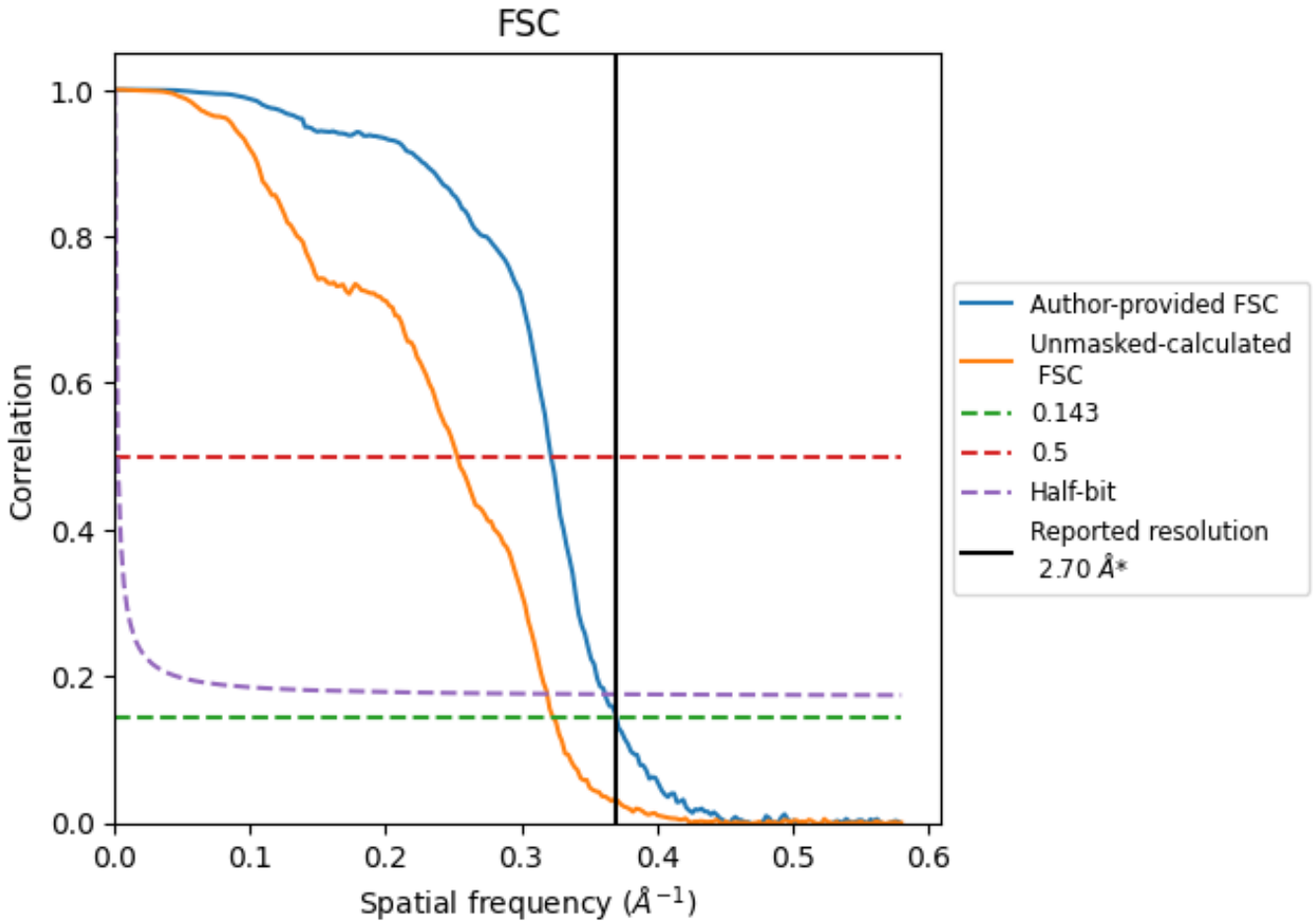


*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8.2 Resolution estimates (i)

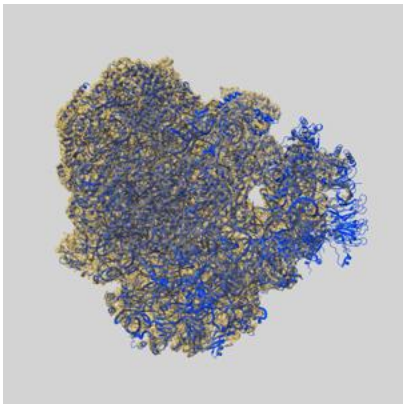
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.11	2.76
Unmasked-calculated*	3.09	3.95	3.13

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.09 differs from the reported value 2.7 by more than 10 %

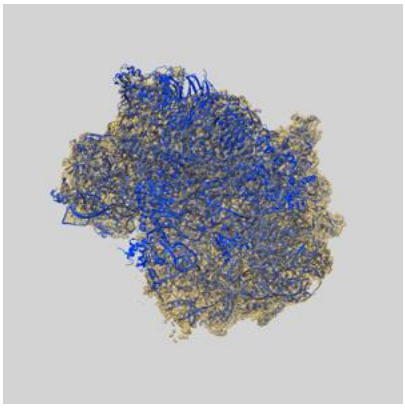
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13936 and PDB model 7QEP. Per-residue inclusion information can be found in section 3 on page 19.

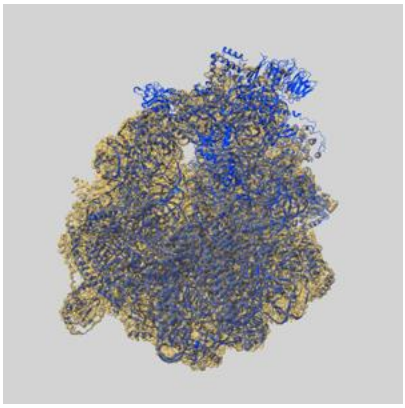
9.1 Map-model overlay



X



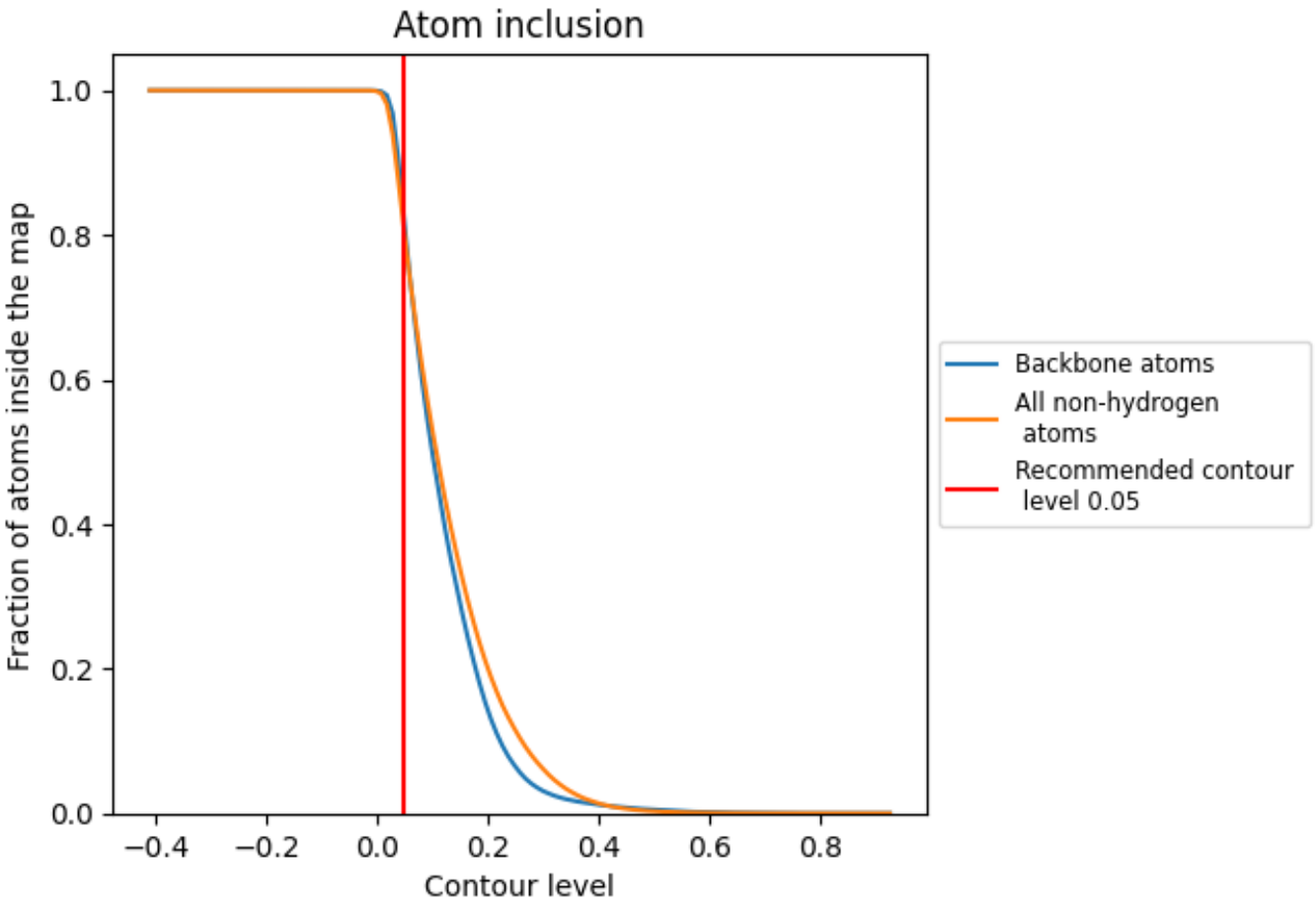
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.