



Full wwPDB EM Validation Report ⓘ

Jun 19, 2026 – 07:21 am BST

PDB ID : 7NSJ / pdb_00007nsj
EMDB ID : EMD-12569
Title : 55S mammalian mitochondrial ribosome with tRNA(P/P) and tRNA(E*)
Authors : Kummer, E.; Schubert, K.; Ban, N.
Deposited on : 2021-03-07
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

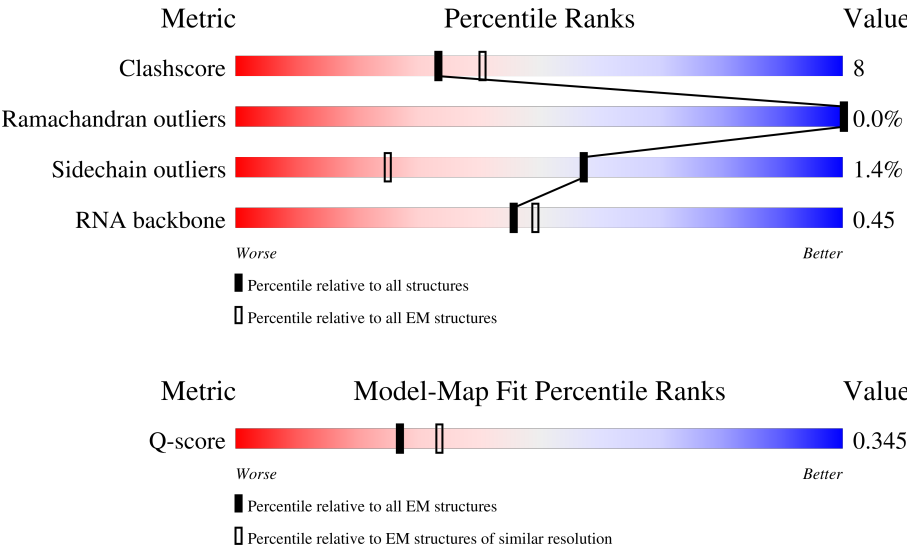
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 Å.

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



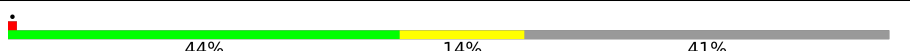
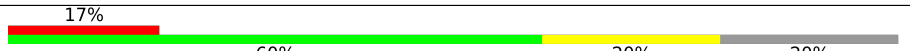
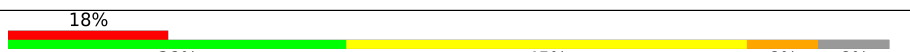
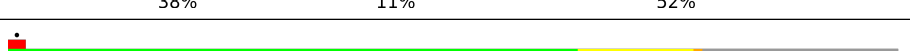
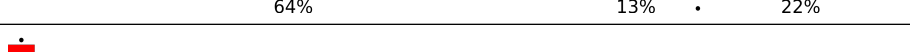
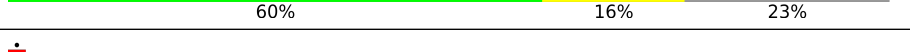
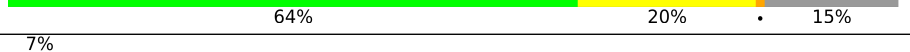
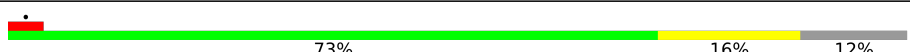
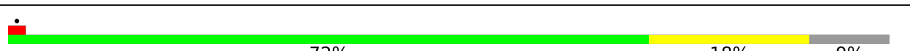
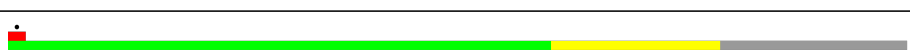
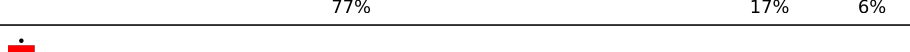
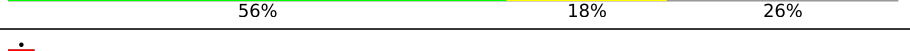
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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

Mol	Chain	Length	Quality of chain
1	B0	148	
2	B1	256	
3	B2	252	

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Mol	Chain	Length	Quality of chain
4	B3	161	
5	B4	126	
6	B5	188	
7	B6	65	
8	BB	73	
9	B7	95	
10	BD	306	
11	BE	399	
12	BF	294	
13	BI	268	
14	BJ	262	
15	BK	192	
16	BN	178	
17	BO	145	
18	BP	296	
19	BQ	251	
20	BR	169	
21	BS	180	
22	BT	292	
23	BU	149	
24	BV	209	
25	BW	210	
26	BX	150	
27	BY	216	
28	Ba	423	

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Mol	Chain	Length	Quality of chain
29	Bb	380	
30	Bc	334	
31	Bd	206	
32	Be	135	
33	Bf	142	
34	Bg	159	
35	Bh	332	
36	B8	188	
37	Bi	306	
38	Bj	279	
39	Bk	269	
40	Bl	166	
41	Bm	198	
42	Bn	128	
43	Bo	124	
44	Bp	112	
45	Bq	138	
46	Bt	102	
47	Bu	205	
48	Bv	222	
49	Bw	433	
50	Bx	196	
51	AA	962	
52	B9	100	
53	BA	1571	

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Mol	Chain	Length	Quality of chain
54	AB	289	
55	AC	167	
56	AE	430	
57	AF	276	
58	AG	242	
59	AI	397	
60	AJ	200	
61	AK	196	
62	AL	139	
63	AN	128	
64	AO	239	
65	AP	135	
66	AQ	130	
67	AR	143	
68	AU	87	
69	AZ	18	
70	Aa	382	
71	Ab	190	
72	Ac	173	
73	Ad	205	
74	Ae	455	
75	Af	188	
76	Ag	410	
77	Ah	387	
78	Ai	106	

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Mol	Chain	Length	Quality of chain
79	Aj	218	
80	Ak	325	
81	Am	118	
82	An	199	
83	Ao	690	
84	Ap	258	
85	CL	198	
85	DL	198	
85	EL	198	
85	FL	198	
85	GL	198	
85	HL	198	
86	AV	71	
86	AY	71	
87	AX	6	

2 Entry composition

There are 93 unique types of molecules in this entry. The entry contains 174837 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Mitochondrial ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B0	110	Total	C	N	O	S	0	0
			857	553	156	145	3		

- Molecule 2 is a protein called Mitochondrial ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B1	244	Total	C	N	O	S	0	0
			2036	1315	363	353	5		

- Molecule 3 is a protein called Mitochondrial ribosomal protein L47.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B2	179	Total	C	N	O	S	0	0
			1548	992	290	260	6		

- Molecule 4 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B3	118	Total	C	N	O	S	0	0
			968	622	178	165	3		

- Molecule 5 is a protein called bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B4	62	Total	C	N	O	S	0	0
			474	296	94	81	3		

- Molecule 6 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B5	110	Total	C	N	O	S	0	0
			902	553	181	162	6		

- Molecule 7 is a protein called bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B6	52	Total	C	N	O	S	0	0
			425	274	78	71	2		

- Molecule 8 is a RNA chain called CP tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BB	67	Total	C	N	O	P	0	0
			1427	640	261	459	67		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	71	C	-	insertion	GB 76262549

- Molecule 9 is a protein called Mitochondrial ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B7	46	Total	C	N	O	S	0	0
			387	239	89	58	1		

- Molecule 10 is a protein called uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BD	240	Total	C	N	O	S	0	0
			1860	1160	371	319	10		

- Molecule 11 is a protein called ICT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BE	307	Total	C	N	O	S	0	0
			2420	1554	426	430	10		

- Molecule 12 is a protein called Mitochondrial ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BF	250	Total	C	N	O	S	0	0
			2011	1294	367	344	6		

- Molecule 13 is a protein called Mitochondrial ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	BI	98	Total	C	N	O		
			805	509	155	141	0	0

- Molecule 14 is a protein called Mitochondrial ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BJ	212	Total	C	N	O	S		
			1705	1100	306	290	9	0	0

- Molecule 15 is a protein called Mitochondrial ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BK	176	Total	C	N	O	S		
			1303	830	236	235	2	0	0

- Molecule 16 is a protein called uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BN	177	Total	C	N	O	S		
			1444	926	258	253	7	0	0

- Molecule 17 is a protein called uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BO	115	Total	C	N	O	S		
			896	562	176	154	4	0	0

- Molecule 18 is a protein called uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BP	288	Total	C	N	O	S		
			2312	1473	430	403	6	0	0

- Molecule 19 is a protein called uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BQ	222	Total	C	N	O	S		
			1803	1156	331	306	10	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	237	HIS	TYR	conflict	UNP F1RI89

- Molecule 20 is a protein called bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BR	153	Total	C	N	O	S	0	0
			1240	777	236	222	5		

- Molecule 21 is a protein called Mitochondrial ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BS	143	Total	C	N	O	S	0	0
			1168	733	227	204	4		

- Molecule 22 is a protein called Mitochondrial ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BT	230	Total	C	N	O	S	0	0
			1890	1215	325	341	9		

- Molecule 23 is a protein called Mitochondrial ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BU	140	Total	C	N	O	S	0	0
			1159	732	239	185	3		

- Molecule 24 is a protein called Mitochondrial ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BV	155	Total	C	N	O	S	0	0
			1231	789	219	219	4		

- Molecule 25 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BW	166	Total	C	N	O	S	0	0
			1374	876	258	234	6		

- Molecule 26 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BX	149	Total	C	N	O	S	0	0
			1181	752	227	200	2		

- Molecule 27 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BY	206	Total	C	N	O	S	0	0
			1678	1056	308	309	5		

- Molecule 28 is a protein called Mitochondrial ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ba	393	Total	C	N	O	S	0	0
			3173	2040	556	565	12		

- Molecule 29 is a protein called Mitochondrial ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Bb	354	Total	C	N	O	S	0	0
			2952	1876	542	525	9		

- Molecule 30 is a protein called Mitochondrial ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bc	295	Total	C	N	O	S	0	0
			2408	1541	410	441	16		

- Molecule 31 is a protein called Mitochondrial ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bd	141	Total	C	N	O	S	0	0
			1183	746	216	220	1		

- Molecule 32 is a protein called Mitochondrial ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Be	122	Total	C	N	O	S	0	0
			972	628	168	173	3		

- Molecule 33 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bf	108	Total	C	N	O	S	0	0
			827	519	154	150	4		

- Molecule 34 is a protein called Mitochondrial ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bg	148	Total	C	N	O	S	0	0
			1167	727	225	212	3		

- Molecule 35 is a protein called mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bh	289	Total	C	N	O	S	0	0
			2319	1486	399	426	8		

- Molecule 36 is a protein called Mitochondrial ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B8	95	Total	C	N	O	S	0	0
			833	539	163	129	2		

- Molecule 37 is a protein called Mitochondrial ribosomal protein L45.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bi	260	Total	C	N	O	S	0	0
			2138	1370	379	379	10		

- Molecule 38 is a protein called Mitochondrial ribosomal protein L46.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bj	228	Total	C	N	O	S	0	0
			1872	1197	324	345	6		

- Molecule 39 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bk	165	Total	C	N	O	S	0	0
			1327	848	229	245	5		

- Molecule 40 is a protein called Mrpl34.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bl	133	Total	C	N	O	S	0	0
			1097	709	192	194	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bl	59	ARG	LYS	conflict	UNP A0A0R4J8D6

- Molecule 41 is a protein called Mitochondrial ribosomal protein L50.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bm	109	Total	C	N	O	S	0	0
			893	568	160	162	3		

- Molecule 42 is a protein called Mitochondrial ribosomal protein L51.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Bn	97	Total	C	N	O	S	0	0
			837	539	166	128	4		

- Molecule 43 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bo	97	Total	C	N	O	S	0	0
			772	481	148	141	2		

- Molecule 44 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Bp	97	Total	C	N	O	S	0	0
			742	459	143	134	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bp	12	ALA	SER	conflict	UNP A0A341D604
Bp	107	SER	GLY	conflict	UNP A0A341D604

- Molecule 45 is a protein called mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bq	80	Total	C	N	O	S	0	0
			672	431	123	116	2		

- Molecule 46 is a protein called Mitochondrial ribosomal protein L57.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Bt	94	Total	C	N	O	S	0	0
			780	485	168	126	1		

- Molecule 47 is a protein called mL62 (ICT1).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Bu	151	Total	C	N	O	S	0	0
			1198	738	233	222	5		

- Molecule 48 is a protein called mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Bv	135	Total	C	N	O	S	0	0
			1131	692	223	211	5		

- Molecule 49 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Bw	387	Total	C	N	O	S	0	0
			3126	2011	548	555	12		

- Molecule 50 is a protein called Mitochondrial ribosomal protein S18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Bx	162	Total	C	N	O	S	0	0
			1325	845	249	224	7		

- Molecule 51 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AA	960	Total	C	N	O	P	0	0
			20411	9162	3708	6581	960		

- Molecule 52 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B9	38	Total	C	N	O	S	0	0
			335	214	70	47	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BA	1544	Total	C	N	O	P	0	0
			32844	14750	5972	10578	1544		

- Molecule 54 is a protein called Mitochondrial ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AB	220	Total	C	N	O	S	0	0
			1762	1126	326	304	6		

- Molecule 55 is a protein called Mitochondrial ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AC	132	Total	C	N	O	S	0	0
			1075	695	195	181	4		

- Molecule 56 is a protein called 28S ribosomal protein S5, mitochondrial isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AE	343	Total	C	N	O	S	0	0
			2732	1707	527	487	11		

- Molecule 57 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AF	122	Total	C	N	O	S	0	0
			981	620	178	177	6		

- Molecule 58 is a protein called Mitochondrial ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AG	208	Total	C	N	O	S	0	0
			1721	1097	314	299	11		

- Molecule 59 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AI	328	Total	C	N	O	S	0	0
			2650	1678	478	481	13		

- Molecule 60 is a protein called Mitochondrial ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AJ	140	Total	C	N	O	S	0	0
			1155	746	197	208	4		

- Molecule 61 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AK	137	Total	C	N	O	S	0	0
			1007	631	193	180	3		

- Molecule 62 is a protein called Mitochondrial ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AL	109	Total	C	N	O	S	0	0
			840	524	172	138	6		

- Molecule 63 is a protein called Mitochondrial ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AN	101	Total	C	N	O	S	0	0
			858	534	174	144	6		

- Molecule 64 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AO	175	Total	C	N	O	S	0	0
			1448	919	272	248	9		

- Molecule 65 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AP	117	Total	C	N	O	S	0	0
			932	588	184	155	5		

- Molecule 66 is a protein called uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AQ	112	Total	C	N	O	S	0	0
			875	568	153	151	3		

- Molecule 67 is a protein called Mitochondrial ribosomal protein S18C.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AR	97	Total	C	N	O	S	0	0
			784	507	132	138	7		

- Molecule 68 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AU	86	Total	C	N	O	S	0	0
			734	453	148	125	8		

- Molecule 69 is a protein called unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	AZ	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 70 is a protein called Mitochondrial ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Aa	292	Total	C	N	O	S	0	0
			2378	1518	409	442	9		

- Molecule 71 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ab	135	Total	C	N	O	S	0	0
			1101	709	199	192	1		

- Molecule 72 is a protein called Mitochondrial ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ac	169	Total	C	N	O	S	0	0
			1367	876	236	245	10		

- Molecule 73 is a protein called Mitochondrial ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ad	177	Total	C	N	O	S	0	0
			1467	904	288	273	2		

- Molecule 74 is a protein called Mitochondrial ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ae	388	Total	C	N	O	S	0	0
			3109	1971	535	589	14		

- Molecule 75 is a protein called Mitoribosomal protein ms28, mrps28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Af	99	Total	C	N	O	S	0	0
			778	494	134	146	4		

- Molecule 76 is a protein called Death associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	353	Total	C	N	O	S	0	0
			2875	1837	515	513	10		

- Molecule 77 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ah	120	Total	C	N	O	S	0	0
			1015	659	168	185	3		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ah	133	THR	ALA	conflict	UNP A0A4X1SQW0
Ah	179	ARG	LYS	conflict	UNP A0A4X1SQW0
Ah	180	UNK	ALA	conflict	UNP A0A4X1SQW0

- Molecule 78 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Ai	99	Total	C	N	O	S	0	0
			824	522	156	143	3		

- Molecule 79 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Aj	213	Total	C	N	O	S	0	0
			1788	1131	338	311	8		

- Molecule 80 is a protein called Mitochondrial ribosomal protein S35.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Ak	275	Total	C	N	O	S	0	0
			2222	1414	380	419	9		

- Molecule 81 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Am	116	Total	C	N	O	S	0	0
			930	577	185	160	8		

- Molecule 82 is a protein called Aurora kinase A interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	An	72	Total	C	N	O	S	0	0
			639	407	139	92	1		

- Molecule 83 is a protein called Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,mS39,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Ao	572	Total	C	N	O	S	0	0
			4527	2899	770	834	24		

- Molecule 84 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Ap	190	Total	C	N	O	S	0	0
			1564	991	292	273	8		

- Molecule 85 is a protein called Mitochondrial ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	CL	45	Total	C	N	O	0	0
			317	203	52	62		

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Mol	Chain	Residues	Atoms				AltConf	Trace
85	DL	27	Total	C	N	O	0	0
			213	137	33	43		
85	EL	28	Total	C	N	O	0	0
			222	143	35	44		
85	FL	27	Total	C	N	O	0	0
			213	137	33	43		
85	GL	27	Total	C	N	O	0	0
			213	137	33	43		
85	HL	26	Total	C	N	O	0	0
			204	131	32	41		

- Molecule 86 is a RNA chain called tRNA(P/P) and tRNA(E*).

Mol	Chain	Residues	Atoms					AltConf	Trace
86	AV	71	Total	C	N	O	P	0	0
			1419	640	147	562	70		
86	AY	71	Total	C	N	O	P	0	0
			1419	640	147	562	70		

- Molecule 87 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	AX	6	Total	C	N	O	P	0	0
			120	54	12	48	6		

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	B3	1	Total	Mg	0
			1	1	
88	BB	1	Total	Mg	0
			1	1	
88	BD	3	Total	Mg	0
			3	3	
88	BE	1	Total	Mg	0
			1	1	
88	BJ	1	Total	Mg	0
			1	1	
88	BP	2	Total	Mg	0
			2	2	
88	BQ	1	Total	Mg	0
			1	1	

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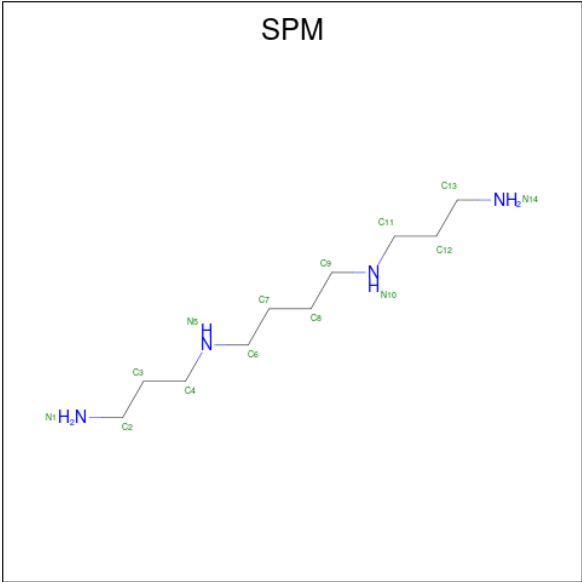
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Mol	Chain	Residues	Atoms		AltConf
88	Be	2	Total 2	Mg 2	0
88	Bl	1	Total 1	Mg 1	0
88	Bt	1	Total 1	Mg 1	0
88	AA	102	Total 102	Mg 102	0
88	BA	203	Total 203	Mg 203	0
88	AB	1	Total 1	Mg 1	0
88	AL	1	Total 1	Mg 1	0
88	Ag	1	Total 1	Mg 1	0
88	Am	1	Total 1	Mg 1	0
88	An	1	Total 1	Mg 1	0

- Molecule 89 is ZINC ION (CCD ID: ZN) (formula: Zn).

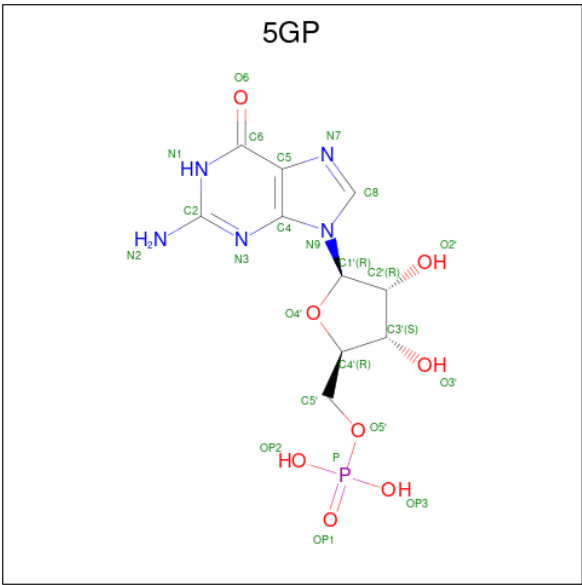
Mol	Chain	Residues	Atoms		AltConf
89	B5	1	Total 1	Zn 1	0
89	Bx	1	Total 1	Zn 1	0
89	B9	1	Total 1	Zn 1	0
89	AR	1	Total 1	Zn 1	0
89	Ac	1	Total 1	Zn 1	0
89	Ap	1	Total 1	Zn 1	0

- Molecule 90 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄).



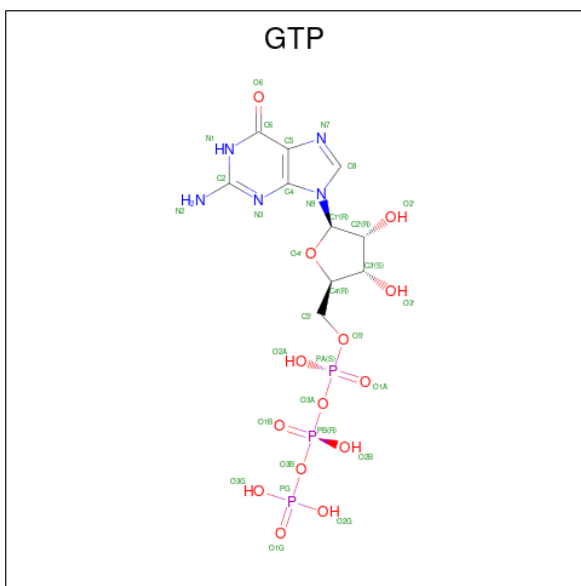
Mol	Chain	Residues	Atoms			AltConf
90	AA	1	Total	C	N	0
			14	10	4	
90	BA	1	Total	C	N	0
			14	10	4	
90	BA	1	Total	C	N	0
			14	10	4	

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: C₁₀H₁₄N₅O₈P).



Mol	Chain	Residues	Atoms					AltConf
91	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 92 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

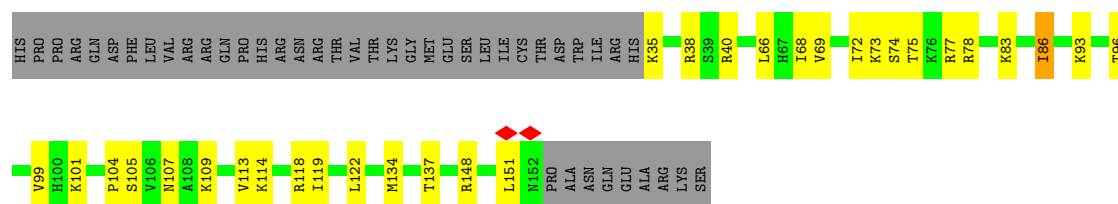


Mol	Chain	Residues	Atoms					AltConf
92	Ag	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 93 is water.

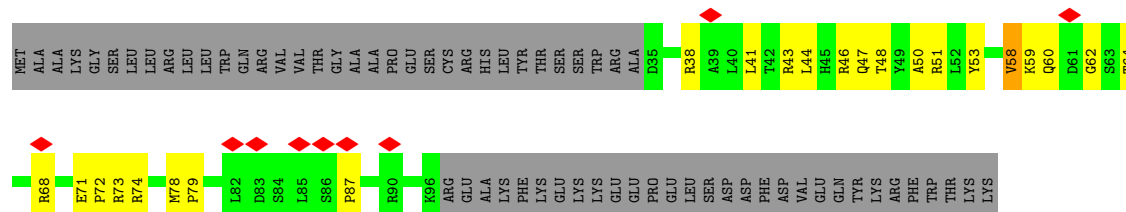
Mol	Chain	Residues	Atoms		AltConf
93	Ag	3	Total	O	0
			3	3	

Chain B3: 

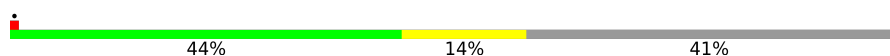


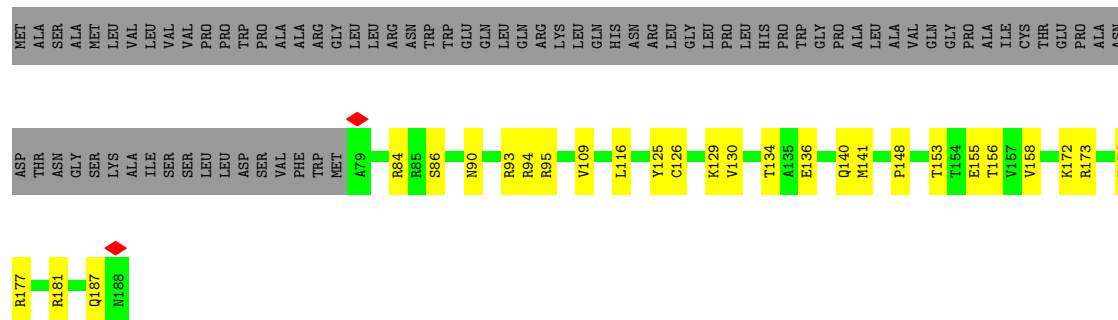
• Molecule 5: bL31m

Chain B4: 



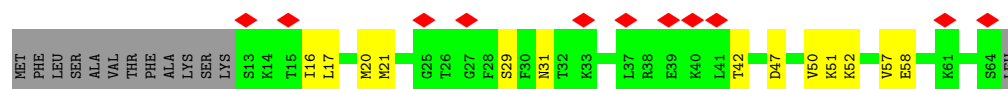
• Molecule 6: bL32m

Chain B5: 



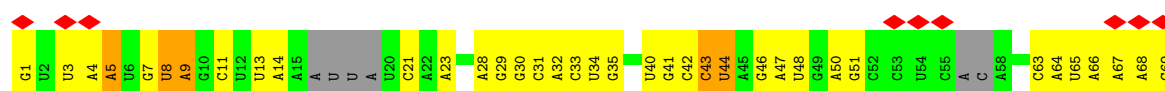
• Molecule 7: bL33m

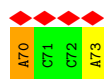
Chain B6: 



• Molecule 8: CP tRNA^{Phe}

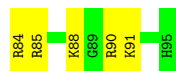
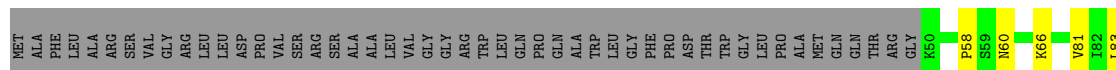
Chain BB: 





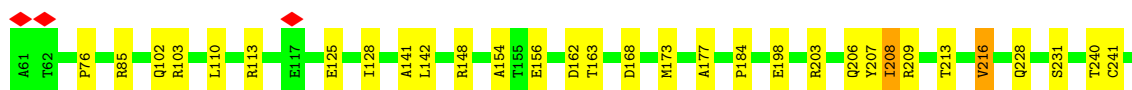
• Molecule 9: Mitochondrial ribosomal protein L34

Chain B7: 38% 11% 52%



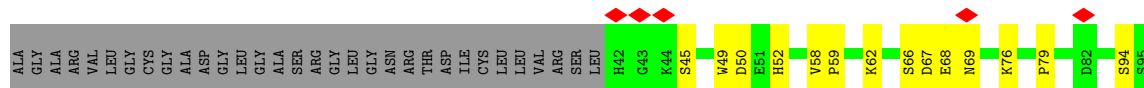
• Molecule 10: uL2m

Chain BD: 64% 13% 22%



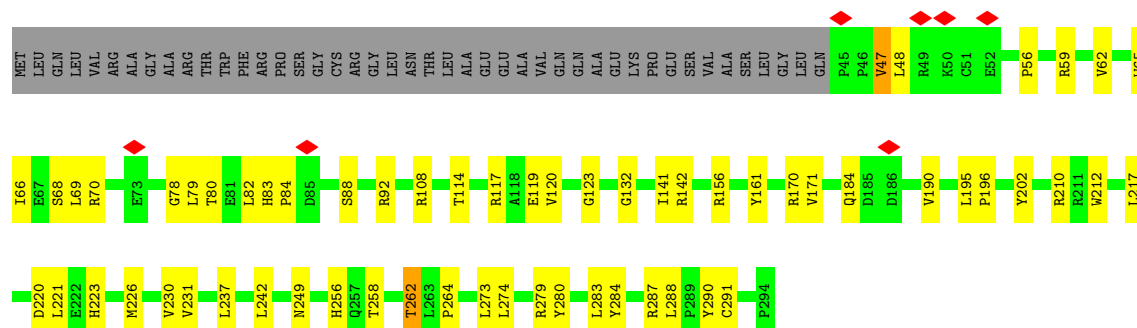
• Molecule 11: ICT1

Chain BE: 60% 16% 23%

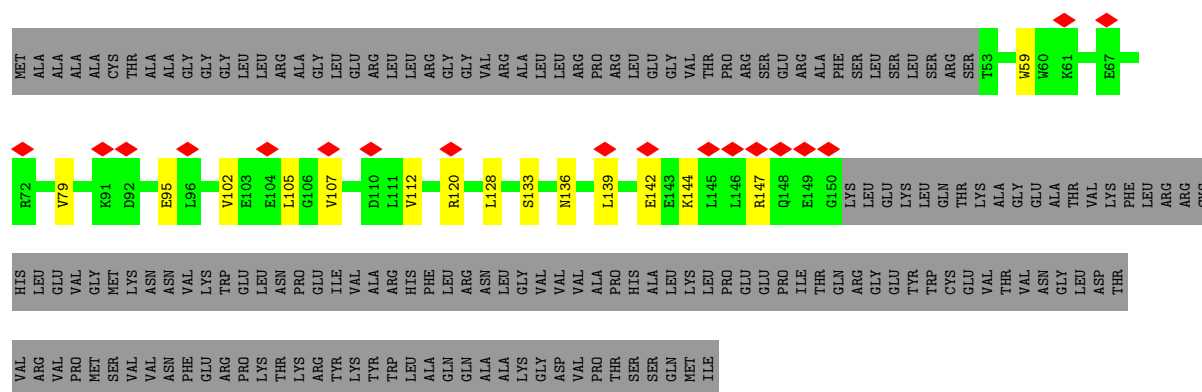


• Molecule 12: Mitochondrial ribosomal protein L4

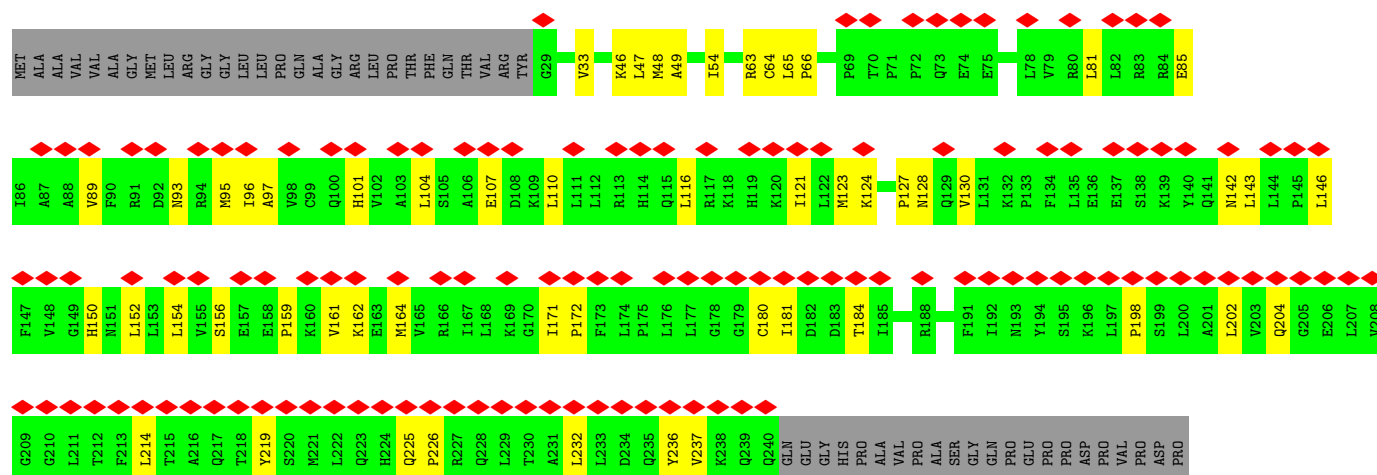
Chain BF: 64% 20% 15%



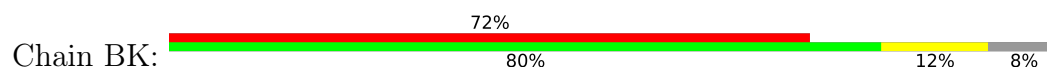
• Molecule 13: Mitochondrial ribosomal protein L9

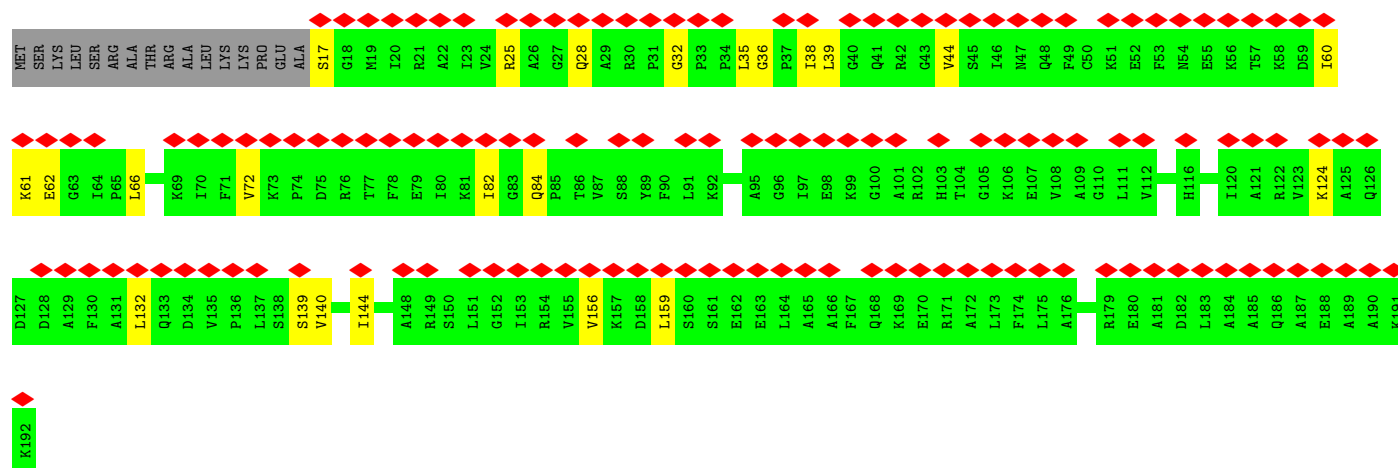


• Molecule 14: Mitochondrial ribosomal protein L10



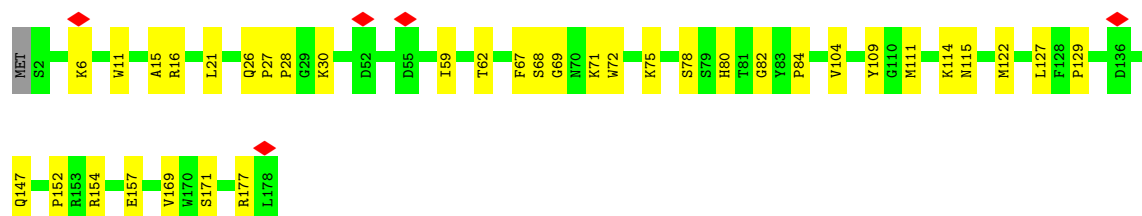
• Molecule 15: Mitochondrial ribosomal protein L11





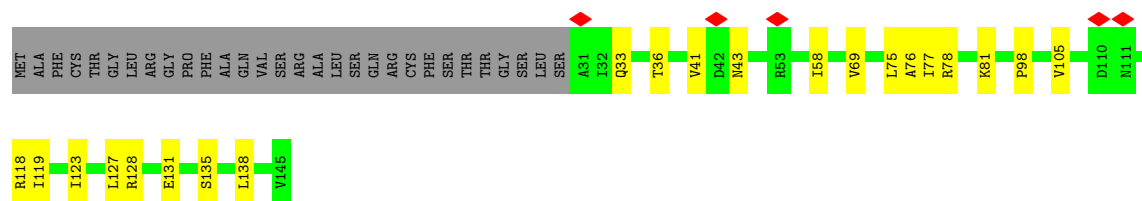
• Molecule 16: uL13m

Chain BN: 79% 20% .



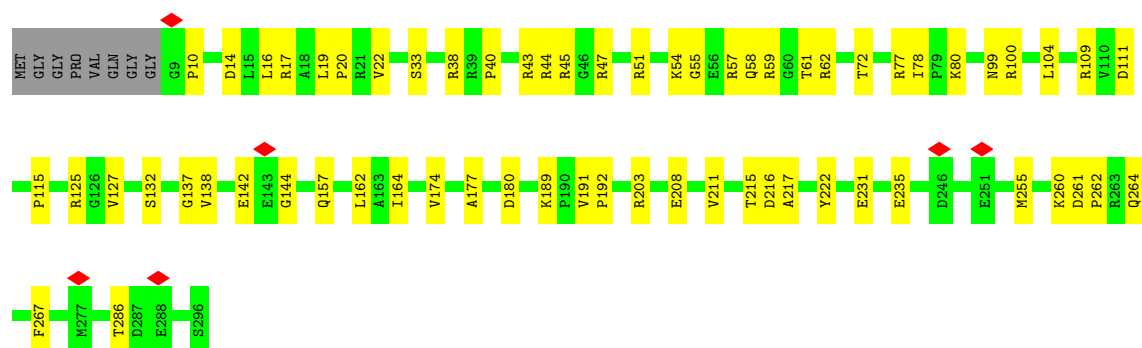
• Molecule 17: uL14m

Chain BO: 65% 14% 21% .

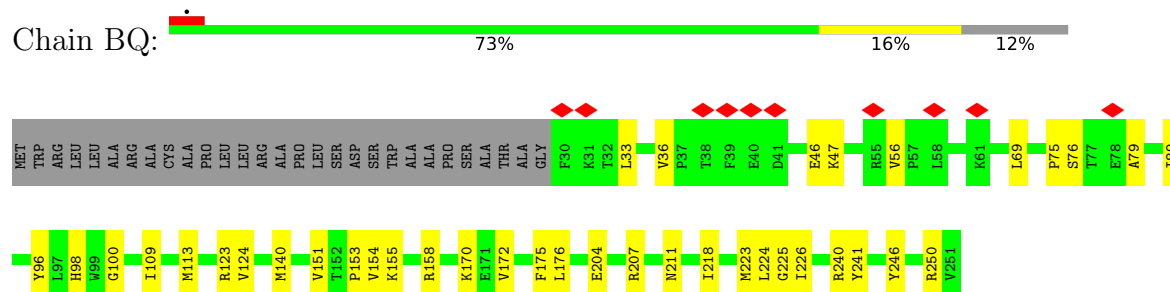


• Molecule 18: uL15m

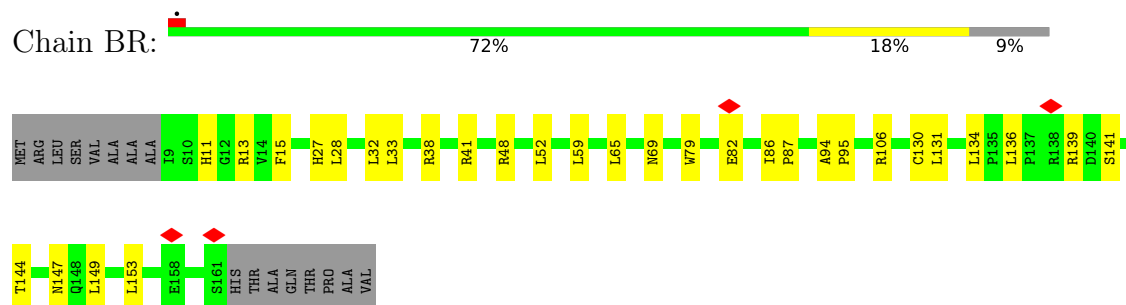
Chain BP: 76% 22% .



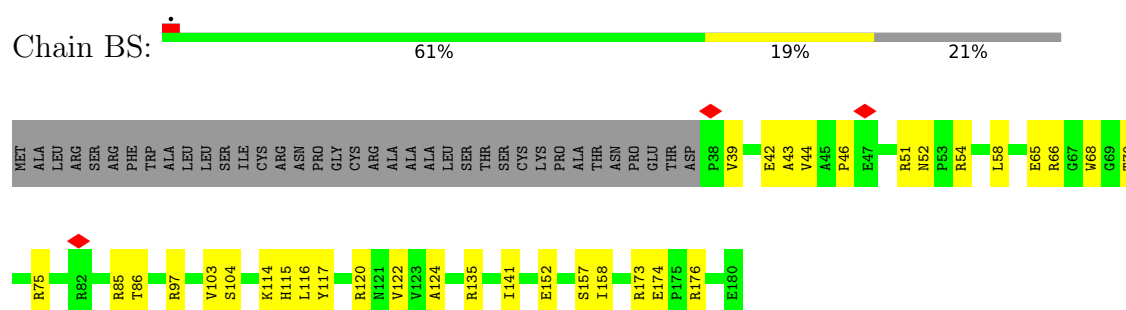
- Molecule 19: uL16m



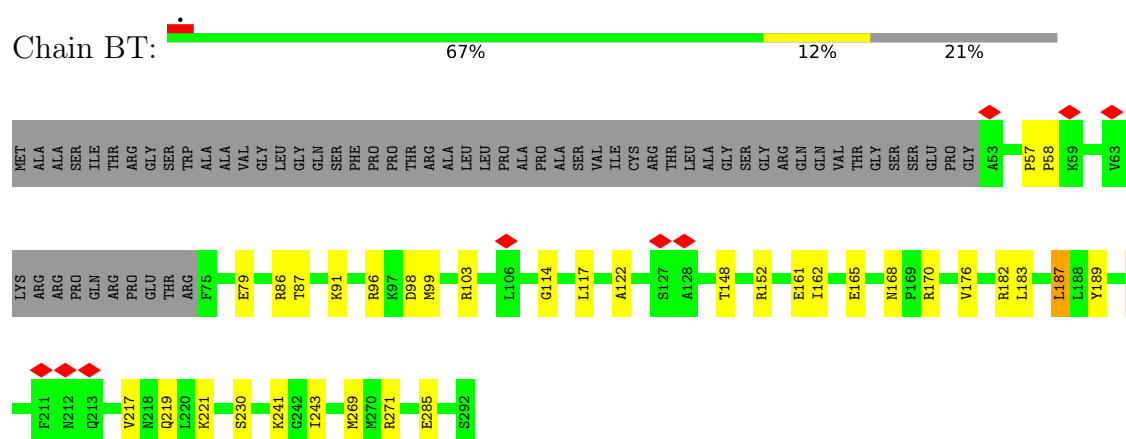
- Molecule 20: bL17m



- Molecule 21: Mitochondrial ribosomal protein L18



- Molecule 22: Mitochondrial ribosomal protein L19



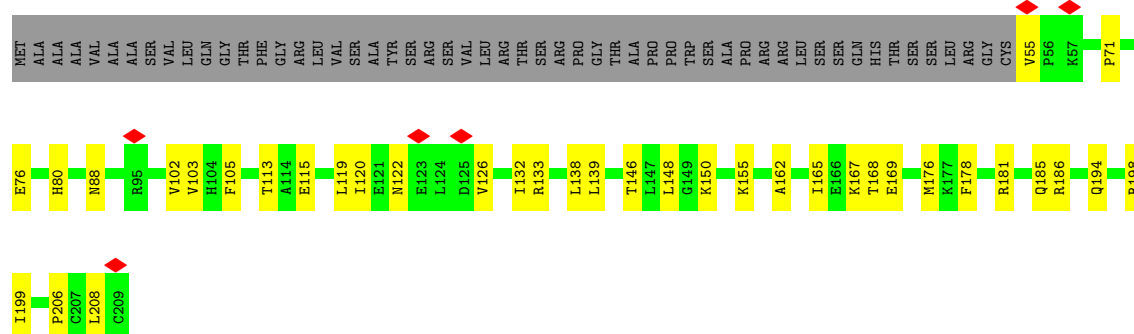
- Molecule 23: Mitochondrial ribosomal protein L20

Chain BU: 



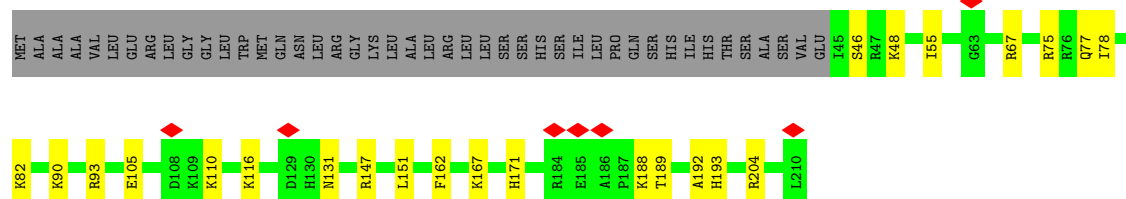
- Molecule 24: Mitochondrial ribosomal protein L21

Chain BV: 



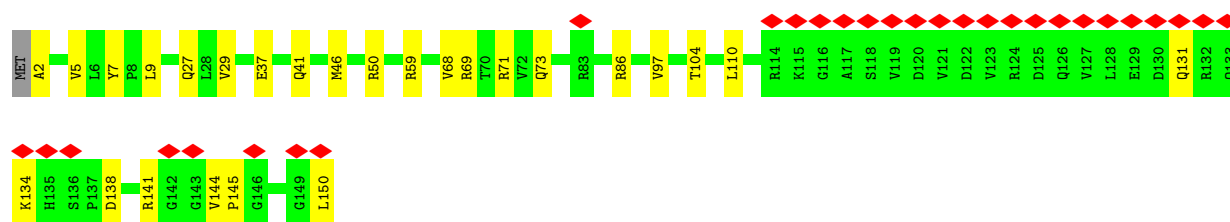
- Molecule 25: uL22m

Chain BW: 



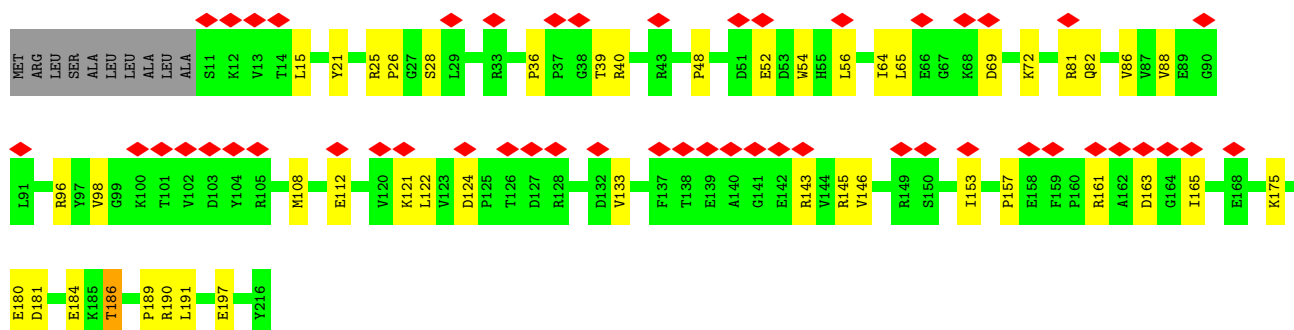
- Molecule 26: uL23m

Chain BX: 



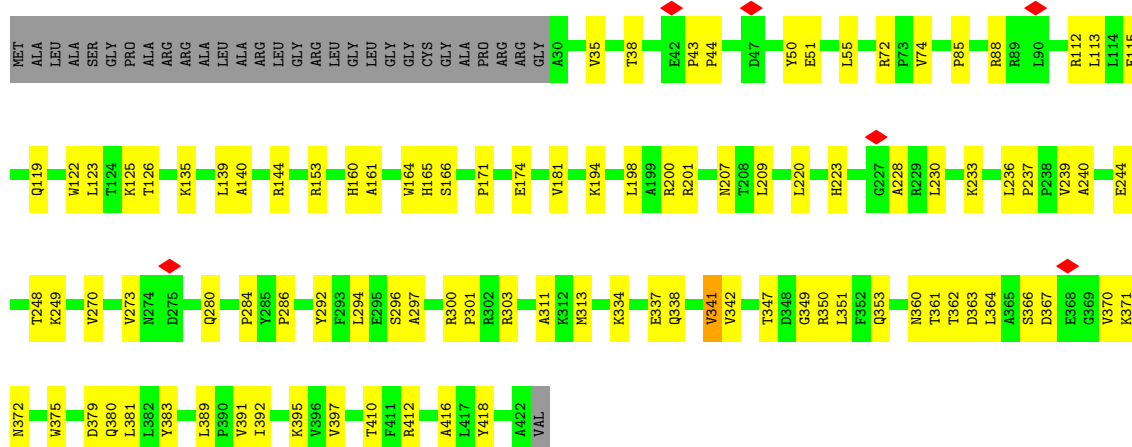
- Molecule 27: uL24m

Chain BY: 



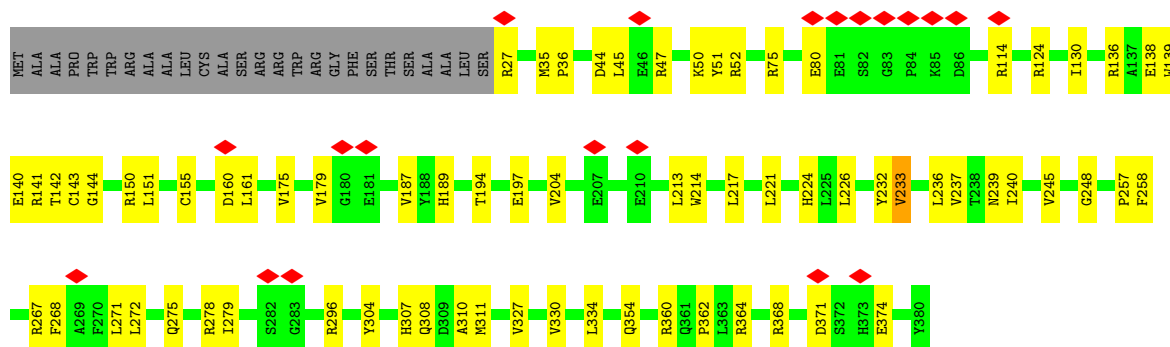
• Molecule 28: Mitochondrial ribosomal protein L37

Chain Ba: 70% 23% 7%



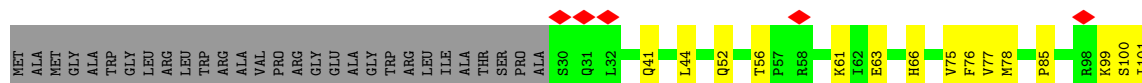
• Molecule 29: Mitochondrial ribosomal protein L38

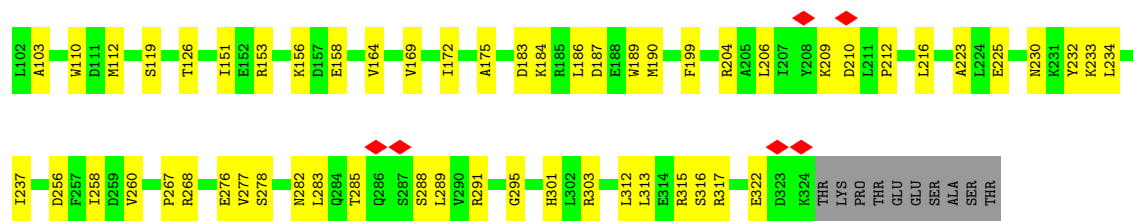
Chain Bb: 74% 19% 7%



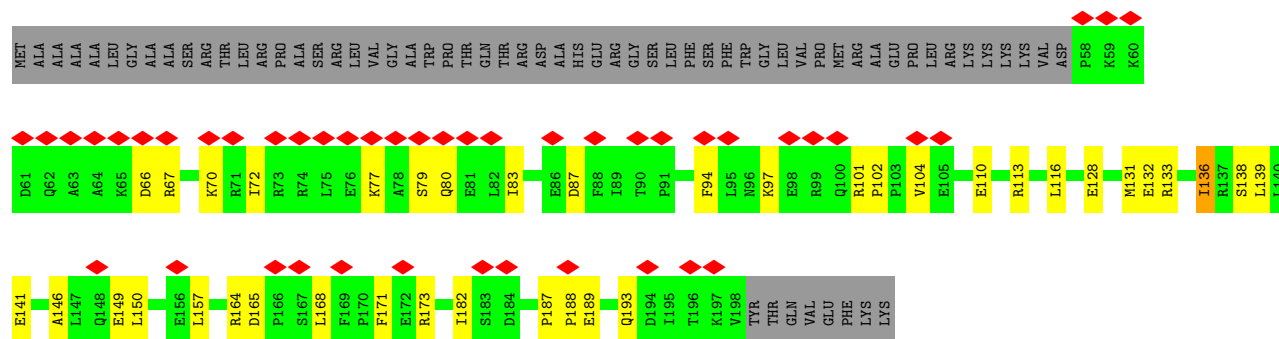
• Molecule 30: Mitochondrial ribosomal protein L39

Chain Bc: 67% 21% 12%

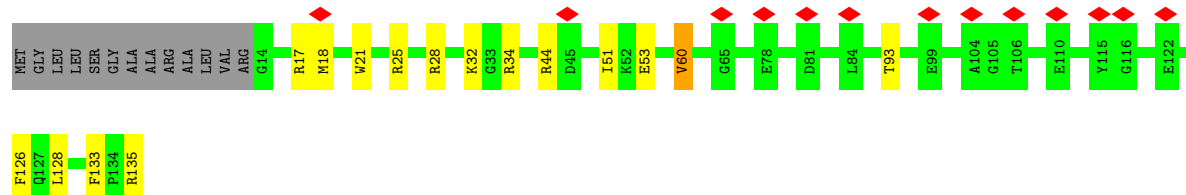
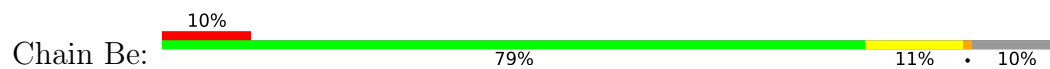




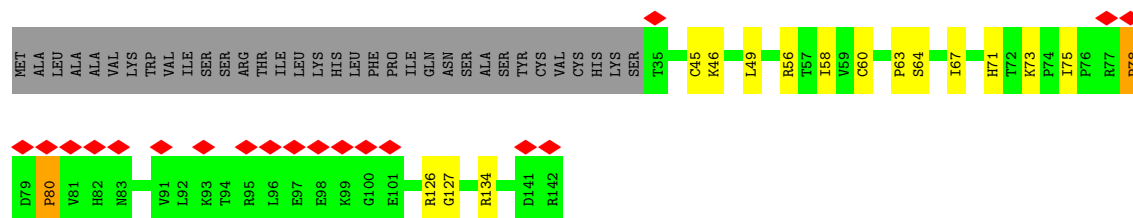
• Molecule 31: Mitochondrial ribosomal protein L40



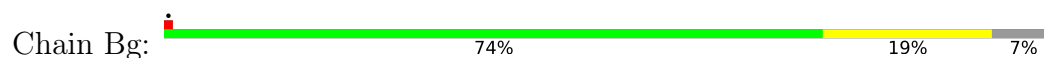
• Molecule 32: Mitochondrial ribosomal protein L41



• Molecule 33: mL42

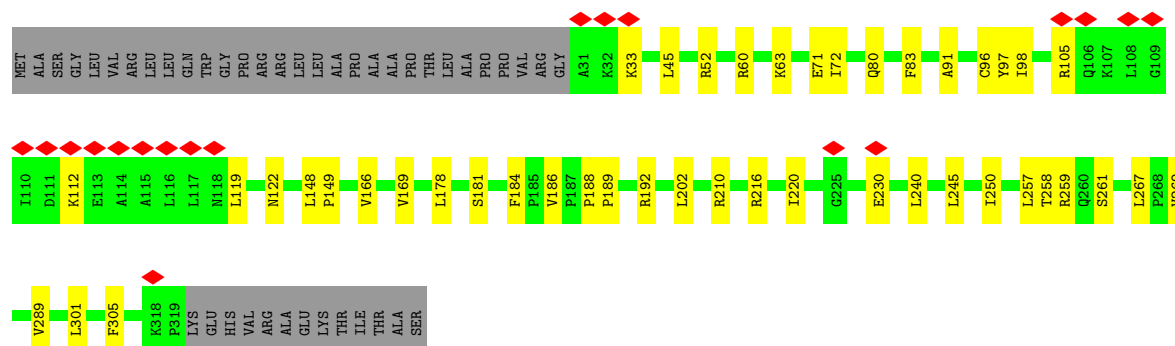
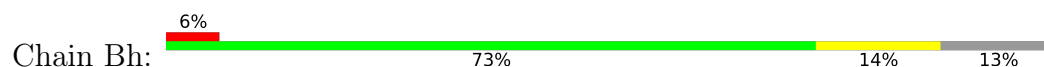


• Molecule 34: Mitochondrial ribosomal protein L43

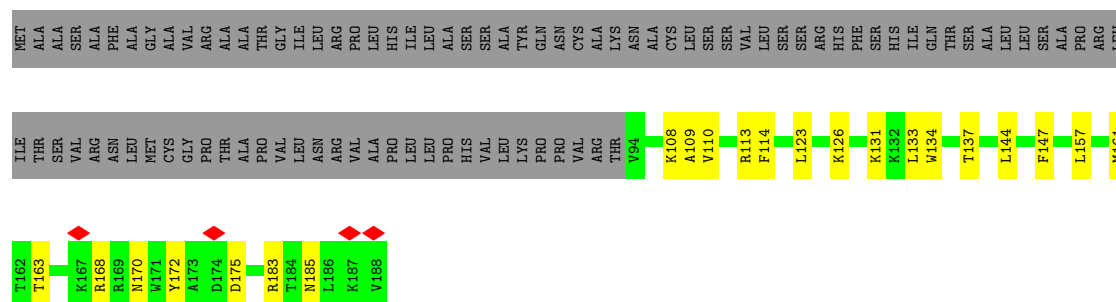




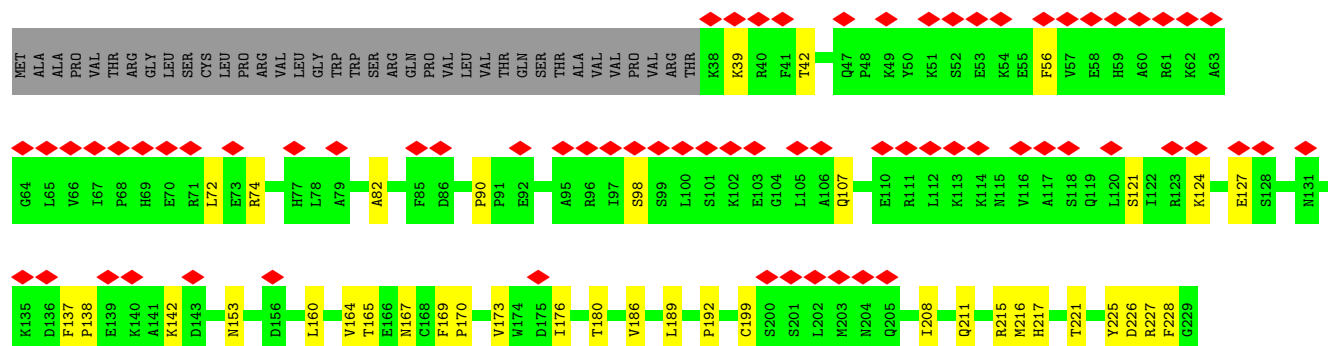
• Molecule 35: mL44



• Molecule 36: Mitochondrial ribosomal protein L35

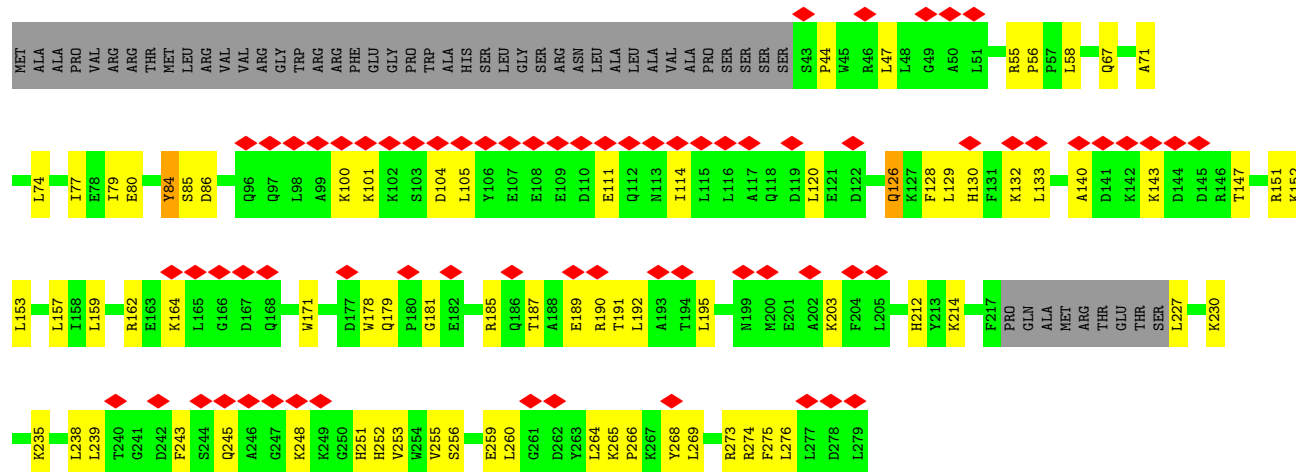


• Molecule 37: Mitochondrial ribosomal protein L45

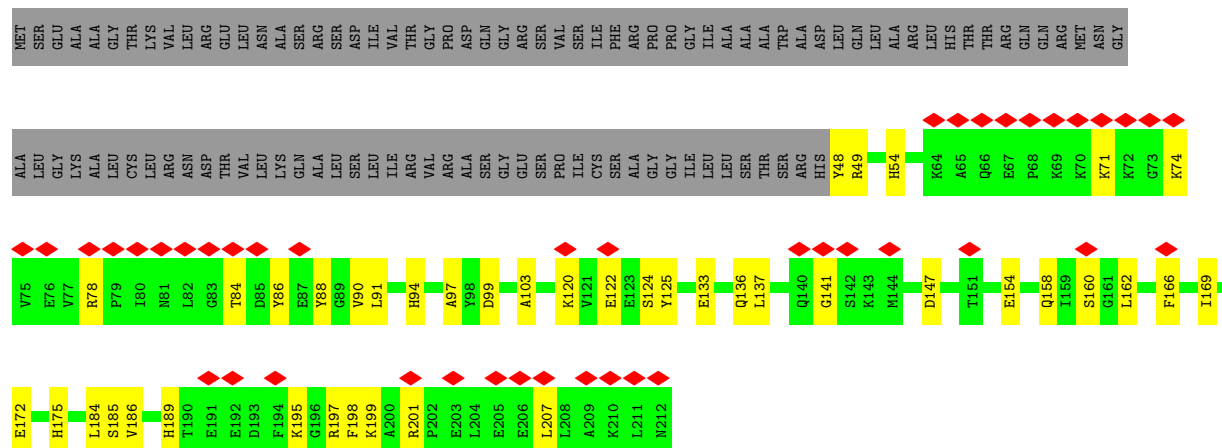




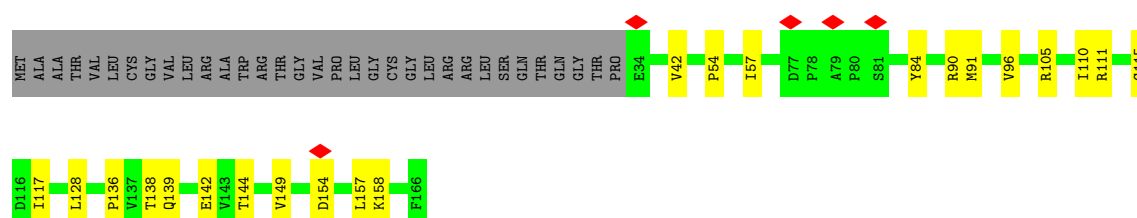
• Molecule 38: Mitochondrial ribosomal protein L46



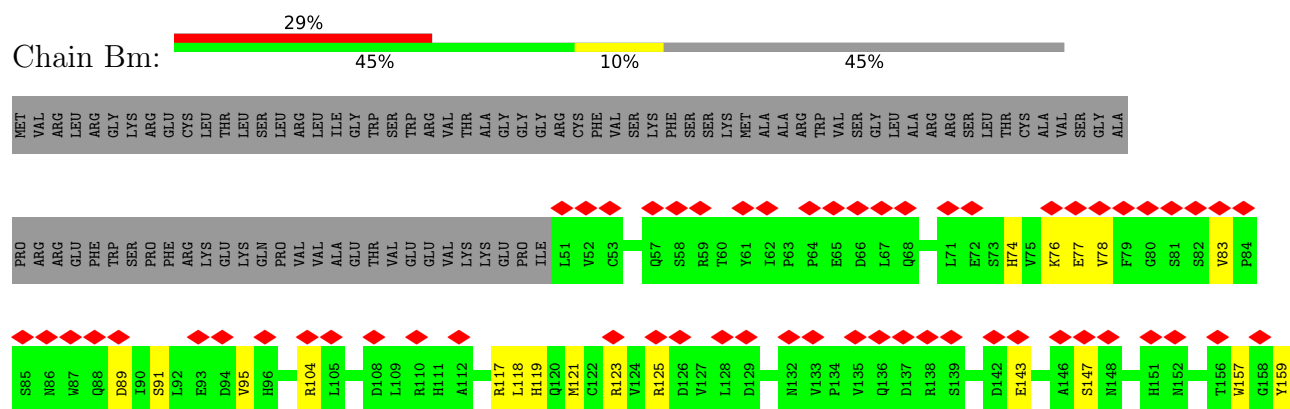
• Molecule 39: 39S ribosomal protein L48, mitochondrial



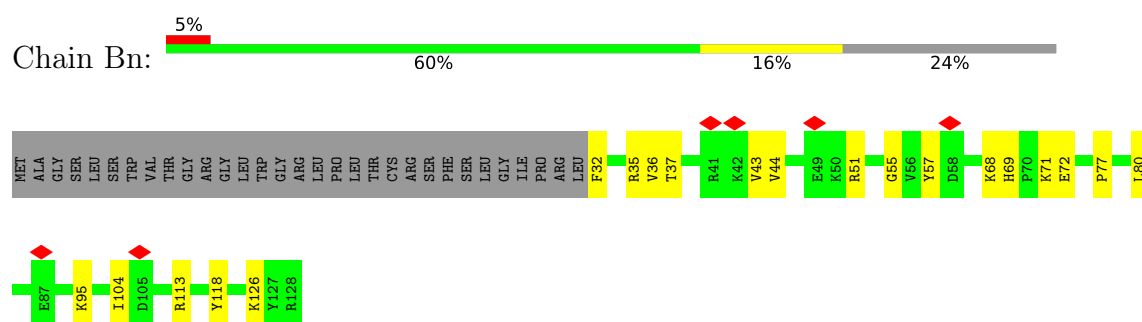
• Molecule 40: Mrpl34



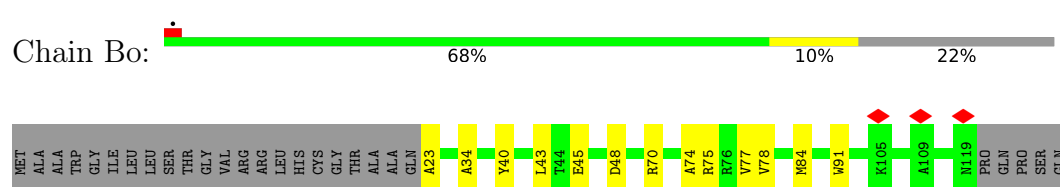
- Molecule 41: Mitochondrial ribosomal protein L50



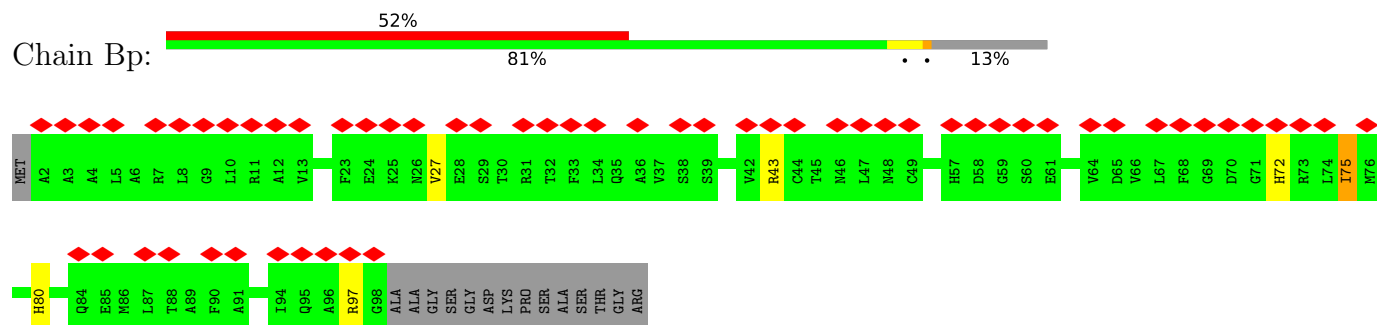
- Molecule 42: Mitochondrial ribosomal protein L51



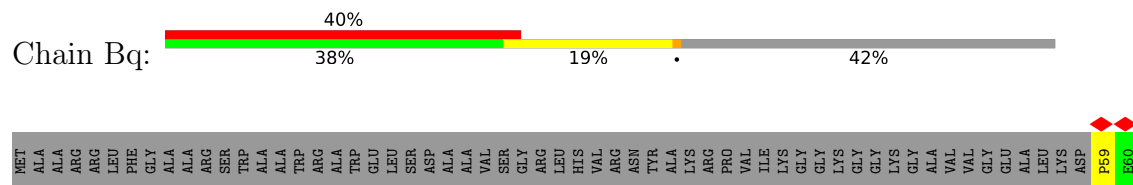
- Molecule 43: mL52

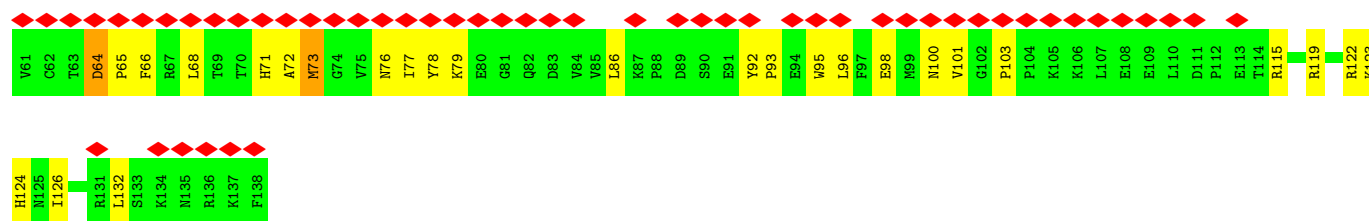


- Molecule 44: mL53

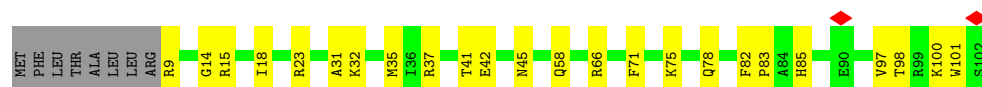


- Molecule 45: mL54

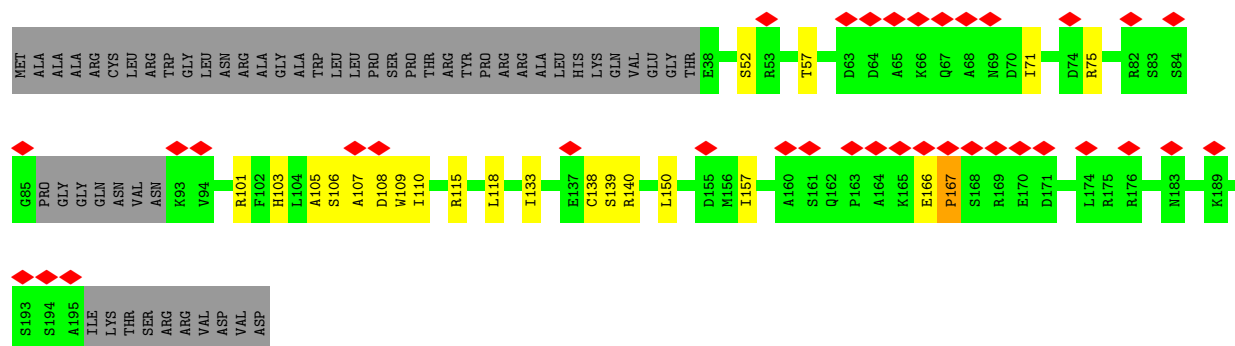




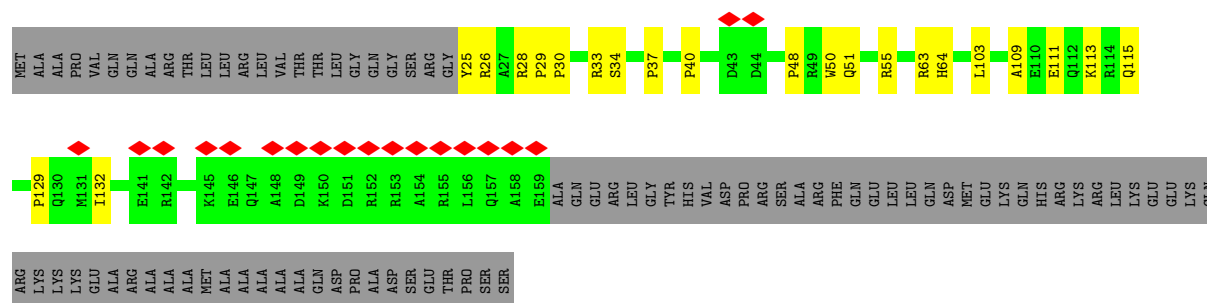
- Molecule 46: Mitochondrial ribosomal protein L57



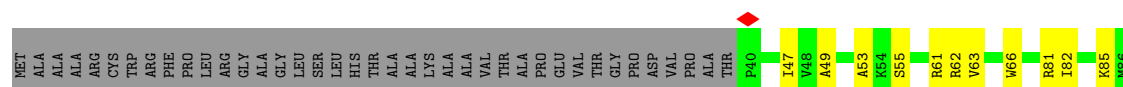
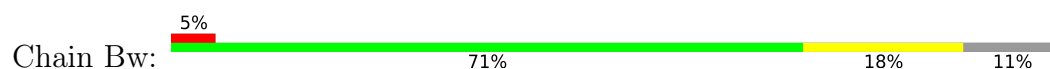
- Molecule 47: mL62 (ICT1)

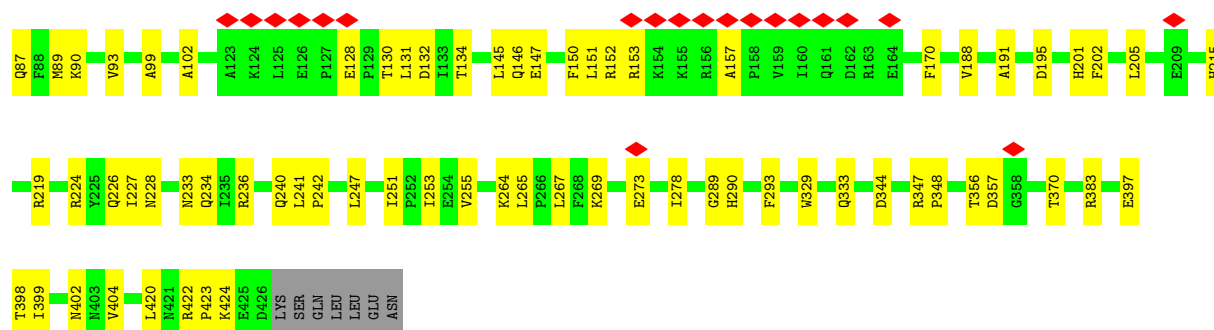


- Molecule 48: mL64

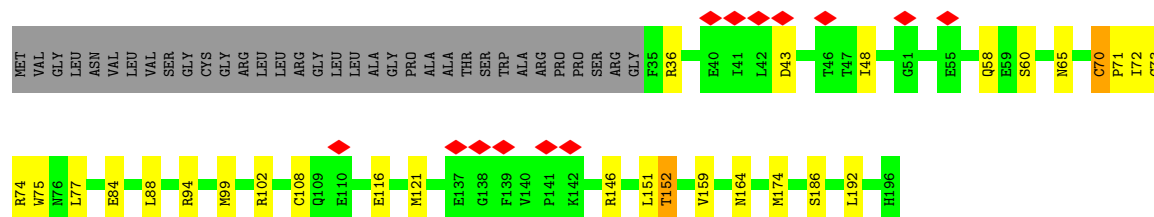


- Molecule 49: 39S ribosomal protein S30, mitochondrial

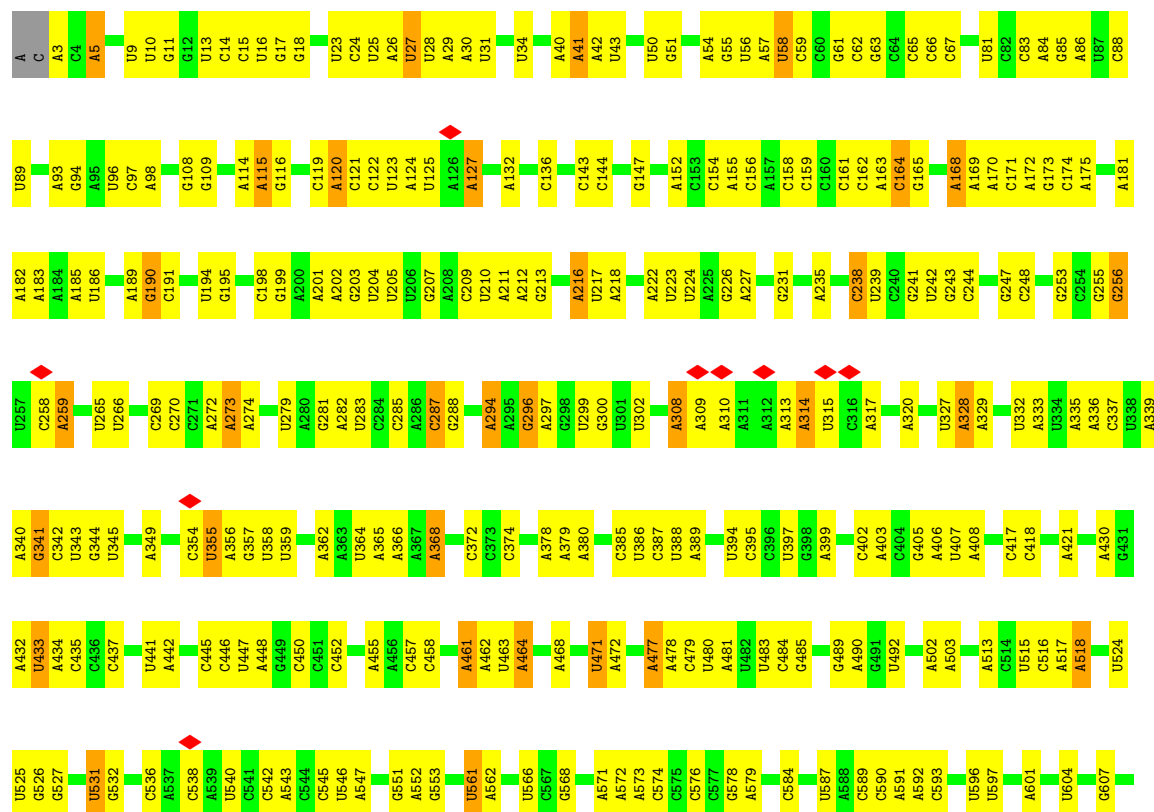


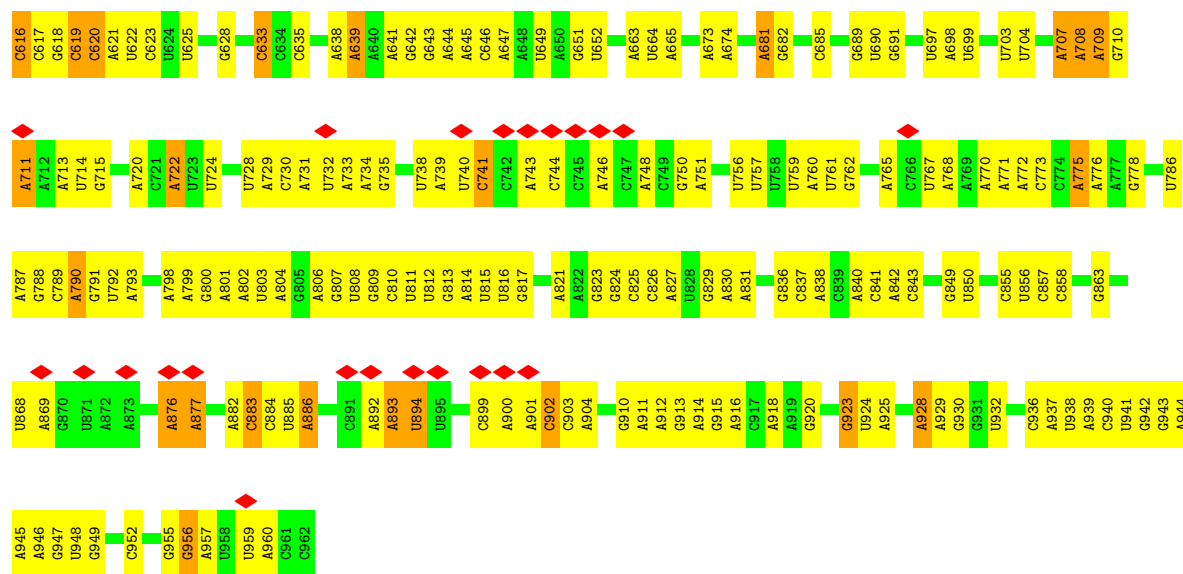


• Molecule 50: Mitochondrial ribosomal protein S18A

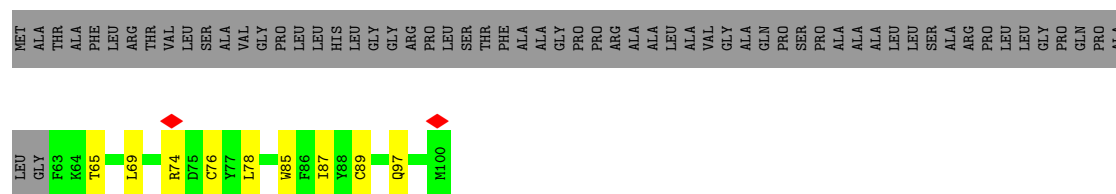


• Molecule 51: 12S rRNA

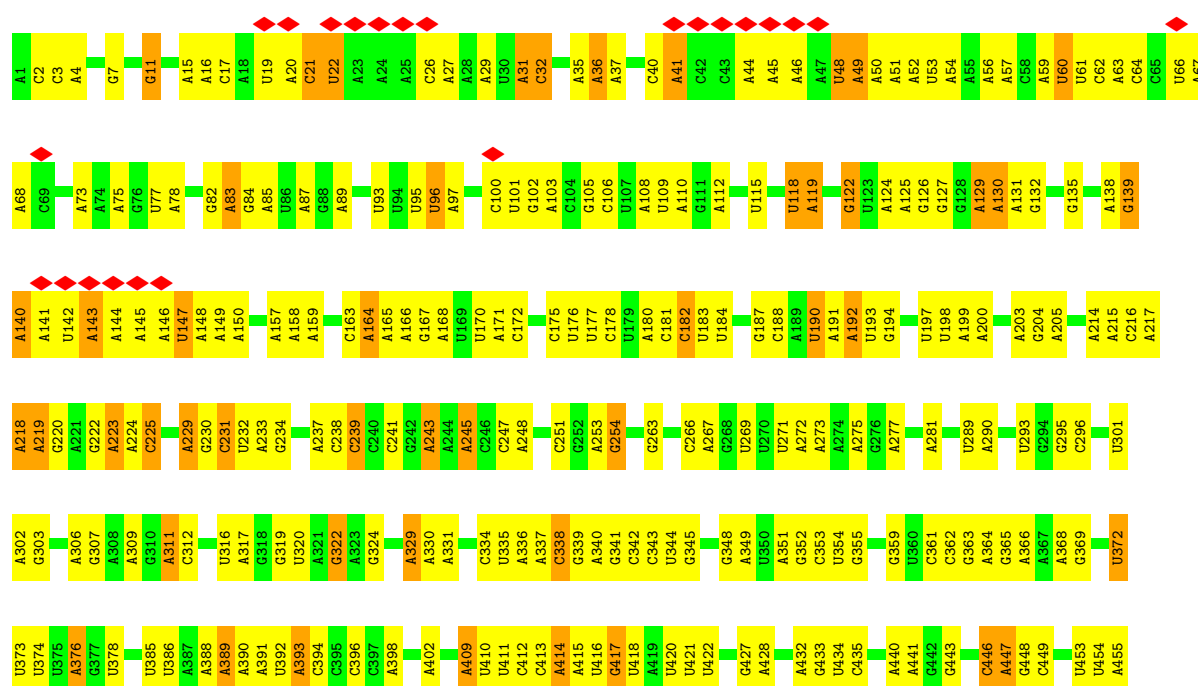


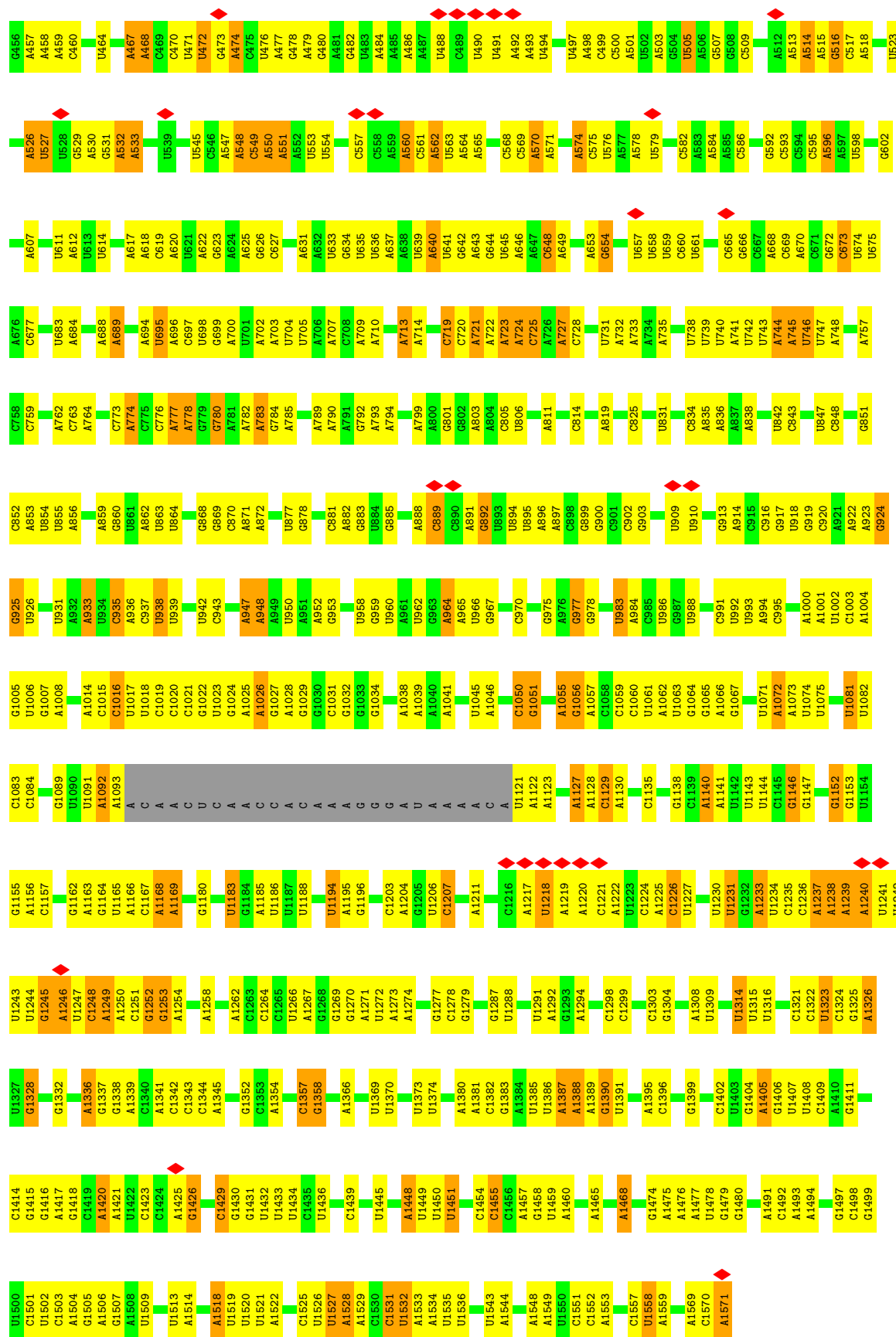


• Molecule 52: Ribosomal protein

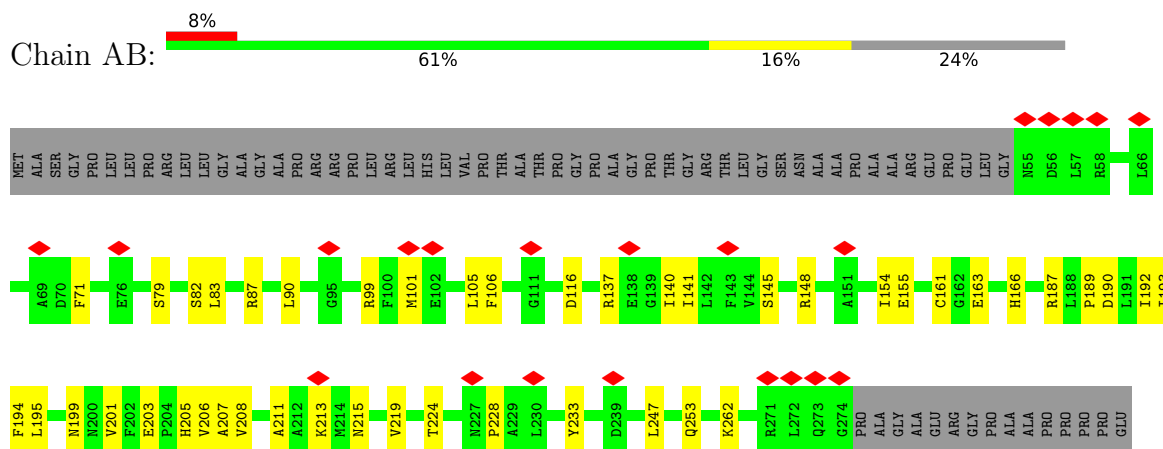


• Molecule 53: 16S rRNA

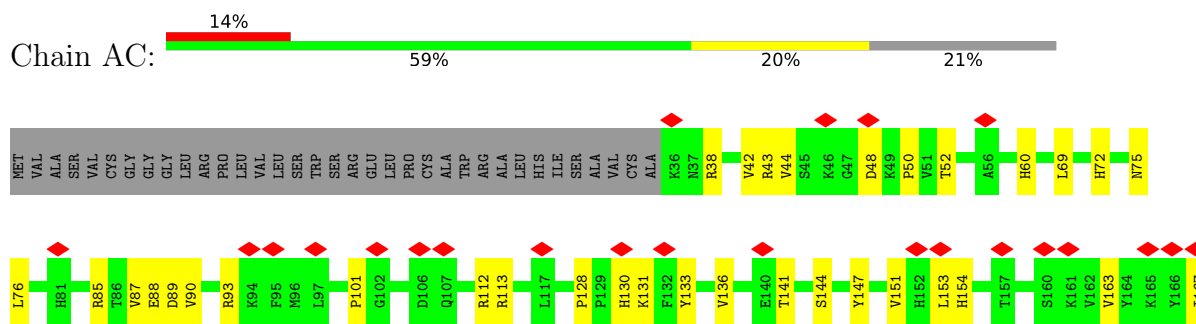




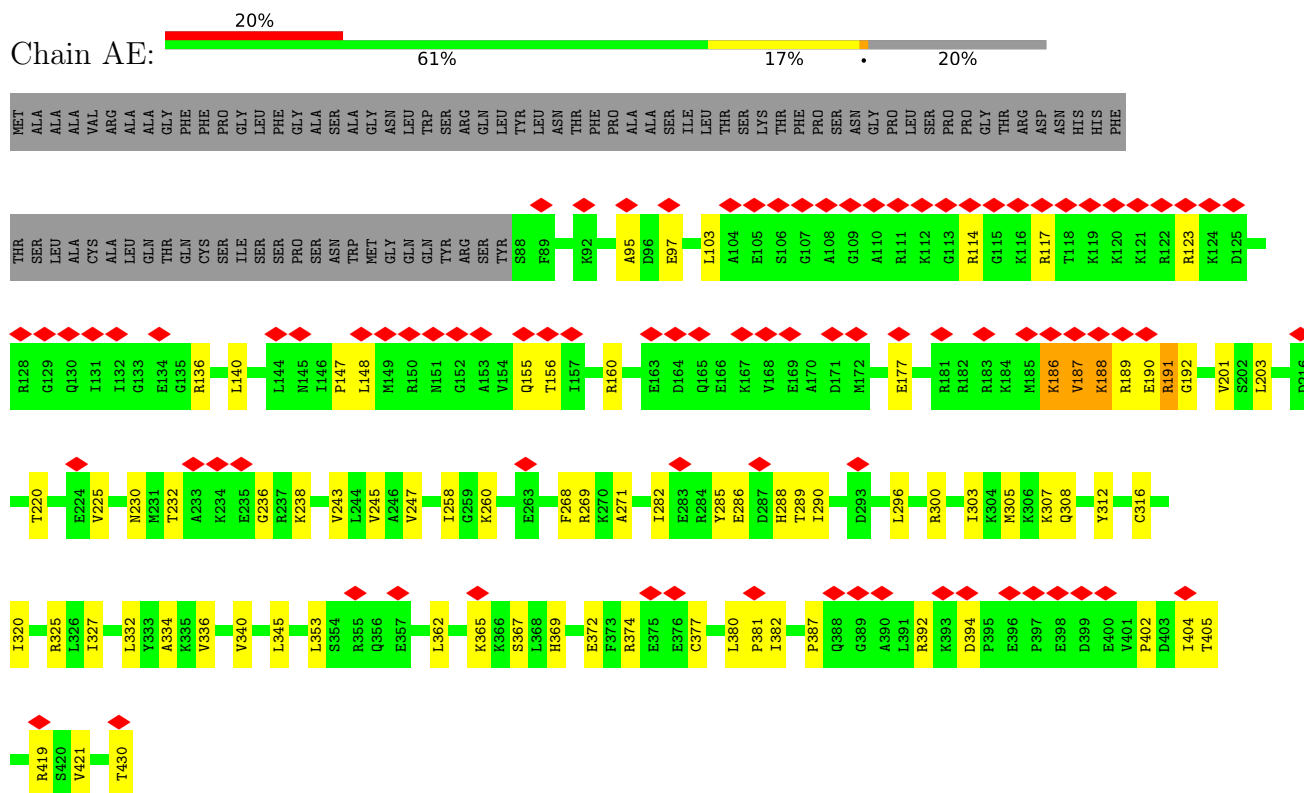
- Molecule 54: Mitochondrial ribosomal protein S2

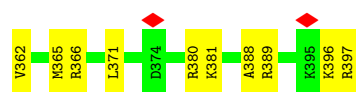


- Molecule 55: Mitochondrial ribosomal protein S24

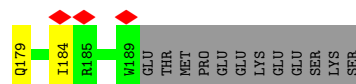
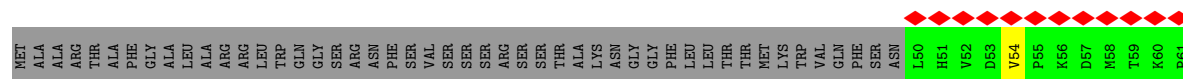


- Molecule 56: 28S ribosomal protein S5, mitochondrial isoform X2

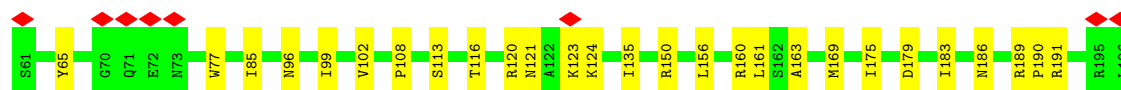
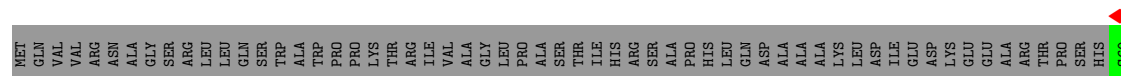




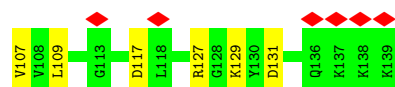
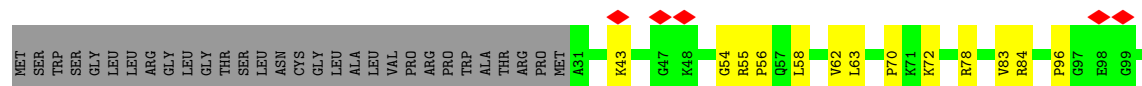
- Molecule 60: Mitochondrial ribosomal protein S10



- Molecule 61: uS11m



- Molecule 62: Mitochondrial ribosomal protein S12

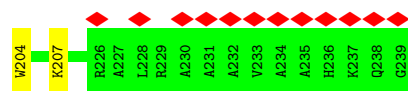
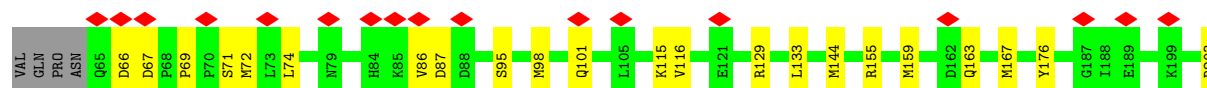


- Molecule 63: Mitochondrial ribosomal protein S14

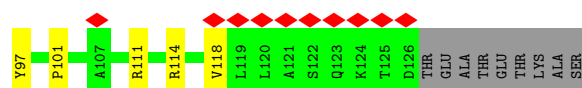
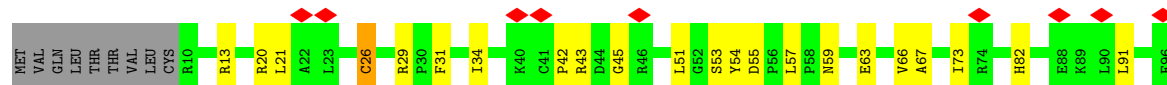




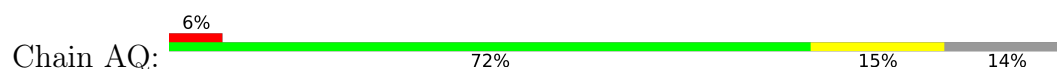
• Molecule 64: uS15m



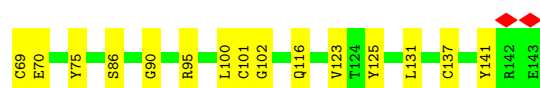
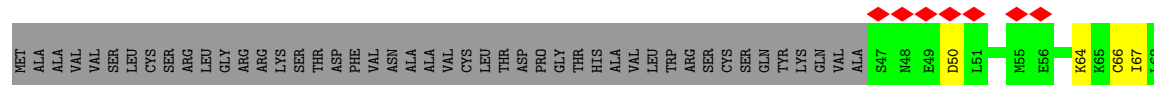
• Molecule 65: 28S ribosomal protein S16, mitochondrial



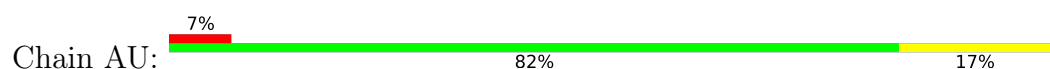
• Molecule 66: uS17m

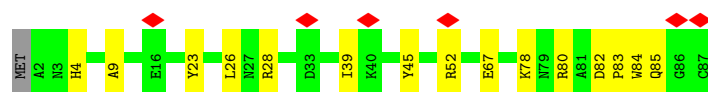


• Molecule 67: Mitochondrial ribosomal protein S18C

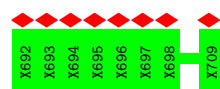


• Molecule 68: bS21m

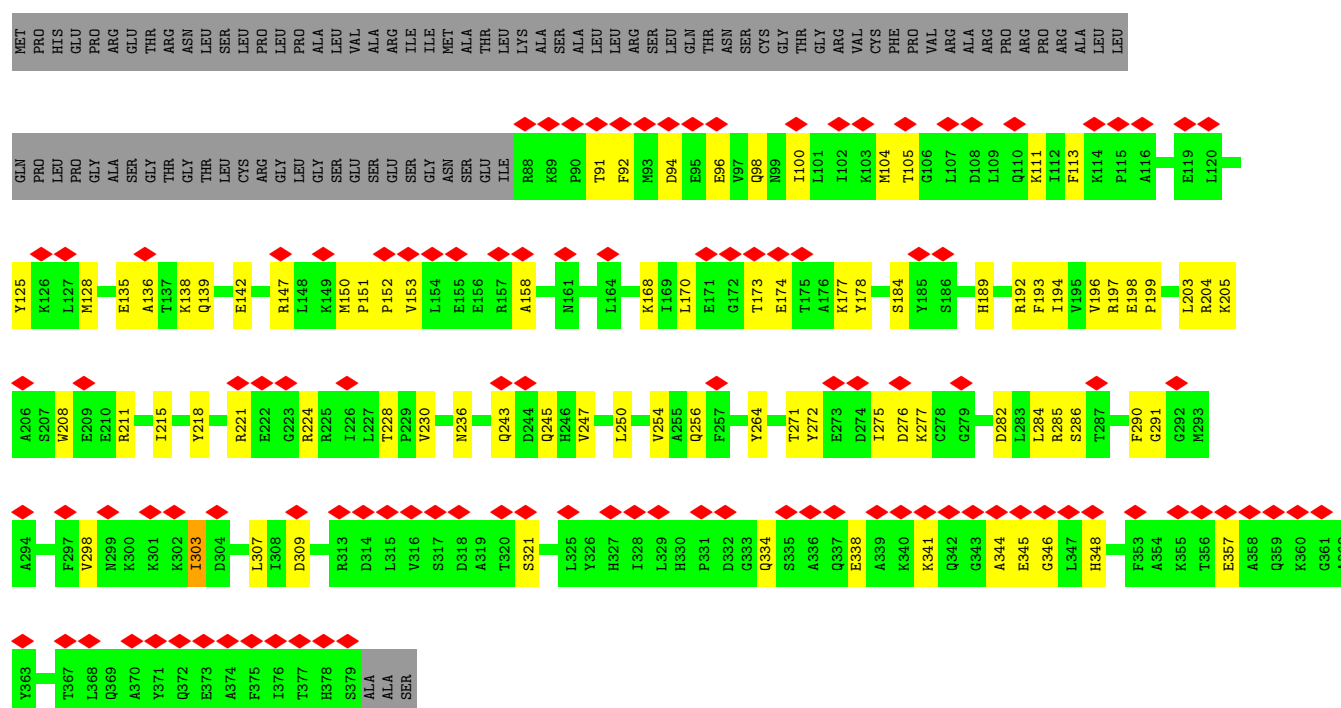




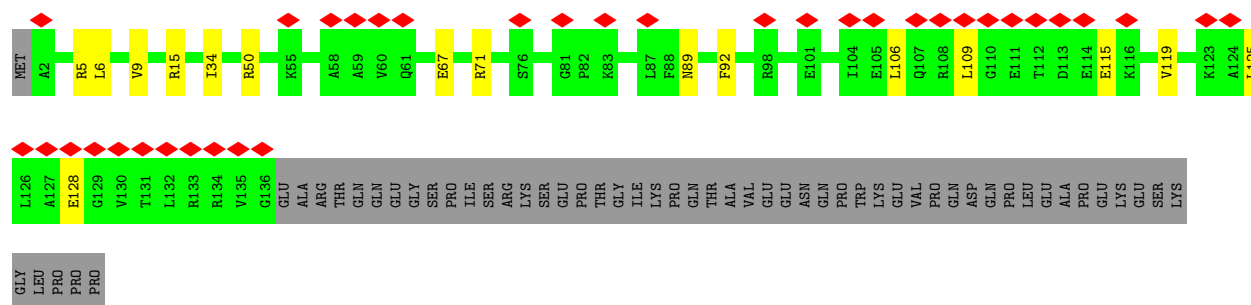
- Molecule 69: unknown



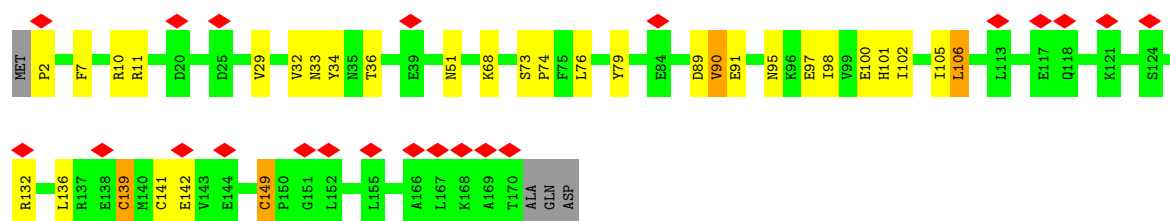
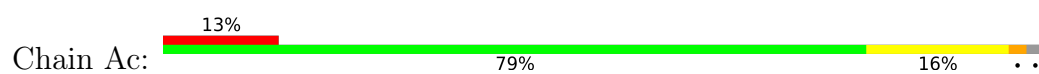
- Molecule 70: Mitochondrial ribosomal protein S22



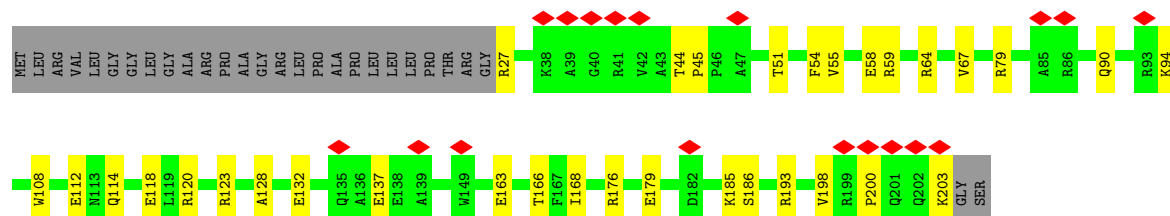
- Molecule 71: mS23



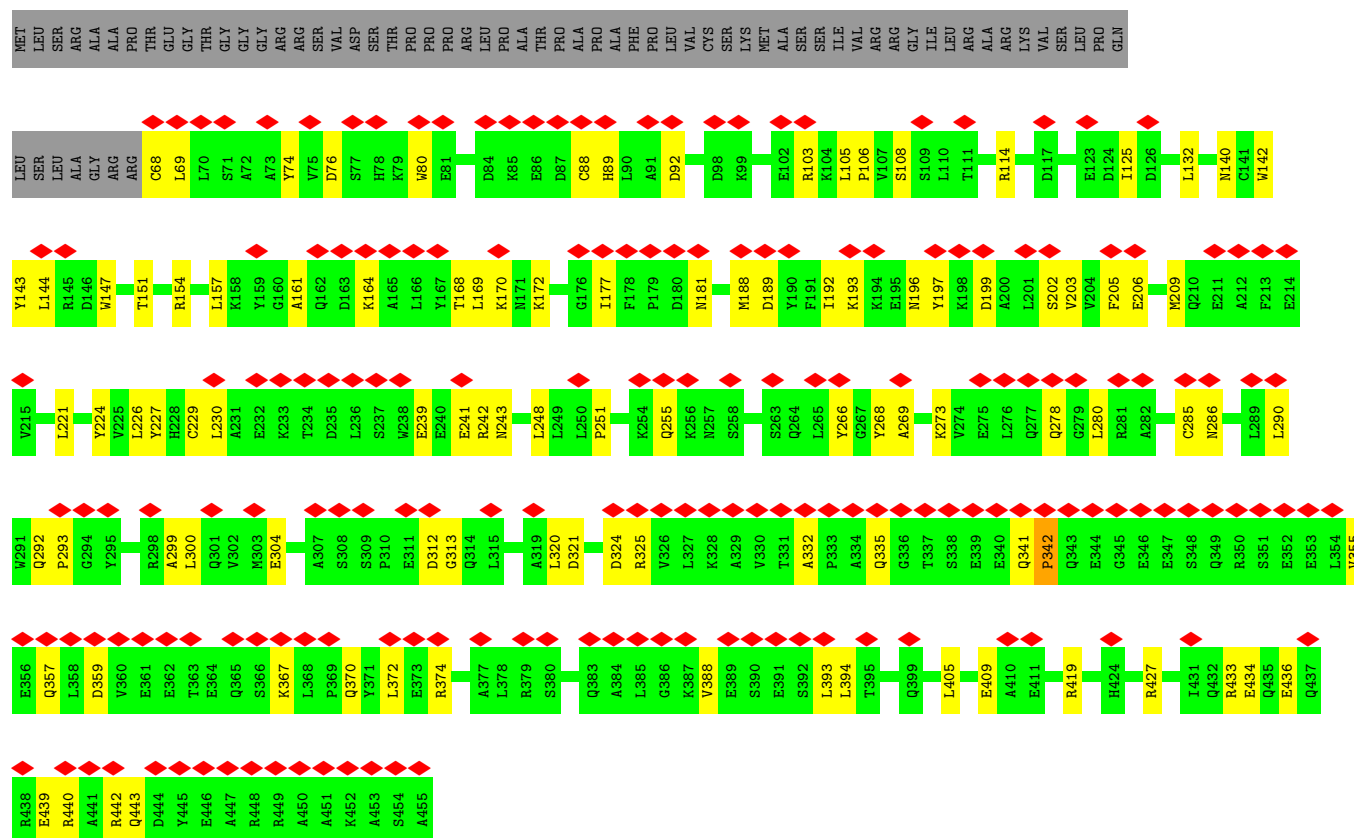
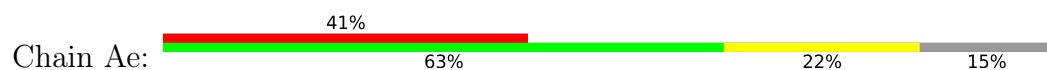
- Molecule 72: Mitochondrial ribosomal protein S25



- Molecule 73: Mitochondrial ribosomal protein S26

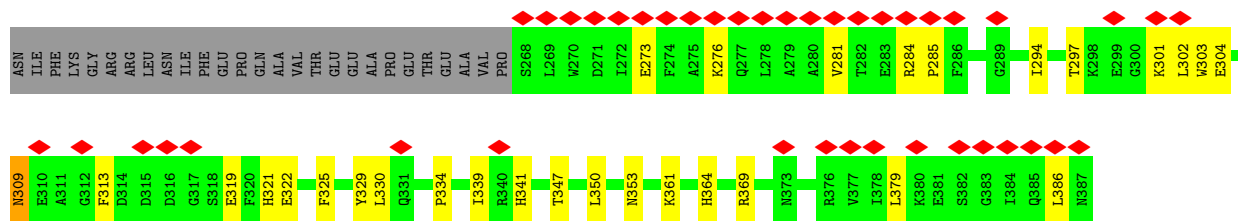


- Molecule 74: Mitochondrial ribosomal protein S27

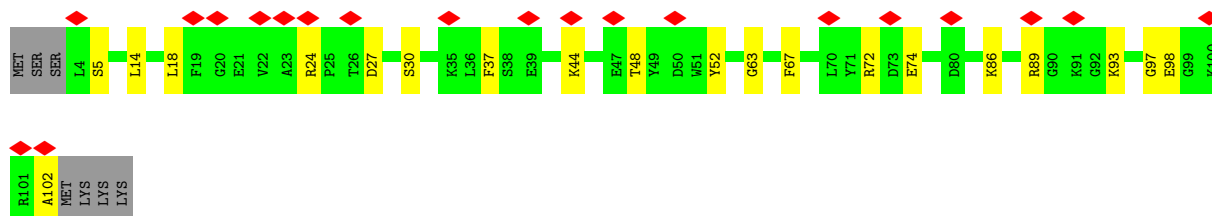
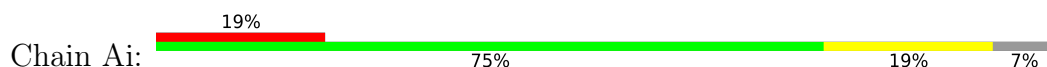


- Molecule 75: Mitochondrial ribosomal protein ms28, mrps28

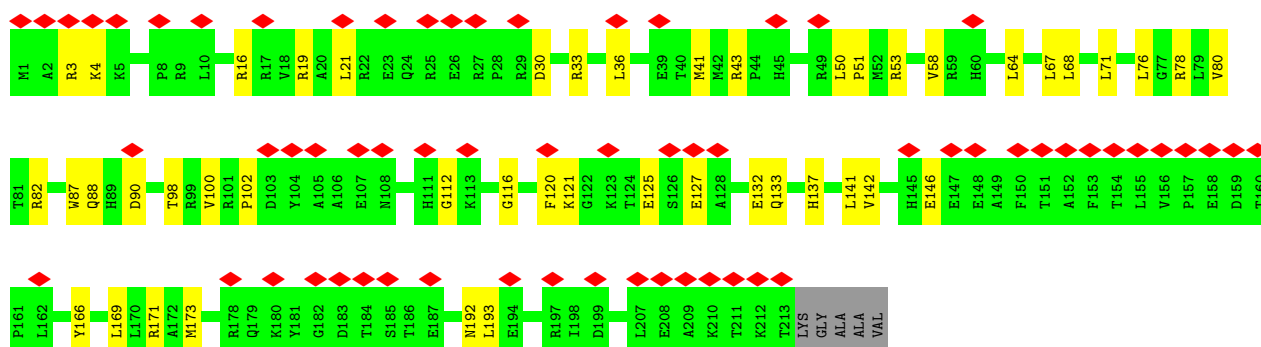
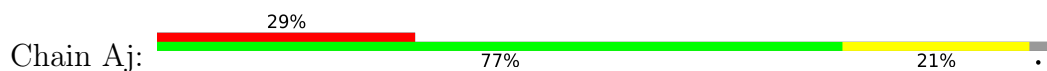




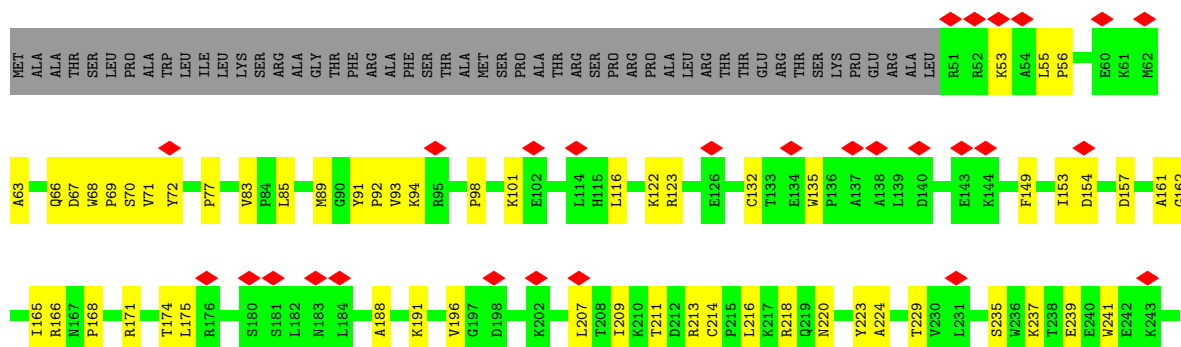
• Molecule 78: mS33

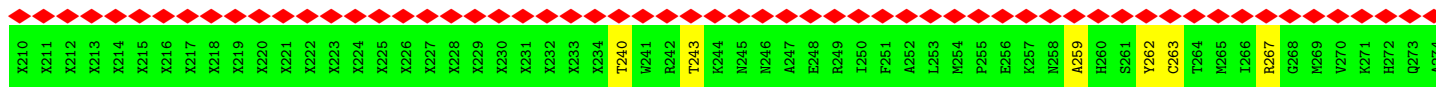


• Molecule 79: mS34

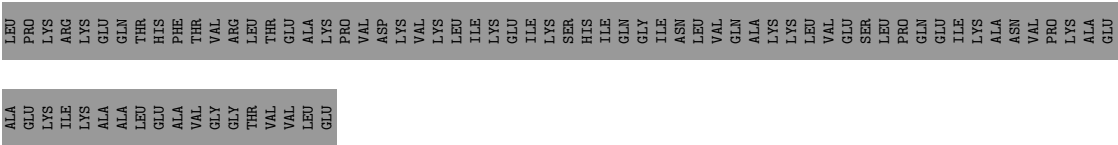


• Molecule 80: Mitochondrial ribosomal protein S35

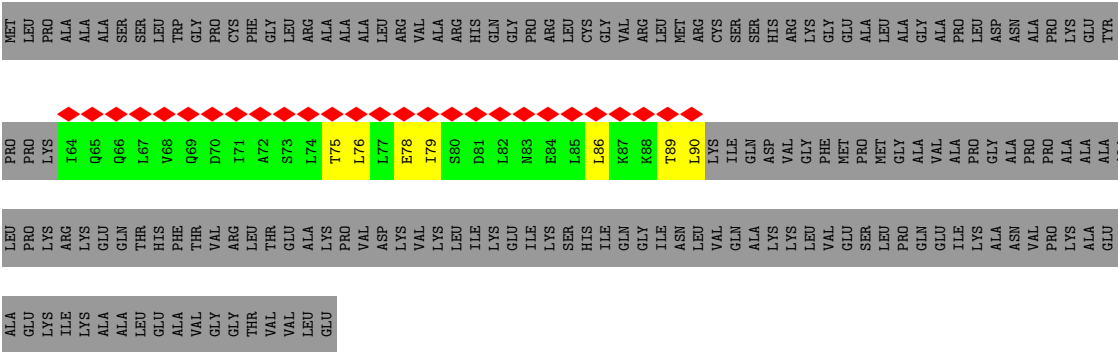




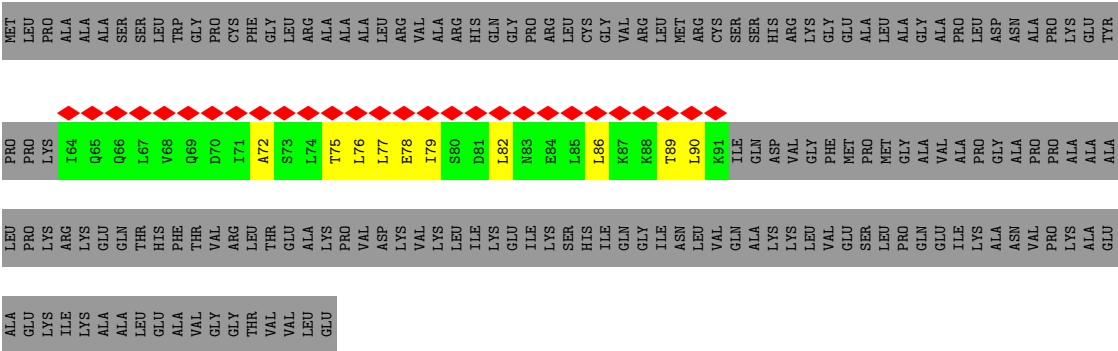




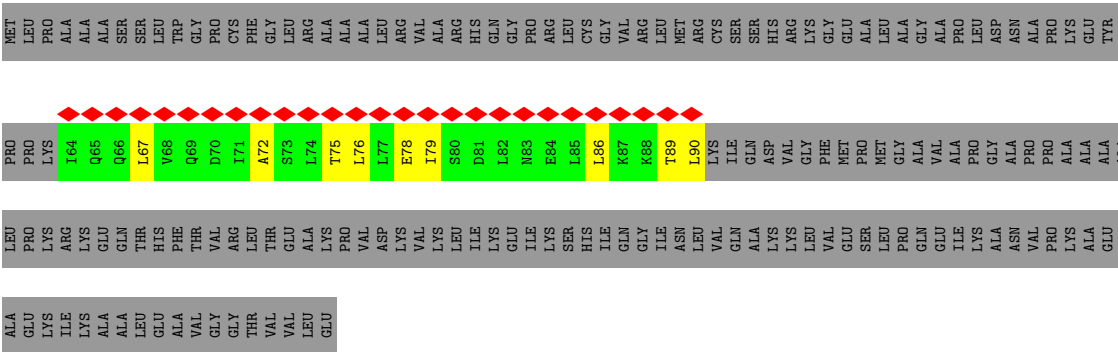
• Molecule 85: Mitochondrial ribosomal protein L12



• Molecule 85: Mitochondrial ribosomal protein L12

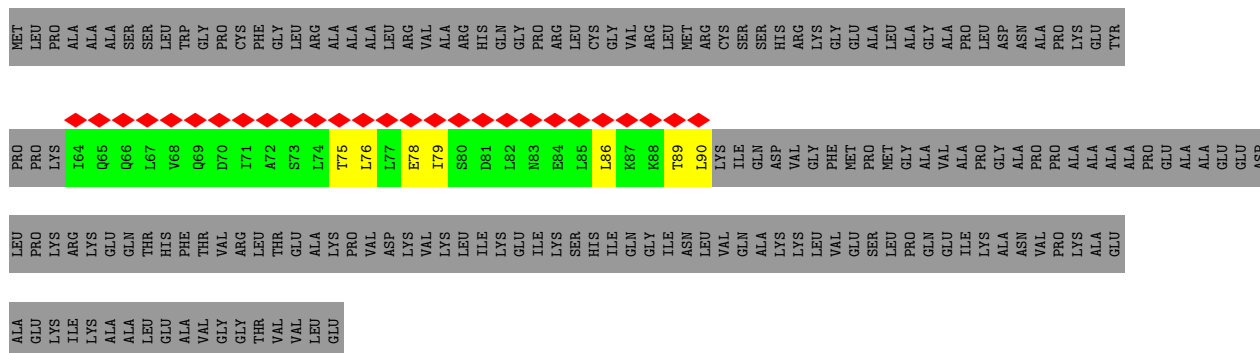


• Molecule 85: Mitochondrial ribosomal protein L12

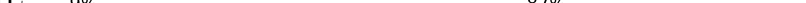


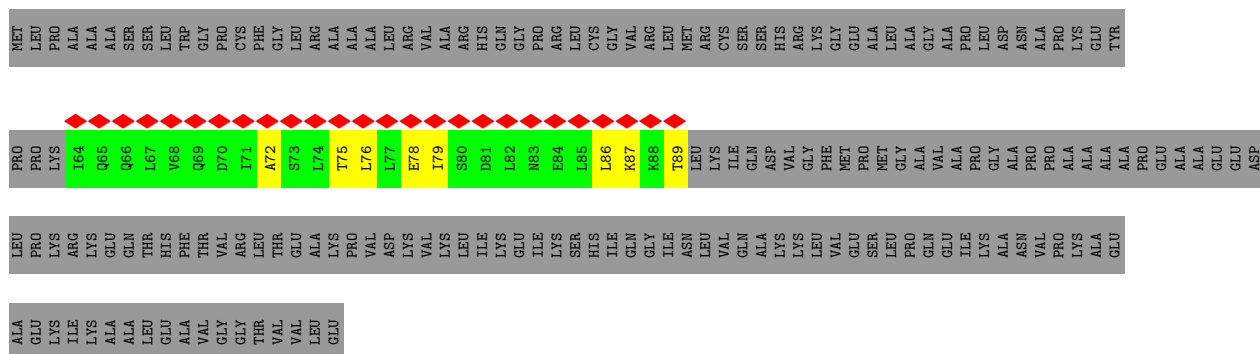
• Molecule 85: Mitochondrial ribosomal protein L12

Chain GL: 14% 10% 86%

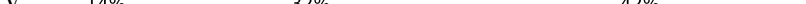


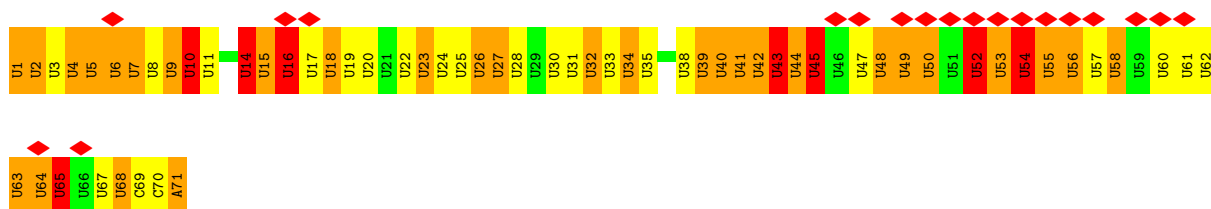
- Molecule 85: Mitochondrial ribosomal protein L12

Chain HL: 

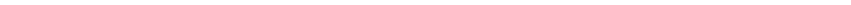


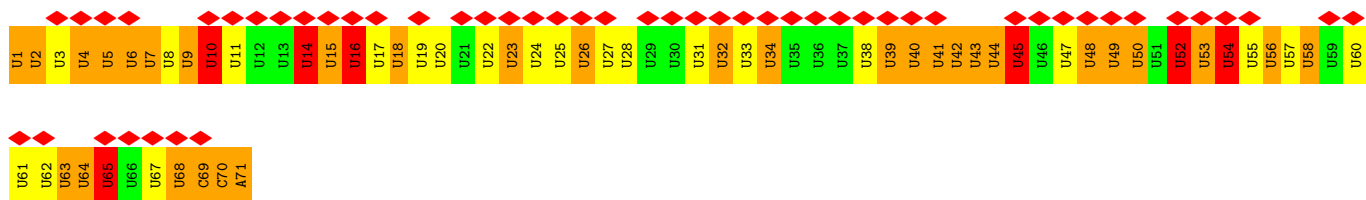
- Molecule 86: tRNA(P/P) and tRNA(E*)

Chain AV: 

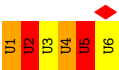


- Molecule 86: tRNA(P/P) and tRNA(E*)

Chain AY: 



- Molecule 87: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26001	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.055	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	521.76, 521.76, 521.76	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GTP, 5GP, SPM, 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	B0	0.08	0/880	0.25	0/1189
2	B1	0.08	0/2093	0.23	0/2835
3	B2	0.08	0/1586	0.22	0/2123
4	B3	0.09	0/993	0.27	0/1341
5	B4	0.12	0/481	0.41	1/653 (0.2%)
6	B5	0.09	0/917	0.24	0/1227
7	B6	0.10	0/430	0.27	0/570
8	BB	0.07	0/1595	0.20	0/2475
9	B7	0.08	0/395	0.22	0/524
10	BD	0.10	0/1898	0.28	0/2555
11	BE	0.11	0/2493	0.30	0/3387
12	BF	0.10	0/2069	0.30	0/2816
13	BI	0.08	0/819	0.26	0/1101
14	BJ	0.10	0/1742	0.29	0/2358
15	BK	0.11	0/1323	0.29	0/1785
16	BN	0.10	0/1487	0.25	0/2017
17	BO	0.09	0/912	0.25	0/1231
18	BP	0.10	0/2368	0.27	0/3198
19	BQ	0.10	0/1850	0.27	0/2491
20	BR	0.09	0/1262	0.28	0/1700
21	BS	0.10	0/1197	0.31	0/1624
22	BT	0.09	0/1936	0.24	0/2615
23	BU	0.10	0/1179	0.24	0/1578
24	BV	0.11	0/1256	0.28	0/1706
25	BW	0.09	0/1407	0.24	0/1891
26	BX	0.12	0/1211	0.28	0/1646
27	BY	0.09	0/1719	0.27	0/2329
28	Ba	0.10	0/3267	0.27	0/4455
29	Bb	0.10	0/3047	0.26	0/4139
30	Bc	0.09	0/2464	0.26	0/3330
31	Bd	0.11	0/1209	0.28	0/1627
32	Be	0.10	0/1000	0.26	0/1345

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bf	0.11	0/851	0.46	2/1159 (0.2%)
34	Bg	0.11	0/1191	0.30	0/1614
35	Bh	0.10	0/2372	0.27	0/3211
36	B8	0.08	0/853	0.22	0/1136
37	Bi	0.09	0/2199	0.28	0/2980
38	Bj	0.10	0/1910	0.29	0/2572
39	Bk	0.11	0/1353	0.29	0/1823
40	Bl	0.12	0/1135	0.28	0/1549
41	Bm	0.09	0/917	0.24	0/1248
42	Bn	0.09	0/860	0.25	0/1150
43	Bo	0.09	0/787	0.26	0/1056
44	Bp	0.10	0/752	0.33	0/1013
45	Bq	0.13	0/692	0.42	1/936 (0.1%)
46	Bt	0.10	0/798	0.26	0/1073
47	Bu	0.09	0/1214	0.33	1/1630 (0.1%)
48	Bv	0.08	0/1157	0.20	0/1560
49	Bw	0.10	0/3206	0.27	0/4354
50	Bx	0.10	0/1364	0.29	0/1849
51	AA	0.08	0/22852	0.20	0/35580
52	B9	0.08	0/342	0.22	0/450
53	BA	0.10	0/36784	0.24	0/57270
54	AB	0.10	0/1804	0.29	0/2445
55	AC	0.10	0/1105	0.30	0/1496
56	AE	0.16	0/2785	0.30	0/3735
57	AF	0.10	0/999	0.28	0/1347
58	AG	0.09	0/1763	0.26	0/2368
59	AI	0.17	0/2707	0.31	0/3636
60	AJ	0.11	0/1181	0.30	0/1597
61	AK	0.09	0/1027	0.26	0/1389
62	AL	0.10	0/858	0.28	0/1152
63	AN	0.08	0/874	0.24	0/1171
64	AO	0.10	0/1473	0.31	0/1970
65	AP	0.10	0/954	0.30	0/1284
66	AQ	0.09	0/894	0.24	0/1213
67	AR	0.10	0/802	0.32	0/1079
68	AU	0.08	0/745	0.26	0/993
70	Aa	0.10	0/2428	0.29	0/3279
71	Ab	0.09	0/1126	0.26	0/1514
72	Ac	0.10	0/1399	0.32	0/1881
73	Ad	0.10	0/1490	0.27	0/2005
74	Ae	0.12	0/3171	0.34	1/4292 (0.0%)
75	Af	0.10	0/790	0.29	0/1064
76	Ag	0.10	0/2945	0.30	0/3984

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	Ah	0.10	0/1045	0.29	0/1409
78	Ai	0.09	0/841	0.26	0/1121
79	Aj	0.08	0/1835	0.27	0/2484
80	Ak	0.10	0/2268	0.29	0/3069
81	Am	0.09	0/947	0.30	0/1268
82	An	0.09	0/650	0.28	0/858
83	Ao	0.10	0/4458	0.32	0/6036
84	Ap	0.10	0/1616	0.27	0/2195
85	CL	0.10	0/319	0.34	0/435
85	DL	0.09	0/212	0.32	0/286
85	EL	0.10	0/221	0.34	0/297
85	FL	0.10	0/212	0.31	0/286
85	GL	0.09	0/212	0.31	0/286
85	HL	0.10	0/203	0.32	0/273
86	AV	0.91	33/1561 (2.1%)	0.41	0/2411
86	AY	0.91	33/1561 (2.1%)	0.41	0/2411
87	AX	1.07	3/131 (2.3%)	0.69	0/200
All	All	0.16	69/183686 (0.0%)	0.27	6/261293 (0.0%)

All (69) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	AV	14	U	C1'-N1	6.58	1.58	1.48
86	AV	16	U	C1'-N1	6.51	1.57	1.47
86	AY	16	U	C1'-N1	6.50	1.57	1.47
86	AY	14	U	C1'-N1	6.49	1.58	1.48
86	AY	40	U	C1'-N1	6.48	1.58	1.48
86	AV	41	U	C1'-N1	6.45	1.58	1.48
86	AY	5	U	C1'-N1	6.44	1.58	1.48
86	AV	5	U	C1'-N1	6.43	1.58	1.48
86	AV	40	U	C1'-N1	6.43	1.58	1.48
86	AY	41	U	C1'-N1	6.41	1.58	1.48
87	AX	5	U	C1'-N1	6.37	1.58	1.48
86	AY	32	U	C1'-N1	6.26	1.57	1.48
86	AV	54	U	C1'-N1	6.24	1.57	1.48
86	AY	54	U	C1'-N1	6.24	1.57	1.48
86	AY	19	U	C1'-N1	6.23	1.57	1.48
86	AV	19	U	C1'-N1	6.22	1.57	1.48
86	AY	42	U	C1'-N1	6.21	1.57	1.48
86	AV	42	U	C1'-N1	6.21	1.57	1.48
86	AY	65	U	C1'-N1	6.20	1.57	1.48
86	AV	34	U	C1'-N1	6.20	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	AV	32	U	C1'-N1	6.18	1.57	1.48
86	AV	65	U	C1'-N1	6.18	1.57	1.48
86	AV	23	U	C1'-N1	6.17	1.57	1.48
86	AY	34	U	C1'-N1	6.17	1.57	1.48
86	AY	1	U	C1'-N1	6.13	1.57	1.48
86	AV	1	U	C1'-N1	6.13	1.57	1.48
86	AY	23	U	C1'-N1	6.12	1.57	1.48
86	AV	10	U	C1'-N1	6.11	1.57	1.48
86	AV	4	U	C1'-N1	6.11	1.57	1.48
86	AY	10	U	C1'-N1	6.09	1.57	1.48
86	AY	15	U	C1'-N1	6.09	1.56	1.47
86	AV	15	U	C1'-N1	6.09	1.56	1.47
86	AV	48	U	C1'-N1	6.06	1.57	1.48
86	AV	6	U	C1'-N1	6.06	1.57	1.48
86	AY	4	U	C1'-N1	6.05	1.57	1.48
86	AY	6	U	C1'-N1	6.04	1.57	1.48
86	AV	18	U	C1'-N1	6.03	1.57	1.48
86	AY	18	U	C1'-N1	6.02	1.57	1.48
86	AY	48	U	C1'-N1	6.00	1.57	1.48
86	AV	45	U	C1'-N1	5.97	1.57	1.48
86	AV	49	U	C1'-N1	5.93	1.57	1.48
86	AY	45	U	C1'-N1	5.93	1.57	1.48
86	AY	49	U	C1'-N1	5.88	1.57	1.48
86	AV	11	U	C1'-N1	5.88	1.57	1.48
86	AY	26	U	C1'-N1	5.86	1.57	1.48
86	AY	43	U	C1'-N1	5.86	1.57	1.48
86	AV	20	U	C1'-N1	5.84	1.57	1.48
86	AV	43	U	C1'-N1	5.83	1.57	1.48
86	AY	28	U	C1'-N1	5.82	1.57	1.48
86	AY	11	U	C1'-N1	5.82	1.57	1.48
86	AY	27	U	C1'-N1	5.82	1.57	1.48
86	AV	26	U	C1'-N1	5.81	1.57	1.48
86	AY	20	U	C1'-N1	5.80	1.57	1.48
86	AV	28	U	C1'-N1	5.79	1.57	1.48
86	AV	39	U	C1'-N1	5.79	1.57	1.48
86	AV	52	U	C1'-N1	5.79	1.57	1.48
86	AY	39	U	C1'-N1	5.78	1.57	1.48
86	AV	27	U	C1'-N1	5.77	1.57	1.48
86	AY	52	U	C1'-N1	5.77	1.57	1.48
86	AY	63	U	C1'-N1	5.76	1.57	1.48
86	AV	2	U	C1'-N1	5.75	1.57	1.48
86	AY	2	U	C1'-N1	5.74	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	AY	7	U	C1'-N1	5.74	1.56	1.47
86	AV	7	U	C1'-N1	5.71	1.56	1.47
86	AV	63	U	C1'-N1	5.70	1.57	1.48
86	AV	68	U	C1'-N1	5.54	1.56	1.48
86	AY	68	U	C1'-N1	5.50	1.56	1.48
87	AX	1	U	C1'-N1	5.12	1.56	1.48
87	AX	2	U	C1'-N1	5.12	1.56	1.48

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	Bf	80	PRO	N-CA-CB	7.59	111.22	103.25
47	Bu	167	PRO	N-CA-CB	7.44	111.06	103.25
33	Bf	78	PRO	N-CA-CB	7.42	111.04	103.25
74	Ae	342	PRO	N-CA-CB	7.35	110.97	103.25
45	Bq	59	PRO	N-CA-CB	6.63	110.30	103.00
5	B4	87	PRO	N-CA-CB	6.36	110.04	103.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B0	857	0	878	16	0
2	B1	2036	0	2058	17	0
3	B2	1548	0	1583	25	0
4	B3	968	0	1018	25	0
5	B4	474	0	454	20	0
6	B5	902	0	916	21	0
7	B6	425	0	471	6	0
8	BB	1427	0	726	22	0
9	B7	387	0	413	13	0
10	BD	1860	0	1923	30	0
11	BE	2420	0	2418	52	0
12	BF	2011	0	2049	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	BI	805	0	845	11	0
14	BJ	1705	0	1804	42	0
15	BK	1303	0	1343	15	0
16	BN	1444	0	1437	31	0
17	BO	896	0	946	15	0
18	BP	2312	0	2373	45	0
19	BQ	1803	0	1841	26	0
20	BR	1240	0	1260	23	0
21	BS	1168	0	1159	30	0
22	BT	1890	0	1898	23	0
23	BU	1159	0	1228	21	0
24	BV	1231	0	1278	26	0
25	BW	1374	0	1405	18	0
26	BX	1181	0	1139	20	0
27	BY	1678	0	1683	31	0
28	Ba	3173	0	3153	58	0
29	Bb	2952	0	2840	52	0
30	Bc	2408	0	2415	47	0
31	Bd	1183	0	1200	42	0
32	Be	972	0	971	19	0
33	Bf	827	0	736	15	0
34	Bg	1167	0	1173	25	0
35	Bh	2319	0	2332	33	0
36	B8	833	0	883	17	0
37	Bi	2138	0	2139	37	0
38	Bj	1872	0	1882	50	0
39	Bk	1327	0	1348	33	0
40	Bl	1097	0	1080	19	0
41	Bm	893	0	878	14	0
42	Bn	837	0	860	16	0
43	Bo	772	0	773	11	0
44	Bp	742	0	749	4	0
45	Bq	672	0	647	20	0
46	Bt	780	0	792	23	0
47	Bu	1198	0	1192	13	0
48	Bv	1131	0	1093	18	0
49	Bw	3126	0	3153	50	0
50	Bx	1325	0	1354	28	0
51	AA	20411	0	10344	339	0
52	B9	335	0	359	6	0
53	BA	32844	0	16616	562	0
54	AB	1762	0	1774	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	AC	1075	0	1087	25	0
56	AE	2732	0	2774	54	0
57	AF	981	0	1012	20	0
58	AG	1721	0	1747	21	0
59	AI	2650	0	2613	45	0
60	AJ	1155	0	1193	29	0
61	AK	1007	0	1042	21	0
62	AL	840	0	890	15	0
63	AN	858	0	883	20	0
64	AO	1448	0	1536	16	0
65	AP	932	0	951	23	0
66	AQ	875	0	931	11	0
67	AR	784	0	813	15	0
68	AU	734	0	745	17	0
69	AZ	90	0	20	0	0
70	Aa	2378	0	2392	46	0
71	Ab	1101	0	1118	12	0
72	Ac	1367	0	1385	21	0
73	Ad	1467	0	1466	25	0
74	Ae	3109	0	3029	63	0
75	Af	778	0	791	14	0
76	Ag	2875	0	2886	68	0
77	Ah	1015	0	969	23	0
78	Ai	824	0	842	17	0
79	Aj	1788	0	1799	36	0
80	Ak	2222	0	2270	50	0
81	Am	930	0	959	10	0
82	An	639	0	709	6	0
83	Ao	4527	0	4391	73	0
84	Ap	1564	0	1531	30	0
85	CL	317	0	309	9	0
85	DL	213	0	234	4	0
85	EL	222	0	247	10	0
85	FL	213	0	234	6	0
85	GL	213	0	234	4	0
85	HL	204	0	221	8	0
86	AV	1419	0	715	62	0
86	AY	1419	0	715	67	0
87	AX	120	0	61	11	0
88	AA	102	0	0	0	0
88	AB	1	0	0	0	0
88	AL	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	Ag	1	0	0	0	0
88	Am	1	0	0	0	0
88	An	1	0	0	0	0
88	B3	1	0	0	0	0
88	BA	203	0	0	0	0
88	BB	1	0	0	0	0
88	BD	3	0	0	0	0
88	BE	1	0	0	0	0
88	BJ	1	0	0	0	0
88	BP	2	0	0	0	0
88	BQ	1	0	0	0	0
88	Be	2	0	0	0	0
88	Bl	1	0	0	0	0
88	Bt	1	0	0	0	0
89	AR	1	0	0	0	0
89	Ac	1	0	0	0	0
89	Ap	1	0	0	0	0
89	B5	1	0	0	0	0
89	B9	1	0	0	0	0
89	Bx	1	0	0	0	0
90	AA	14	0	26	1	0
90	BA	28	0	52	2	0
91	BA	24	0	11	0	0
92	Ag	32	0	12	1	0
93	Ag	3	0	0	0	0
All	All	174837	0	147127	2628	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 (2628) 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)
86:AV:52:U:H5	86:AV:53:U:C4	1.74	1.06
86:AY:52:U:H5	86:AY:53:U:C4	1.74	1.05
86:AV:9:U:O2'	86:AV:10:U:C5	2.10	1.05
86:AY:9:U:O2'	86:AY:10:U:C5	2.10	1.03
51:AA:924:U:OP2	87:AX:1:U:H4'	1.60	1.01
51:AA:405:G:H1	51:AA:452:C:HO2'	1.04	0.97
51:AA:924:U:P	87:AX:1:U:H4'	2.08	0.93
86:AV:52:U:C5	86:AV:53:U:C4	2.57	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:AY:52:U:C5	86:AY:53:U:C4	2.57	0.91
26:BX:2:ALA:N	26:BX:7:TYR:HH	1.75	0.83
52:B9:76:CYS:SG	52:B9:89:CYS:HB2	2.17	0.83
86:AV:64:U:C4	86:AV:65:U:O4	2.32	0.83
86:AY:64:U:C4	86:AY:65:U:O4	2.32	0.83
51:AA:924:U:OP2	87:AX:1:U:C4'	2.27	0.82
37:Bi:39:LYS:HE2	53:BA:834:C:H41	1.44	0.81
62:AL:72:LYS:CE	87:AX:5:U:O2'	2.30	0.79
62:AL:72:LYS:HE2	87:AX:5:U:O2'	1.82	0.79
86:AY:52:U:H5	86:AY:53:U:O4	1.66	0.79
86:AV:52:U:H5	86:AV:53:U:O4	1.66	0.79
86:AY:16:U:H5	86:AY:44:U:C4	2.01	0.78
86:AV:16:U:H5	86:AV:44:U:C4	2.01	0.78
86:AY:50:U:O4	86:AY:54:U:H5	1.67	0.77
53:BA:118:U:H3	53:BA:129:A:H62	1.32	0.77
86:AV:50:U:O4	86:AV:54:U:H5	1.67	0.77
53:BA:1236:C:H2'	53:BA:1237:A:H8	1.50	0.77
51:AA:227:A:H61	51:AA:270:C:H42	1.30	0.76
86:AV:16:U:H5	86:AV:44:U:O4	1.68	0.76
53:BA:1236:C:H2'	53:BA:1237:A:C8	2.21	0.76
28:Ba:126:THR:HG22	28:Ba:372:ASN:HB2	1.68	0.76
53:BA:920:C:H42	53:BA:924:G:H22	1.32	0.76
86:AV:16:U:C5	86:AV:44:U:O4	2.39	0.76
86:AY:16:U:H5	86:AY:44:U:O4	1.68	0.75
86:AY:16:U:C5	86:AY:44:U:O4	2.39	0.75
51:AA:536:C:O2	51:AA:829:G:N2	2.12	0.75
45:Bq:126:ILE:HD11	53:BA:548:A:H5''	1.66	0.75
53:BA:529:G:H1'	53:BA:549:C:H1'	1.69	0.74
53:BA:1233:A:N6	86:AY:71:A:O3'	2.21	0.74
14:BJ:101:HIS:HB3	14:BJ:150:HIS:HB3	1.70	0.74
51:AA:50:U:H2'	51:AA:51:G:H8	1.53	0.73
53:BA:486:A:H61	53:BA:582:C:H42	1.36	0.73
53:BA:392:U:H2'	53:BA:393:A:H8	1.53	0.73
86:AY:4:U:H2'	86:AY:5:U:H6	1.54	0.73
86:AV:48:U:H2'	86:AV:49:U:C6	2.25	0.72
86:AY:48:U:H2'	86:AY:49:U:C6	2.25	0.72
51:AA:84:A:N6	51:AA:98:A:O2'	2.23	0.72
72:Ac:105:ILE:HG13	72:Ac:106:LEU:HG	1.71	0.72
27:BY:161:ARG:HH21	27:BY:165:ILE:HB	1.55	0.71
11:BE:69:ASN:ND2	53:BA:1569:A:N1	2.37	0.71
38:Bj:264:LEU:HD13	38:Bj:269:LEU:HB3	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:89:U:H3	51:AA:93:A:H61	1.37	0.71
86:AV:4:U:H2'	86:AV:5:U:H6	1.54	0.71
24:BV:150:LYS:HE3	33:Bf:58:ILE:HD11	1.71	0.71
31:Bd:173:ARG:HH22	38:Bj:56:PRO:HB3	1.54	0.71
83:Ao:614:LEU:HD22	83:Ao:633:LEU:HD11	1.71	0.71
37:Bi:121:SER:HG	37:Bi:199:CYS:HG	1.38	0.71
49:Bw:146:GLN:HA	49:Bw:150:PHE:HB2	1.72	0.71
53:BA:831:U:OP2	53:BA:836:A:N6	2.22	0.70
70:Aa:184:SER:H	70:Aa:192:ARG:HH12	1.36	0.70
35:Bh:97:TYR:HB2	35:Bh:181:SER:HA	1.72	0.70
53:BA:803:A:N3	53:BA:805:C:N4	2.38	0.70
19:BQ:33:LEU:HD21	45:Bq:122:ARG:HG3	1.72	0.70
53:BA:112:A:N6	53:BA:115:U:OP2	2.25	0.69
38:Bj:55:ARG:HG3	38:Bj:238:LEU:HD23	1.75	0.69
53:BA:1245:G:O2'	86:AY:69:C:O5'	2.10	0.69
27:BY:191:LEU:HG	32:Be:93:THR:HG21	1.74	0.69
42:Bn:69:HIS:HD2	42:Bn:71:LYS:HG3	1.56	0.69
53:BA:877:U:H5''	53:BA:878:G:H5'	1.75	0.69
83:Ao:427:SER:HA	83:Ao:467:LEU:HD11	1.72	0.69
86:AY:3:U:C4	86:AY:4:U:O4	2.46	0.69
3:B2:228:LEU:HD11	53:BA:11:G:H5'	1.75	0.69
4:B3:78:ARG:HH12	19:BQ:225:GLY:HA3	1.58	0.69
6:B5:140:GLN:NE2	6:B5:176:GLU:O	2.26	0.68
16:BN:27:PRO:HG2	16:BN:30:LYS:HB2	1.76	0.68
60:AJ:176:LYS:HB3	80:Ak:153:ILE:HB	1.75	0.68
65:AP:118:VAL:HG11	84:Ap:236:PRO:HB2	1.75	0.68
83:Ao:469:CYS:HB3	83:Ao:502:ALA:HB2	1.74	0.68
18:BP:72:THR:HB	18:BP:77:ARG:HH21	1.58	0.68
51:AA:195:G:H5''	65:AP:20:ARG:HB2	1.74	0.68
4:B3:69:VAL:HG12	4:B3:119:ILE:HG12	1.76	0.68
29:Bb:221:LEU:HB2	29:Bb:267:ARG:HG3	1.75	0.68
5:B4:38:ARG:NH1	31:Bd:132:GLU:OE1	2.27	0.68
5:B4:73:ARG:NH1	39:Bk:147:ASP:OD1	2.26	0.68
86:AV:3:U:C4	86:AV:4:U:O4	2.46	0.68
48:Bv:63:ARG:NH2	53:BA:95:U:OP1	2.27	0.68
49:Bw:53:ALA:O	49:Bw:62:ARG:NH2	2.26	0.68
53:BA:789:A:N6	53:BA:1000:A:O2'	2.27	0.68
70:Aa:194:ILE:HG13	70:Aa:211:ARG:HG3	1.76	0.68
51:AA:924:U:C4	87:AX:2:U:H5'	2.29	0.68
21:BS:68:TRP:CD1	21:BS:68:TRP:H	2.12	0.67
51:AA:255:G:OP1	56:AE:117:ARG:NH1	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:821:A:OP1	58:AG:177:ARG:NH1	2.27	0.67
86:AY:16:U:C5	86:AY:44:U:C4	2.83	0.67
21:BS:173:ARG:HE	53:BA:1218:U:H5'	1.59	0.67
31:Bd:79:SER:O	39:Bk:201:ARG:NH2	2.26	0.67
53:BA:1233:A:N6	86:AY:71:A:HO3'	1.93	0.67
1:B0:121:PRO:HA	29:Bb:50:LYS:HG3	1.76	0.67
5:B4:62:GLY:HA3	31:Bd:182:ILE:H	1.59	0.67
29:Bb:27:ARG:N	53:BA:1168:A:N1	2.43	0.67
37:Bi:267:PRO:HG2	37:Bi:270:ALA:HB2	1.76	0.67
38:Bj:256:SER:O	38:Bj:260:LEU:HB2	1.94	0.67
71:Ab:71:ARG:HH12	75:Af:91:THR:HG22	1.59	0.67
74:Ae:325:ARG:HH21	74:Ae:372:LEU:HB3	1.58	0.67
77:Ah:284:ARG:HH21	83:Ao:451:ILE:HB	1.59	0.67
53:BA:889:C:H41	53:BA:1082:U:H4'	1.59	0.67
11:BE:238:ARG:NH2	53:BA:993:U:OP2	2.28	0.66
83:Ao:485:ILE:HD12	83:Ao:491:PRO:HG3	1.75	0.66
40:Bl:138:THR:HG22	40:Bl:149:VAL:HG12	1.76	0.66
51:AA:342:C:OP1	61:AK:96:ASN:ND2	2.28	0.66
76:Ag:191:LYS:HE3	76:Ag:226:GLU:HG2	1.77	0.66
85:HL:76:LEU:HD12	85:HL:79:ILE:HD11	1.78	0.66
86:AV:16:U:C5	86:AV:44:U:C4	2.82	0.66
55:AC:76:LEU:O	63:AN:103:ARG:NH2	2.26	0.66
10:BD:258:ILE:O	53:BA:843:C:O2'	2.13	0.66
46:Bt:78:GLN:NE2	53:BA:420:U:O4	2.28	0.66
51:AA:724:U:OP1	58:AG:195:LYS:NZ	2.28	0.66
28:Ba:160:HIS:HA	28:Ba:164:TRP:HB2	1.78	0.66
34:Bg:28:ARG:HG2	34:Bg:78:GLU:HB2	1.78	0.66
51:AA:882:A:O2'	74:Ae:140:ASN:ND2	2.28	0.66
53:BA:743:U:H3'	53:BA:744:A:H5''	1.78	0.66
85:FL:76:LEU:HD12	85:FL:79:ILE:HD11	1.78	0.66
12:BF:170:ARG:NH2	53:BA:222:G:N7	2.42	0.66
51:AA:374:C:OP2	81:Am:9:ARG:NH2	2.29	0.66
23:BU:33:GLY:O	23:BU:36:ASN:ND2	2.28	0.66
30:Bc:175:ALA:HB2	30:Bc:316:SER:HB2	1.76	0.66
42:Bn:35:ARG:NH1	42:Bn:37:THR:O	2.28	0.66
86:AV:4:U:H2'	86:AV:5:U:C6	2.30	0.66
86:AY:4:U:H2'	86:AY:5:U:C6	2.30	0.66
32:Be:44:ARG:HH12	49:Bw:157:ALA:HB3	1.59	0.66
53:BA:198:U:H2'	53:BA:199:A:H8	1.61	0.66
53:BA:388:A:H2'	53:BA:389:A:H8	1.61	0.66
27:BY:146:VAL:HG22	27:BY:153:ILE:HG22	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Bu:52:SER:HB3	47:Bu:57:THR:HG21	1.78	0.65
80:Ak:83:VAL:O	80:Ak:101:LYS:NZ	2.28	0.65
4:B3:75:THR:HG21	4:B3:86:ILE:HG21	1.78	0.65
14:BJ:47:LEU:HD22	19:BQ:226:ILE:HG12	1.78	0.65
30:Bc:278:SER:O	30:Bc:317:ARG:NH1	2.29	0.65
51:AA:16:U:O2'	51:AA:294:A:N6	2.28	0.65
86:AY:52:U:C5	86:AY:53:U:O4	2.48	0.65
51:AA:551:G:N2	51:AA:778:G:O2'	2.29	0.65
86:AY:40:U:H2'	86:AY:41:U:C6	2.31	0.65
75:Af:105:ILE:HG12	75:Af:115:ILE:HG12	1.78	0.65
86:AV:9:U:O2'	86:AV:10:U:H5	1.77	0.65
86:AV:40:U:H2'	86:AV:41:U:C6	2.31	0.65
85:DL:76:LEU:HD12	85:DL:79:ILE:HD11	1.78	0.65
51:AA:272:A:H4'	51:AA:274:A:H4'	1.78	0.65
55:AC:75:ASN:HD21	63:AN:104:TRP:HE1	1.45	0.65
4:B3:134:MET:HG3	43:Bo:75:ARG:HE	1.61	0.65
10:BD:76:PRO:HB2	10:BD:103:ARG:HD2	1.79	0.65
53:BA:1369:U:H5''	53:BA:1370:U:H5'	1.78	0.65
85:GL:76:LEU:HD12	85:GL:79:ILE:HD11	1.78	0.65
18:BP:142:GLU:HG3	18:BP:162:LEU:HD23	1.77	0.65
8:BB:35:G:N2	39:Bk:124:SER:O	2.30	0.65
15:BK:25:ARG:HB3	15:BK:28:GLN:HB2	1.78	0.65
4:B3:148:ARG:HB3	4:B3:151:LEU:HD21	1.79	0.65
12:BF:132:GLY:HA3	37:Bi:42:THR:HG21	1.78	0.65
51:AA:11:G:H1	51:AA:524:U:H3	1.45	0.65
14:BJ:121:ILE:HD13	14:BJ:164:MET:HE3	1.78	0.64
18:BP:44:ARG:NH2	53:BA:602:G:N7	2.41	0.64
53:BA:1066:A:H2'	53:BA:1067:G:H8	1.61	0.64
85:EL:76:LEU:HD12	85:EL:79:ILE:HD11	1.78	0.64
21:BS:122:VAL:HG13	21:BS:157:SER:HA	1.79	0.64
31:Bd:171:PHE:HB3	39:Bk:186:VAL:HB	1.79	0.64
38:Bj:214:LYS:HZ3	38:Bj:230:LYS:HD3	1.62	0.64
75:Af:141:VAL:HA	75:Af:173:LEU:HA	1.80	0.64
52:B9:69:LEU:H	53:BA:560:A:H62	1.45	0.64
86:AY:7:U:O2'	86:AY:45:U:O4'	2.15	0.64
76:Ag:358:TYR:O	76:Ag:362:ASN:ND2	2.31	0.64
36:B8:113:ARG:NH2	53:BA:84:G:OP2	2.31	0.64
86:AY:50:U:C4	86:AY:54:U:H5	2.15	0.64
51:AA:202:A:N1	79:Aj:53:ARG:NH2	2.46	0.64
51:AA:579:A:OP2	63:AN:108:ARG:NH1	2.31	0.64
60:AJ:184:ILE:HD11	80:Ak:229:THR:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Bj:162:ARG:HB3	38:Bj:251:HIS:HB2	1.80	0.64
51:AA:924:U:P	87:AX:1:U:C4'	2.84	0.64
72:Ac:132:ARG:NH1	72:Ac:136:LEU:O	2.31	0.64
12:BF:142:ARG:NH2	53:BA:129:A:OP1	2.31	0.64
26:BX:145:PRO:HG3	37:Bi:176:ILE:HD13	1.80	0.64
34:Bg:133:PHE:HZ	35:Bh:261:SER:HB2	1.63	0.64
51:AA:647:A:OP2	59:AI:221:GLN:NE2	2.31	0.64
85:CL:60:TYR:HB3	85:CL:64:ILE:HD11	1.80	0.64
23:BU:146:VAL:HG11	33:Bf:56:ARG:HG2	1.80	0.63
28:Ba:174:GLU:HA	28:Ba:296:SER:HB2	1.78	0.63
51:AA:57:A:C8	79:Aj:51:PRO:HB3	2.33	0.63
51:AA:884:C:N4	74:Ae:144:LEU:O	2.31	0.63
53:BA:1418:G:N2	53:BA:1421:A:OP2	2.26	0.63
80:Ak:63:ALA:HB3	80:Ak:66:GLN:HB2	1.80	0.63
6:B5:156:THR:HG22	6:B5:173:ARG:HB3	1.80	0.63
18:BP:203:ARG:HH21	18:BP:262:PRO:HA	1.62	0.63
51:AA:492:U:OP1	82:An:139:ASN:ND2	2.31	0.63
51:AA:884:C:OP1	74:Ae:433:ARG:NH1	2.32	0.63
25:BW:147:ARG:HH12	53:BA:639:U:H5'	1.63	0.63
26:BX:37:GLU:HB3	26:BX:104:THR:HG23	1.80	0.63
35:Bh:52:ARG:NH1	53:BA:148:A:OP1	2.31	0.63
51:AA:194:U:H2'	51:AA:195:G:H8	1.62	0.63
51:AA:942:G:N2	51:AA:945:A:OP2	2.31	0.63
76:Ag:137:LEU:HD11	76:Ag:260:ALA:HB1	1.80	0.63
86:AV:7:U:O2'	86:AV:45:U:O4'	2.15	0.63
57:AF:29:LEU:HG	57:AF:78:MET:HE2	1.79	0.63
73:Ad:166:THR:O	73:Ad:176:ARG:NH2	2.31	0.63
86:AY:9:U:O2'	86:AY:10:U:H5	1.77	0.63
11:BE:239:ARG:NH1	53:BA:1046:A:OP1	2.31	0.63
25:BW:105:GLU:OE1	25:BW:116:LYS:NZ	2.31	0.63
51:AA:587:U:O2	51:AA:707:A:N6	2.31	0.63
56:AE:374:ARG:HB3	56:AE:377:CYS:HB2	1.80	0.63
14:BJ:48:MET:SD	19:BQ:250:ARG:NH1	2.70	0.63
18:BP:208:GLU:HB3	48:Bv:103:LEU:HD21	1.80	0.63
51:AA:25:U:H2'	51:AA:26:A:H8	1.63	0.63
51:AA:29:A:H2'	51:AA:30:A:H8	1.64	0.63
53:BA:869:G:O2'	53:BA:966:U:OP2	2.17	0.63
59:AI:296:VAL:HG12	59:AI:331:CYS:HB2	1.80	0.63
65:AP:111:ARG:NH2	70:Aa:168:LYS:O	2.30	0.63
14:BJ:95:MET:HB2	14:BJ:159:PRO:HB3	1.81	0.63
51:AA:536:C:N3	51:AA:829:G:N1	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Aa:105:THR:HG22	70:Aa:290:PHE:HB3	1.79	0.63
74:Ae:241:GLU:OE2	74:Ae:278:GLN:NE2	2.32	0.63
10:BD:113:ARG:O	10:BD:148:ARG:NH2	2.32	0.63
11:BE:69:ASN:HD21	11:BE:154:HIS:HE1	1.46	0.63
16:BN:26:GLN:NE2	16:BN:147:GLN:OE1	2.32	0.63
22:BT:96:ARG:NH1	22:BT:285:GLU:OE1	2.32	0.63
53:BA:1404:G:N2	53:BA:1404:G:OP2	2.31	0.63
10:BD:177:ALA:HB1	10:BD:245:VAL:HG11	1.81	0.62
11:BE:221:ARG:NH1	11:BE:257:MET:O	2.32	0.62
76:Ag:107:LEU:HD23	76:Ag:140:ILE:HG13	1.80	0.62
14:BJ:237:VAL:HA	85:GL:76:LEU:HD11	1.79	0.62
29:Bb:279:ILE:HD11	29:Bb:310:ALA:HB3	1.81	0.62
45:Bq:64:ASP:H	45:Bq:65:PRO:HD2	1.64	0.62
70:Aa:285:ARG:NH2	70:Aa:309:ASP:OD2	2.32	0.62
86:AV:50:U:C4	86:AV:54:U:H5	2.15	0.62
29:Bb:160:ASP:OD2	29:Bb:267:ARG:NH2	2.32	0.62
38:Bj:159:LEU:HD11	38:Bj:252:HIS:HB2	1.81	0.62
51:AA:800:G:H2'	51:AA:801:A:C8	2.35	0.62
56:AE:147:PRO:O	56:AE:155:GLN:NE2	2.33	0.62
46:Bt:23:ARG:NH1	53:BA:464:U:OP1	2.32	0.62
53:BA:1152:G:H2'	53:BA:1153:G:H8	1.65	0.62
60:AJ:172:VAL:HB	80:Ak:157:ASP:HB3	1.81	0.62
74:Ae:142:TRP:HZ2	79:Aj:76:LEU:HD11	1.63	0.62
28:Ba:367:ASP:O	28:Ba:371:LYS:NZ	2.33	0.62
49:Bw:240:GLN:OE1	49:Bw:347:ARG:NH1	2.33	0.62
1:B0:92:LEU:HB3	21:BS:66:ARG:HH21	1.63	0.62
42:Bn:77:PRO:HG2	42:Bn:80:LEU:HB2	1.82	0.62
53:BA:52:A:O2'	53:BA:349:A:N3	2.32	0.62
53:BA:569:C:N4	53:BA:1020:C:O2	2.33	0.62
53:BA:1246:A:C6	86:AY:70:C:H5	2.18	0.62
74:Ae:290:LEU:HG	74:Ae:292:GLN:H	1.64	0.62
4:B3:74:SER:HB3	53:BA:472:U:H5''	1.81	0.62
53:BA:1278:C:H2'	53:BA:1279:G:H8	1.65	0.62
72:Ac:51:ASN:ND2	72:Ac:95:ASN:OD1	2.33	0.62
74:Ae:304:GLU:HG3	74:Ae:374:ARG:HH21	1.64	0.62
80:Ak:166:ARG:HG2	83:Ao:134:GLU:HG3	1.82	0.62
9:B7:58:PRO:HB2	53:BA:672:G:H4'	1.81	0.62
31:Bd:97:LYS:HB3	38:Bj:84:TYR:HB2	1.82	0.62
53:BA:935:C:H4'	53:BA:1426:G:H1'	1.82	0.62
76:Ag:230:MET:HG3	76:Ag:231:ARG:HG3	1.81	0.62
83:Ao:379:ILE:HD12	83:Ao:396:ILE:HG23	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BJ:85:GLU:OE2	14:BJ:124:LYS:NZ	2.33	0.61
39:Bk:90:VAL:HG12	39:Bk:160:SER:HA	1.82	0.61
68:AU:67:GLU:HG3	75:Af:155:LEU:HG	1.82	0.61
11:BE:152:VAL:O	53:BA:1569:A:N6	2.33	0.61
20:BR:106:ARG:HD3	20:BR:136:LEU:HD11	1.81	0.61
53:BA:1248:C:N3	53:BA:1253:G:H1'	2.15	0.61
56:AE:191:ARG:O	84:Ap:78:ARG:NH1	2.32	0.61
57:AF:37:ARG:NH1	73:Ad:163:GLU:OE1	2.27	0.61
86:AV:52:U:C5	86:AV:53:U:O4	2.48	0.61
11:BE:45:SER:O	30:Bc:303:ARG:NH2	2.33	0.61
3:B2:172:ARG:NH1	53:BA:22:U:O4	2.33	0.61
53:BA:975:G:O2'	53:BA:977:G:OP2	2.17	0.61
62:AL:96:PRO:O	62:AL:127:ARG:NH1	2.34	0.61
50:Bx:70:CYS:SG	50:Bx:108:CYS:N	2.73	0.61
51:AA:798:A:H2'	51:AA:799:A:H8	1.65	0.61
56:AE:367:SER:OG	56:AE:392:ARG:NH1	2.33	0.61
80:Ak:268:LEU:HD13	80:Ak:271:ILE:HD11	1.83	0.61
83:Ao:275:PRO:HG3	83:Ao:306:LEU:HD11	1.83	0.61
83:Ao:376:HIS:HB2	83:Ao:418:PHE:HA	1.81	0.61
14:BJ:95:MET:HB3	14:BJ:156:SER:HB3	1.81	0.61
14:BJ:123:MET:HB2	14:BJ:152:LEU:HD11	1.83	0.61
21:BS:86:THR:O	21:BS:120:ARG:NH1	2.34	0.61
24:BV:88:ASN:ND2	24:BV:206:PRO:O	2.31	0.61
19:BQ:240:ARG:NH2	19:BQ:246:TYR:OH	2.34	0.61
29:Bb:240:ILE:HD12	29:Bb:245:VAL:HA	1.82	0.61
51:AA:826:C:H2'	51:AA:827:A:H8	1.66	0.61
51:AA:876:A:H5'	51:AA:877:A:H5'	1.82	0.61
62:AL:72:LYS:HE3	87:AX:5:U:O2'	2.01	0.61
83:Ao:543:HIS:HB2	83:Ao:588:ARG:HD3	1.81	0.61
49:Bw:63:VAL:HA	49:Bw:66:TRP:CD1	2.35	0.61
53:BA:135:G:N1	53:BA:138:A:OP2	2.31	0.61
53:BA:1026:A:O2'	53:BA:1277:G:N2	2.24	0.61
56:AE:305:MET:HE3	56:AE:332:LEU:HD21	1.83	0.61
53:BA:1245:G:H2'	86:AY:69:C:H3'	1.82	0.61
23:BU:85:ALA:O	23:BU:89:ASN:ND2	2.33	0.61
30:Bc:210:ASP:OD2	30:Bc:268:ARG:NH1	2.33	0.61
53:BA:776:C:O2'	53:BA:778:A:N7	2.34	0.61
54:AB:71:PHE:O	54:AB:262:LYS:NZ	2.33	0.61
74:Ae:147:TRP:HB2	74:Ae:427:ARG:HH21	1.66	0.61
7:B6:42:THR:HG23	7:B6:57:VAL:HG12	1.83	0.60
38:Bj:140:ALA:HA	38:Bj:143:LYS:HE2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:1233:A:H62	53:BA:1248:C:H42	1.48	0.60
65:AP:29:ARG:NH1	65:AP:55:ASP:OD1	2.32	0.60
86:AV:60:U:H2'	86:AV:61:U:C6	2.36	0.60
6:B5:95:ARG:NH1	53:BA:157:A:OP2	2.35	0.60
11:BE:206:VAL:HG11	11:BE:289:VAL:HG13	1.82	0.60
51:AA:66:C:H42	73:Ad:27:ARG:HB2	1.66	0.60
51:AA:952:C:OP1	68:AU:52:ARG:NH2	2.33	0.60
76:Ag:323:LEU:HB2	76:Ag:326:GLU:HG2	1.83	0.60
86:AV:9:U:H1'	86:AV:42:U:H2'	1.83	0.60
29:Bb:194:THR:OG1	29:Bb:197:GLU:OE1	2.19	0.60
5:B4:46:ARG:HH22	31:Bd:87:ASP:HB3	1.65	0.60
14:BJ:97:ALA:HB3	14:BJ:154:LEU:HB2	1.84	0.60
30:Bc:183:ASP:HB3	30:Bc:186:LEU:HD13	1.84	0.60
51:AA:85:G:H2'	51:AA:86:A:H8	1.66	0.60
51:AA:283:U:OP1	56:AE:419:ARG:NH1	2.35	0.60
65:AP:42:PRO:HG2	65:AP:45:GLY:HA3	1.83	0.60
80:Ak:154:ASP:HB2	80:Ak:174:THR:HB	1.84	0.60
80:Ak:216:LEU:O	80:Ak:220:ASN:ND2	2.33	0.60
45:Bq:71:HIS:HA	45:Bq:86:LEU:HG	1.82	0.60
56:AE:187:VAL:HG12	56:AE:188:LYS:NZ	2.16	0.60
60:AJ:76:LEU:HD23	60:AJ:145:LEU:HD12	1.83	0.60
76:Ag:80:HIS:HB3	76:Ag:155:PRO:HG3	1.82	0.60
54:AB:137:ARG:HD3	71:Ab:34:ILE:HD11	1.84	0.60
67:AR:125:TYR:HB3	68:AU:9:ALA:HB2	1.84	0.60
9:B7:85:ARG:HE	9:B7:90:ARG:HG3	1.66	0.60
51:AA:584:C:O2	63:AN:86:ARG:NH1	2.35	0.60
55:AC:141:THR:HG21	83:Ao:114:GLU:HG3	1.83	0.60
62:AL:62:VAL:HA	62:AL:83:VAL:HG12	1.82	0.60
76:Ag:314:SER:HB2	76:Ag:317:LYS:HD2	1.84	0.60
86:AY:9:U:H1'	86:AY:42:U:H2'	1.83	0.60
51:AA:463:U:O4	51:AA:464:A:N6	2.35	0.60
56:AE:367:SER:HG	56:AE:392:ARG:NH1	2.00	0.60
74:Ae:359:ASP:OD2	84:Ap:217:ARG:NH1	2.34	0.60
12:BF:212:TRP:O	12:BF:258:THR:OG1	2.20	0.60
14:BJ:46:LYS:HE3	46:Bt:31:ALA:HB1	1.84	0.60
64:AO:71:SER:HA	64:AO:95:SER:HB2	1.84	0.60
12:BF:223:HIS:HA	12:BF:226:MET:HE3	1.84	0.59
16:BN:68:SER:OG	16:BN:71:LYS:NZ	2.28	0.59
26:BX:41:GLN:NE2	53:BA:703:A:OP1	2.27	0.59
37:Bi:211:GLN:HA	37:Bi:248:PHE:O	2.02	0.59
53:BA:229:A:H4'	53:BA:230:G:H5'	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:550:A:N7	53:BA:551:A:N6	2.49	0.59
60:AJ:107:LYS:HB3	60:AJ:144:GLU:HB2	1.84	0.59
86:AY:60:U:H2'	86:AY:61:U:C6	2.36	0.59
10:BD:102:GLN:NE2	53:BA:733:A:OP1	2.35	0.59
79:Aj:16:ARG:HD3	79:Aj:19:ARG:HH12	1.65	0.59
3:B2:119:GLN:NE2	53:BA:702:A:OP1	2.36	0.59
9:B7:85:ARG:NH1	53:BA:125:A:OP1	2.35	0.59
16:BN:111:MET:HE3	53:BA:571:A:H2	1.67	0.59
40:Bl:110:ILE:HD11	40:Bl:157:LEU:HD13	1.83	0.59
10:BD:103:ARG:NE	53:BA:735:A:OP1	2.36	0.59
39:Bk:48:TYR:N	53:BA:402:A:OP1	2.35	0.59
49:Bw:87:GLN:HE22	49:Bw:273:GLU:HA	1.68	0.59
53:BA:645:U:H2'	53:BA:646:A:H8	1.68	0.59
54:AB:215:ASN:OD1	71:Ab:15:ARG:NH1	2.32	0.59
70:Aa:205:LYS:NZ	84:Ap:182:GLY:O	2.34	0.59
86:AY:3:U:C4	86:AY:4:U:C4	2.91	0.59
25:BW:90:LYS:HD2	25:BW:93:ARG:HD2	1.85	0.59
45:Bq:68:LEU:HA	45:Bq:73:MET:HE2	1.85	0.59
86:AV:3:U:C4	86:AV:4:U:C4	2.91	0.59
1:B0:88:CYS:SG	53:BA:1207:C:O2'	2.60	0.59
6:B5:93:ARG:NH2	53:BA:642:G:OP1	2.36	0.59
43:Bo:23:ALA:N	53:BA:482:G:OP1	2.36	0.59
49:Bw:147:GLU:HG3	49:Bw:170:PHE:HA	1.85	0.59
76:Ag:267:LEU:O	76:Ag:293:ARG:NH2	2.36	0.59
86:AY:15:U:O2'	86:AY:16:U:H5''	2.03	0.59
14:BJ:214:LEU:HB2	85:DL:90:LEU:HD11	1.84	0.59
30:Bc:85:PRO:HG2	30:Bc:112:MET:HA	1.84	0.59
58:AG:119:LYS:NZ	76:Ag:364:TRP:O	2.33	0.59
34:Bg:73:PRO:HB2	34:Bg:89:ILE:HG13	1.84	0.59
51:AA:714:U:H2'	51:AA:715:G:H8	1.68	0.59
53:BA:165:A:H2'	53:BA:166:A:H8	1.68	0.59
2:B1:41:VAL:HG21	2:B1:83:GLU:HB3	1.84	0.59
8:BB:63:C:H2'	8:BB:64:A:H8	1.68	0.59
27:BY:25:ARG:HB3	27:BY:28:SER:HB3	1.85	0.59
42:Bn:32:PHE:HD1	53:BA:199:A:H5''	1.67	0.59
46:Bt:78:GLN:OE1	53:BA:391:A:N6	2.36	0.59
51:AA:327:U:O2'	51:AA:328:A:N7	2.35	0.59
63:AN:81:ASP:HA	63:AN:86:ARG:HD3	1.85	0.59
65:AP:51:LEU:HD13	65:AP:73:ILE:HG12	1.85	0.59
72:Ac:73:SER:OG	73:Ad:120:ARG:NH2	2.36	0.59
86:AV:15:U:O2'	86:AV:16:U:H5''	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B2:204:MET:HE3	3:B2:205:PRO:HD2	1.85	0.59
5:B4:51:ARG:HB3	38:Bj:85:SER:HB2	1.85	0.59
11:BE:215:PHE:O	53:BA:789:A:O2'	2.19	0.59
39:Bk:94:HIS:ND1	39:Bk:154:GLU:OE2	2.30	0.59
51:AA:287:C:N3	72:Ac:11:ARG:NH2	2.50	0.59
51:AA:430:A:OP1	86:AV:35:U:O2'	2.20	0.59
51:AA:902:C:H5''	82:An:171:ARG:HD2	1.85	0.59
53:BA:218:A:N6	53:BA:229:A:O4'	2.36	0.59
53:BA:1387:A:O2'	53:BA:1388:A:O5'	2.15	0.59
15:BK:61:LYS:HB3	45:Bq:79:LYS:HD2	1.84	0.58
38:Bj:58:LEU:HD12	38:Bj:153:LEU:HD22	1.85	0.58
53:BA:215:A:H61	53:BA:231:C:H42	1.51	0.58
83:Ao:404:MET:HG3	83:Ao:441:LEU:HB2	1.85	0.58
12:BF:66:ILE:HD11	12:BF:80:THR:HB	1.85	0.58
23:BU:34:ARG:NH2	53:BA:1014:A:OP1	2.35	0.58
28:Ba:35:VAL:HB	28:Ba:38:THR:HG22	1.83	0.58
82:An:173:LEU:HD12	82:An:191:THR:HG23	1.85	0.58
83:Ao:599:LEU:HB3	83:Ao:603:ARG:HH21	1.68	0.58
4:B3:77:ARG:NH1	53:BA:470:C:OP2	2.36	0.58
22:BT:183:LEU:HD21	22:BT:219:GLN:HG2	1.85	0.58
31:Bd:97:LYS:NZ	38:Bj:86:ASP:OD1	2.35	0.58
39:Bk:48:TYR:HE2	53:BA:409:A:H61	1.51	0.58
42:Bn:113:ARG:NH1	53:BA:348:G:O6	2.31	0.58
1:B0:71:ARG:NH1	53:BA:1162:G:OP1	2.36	0.58
19:BQ:140:MET:HE3	53:BA:447:A:H61	1.69	0.58
30:Bc:282:ASN:HD21	30:Bc:289:LEU:HD12	1.68	0.58
53:BA:376:A:N6	53:BA:1061:U:O2	2.36	0.58
55:AC:128:PRO:HD2	55:AC:131:LYS:HD3	1.84	0.58
63:AN:54:ILE:HG21	63:AN:75:ILE:HB	1.85	0.58
84:Ap:110:ASP:HB3	84:Ap:113:LEU:HD23	1.85	0.58
19:BQ:218:ILE:HG23	19:BQ:223:MET:HB2	1.85	0.58
53:BA:1224:C:H2'	53:BA:1225:A:H8	1.68	0.58
65:AP:59:ASN:HD21	65:AP:63:GLU:HB2	1.68	0.58
70:Aa:224:ARG:NH1	70:Aa:256:GLN:O	2.36	0.58
80:Ak:191:LYS:NZ	80:Ak:237:LYS:O	2.36	0.58
18:BP:109:ARG:NH2	40:Bl:91:MET:SD	2.72	0.58
30:Bc:204:ARG:NH2	30:Bc:276:GLU:OE2	2.36	0.58
51:AA:56:U:H1'	51:AA:198:C:H1'	1.86	0.58
66:AQ:6:SER:O	66:AQ:11:LYS:NZ	2.37	0.58
80:Ak:71:VAL:HG13	80:Ak:72:TYR:HD1	1.67	0.58
47:Bu:107:ALA:O	47:Bu:115:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:525:U:H2'	51:AA:526:G:H8	1.67	0.58
53:BA:29:A:N3	53:BA:35:A:O2'	2.34	0.58
53:BA:165:A:H2'	53:BA:166:A:C8	2.39	0.58
53:BA:416:U:H2'	53:BA:417:G:C8	2.39	0.58
54:AB:155:GLU:OE1	59:AI:163:HIS:ND1	2.37	0.58
31:Bd:67:ARG:HD2	86:AV:43:U:H5'	1.85	0.58
34:Bg:28:ARG:NH1	35:Bh:71:GLU:OE2	2.30	0.58
46:Bt:66:ARG:NH2	53:BA:417:G:OP1	2.34	0.58
53:BA:197:U:H2'	53:BA:198:U:H6	1.68	0.58
54:AB:219:VAL:HG22	54:AB:233:TYR:HB2	1.86	0.58
58:AG:61:GLU:HA	58:AG:64:TYR:HD1	1.69	0.58
4:B3:72:ILE:HD11	4:B3:118:ARG:HB2	1.86	0.58
9:B7:91:LYS:N	53:BA:118:U:OP1	2.35	0.58
21:BS:116:LEU:HD21	21:BS:124:ALA:HA	1.85	0.58
30:Bc:112:MET:HB2	30:Bc:267:PRO:HB3	1.86	0.58
53:BA:388:A:H2'	53:BA:389:A:C8	2.38	0.58
80:Ak:213:ARG:NH1	80:Ak:223:TYR:OH	2.37	0.58
25:BW:131:ASN:O	37:Bi:230:ARG:NH2	2.37	0.58
28:Ba:297:ALA:HB3	28:Ba:303:ARG:HG2	1.86	0.58
67:AR:95:ARG:HH12	67:AR:102:GLY:HA2	1.69	0.58
70:Aa:243:GLN:NE2	70:Aa:245:GLN:OE1	2.37	0.58
81:Am:88:SER:O	81:Am:92:ASN:ND2	2.36	0.58
86:AY:3:U:C2	86:AY:4:U:C5	2.92	0.58
12:BF:92:ARG:NH1	53:BA:215:A:OP1	2.34	0.57
14:BJ:128:ASN:ND2	53:BA:551:A:OP1	2.37	0.57
15:BK:60:ILE:HG22	45:Bq:78:TYR:HA	1.85	0.57
16:BN:177:ARG:HB2	50:Bx:36:ARG:HB3	1.86	0.57
31:Bd:141:GLU:HG3	38:Bj:274:ARG:HH21	1.68	0.57
35:Bh:80:GLN:O	35:Bh:210:ARG:NH2	2.37	0.57
53:BA:49:A:H2'	53:BA:50:A:C8	2.39	0.57
53:BA:243:A:N3	53:BA:1266:U:O2'	2.37	0.57
53:BA:881:C:H4'	53:BA:882:A:H5'	1.86	0.57
70:Aa:282:ASP:HA	70:Aa:285:ARG:HG2	1.85	0.57
71:Ab:89:ASN:HB3	71:Ab:92:PHE:HB2	1.85	0.57
86:AV:3:U:C2	86:AV:4:U:C5	2.92	0.57
1:B0:59:HIS:NE2	53:BA:412:C:O2'	2.37	0.57
10:BD:265:ARG:HE	10:BD:271:PRO:HD3	1.69	0.57
18:BP:132:SER:OG	53:BA:225:C:OP1	2.18	0.57
28:Ba:228:ALA:HB3	28:Ba:292:TYR:HB2	1.86	0.57
29:Bb:233:VAL:O	29:Bb:296:ARG:NH1	2.37	0.57
45:Bq:92:TYR:HB3	45:Bq:96:LEU:HD22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:86:A:O2'	65:AP:13:ARG:O	2.20	0.57
51:AA:868:U:H3	51:AA:902:C:H42	1.52	0.57
53:BA:672:G:H21	53:BA:759:C:H5'	1.68	0.57
60:AJ:75:ARG:H	60:AJ:175:THR:HB	1.69	0.57
60:AJ:122:LYS:O	63:AN:112:ARG:NH1	2.37	0.57
70:Aa:250:LEU:HD11	70:Aa:271:THR:HG21	1.85	0.57
70:Aa:344:ALA:HB1	70:Aa:348:HIS:HB3	1.85	0.57
28:Ba:395:LYS:HD3	53:BA:269:U:H5''	1.85	0.57
38:Bj:100:LYS:NZ	38:Bj:104:ASP:OD2	2.37	0.57
53:BA:843:C:N4	53:BA:871:A:O2'	2.38	0.57
74:Ae:273:LYS:NZ	74:Ae:324:ASP:OD1	2.32	0.57
79:Aj:43:ARG:HE	79:Aj:50:LEU:HD21	1.69	0.57
10:BD:258:ILE:HG23	10:BD:263:ARG:HB3	1.85	0.57
12:BF:114:THR:O	12:BF:156:ARG:NH1	2.38	0.57
22:BT:86:ARG:HH12	53:BA:1557:C:H4'	1.69	0.57
23:BU:16:ASP:OD2	53:BA:607:A:O2'	2.21	0.57
45:Bq:123:LYS:HG3	53:BA:531:G:H5''	1.86	0.57
73:Ad:45:PRO:O	84:Ap:223:ARG:NH2	2.31	0.57
79:Aj:171:ARG:NH2	84:Ap:188:PRO:O	2.38	0.57
4:B3:134:MET:HE1	43:Bo:78:VAL:HG21	1.86	0.57
51:AA:349:A:OP2	61:AK:121:ASN:ND2	2.36	0.57
86:AV:38:U:C2	86:AV:39:U:C5	2.93	0.57
28:Ba:135:LYS:HD2	28:Ba:239:VAL:HG23	1.87	0.57
29:Bb:161:LEU:HD13	29:Bb:271:LEU:HD11	1.87	0.57
33:Bf:127:GLY:N	53:BA:159:A:OP2	2.33	0.57
56:AE:320:ILE:HD11	56:AE:345:LEU:HD11	1.86	0.57
86:AY:1:U:H2'	86:AY:2:U:H6	1.69	0.57
14:BJ:49:ALA:HB1	46:Bt:32:LYS:HE2	1.85	0.57
49:Bw:344:ASP:OD2	49:Bw:383:ARG:NH2	2.38	0.57
53:BA:296:C:OP2	90:BA:1792:SPM:N1	2.37	0.57
53:BA:888:A:O2'	53:BA:891:A:N6	2.35	0.57
54:AB:99:ARG:NH1	71:Ab:50:ARG:O	2.37	0.57
76:Ag:259:VAL:HG23	76:Ag:305:ILE:HA	1.87	0.57
83:Ao:475:ASP:OD1	83:Ao:476:VAL:N	2.37	0.57
4:B3:104:PRO:HA	4:B3:107:ASN:HB2	1.86	0.57
24:BV:138:LEU:HD21	43:Bo:43:LEU:HD11	1.87	0.57
51:AA:61:G:N2	51:AA:198:C:O3'	2.37	0.57
53:BA:220:G:H1'	53:BA:231:C:H1'	1.87	0.57
53:BA:1450:U:H2'	53:BA:1451:U:C6	2.40	0.57
54:AB:101:MET:HE2	54:AB:228:PRO:HD3	1.87	0.57
74:Ae:80:TRP:HH2	74:Ae:151:THR:HG23	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B0:101:LYS:NZ	1:B0:129:THR:OG1	2.32	0.57
10:BD:231:SER:OG	53:BA:851:G:N7	2.37	0.57
25:BW:151:LEU:HB2	25:BW:167:LYS:HB2	1.87	0.57
51:AA:17:G:H2'	51:AA:18:G:C8	2.40	0.57
51:AA:29:A:H2'	51:AA:30:A:C8	2.40	0.57
57:AF:2:PRO:N	57:AF:69:TYR:HH	2.03	0.57
70:Aa:100:ILE:HG23	70:Aa:321:SER:HB3	1.86	0.57
76:Ag:122:ARG:HH11	76:Ag:336:LEU:HD13	1.69	0.57
11:BE:236:THR:HG23	11:BE:239:ARG:HD2	1.87	0.57
18:BP:137:GLY:HA3	18:BP:157:GLN:HG3	1.86	0.57
21:BS:65:GLU:OE1	21:BS:75:ARG:NH1	2.38	0.57
25:BW:67:ARG:NH2	37:Bi:228:PHE:O	2.38	0.57
29:Bb:371:ASP:OD1	36:B8:185:ASN:ND2	2.31	0.57
51:AA:681:A:H62	56:AE:114:ARG:HH11	1.51	0.57
53:BA:611:U:H2'	53:BA:612:A:H8	1.70	0.57
53:BA:1245:G:C2'	86:AY:69:C:H3'	2.35	0.57
77:Ah:350:LEU:HD13	77:Ah:361:LYS:HB3	1.87	0.57
80:Ak:92:PRO:HB3	80:Ak:98:PRO:HD3	1.85	0.57
8:BB:73:A:N3	38:Bj:268:TYR:OH	2.37	0.56
10:BD:203:ARG:HH21	10:BD:206:GLN:HE22	1.51	0.56
23:BU:52:LYS:NZ	53:BA:164:A:OP1	2.37	0.56
29:Bb:175:VAL:HG22	29:Bb:204:VAL:HG12	1.87	0.56
52:B9:78:LEU:HD11	52:B9:85:TRP:HB3	1.87	0.56
56:AE:296:LEU:HD11	56:AE:303:ILE:HD12	1.87	0.56
37:Bi:90:PRO:HB2	37:Bi:269:TRP:HH2	1.70	0.56
53:BA:1399:G:O2'	53:BA:1402:C:OP2	2.18	0.56
5:B4:43:ARG:NH1	5:B4:44:LEU:O	2.39	0.56
9:B7:88:LYS:NZ	53:BA:127:G:OP2	2.31	0.56
12:BF:221:LEU:HD22	12:BF:264:PRO:HB2	1.86	0.56
18:BP:164:ILE:HG12	18:BP:174:VAL:HG11	1.86	0.56
24:BV:126:VAL:HG11	24:BV:132:ILE:HD11	1.87	0.56
28:Ba:144:ARG:O	28:Ba:194:LYS:NZ	2.29	0.56
53:BA:198:U:H2'	53:BA:199:A:C8	2.40	0.56
53:BA:1416:G:H2'	53:BA:1417:A:H8	1.71	0.56
64:AO:176:TYR:HB2	66:AQ:89:GLY:HA3	1.87	0.56
82:An:189:TRP:NE1	82:An:191:THR:OG1	2.38	0.56
86:AV:1:U:H2'	86:AV:2:U:H6	1.69	0.56
6:B5:134:THR:OG1	20:BR:41:ARG:NH2	2.38	0.56
11:BE:50:ASP:O	20:BR:139:ARG:NH1	2.38	0.56
20:BR:28:LEU:HD13	20:BR:48:ARG:HH12	1.70	0.56
26:BX:2:ALA:N	26:BX:7:TYR:OH	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:644:G:N2	53:BA:1008:A:OP2	2.35	0.56
84:Ap:116:ASP:OD2	84:Ap:118:ARG:NH1	2.39	0.56
86:AY:38:U:C2	86:AY:39:U:C5	2.93	0.56
3:B2:231:LYS:NZ	53:BA:11:G:O6	2.39	0.56
5:B4:60:GLN:NE2	5:B4:79:PRO:O	2.37	0.56
28:Ba:200:ARG:HD2	28:Ba:233:LYS:HD2	1.86	0.56
38:Bj:245:GLN:HG3	38:Bj:248:LYS:HB3	1.87	0.56
38:Bj:260:LEU:HD22	38:Bj:273:ARG:HD2	1.87	0.56
46:Bt:15:ARG:NH1	53:BA:1025:A:OP1	2.38	0.56
81:Am:100:PRO:HD2	81:Am:103:LYS:HD3	1.88	0.56
1:B0:85:LYS:NZ	53:BA:1207:C:OP1	2.38	0.56
7:B6:21:MET:HG2	7:B6:29:SER:HB3	1.86	0.56
36:B8:172:TYR:HB2	36:B8:175:ASP:HB2	1.88	0.56
51:AA:386:U:H4'	57:AF:94:VAL:HG12	1.88	0.56
51:AA:812:U:OP1	59:AI:380:ARG:NH2	2.39	0.56
51:AA:923:G:H1'	51:AA:944:A:H2	1.70	0.56
53:BA:130:A:H2'	53:BA:131:A:O4'	2.05	0.56
53:BA:699:G:H2'	53:BA:700:A:H8	1.70	0.56
21:BS:39:VAL:HB	21:BS:42:GLU:HB2	1.88	0.56
61:AK:160:ARG:NH2	61:AK:179:ASP:OD1	2.38	0.56
70:Aa:230:VAL:O	70:Aa:236:ASN:ND2	2.38	0.56
76:Ag:323:LEU:HD13	80:Ak:306:ASP:HB2	1.87	0.56
46:Bt:41:THR:O	46:Bt:45:ASN:ND2	2.36	0.56
51:AA:468:A:OP2	54:AB:99:ARG:NH2	2.38	0.56
53:BA:53:U:O4	53:BA:62:C:N3	2.39	0.56
53:BA:918:U:H2'	53:BA:919:G:H8	1.70	0.56
70:Aa:338:GLU:HG2	70:Aa:341:LYS:HE2	1.86	0.56
3:B2:194:LYS:HG2	53:BA:41:A:H4'	1.87	0.56
15:BK:17:SER:N	15:BK:72:VAL:O	2.38	0.56
24:BV:198:ARG:NH2	34:Bg:13:SER:OG	2.39	0.56
51:AA:162:C:OP2	51:AA:163:A:N6	2.34	0.56
53:BA:1454:C:H2'	53:BA:1455:C:C6	2.41	0.56
64:AO:155:ARG:NE	64:AO:159:MET:SD	2.79	0.56
74:Ae:242:ARG:NH1	74:Ae:278:GLN:OE1	2.37	0.56
74:Ae:300:LEU:HD13	74:Ae:374:ARG:HD3	1.88	0.56
86:AV:3:U:N3	86:AV:4:U:C4	2.74	0.56
3:B2:115:LEU:HB3	26:BX:27:GLN:HG2	1.86	0.56
11:BE:210:THR:OG1	11:BE:262:GLY:O	2.21	0.56
26:BX:150:LEU:HD13	37:Bi:240:ARG:HG2	1.88	0.56
28:Ba:347:THR:HG22	28:Ba:349:GLY:H	1.71	0.56
29:Bb:50:LYS:O	29:Bb:52:ARG:NH1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:328:A:H2'	51:AA:329:A:H8	1.70	0.56
51:AA:552:A:H2'	51:AA:553:G:C8	2.41	0.56
79:Aj:78:ARG:NH2	79:Aj:142:VAL:O	2.39	0.56
5:B4:71:GLU:O	5:B4:73:ARG:N	2.38	0.55
28:Ba:360:ASN:HD22	28:Ba:372:ASN:HA	1.71	0.55
51:AA:635:C:H5''	54:AB:213:LYS:HE2	1.88	0.55
51:AA:647:A:N6	68:AU:80:ARG:O	2.36	0.55
54:AB:106:PHE:HB2	54:AB:116:ASP:HB3	1.88	0.55
57:AF:26:LEU:HD12	57:AF:36:VAL:HG21	1.87	0.55
60:AJ:79:LEU:HD11	60:AJ:140:TYR:HB3	1.87	0.55
62:AL:70:PRO:HB3	62:AL:117:ASP:HB3	1.87	0.55
74:Ae:293:PRO:HG3	74:Ae:357:GLN:HE22	1.70	0.55
76:Ag:79:PRO:HG2	76:Ag:193:ALA:HA	1.87	0.55
80:Ak:239:GLU:OE1	80:Ak:241:TRP:NE1	2.34	0.55
86:AV:67:U:C5	86:AV:68:U:C5	2.94	0.55
41:Bm:91:SER:HB2	41:Bm:123:ARG:HH11	1.71	0.55
51:AA:313:A:O2'	51:AA:314:A:O4'	2.23	0.55
53:BA:187:G:H1'	53:BA:467:A:N6	2.21	0.55
77:Ah:329:TYR:O	77:Ah:369:ARG:NH2	2.39	0.55
2:B1:167:LEU:HD21	2:B1:202:GLU:HB3	1.88	0.55
14:BJ:54:ILE:HD12	19:BQ:211:ASN:HB3	1.87	0.55
35:Bh:60:ARG:HD2	35:Bh:63:LYS:HD2	1.87	0.55
37:Bi:124:LYS:HE2	37:Bi:208:ILE:HD13	1.88	0.55
49:Bw:82:ILE:O	53:BA:777:A:N6	2.24	0.55
49:Bw:236:ARG:HA	49:Bw:289:GLY:HA2	1.87	0.55
50:Bx:164:ASN:O	53:BA:568:C:O2'	2.19	0.55
53:BA:354:U:O2'	53:BA:1055:A:N1	2.38	0.55
56:AE:307:LYS:NZ	70:Aa:125:TYR:OH	2.39	0.55
59:AI:158:TYR:CZ	59:AI:218:ASP:HB2	2.42	0.55
63:AN:63:LEU:HB3	63:AN:67:LEU:HD11	1.89	0.55
5:B4:43:ARG:NH2	8:BB:32:A:OP1	2.34	0.55
20:BR:13:ARG:NH2	53:BA:995:C:OP1	2.39	0.55
34:Bg:27:GLN:HB2	34:Bg:80:LEU:HD12	1.87	0.55
51:AA:3:A:O2'	51:AA:5:A:OP2	2.24	0.55
51:AA:121:C:O2'	66:AQ:23:GLN:O	2.24	0.55
61:AK:179:ASP:HB2	68:AU:26:LEU:HD21	1.88	0.55
83:Ao:613:LEU:HD23	83:Ao:614:LEU:HD23	1.88	0.55
86:AY:3:U:N3	86:AY:4:U:C4	2.74	0.55
11:BE:52:HIS:NE2	30:Bc:301:HIS:O	2.40	0.55
12:BF:123:GLY:HA2	12:BF:141:ILE:HG12	1.89	0.55
48:Bv:55:ARG:NH1	53:BA:93:U:OP2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AC:112:ARG:HG2	80:Ak:161:ALA:HB1	1.88	0.55
68:AU:80:ARG:NH1	75:Af:112:ASP:OD2	2.39	0.55
70:Aa:198:GLU:OE2	70:Aa:204:ARG:NH1	2.33	0.55
74:Ae:239:GLU:O	74:Ae:243:ASN:ND2	2.32	0.55
4:B3:99:VAL:HG21	43:Bo:77:VAL:HG22	1.88	0.55
16:BN:114:LYS:NZ	53:BA:1034:G:OP1	2.39	0.55
51:AA:57:A:O2'	51:AA:59:C:OP1	2.25	0.55
70:Aa:303:ILE:HG22	70:Aa:307:LEU:HG	1.87	0.55
73:Ad:166:THR:OG1	73:Ad:176:ARG:NH2	2.39	0.55
84:Ap:105:CYS:HB3	84:Ap:142:VAL:HA	1.88	0.55
86:AY:9:U:O2'	86:AY:10:U:C4	2.52	0.55
11:BE:76:LYS:HG3	11:BE:170:LEU:HD21	1.88	0.55
27:BY:69:ASP:HB3	27:BY:72:LYS:HD2	1.89	0.55
60:AJ:147:HIS:HB3	80:Ak:135:TRP:CE2	2.41	0.55
19:BQ:124:VAL:HG12	19:BQ:158:ARG:HE	1.71	0.55
31:Bd:80:GLN:HG3	39:Bk:201:ARG:HH21	1.71	0.55
35:Bh:33:LYS:NZ	53:BA:106:C:OP1	2.39	0.55
53:BA:233:A:H2'	53:BA:234:G:H8	1.72	0.55
54:AB:145:SER:HB2	54:AB:195:LEU:HB2	1.89	0.55
55:AC:38:ARG:HG2	55:AC:43:ARG:HH21	1.71	0.55
55:AC:113:ARG:HB2	60:AJ:166:GLU:HB3	1.89	0.55
67:AR:141:TYR:O	68:AU:28:ARG:NH1	2.40	0.55
4:B3:137:THR:HG21	43:Bo:74:ALA:HB2	1.87	0.55
18:BP:211:VAL:O	18:BP:215:THR:OG1	2.20	0.55
19:BQ:98:HIS:HB3	19:BQ:151:VAL:HG12	1.89	0.55
27:BY:81:ARG:HD3	27:BY:81:ARG:H	1.71	0.55
29:Bb:139:TRP:O	29:Bb:144:GLY:N	2.37	0.55
47:Bu:101:ARG:HG2	47:Bu:133:ILE:HG12	1.89	0.55
50:Bx:72:ILE:HG23	50:Bx:77:LEU:HB2	1.89	0.55
53:BA:1354:A:H61	53:BA:1465:A:H61	1.53	0.55
76:Ag:173:ASN:O	76:Ag:176:ARG:NH1	2.37	0.55
12:BF:70:ARG:O	12:BF:202:TYR:OH	2.24	0.55
27:BY:112:GLU:OE1	37:Bi:74:ARG:NH1	2.39	0.55
70:Aa:334:GLN:NE2	70:Aa:357:GLU:OE2	2.40	0.55
27:BY:65:LEU:HD11	27:BY:121:LYS:HG3	1.88	0.54
53:BA:203:A:O2'	53:BA:239:C:O2	2.24	0.54
76:Ag:221:LEU:HD11	76:Ag:242:VAL:HG23	1.88	0.54
29:Bb:240:ILE:HD13	29:Bb:248:GLY:HA3	1.89	0.54
36:B8:157:LEU:HG	36:B8:161:MET:HE2	1.89	0.54
51:AA:355:U:H2'	51:AA:356:A:H8	1.71	0.54
67:AR:66:CYS:HB3	67:AR:101:CYS:H	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BP:44:ARG:HD3	18:BP:45:ARG:HG3	1.90	0.54
30:Bc:100:SER:HA	30:Bc:126:THR:HG22	1.89	0.54
30:Bc:230:ASN:HB3	30:Bc:233:LYS:HB2	1.88	0.54
36:B8:108:LYS:NZ	53:BA:77:U:OP2	2.33	0.54
40:Bl:84:TYR:HA	40:Bl:115:GLY:HA3	1.88	0.54
41:Bm:76:LYS:HE2	41:Bm:83:VAL:HG21	1.89	0.54
53:BA:740:U:H2'	53:BA:741:A:H8	1.72	0.54
73:Ad:168:ILE:HG12	73:Ad:176:ARG:HG3	1.89	0.54
16:BN:154:ARG:NH1	16:BN:157:GLU:OE2	2.41	0.54
37:Bi:142:LYS:HD2	37:Bi:216:MET:HE3	1.89	0.54
51:AA:607:G:O6	78:Ai:93:LYS:NZ	2.41	0.54
61:AK:156:LEU:HD13	68:AU:39:ILE:HG21	1.88	0.54
86:AY:67:U:C5	86:AY:68:U:C5	2.94	0.54
22:BT:79:GLU:OE2	22:BT:103:ARG:NH2	2.40	0.54
29:Bb:330:VAL:HG13	29:Bb:334:LEU:HD12	1.88	0.54
33:Bf:73:LYS:HE3	35:Bh:257:LEU:HD23	1.90	0.54
50:Bx:99:MET:HE3	50:Bx:116:GLU:HG3	1.90	0.54
51:AA:590:C:H2'	51:AA:591:A:C8	2.41	0.54
53:BA:343:C:H2'	53:BA:344:U:C6	2.42	0.54
12:BF:287:ARG:HH21	53:BA:223:A:H62	1.56	0.54
16:BN:104:VAL:HG13	16:BN:127:LEU:HD13	1.90	0.54
28:Ba:280:GLN:HG2	49:Bw:152:ARG:HE	1.71	0.54
30:Bc:76:PHE:HB3	30:Bc:78:MET:HE2	1.89	0.54
31:Bd:173:ARG:NH2	38:Bj:56:PRO:HB3	2.23	0.54
38:Bj:129:LEU:O	38:Bj:132:LYS:NZ	2.36	0.54
49:Bw:202:PHE:O	49:Bw:226:GLN:NE2	2.41	0.54
51:AA:759:U:H2'	51:AA:760:A:H8	1.72	0.54
53:BA:1140:A:H2'	53:BA:1141:A:H8	1.73	0.54
53:BA:1506:A:H2'	53:BA:1507:G:C8	2.42	0.54
80:Ak:175:LEU:HD23	80:Ak:209:ILE:HD12	1.88	0.54
83:Ao:353:LYS:HD3	83:Ao:381:LEU:HB3	1.90	0.54
24:BV:119:LEU:HD11	24:BV:194:GLN:HB3	1.90	0.54
25:BW:48:LYS:N	53:BA:2:C:OP1	2.33	0.54
29:Bb:304:TYR:O	29:Bb:308:GLN:HB2	2.08	0.54
35:Bh:148:LEU:HD13	35:Bh:149:PRO:HD2	1.88	0.54
51:AA:948:U:H2'	51:AA:949:G:H8	1.72	0.54
53:BA:266:C:O2'	53:BA:281:A:N6	2.37	0.54
59:AI:366:ARG:HB3	59:AI:371:LEU:HD12	1.88	0.54
61:AK:102:VAL:HG12	61:AK:108:PRO:HA	1.89	0.54
67:AR:116:GLN:HB3	67:AR:123:VAL:HG22	1.90	0.54
83:Ao:137:ILE:HD12	83:Ao:138:PRO:HD2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BW:77:GLN:H	25:BW:171:HIS:CD2	2.26	0.54
25:BW:189:THR:HG23	25:BW:192:ALA:H	1.73	0.54
51:AA:302:U:OP1	64:AO:163:GLN:NE2	2.40	0.54
57:AF:3:ARG:NH1	64:AO:98:MET:O	2.41	0.54
59:AI:120:ARG:NH2	80:Ak:91:TYR:OH	2.41	0.54
59:AI:396:LYS:NZ	86:AV:31:U:OP2	2.37	0.54
74:Ae:221:LEU:HD23	74:Ae:251:PRO:HB3	1.90	0.54
83:Ao:346:ARG:HA	83:Ao:381:LEU:HD21	1.90	0.54
83:Ao:404:MET:HA	83:Ao:441:LEU:HD13	1.90	0.54
22:BT:152:ARG:HD3	22:BT:161:GLU:HG2	1.89	0.54
26:BX:68:VAL:HG22	26:BX:97:VAL:HG12	1.90	0.54
26:BX:71:ARG:NH2	26:BX:73:GLN:OE1	2.41	0.54
28:Ba:361:THR:OG1	28:Ba:363:ASP:OD1	2.26	0.54
38:Bj:265:LYS:HG3	38:Bj:266:PRO:HD3	1.90	0.54
40:Bl:111:ARG:NH2	53:BA:216:C:OP2	2.41	0.54
53:BA:1072:A:H2'	53:BA:1073:A:H8	1.73	0.54
56:AE:289:THR:HG21	56:AE:308:GLN:H	1.71	0.54
2:B1:215:GLN:NE2	2:B1:219:GLU:OE2	2.32	0.54
8:BB:65:U:H2'	8:BB:66:A:C8	2.42	0.54
12:BF:262:THR:HG22	12:BF:264:PRO:HD2	1.89	0.54
12:BF:287:ARG:HD2	48:Bv:33:ARG:HH12	1.72	0.54
16:BN:171:SER:OG	50:Bx:58:GLN:OE1	2.21	0.54
28:Ba:350:ARG:HH12	28:Ba:381:LEU:HD23	1.72	0.54
48:Bv:28:ARG:NH1	53:BA:100:C:O2'	2.41	0.54
51:AA:85:G:H2'	51:AA:86:A:C8	2.43	0.54
53:BA:1557:C:O2'	53:BA:1558:U:O2	2.25	0.54
1:B0:59:HIS:HE2	53:BA:412:C:HO2'	1.55	0.53
29:Bb:139:TRP:CD1	29:Bb:143:CYS:HG	2.26	0.53
49:Bw:242:PRO:HD3	49:Bw:423:PRO:HA	1.90	0.53
51:AA:799:A:H2'	51:AA:800:G:H8	1.73	0.53
53:BA:920:C:N4	53:BA:924:G:H22	2.05	0.53
60:AJ:163:ASN:HB3	80:Ak:116:LEU:HD11	1.89	0.53
83:Ao:369:GLU:OE2	83:Ao:411:ARG:NH1	2.41	0.53
2:B1:96:LYS:O	53:BA:60:U:O2'	2.24	0.53
6:B5:93:ARG:NH1	53:BA:644:G:OP1	2.41	0.53
16:BN:62:THR:HB	16:BN:129:PRO:HA	1.90	0.53
21:BS:173:ARG:NE	53:BA:1218:U:H5'	2.23	0.53
22:BT:271:ARG:NH1	53:BA:1491:A:O2'	2.40	0.53
24:BV:71:PRO:HB2	24:BV:76:GLU:HG2	1.91	0.53
25:BW:147:ARG:O	53:BA:2:C:O2'	2.16	0.53
51:AA:15:C:H4'	56:AE:300:ARG:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:122:C:H4'	66:AQ:24:LYS:HD2	1.89	0.53
53:BA:344:U:H2'	53:BA:345:G:C8	2.43	0.53
60:AJ:179:GLN:HA	80:Ak:149:PHE:HA	1.88	0.53
15:BK:39:LEU:HD12	15:BK:44:VAL:HB	1.89	0.53
29:Bb:217:LEU:HD11	29:Bb:233:VAL:HG12	1.90	0.53
35:Bh:96:CYS:SG	35:Bh:181:SER:OG	2.64	0.53
49:Bw:241:LEU:HD11	49:Bw:290:HIS:HD1	1.73	0.53
51:AA:58:U:OP1	79:Aj:53:ARG:NH1	2.42	0.53
51:AA:248:C:H41	62:AL:78:ARG:HH22	1.56	0.53
51:AA:590:C:H2'	51:AA:591:A:H8	1.72	0.53
51:AA:767:U:O2'	51:AA:806:A:O2'	2.25	0.53
53:BA:158:A:N3	53:BA:1039:A:O2'	2.37	0.53
53:BA:1072:A:H2'	53:BA:1073:A:C8	2.43	0.53
53:BA:1570:C:H3'	53:BA:1571:A:H2'	1.89	0.53
54:AB:192:ILE:HD12	54:AB:211:ALA:HB2	1.91	0.53
83:Ao:622:LYS:HD3	83:Ao:655:GLU:HB2	1.91	0.53
84:Ap:89:ARG:HD3	84:Ap:144:MET:HE3	1.91	0.53
4:B3:68:ILE:HD11	4:B3:122:LEU:HD13	1.91	0.53
30:Bc:190:MET:HG2	30:Bc:291:ARG:HH12	1.73	0.53
31:Bd:110:GLU:HA	31:Bd:113:ARG:HG2	1.91	0.53
51:AA:807:G:H2'	51:AA:809:G:C8	2.43	0.53
53:BA:790:A:N6	53:BA:1000:A:O2'	2.42	0.53
55:AC:136:VAL:HG23	55:AC:153:LEU:HD23	1.90	0.53
86:AV:1:U:H2'	86:AV:2:U:C6	2.43	0.53
86:AV:9:U:O2'	86:AV:10:U:C4	2.52	0.53
40:Bl:96:VAL:HG22	40:Bl:110:ILE:HG12	1.90	0.53
51:AA:561:U:H3'	51:AA:562:A:C2	2.44	0.53
53:BA:1121:U:H2'	53:BA:1122:A:C8	2.44	0.53
74:Ae:69:LEU:HB3	74:Ae:405:LEU:HD23	1.91	0.53
80:Ak:67:ASP:OD2	80:Ak:70:SER:OG	2.26	0.53
4:B3:78:ARG:O	4:B3:83:LYS:NZ	2.42	0.53
30:Bc:103:ALA:O	30:Bc:110:TRP:N	2.42	0.53
36:B8:110:VAL:O	36:B8:114:PHE:HB2	2.09	0.53
38:Bj:179:GLN:HG2	38:Bj:181:GLY:H	1.74	0.53
40:Bl:91:MET:HE3	53:BA:219:A:H5''	1.91	0.53
49:Bw:63:VAL:HA	49:Bw:66:TRP:HD1	1.73	0.53
53:BA:73:A:O2'	53:BA:224:A:O2'	2.26	0.53
60:AJ:123:SER:HB3	60:AJ:127:PHE:HB2	1.91	0.53
76:Ag:383:SER:HB3	76:Ag:393:LEU:HD12	1.89	0.53
5:B4:68:ARG:NH1	39:Bk:99:ASP:OD2	2.40	0.53
14:BJ:236:TYR:OH	85:HL:86:LEU:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Be:32:LYS:NZ	53:BA:35:A:OP1	2.33	0.53
51:AA:88:C:O2'	65:AP:82:HIS:NE2	2.36	0.53
51:AA:552:A:H2'	51:AA:553:G:H8	1.74	0.53
53:BA:164:A:H4'	53:BA:165:A:C8	2.43	0.53
2:B1:40:PRO:HG3	2:B1:45:PRO:HG3	1.89	0.53
14:BJ:219:TYR:CE1	85:EL:86:LEU:HD13	2.44	0.53
20:BR:33:LEU:HD21	20:BR:59:LEU:HD22	1.90	0.53
51:AA:11:G:O4'	51:AA:840:A:O2'	2.26	0.53
51:AA:226:G:H2'	51:AA:227:A:H8	1.73	0.53
51:AA:524:U:H2'	51:AA:525:U:C6	2.44	0.53
53:BA:301:U:H2'	53:BA:302:A:H8	1.73	0.53
53:BA:1121:U:H2'	53:BA:1122:A:H8	1.74	0.53
53:BA:1163:A:N6	53:BA:1164:G:O6	2.42	0.53
53:BA:1224:C:H2'	53:BA:1225:A:C8	2.42	0.53
59:AI:302:LEU:HD22	76:Ag:384:ASN:HB3	1.90	0.53
48:Bv:33:ARG:NH2	53:BA:96:U:OP1	2.42	0.53
51:AA:340:A:H4'	61:AK:116:THR:HG22	1.91	0.53
51:AA:938:U:H2'	51:AA:939:A:C8	2.43	0.53
3:B2:200:ARG:N	53:BA:31:A:N1	2.45	0.53
11:BE:231:HIS:NE2	53:BA:805:C:O2	2.35	0.53
12:BF:92:ARG:NH2	40:Bl:144:THR:OG1	2.42	0.53
12:BF:249:ASN:ND2	42:Bn:55:GLY:O	2.42	0.53
18:BP:16:LEU:HD23	18:BP:19:LEU:HD12	1.90	0.53
28:Ba:240:ALA:HB2	28:Ba:375:TRP:HH2	1.73	0.53
38:Bj:273:ARG:HA	38:Bj:276:LEU:HB3	1.90	0.53
51:AA:182:A:C6	62:AL:56:PRO:HD2	2.44	0.53
53:BA:699:G:H2'	53:BA:700:A:C8	2.44	0.53
53:BA:740:U:H2'	53:BA:741:A:C8	2.44	0.53
67:AR:137:CYS:O	73:Ad:193:ARG:NH2	2.40	0.53
11:BE:96:ARG:HH22	11:BE:202:GLN:HE22	1.57	0.52
11:BE:252:TRP:HB3	16:BN:84:PRO:HD3	1.91	0.52
12:BF:171:VAL:HG13	12:BF:273:LEU:HD22	1.90	0.52
30:Bc:66:HIS:HB2	30:Bc:76:PHE:HE1	1.74	0.52
44:Bp:80:HIS:O	50:Bx:36:ARG:NH1	2.39	0.52
49:Bw:151:LEU:HD23	49:Bw:153:ARG:HH21	1.74	0.52
53:BA:197:U:H2'	53:BA:198:U:C6	2.43	0.52
57:AF:3:ARG:NH1	57:AF:70:ALA:O	2.43	0.52
16:BN:6:LYS:NZ	35:Bh:230:GLU:OE2	2.42	0.52
27:BY:145:ARG:HH22	27:BY:157:PRO:HD3	1.74	0.52
45:Bq:72:ALA:HA	45:Bq:73:MET:HE3	1.91	0.52
51:AA:441:U:H2'	51:AA:442:A:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:677:C:OP1	53:BA:695:U:O2'	2.20	0.52
55:AC:69:LEU:HB3	55:AC:93:ARG:HH22	1.73	0.52
56:AE:380:LEU:HD12	56:AE:381:PRO:HD2	1.90	0.52
59:AI:203:LYS:NZ	59:AI:207:GLU:OE2	2.38	0.52
74:Ae:68:CYS:HB2	74:Ae:192:ILE:HG21	1.90	0.52
14:BJ:65:LEU:HD12	14:BJ:66:PRO:HD2	1.90	0.52
16:BN:115:ASN:HB2	53:BA:175:C:H5''	1.92	0.52
20:BR:153:LEU:HG	30:Bc:315:ARG:HD2	1.91	0.52
23:BU:73:THR:HG22	23:BU:83:TYR:HB2	1.90	0.52
28:Ba:207:ASN:HB3	49:Bw:151:LEU:HD11	1.91	0.52
38:Bj:235:LYS:HE3	38:Bj:275:PHE:HD1	1.74	0.52
55:AC:154:HIS:CG	80:Ak:77:PRO:HG3	2.45	0.52
79:Aj:98:THR:HG22	79:Aj:116:GLY:HA2	1.90	0.52
22:BT:221:LYS:NZ	22:BT:241:LYS:O	2.38	0.52
32:Be:51:ILE:HG23	53:BA:747:U:H3	1.75	0.52
36:B8:123:LEU:HD11	36:B8:147:PHE:HB3	1.91	0.52
51:AA:120:A:N6	51:AA:132:A:N1	2.57	0.52
51:AA:800:G:H2'	51:AA:801:A:H8	1.73	0.52
53:BA:343:C:H2'	53:BA:344:U:H6	1.74	0.52
53:BA:1338:G:H2'	53:BA:1339:A:H8	1.75	0.52
53:BA:1405:A:H2'	53:BA:1406:G:C8	2.43	0.52
25:BW:55:ILE:O	37:Bi:227:ARG:NH2	2.42	0.52
30:Bc:186:LEU:HG	30:Bc:189:TRP:HE1	1.73	0.52
34:Bg:48:GLU:OE2	46:Bt:101:TRP:NE1	2.36	0.52
49:Bw:93:VAL:HB	49:Bw:227:ILE:HG12	1.90	0.52
51:AA:913:G:H2'	51:AA:914:A:C8	2.44	0.52
53:BA:289:U:H2'	53:BA:290:A:H8	1.73	0.52
53:BA:1246:A:H5''	86:AY:70:C:H5'	1.92	0.52
53:BA:1459:U:O2	53:BA:1468:A:N7	2.42	0.52
83:Ao:66:ASP:OD1	83:Ao:67:LYS:N	2.43	0.52
86:AY:1:U:H2'	86:AY:2:U:C6	2.43	0.52
23:BU:54:THR:HG21	24:BV:176:MET:H	1.75	0.52
35:Bh:105:ARG:HB2	35:Bh:112:LYS:HD2	1.91	0.52
53:BA:925:G:N2	53:BA:964:A:OP2	2.36	0.52
53:BA:1326:A:O2'	53:BA:1328:G:OP2	2.22	0.52
53:BA:1414:C:N4	53:BA:1415:G:O6	2.43	0.52
60:AJ:155:VAL:HG11	80:Ak:132:CYS:HB3	1.92	0.52
65:AP:63:GLU:HG2	70:Aa:177:LYS:HE3	1.92	0.52
76:Ag:347:TYR:CZ	76:Ag:387:PRO:HB3	2.44	0.52
83:Ao:559:LYS:HD3	83:Ao:598:MET:HE2	1.91	0.52
8:BB:42:C:OP2	21:BS:85:ARG:NH2	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BJ:127:PRO:HG2	14:BJ:130:VAL:HG12	1.92	0.52
51:AA:936:C:H2'	51:AA:937:A:C8	2.44	0.52
53:BA:916:C:H2'	53:BA:917:G:H8	1.75	0.52
74:Ae:188:MET:O	74:Ae:192:ILE:HG12	2.10	0.52
18:BP:261:ASP:HB3	18:BP:264:GLN:HB2	1.92	0.52
19:BQ:89:ILE:HD11	19:BQ:176:LEU:HD22	1.91	0.52
19:BQ:98:HIS:CD2	19:BQ:100:GLY:H	2.27	0.52
28:Ba:249:LYS:HE2	28:Ba:370:VAL:HG22	1.92	0.52
51:AA:332:U:H2'	51:AA:333:A:H8	1.74	0.52
51:AA:738:U:H3'	58:AG:198:ARG:HH21	1.74	0.52
52:B9:69:LEU:HD22	52:B9:97:GLN:HB3	1.92	0.52
53:BA:1234:U:H3'	53:BA:1235:C:H6	1.75	0.52
53:BA:1262:A:O2'	53:BA:1423:C:OP1	2.24	0.52
53:BA:1450:U:H2'	53:BA:1451:U:H6	1.74	0.52
55:AC:101:PRO:HB2	78:Ai:72:ARG:HH21	1.74	0.52
79:Aj:3:ARG:HE	79:Aj:4:LYS:H	1.58	0.52
18:BP:57:ARG:HB3	18:BP:62:ARG:HH21	1.75	0.52
28:Ba:236:LEU:HB3	28:Ba:341:VAL:HG13	1.92	0.52
49:Bw:49:ALA:O	49:Bw:61:ARG:NH1	2.43	0.52
53:BA:1292:A:N6	53:BA:1304:G:O2'	2.41	0.52
55:AC:89:ASP:O	55:AC:93:ARG:HG2	2.10	0.52
80:Ak:55:LEU:HD12	80:Ak:56:PRO:HD2	1.92	0.52
10:BD:262:GLY:HA2	53:BA:311:A:H5'	1.91	0.52
12:BF:68:SER:O	12:BF:210:ARG:NH2	2.37	0.52
29:Bb:35:MET:HE3	29:Bb:36:PRO:HD2	1.92	0.52
53:BA:993:U:H2'	53:BA:994:A:H8	1.75	0.52
79:Aj:41:MET:HE3	79:Aj:50:LEU:HD12	1.91	0.52
82:An:159:GLU:HG3	82:An:163:ARG:HH21	1.75	0.52
83:Ao:586:PHE:HD2	83:Ao:591:ARG:HB2	1.74	0.52
85:DL:86:LEU:HA	85:DL:89:THR:HG22	1.92	0.52
7:B6:17:LEU:HD11	7:B6:31:ASN:HB3	1.91	0.51
28:Ba:201:ARG:HD3	28:Ba:230:LEU:HD21	1.91	0.51
34:Bg:78:GLU:HG2	34:Bg:84:VAL:HG22	1.91	0.51
48:Bv:37:PRO:HG3	48:Bv:64:HIS:CG	2.44	0.51
51:AA:122:C:H2'	51:AA:123:U:C6	2.44	0.51
51:AA:158:C:O3'	51:AA:172:A:N6	2.43	0.51
51:AA:728:U:H2'	51:AA:729:A:C8	2.45	0.51
51:AA:799:A:H2'	51:AA:800:G:C8	2.44	0.51
53:BA:157:A:H2'	53:BA:158:A:H8	1.74	0.51
53:BA:220:G:N3	53:BA:231:C:O2'	2.44	0.51
55:AC:85:ARG:HH21	80:Ak:162:GLY:HA3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:AQ:13:VAL:HG23	66:AQ:66:LEU:HB2	1.93	0.51
79:Aj:68:LEU:HD21	79:Aj:100:VAL:HG21	1.92	0.51
81:Am:11:ALA:O	81:Am:12:ARG:NH1	2.38	0.51
8:BB:31:C:H2'	8:BB:32:A:H8	1.75	0.51
12:BF:84:PRO:HA	12:BF:88:SER:HB3	1.91	0.51
21:BS:43:ALA:HB1	29:Bb:226:LEU:HD21	1.92	0.51
33:Bf:49:LEU:HD23	33:Bf:60:CYS:HB3	1.92	0.51
35:Bh:245:LEU:HB3	35:Bh:250:ILE:HB	1.91	0.51
39:Bk:120:LYS:HB3	39:Bk:160:SER:HB3	1.93	0.51
51:AA:194:U:H2'	51:AA:195:G:C8	2.45	0.51
51:AA:620:C:H2'	51:AA:621:A:H8	1.75	0.51
53:BA:233:A:H2'	53:BA:234:G:C8	2.45	0.51
55:AC:76:LEU:HD13	60:AJ:81:LYS:HG3	1.92	0.51
79:Aj:166:TYR:O	84:Ap:199:TRP:NE1	2.31	0.51
85:HL:86:LEU:HA	85:HL:89:THR:HG22	1.92	0.51
3:B2:71:ASP:OD1	27:BY:175:LYS:NZ	2.36	0.51
51:AA:787:A:H2'	51:AA:788:G:C8	2.45	0.51
55:AC:133:TYR:HA	55:AC:136:VAL:HG12	1.93	0.51
56:AE:203:LEU:HD21	56:AE:268:PHE:HB3	1.91	0.51
59:AI:198:SER:HB3	59:AI:246:ARG:HD2	1.93	0.51
59:AI:206:LEU:HD12	59:AI:219:TYR:HD1	1.75	0.51
60:AJ:80:VAL:HG23	60:AJ:141:ARG:HB2	1.90	0.51
60:AJ:124:VAL:O	63:AN:108:ARG:NH2	2.43	0.51
76:Ag:318:PRO:HG2	76:Ag:321:ALA:HB2	1.92	0.51
80:Ak:175:LEU:HB3	80:Ak:209:ILE:HB	1.93	0.51
3:B2:176:GLY:O	53:BA:22:U:N3	2.30	0.51
3:B2:230:ARG:NH2	53:BA:101:U:O3'	2.44	0.51
10:BD:173:MET:HE1	57:AF:86:ILE:HG12	1.93	0.51
13:BI:144:LYS:HG2	13:BI:147:ARG:HH12	1.76	0.51
14:BJ:171:ILE:HD12	14:BJ:172:PRO:HD2	1.92	0.51
49:Bw:265:LEU:HD23	49:Bw:267:LEU:HG	1.92	0.51
51:AA:641:A:N7	56:AE:260:LYS:NZ	2.54	0.51
51:AA:830:A:H2'	51:AA:831:A:H8	1.76	0.51
51:AA:924:U:O5'	87:AX:1:U:H4'	2.11	0.51
51:AA:939:A:H2'	51:AA:940:C:H6	1.75	0.51
53:BA:192:A:OP2	53:BA:1322:C:O2'	2.25	0.51
80:Ak:70:SER:HA	83:Ao:78:VAL:HG23	1.93	0.51
5:B4:47:GLN:NE2	8:BB:33:C:OP1	2.30	0.51
6:B5:126:CYS:HA	6:B5:129:LYS:HE2	1.92	0.51
31:Bd:101:ARG:NH2	38:Bj:79:ILE:O	2.43	0.51
46:Bt:9:ARG:NH2	53:BA:564:A:OP1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:939:A:H2'	51:AA:940:C:C6	2.45	0.51
53:BA:289:U:H2'	53:BA:290:A:C8	2.45	0.51
53:BA:301:U:H2'	53:BA:302:A:C8	2.45	0.51
53:BA:344:U:H2'	53:BA:345:G:H8	1.75	0.51
53:BA:1081:U:O4	53:BA:1135:C:N3	2.43	0.51
63:AN:48:ALA:HB3	78:Ai:44:LYS:HE2	1.92	0.51
74:Ae:197:TYR:O	74:Ae:224:TYR:OH	2.28	0.51
86:AY:67:U:C4	86:AY:68:U:C4	2.98	0.51
2:B1:177:HIS:O	2:B1:184:ARG:NH2	2.44	0.51
51:AA:115:A:H5''	64:AO:204:TRP:HD1	1.76	0.51
51:AA:216:A:N7	51:AA:273:A:O2'	2.37	0.51
51:AA:761:U:H2'	51:AA:762:G:C8	2.46	0.51
84:Ap:215:ARG:HG3	84:Ap:218:ARG:HH21	1.76	0.51
85:EL:86:LEU:HA	85:EL:89:THR:HG22	1.92	0.51
85:EL:89:THR:HG23	85:EL:90:LEU:HG	1.92	0.51
13:BI:95:GLU:OE1	13:BI:95:GLU:N	2.40	0.51
14:BJ:198:PRO:HB3	14:BJ:202:LEU:HD23	1.92	0.51
15:BK:139:SER:HB3	53:BA:526:A:H4'	1.92	0.51
34:Bg:35:ARG:O	34:Bg:44:ARG:NH1	2.43	0.51
51:AA:28:U:H2'	51:AA:29:A:H8	1.75	0.51
51:AA:61:G:OP1	79:Aj:33:ARG:NH2	2.42	0.51
51:AA:394:U:H2'	64:AO:129:ARG:HD3	1.92	0.51
53:BA:619:C:H2'	53:BA:620:A:H8	1.76	0.51
53:BA:1226:C:OP1	53:BA:1227:U:N3	2.44	0.51
70:Aa:174:GLU:HG2	70:Aa:178:TYR:HE1	1.76	0.51
74:Ae:248:LEU:HD13	74:Ae:266:TYR:HB3	1.93	0.51
85:FL:89:THR:HG23	85:FL:90:LEU:HG	1.92	0.51
13:BI:102:VAL:HG22	13:BI:128:LEU:HD12	1.93	0.51
19:BQ:36:VAL:HG11	45:Bq:124:HIS:HB3	1.92	0.51
55:AC:72:HIS:NE2	55:AC:75:ASN:OD1	2.43	0.51
56:AE:308:GLN:HB3	56:AE:312:TYR:HB3	1.93	0.51
74:Ae:88:CYS:SG	74:Ae:89:HIS:N	2.83	0.51
74:Ae:226:LEU:HB3	74:Ae:394:LEU:HD13	1.93	0.51
51:AA:181:A:O2'	51:AA:183:A:N7	2.37	0.51
51:AA:368:A:OP1	61:AK:186:ASN:ND2	2.44	0.51
53:BA:983:U:O4	53:BA:984:A:N6	2.44	0.51
59:AI:318:LEU:HD21	59:AI:329:MET:HE1	1.91	0.51
74:Ae:268:TYR:HB3	74:Ae:299:ALA:HB2	1.91	0.51
83:Ao:446:ASP:N	83:Ao:446:ASP:OD1	2.43	0.51
86:AV:67:U:C4	86:AV:68:U:C4	2.98	0.51
12:BF:284:TYR:O	12:BF:290:TYR:OH	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BJ:110:LEU:HB3	15:BK:132:LEU:HD23	1.92	0.51
28:Ba:112:ARG:HG3	53:BA:719:C:O2'	2.11	0.51
28:Ba:300:ARG:NH2	53:BA:727:A:OP2	2.44	0.51
36:B8:133:LEU:HD12	53:BA:1243:U:H5'	1.93	0.51
53:BA:1269:G:N2	53:BA:1272:U:O2	2.40	0.51
55:AC:163:VAL:HG11	55:AC:167:ILE:HD12	1.92	0.51
64:AO:69:PRO:HD2	64:AO:72:MET:HG2	1.93	0.51
74:Ae:255:GLN:OE1	74:Ae:255:GLN:N	2.43	0.51
74:Ae:332:ALA:O	74:Ae:335:GLN:NE2	2.44	0.51
84:Ap:90:THR:H	84:Ap:144:MET:HE2	1.75	0.51
24:BV:148:LEU:HB2	33:Bf:58:ILE:HB	1.93	0.50
70:Aa:272:TYR:HA	70:Aa:275:ILE:HG12	1.92	0.50
85:FL:86:LEU:HA	85:FL:89:THR:HG22	1.92	0.50
12:BF:56:PRO:HG2	12:BF:59:ARG:HB3	1.93	0.50
49:Bw:85:LYS:HE2	53:BA:777:A:H62	1.75	0.50
51:AA:93:A:N3	73:Ad:79:ARG:NH2	2.59	0.50
53:BA:53:U:H2'	53:BA:54:A:H8	1.76	0.50
53:BA:148:A:H4'	53:BA:149:A:H5''	1.93	0.50
56:AE:95:ALA:HB2	78:Ai:74:GLU:HB3	1.93	0.50
61:AK:190:PRO:HG2	68:AU:45:TYR:HB2	1.93	0.50
76:Ag:271:THR:HG22	76:Ag:273:LEU:H	1.77	0.50
83:Ao:343:LYS:HD2	83:Ao:346:ARG:HH21	1.75	0.50
18:BP:216:ASP:OD1	18:BP:217:ALA:N	2.44	0.50
20:BR:27:HIS:HD1	53:BA:661:U:HO2'	1.47	0.50
24:BV:178:PHE:HD1	24:BV:185:GLN:HG2	1.75	0.50
26:BX:138:ASP:HB3	26:BX:141:ARG:HG2	1.94	0.50
30:Bc:61:LYS:HD2	30:Bc:77:VAL:HG12	1.93	0.50
51:AA:55:G:H2'	51:AA:56:U:C6	2.46	0.50
51:AA:344:G:O6	61:AK:124:LYS:NZ	2.31	0.50
51:AA:710:G:N2	51:AA:711:A:N7	2.51	0.50
53:BA:176:U:H2'	53:BA:177:U:C6	2.46	0.50
53:BA:385:U:H2'	53:BA:386:U:H6	1.77	0.50
70:Aa:91:THR:OG1	70:Aa:94:ASP:OD1	2.18	0.50
18:BP:104:LEU:HD22	18:BP:109:ARG:HD2	1.93	0.50
27:BY:52:GLU:O	27:BY:143:ARG:NH2	2.45	0.50
28:Ba:181:VAL:HG21	28:Ba:294:LEU:HD22	1.92	0.50
30:Bc:41:GLN:HB3	30:Bc:258:ILE:HD12	1.92	0.50
43:Bo:45:GLU:OE2	43:Bo:70:ARG:NH2	2.42	0.50
51:AA:121:C:H2'	51:AA:122:C:C6	2.46	0.50
51:AA:893:A:H2'	51:AA:894:U:O4'	2.12	0.50
53:BA:657:U:H1'	53:BA:658:U:C5	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:Ag:154:ILE:HD13	76:Ag:261:VAL:HG12	1.93	0.50
23:BU:34:ARG:HH21	53:BA:1014:A:H5''	1.75	0.50
29:Bb:214:TRP:HB3	29:Bb:272:LEU:HD11	1.93	0.50
29:Bb:237:VAL:HG22	29:Bb:240:ILE:HD11	1.94	0.50
29:Bb:364:ARG:HD2	53:BA:1194:U:H5''	1.93	0.50
30:Bc:151:ILE:HA	30:Bc:199:PHE:HE1	1.76	0.50
51:AA:941:U:H2'	51:AA:942:G:C8	2.47	0.50
70:Aa:189:HIS:HB3	70:Aa:215:ILE:HD13	1.92	0.50
71:Ab:67:GLU:OE1	71:Ab:71:ARG:NH2	2.44	0.50
11:BE:238:ARG:N	53:BA:792:G:OP1	2.43	0.50
51:AA:527:G:O2'	51:AA:843:C:OP2	2.27	0.50
51:AA:546:U:H2'	51:AA:547:A:C8	2.47	0.50
53:BA:474:A:O2'	53:BA:596:A:O4'	2.30	0.50
55:AC:50:PRO:HB3	55:AC:167:ILE:HG13	1.93	0.50
59:AI:91:MET:HE1	80:Ak:85:LEU:HD11	1.94	0.50
62:AL:55:ARG:HD2	62:AL:58:LEU:HD21	1.93	0.50
76:Ag:103:PRO:HA	76:Ag:342:ILE:HD11	1.93	0.50
77:Ah:285:PRO:HB3	83:Ao:88:VAL:HG11	1.93	0.50
4:B3:40:ARG:NH1	53:BA:410:U:OP2	2.38	0.50
11:BE:334:ASP:OD1	11:BE:335:GLU:N	2.44	0.50
25:BW:75:ARG:HB3	25:BW:78:ILE:HD11	1.92	0.50
36:B8:131:LYS:NZ	53:BA:1234:U:OP2	2.44	0.50
51:AA:471:U:OP2	71:Ab:50:ARG:NH2	2.45	0.50
52:B9:87:ILE:HB	52:B9:97:GLN:HB2	1.93	0.50
53:BA:396:C:O2'	53:BA:415:A:N6	2.45	0.50
53:BA:1230:U:H5'	53:BA:1231:U:H5'	1.94	0.50
54:AB:105:LEU:HD21	54:AB:224:THR:HG22	1.94	0.50
59:AI:381:LYS:HA	59:AI:388:ALA:HB2	1.93	0.50
61:AK:99:ILE:HD11	61:AK:163:ALA:HB1	1.92	0.50
70:Aa:150:MET:HE1	70:Aa:291:GLY:HA3	1.93	0.50
73:Ad:108:TRP:O	73:Ad:112:GLU:HG2	2.12	0.50
83:Ao:499:LEU:HD21	83:Ao:515:ILE:HD12	1.93	0.50
11:BE:274:TRP:HE1	11:BE:286:ASN:HB2	1.75	0.50
24:BV:139:LEU:HD13	24:BV:148:LEU:HD23	1.94	0.50
27:BY:52:GLU:HG3	27:BY:143:ARG:HH12	1.76	0.50
31:Bd:189:GLU:HG2	39:Bk:137:LEU:HD13	1.94	0.50
59:AI:276:LYS:HE2	59:AI:281:LYS:HD3	1.93	0.50
62:AL:107:VAL:N	62:AL:131:ASP:OD2	2.39	0.50
76:Ag:300:TRP:HE1	76:Ag:303:GLY:HA3	1.75	0.50
85:GL:86:LEU:HA	85:GL:89:THR:HG22	1.92	0.50
11:BE:105:GLY:HA3	22:BT:91:LYS:HD2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BJ:121:ILE:HD12	14:BJ:156:SER:HB2	1.93	0.50
29:Bb:45:LEU:O	29:Bb:50:LYS:NZ	2.36	0.50
30:Bc:156:LYS:HD2	30:Bc:158:GLU:HG2	1.93	0.50
51:AA:798:A:H2'	51:AA:799:A:C8	2.46	0.50
53:BA:122:G:N2	53:BA:125:A:OP2	2.42	0.50
53:BA:698:U:H2'	53:BA:699:G:H8	1.76	0.50
59:AI:115:GLY:HA3	60:AJ:84:ASP:HB2	1.92	0.50
74:Ae:205:PHE:O	74:Ae:209:MET:HG2	2.12	0.50
80:Ak:196:VAL:HG11	80:Ak:207:LEU:HD11	1.93	0.50
17:BO:98:PRO:HA	22:BT:162:ILE:HG12	1.94	0.49
24:BV:102:VAL:HB	24:BV:139:LEU:HB3	1.93	0.49
36:B8:113:ARG:NH1	53:BA:1234:U:O2'	2.46	0.49
42:Bn:69:HIS:CD2	42:Bn:71:LYS:HG3	2.44	0.49
53:BA:942:U:H2'	53:BA:943:C:C6	2.47	0.49
86:AV:39:U:H2'	86:AV:40:U:C6	2.47	0.49
3:B2:100:LEU:HB3	3:B2:144:LEU:HD11	1.94	0.49
22:BT:165:GLU:HB2	22:BT:168:ASN:HB2	1.94	0.49
28:Ba:123:LEU:HD22	28:Ba:220:LEU:HD11	1.94	0.49
30:Bc:183:ASP:OD1	30:Bc:184:LYS:N	2.44	0.49
35:Bh:184:PHE:O	35:Bh:186:VAL:HG23	2.12	0.49
51:AA:855:C:H2'	51:AA:856:U:C6	2.48	0.49
53:BA:52:A:H4'	53:BA:245:A:H2	1.77	0.49
53:BA:1249:A:P	53:BA:1250:A:H2'	2.52	0.49
65:AP:59:ASN:ND2	65:AP:63:GLU:O	2.45	0.49
70:Aa:221:ARG:HH22	70:Aa:224:ARG:HE	1.59	0.49
3:B2:95:LYS:NZ	27:BY:181:ASP:O	2.38	0.49
23:BU:114:LYS:HD3	33:Bf:45:CYS:SG	2.52	0.49
30:Bc:44:LEU:HD21	30:Bc:225:GLU:HG3	1.95	0.49
30:Bc:285:THR:OG1	30:Bc:288:SER:O	2.28	0.49
31:Bd:157:LEU:HD11	38:Bj:178:TRP:HH2	1.77	0.49
41:Bm:117:ARG:O	41:Bm:121:MET:HG2	2.13	0.49
51:AA:641:A:H2'	51:AA:642:G:C8	2.47	0.49
51:AA:708:A:H3'	51:AA:709:A:H8	1.77	0.49
53:BA:842:U:OP2	53:BA:871:A:N6	2.26	0.49
53:BA:1344:C:H2'	53:BA:1345:A:C8	2.48	0.49
56:AE:392:ARG:HG2	56:AE:394:ASP:H	1.76	0.49
58:AG:176:ASP:N	58:AG:176:ASP:OD1	2.44	0.49
73:Ad:64:ARG:HA	73:Ad:67:VAL:HG22	1.94	0.49
76:Ag:129:LYS:HZ2	76:Ag:319:ARG:HE	1.60	0.49
80:Ak:123:ARG:HG2	83:Ao:77:THR:HB	1.94	0.49
86:AV:3:U:H2'	86:AV:4:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:AY:56:U:H2'	86:AY:57:U:C6	2.47	0.49
27:BY:40:ARG:HH22	53:BA:108:A:H61	1.60	0.49
28:Ba:392:ILE:HG12	28:Ba:397:VAL:HG22	1.93	0.49
53:BA:16:A:H2'	53:BA:17:C:C6	2.47	0.49
62:AL:63:LEU:HD11	62:AL:84:ARG:HB2	1.95	0.49
76:Ag:133:LYS:HG2	76:Ag:344:VAL:HG11	1.95	0.49
5:B4:53:TYR:CG	5:B4:72:PRO:HB3	2.47	0.49
7:B6:47:ASP:O	7:B6:51:LYS:N	2.46	0.49
11:BE:104:LEU:HB2	11:BE:121:LEU:HB2	1.93	0.49
17:BO:36:THR:HG22	53:BA:801:G:H4'	1.94	0.49
28:Ba:363:ASP:OD1	28:Ba:363:ASP:N	2.45	0.49
37:Bi:170:PRO:HA	37:Bi:173:VAL:HG12	1.93	0.49
50:Bx:192:LEU:HB3	53:BA:574:A:C8	2.48	0.49
51:AA:96:U:H2'	51:AA:97:C:C6	2.47	0.49
51:AA:365:A:H2'	51:AA:366:A:C8	2.48	0.49
51:AA:936:C:H2'	51:AA:937:A:H8	1.77	0.49
53:BA:1528:A:H2'	53:BA:1529:A:H8	1.78	0.49
86:AV:56:U:H2'	86:AV:57:U:C6	2.48	0.49
10:BD:216:VAL:HG13	10:BD:228:GLN:HB3	1.93	0.49
11:BE:206:VAL:HG13	11:BE:297:VAL:HG13	1.93	0.49
19:BQ:170:LYS:HB2	45:Bq:132:LEU:HD22	1.93	0.49
27:BY:190:ARG:NE	27:BY:197:GLU:OE2	2.38	0.49
53:BA:783:A:O2'	53:BA:785:A:OP2	2.26	0.49
70:Aa:111:LYS:HD3	70:Aa:286:SER:HB2	1.93	0.49
76:Ag:152:LEU:HB3	76:Ag:259:VAL:HG12	1.95	0.49
12:BF:237:LEU:O	48:Bv:25:TYR:N	2.46	0.49
29:Bb:124:ARG:HH22	31:Bd:116:LEU:HD23	1.77	0.49
53:BA:83:A:OP2	53:BA:1235:C:O2'	2.21	0.49
59:AI:300:ASP:OD1	59:AI:300:ASP:N	2.45	0.49
77:Ah:341:HIS:CD2	78:Ai:24:ARG:HD2	2.48	0.49
81:Am:69:GLU:OE1	81:Am:69:GLU:N	2.44	0.49
85:CL:80:SER:HA	85:CL:83:ASN:ND2	2.28	0.49
86:AY:3:U:H2'	86:AY:4:U:C6	2.48	0.49
11:BE:230:THR:HG22	53:BA:988:U:H4'	1.95	0.49
12:BF:69:LEU:HB2	12:BF:190:VAL:HG11	1.94	0.49
35:Bh:83:PHE:HE2	35:Bh:202:LEU:HB2	1.78	0.49
51:AA:912:A:H2'	51:AA:913:G:H8	1.78	0.49
53:BA:414:A:H3'	53:BA:415:A:H8	1.77	0.49
59:AI:277:ARG:HD3	59:AI:343:GLY:HA3	1.93	0.49
76:Ag:166:ASP:OD1	76:Ag:166:ASP:N	2.45	0.49
76:Ag:357:GLN:O	76:Ag:361:GLU:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Ah:313:PHE:HB2	80:Ak:166:ARG:HH21	1.77	0.49
77:Ah:353:ASN:ND2	78:Ai:37:PHE:O	2.45	0.49
12:BF:119:GLU:OE2	12:BF:156:ARG:NH2	2.41	0.49
14:BJ:89:VAL:O	14:BJ:93:ASN:ND2	2.46	0.49
15:BK:32:GLY:O	15:BK:36:GLY:N	2.45	0.49
49:Bw:397:GLU:HG2	49:Bw:398:THR:HG22	1.93	0.49
53:BA:150:A:N3	53:BA:198:U:O2'	2.43	0.49
53:BA:920:C:H42	53:BA:924:G:N2	2.05	0.49
53:BA:1238:A:H3'	53:BA:1239:A:H5''	1.94	0.49
85:CL:60:TYR:HB2	85:CL:65:GLN:HE22	1.77	0.49
20:BR:32:LEU:HB3	20:BR:52:LEU:HD22	1.93	0.49
35:Bh:166:VAL:HG11	35:Bh:192:ARG:HG3	1.95	0.49
49:Bw:215:HIS:ND1	53:BA:757:A:OP1	2.38	0.49
49:Bw:240:GLN:NE2	49:Bw:348:PRO:O	2.46	0.49
51:AA:525:U:H2'	51:AA:526:G:C8	2.47	0.49
53:BA:935:C:H2'	53:BA:936:A:C8	2.48	0.49
59:AI:397:ARG:NH2	86:AV:30:U:OP2	2.46	0.49
65:AP:67:ALA:HB2	70:Aa:218:TYR:CZ	2.48	0.49
11:BE:94:SER:HA	11:BE:182:THR:HG21	1.95	0.48
12:BF:220:ASP:OD1	12:BF:221:LEU:N	2.45	0.48
16:BN:69:GLY:HA2	50:Bx:152:THR:HA	1.94	0.48
28:Ba:380:GLN:HB3	28:Ba:410:THR:HG22	1.95	0.48
31:Bd:133:ARG:HA	31:Bd:136:ILE:HG22	1.93	0.48
49:Bw:233:ASN:HB2	49:Bw:293:PHE:HB2	1.95	0.48
51:AA:734:A:H2'	51:AA:735:G:H8	1.77	0.48
53:BA:799:A:H61	53:BA:991:C:N4	2.10	0.48
74:Ae:125:ILE:HG22	74:Ae:164:LYS:HD2	1.95	0.48
10:BD:141:ALA:HB2	10:BD:154:ALA:HB2	1.95	0.48
12:BF:217:LEU:HB2	12:BF:256:HIS:CG	2.48	0.48
20:BR:141:SER:O	20:BR:147:ASN:ND2	2.42	0.48
49:Bw:219:ARG:NH2	53:BA:780:G:OP2	2.44	0.48
51:AA:546:U:H2'	51:AA:547:A:H8	1.78	0.48
51:AA:913:G:H2'	51:AA:914:A:H8	1.77	0.48
51:AA:941:U:H2'	51:AA:942:G:H8	1.78	0.48
59:AI:228:ARG:HH11	68:AU:85:GLN:HB3	1.77	0.48
78:Ai:98:GLU:HB2	78:Ai:102:ALA:HB3	1.95	0.48
83:Ao:259:ALA:HA	83:Ao:262:TYR:CZ	2.48	0.48
86:AV:8:U:O4	86:AV:14:U:C5	2.67	0.48
86:AY:8:U:O4	86:AY:14:U:C5	2.66	0.48
86:AY:39:U:H2'	86:AY:40:U:C6	2.48	0.48
13:BI:133:SER:HG	13:BI:136:ASN:HD22	1.54	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:BO:77:ILE:HG22	17:BO:78:ARG:HG3	1.93	0.48
21:BS:75:ARG:NH2	21:BS:97:ARG:O	2.46	0.48
26:BX:46:MET:HG3	32:Be:34:ARG:HB3	1.94	0.48
30:Bc:313:LEU:O	30:Bc:317:ARG:HG2	2.13	0.48
40:Bl:154:ASP:OD1	40:Bl:154:ASP:N	2.46	0.48
63:AN:40:ARG:NH1	63:AN:86:ARG:HH21	2.11	0.48
70:Aa:92:PHE:O	70:Aa:98:GLN:NE2	2.33	0.48
77:Ah:379:LEU:HD13	77:Ah:386:LEU:HB2	1.95	0.48
12:BF:123:GLY:HA3	12:BF:142:ARG:HG2	1.95	0.48
31:Bd:66:ASP:OD2	31:Bd:70:LYS:NZ	2.45	0.48
36:B8:109:ALA:O	36:B8:113:ARG:HG2	2.13	0.48
47:Bu:138:CYS:SG	47:Bu:139:SER:N	2.87	0.48
51:AA:545:C:OP1	58:AG:185:LYS:NZ	2.46	0.48
51:AA:578:G:H2'	51:AA:579:A:H2'	1.95	0.48
53:BA:1387:A:H2'	53:BA:1388:A:C8	2.48	0.48
59:AI:100:THR:OG1	59:AI:101:GLN:N	2.46	0.48
74:Ae:440:ARG:HA	74:Ae:443:GLN:HG2	1.96	0.48
86:AY:22:U:C4	86:AY:23:U:C5	3.01	0.48
3:B2:236:LEU:HD13	27:BY:48:PRO:HG3	1.94	0.48
5:B4:41:LEU:HD11	38:Bj:67:GLN:HB3	1.95	0.48
35:Bh:72:ILE:HD13	35:Bh:178:LEU:HD23	1.95	0.48
41:Bm:89:ASP:OD1	41:Bm:125:ARG:NH2	2.42	0.48
51:AA:154:C:H2'	51:AA:155:A:H8	1.77	0.48
53:BA:232:U:H2'	53:BA:233:A:C8	2.48	0.48
62:AL:72:LYS:HE3	87:AX:5:U:H4'	1.96	0.48
83:Ao:67:LYS:HG3	83:Ao:68:VAL:HG13	1.95	0.48
83:Ao:263:CYS:O	83:Ao:267:ARG:NH1	2.47	0.48
83:Ao:423:MET:HE1	83:Ao:463:LYS:HG3	1.96	0.48
21:BS:104:SER:O	21:BS:135:ARG:NH1	2.47	0.48
51:AA:25:U:H2'	51:AA:26:A:C8	2.46	0.48
51:AA:339:A:H2'	51:AA:340:A:C8	2.49	0.48
53:BA:230:G:H2'	53:BA:231:C:C6	2.48	0.48
53:BA:476:U:H2'	53:BA:477:A:H8	1.79	0.48
56:AE:402:PRO:HB2	56:AE:404:ILE:HG12	1.96	0.48
83:Ao:396:ILE:HG21	83:Ao:425:VAL:HG21	1.95	0.48
86:AV:50:U:N3	86:AV:54:U:C5	2.81	0.48
87:AX:4:U:HO2'	87:AX:5:U:H6	1.61	0.48
4:B3:35:LYS:HE2	53:BA:453:U:H1'	1.96	0.48
6:B5:181:ARG:NH1	6:B5:187:GLN:OE1	2.46	0.48
10:BD:162:ASP:OD1	10:BD:163:THR:N	2.44	0.48
10:BD:207:TYR:OH	10:BD:296:TYR:OH	2.16	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BP:99:ASN:HB2	18:BP:144:GLY:HA3	1.94	0.48
31:Bd:104:VAL:HG11	38:Bj:80:GLU:HG2	1.96	0.48
34:Bg:133:PHE:HB3	35:Bh:259:ARG:HD2	1.96	0.48
51:AA:386:U:H2'	51:AA:387:C:H6	1.79	0.48
53:BA:505:U:C2	53:BA:507:G:H5'	2.49	0.48
53:BA:622:A:N6	53:BA:623:G:O6	2.47	0.48
56:AE:282:ILE:HG13	56:AE:327:ILE:HD13	1.93	0.48
61:AK:113:SER:O	61:AK:116:THR:OG1	2.29	0.48
65:AP:29:ARG:NH1	65:AP:57:LEU:HB2	2.28	0.48
85:CL:63:LYS:O	85:CL:66:GLN:HG3	2.14	0.48
19:BQ:172:VAL:HA	19:BQ:175:PHE:CE2	2.48	0.48
25:BW:188:LYS:HD2	25:BW:193:HIS:CE1	2.49	0.48
37:Bi:98:SER:HB3	37:Bi:215:ARG:HH22	1.78	0.48
42:Bn:51:ARG:NE	53:BA:612:A:OP1	2.47	0.48
51:AA:154:C:H2'	51:AA:155:A:C8	2.49	0.48
51:AA:477:A:H2'	51:AA:478:A:C8	2.48	0.48
51:AA:792:U:H2'	51:AA:793:A:H8	1.78	0.48
51:AA:883:C:H1'	51:AA:886:A:N6	2.28	0.48
53:BA:247:C:H2'	53:BA:248:A:C8	2.49	0.48
53:BA:1344:C:O2'	53:BA:1387:A:N3	2.39	0.48
79:Aj:30:ASP:N	79:Aj:30:ASP:OD1	2.46	0.48
6:B5:156:THR:OG1	20:BR:130:CYS:SG	2.51	0.48
12:BF:79:LEU:HD23	41:Bm:95:VAL:HG13	1.96	0.48
21:BS:52:ASN:HD22	29:Bb:267:ARG:HD3	1.79	0.48
29:Bb:138:GLU:O	29:Bb:142:THR:HG22	2.13	0.48
34:Bg:35:ARG:HD3	41:Bm:157:TRP:HH2	1.79	0.48
34:Bg:93:SER:O	34:Bg:97:ILE:HG12	2.14	0.48
45:Bq:73:MET:SD	45:Bq:73:MET:N	2.86	0.48
51:AA:199:G:N2	51:AA:202:A:OP2	2.25	0.48
53:BA:1152:G:H2'	53:BA:1153:G:C8	2.47	0.48
53:BA:1388:A:H8	53:BA:1388:A:OP2	1.96	0.48
70:Aa:128:MET:HE1	70:Aa:136:ALA:HB2	1.96	0.48
70:Aa:247:VAL:HG22	70:Aa:284:LEU:HD23	1.96	0.48
73:Ad:185:LYS:NZ	73:Ad:186:SER:O	2.47	0.48
77:Ah:294:ILE:HD13	83:Ao:72:GLN:HG2	1.95	0.48
14:BJ:232:LEU:HD21	85:HL:87:LYS:NZ	2.29	0.48
51:AA:483:U:H2'	51:AA:484:C:C6	2.49	0.48
51:AA:843:C:O2	51:AA:928:A:N6	2.46	0.48
51:AA:882:A:H4'	74:Ae:108:SER:HB2	1.96	0.48
53:BA:570:A:H2'	53:BA:571:A:C8	2.49	0.48
54:AB:199:ASN:ND2	54:AB:203:GLU:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AI:157:SER:HB3	59:AI:210:LEU:HD22	1.95	0.48
64:AO:144:MET:HE2	64:AO:144:MET:HA	1.96	0.48
79:Aj:36:LEU:HD11	79:Aj:50:LEU:HD11	1.94	0.48
86:AV:47:U:C4	86:AV:48:U:C4	3.02	0.48
1:B0:71:ARG:NH2	53:BA:1163:A:OP1	2.47	0.47
5:B4:46:ARG:NH1	31:Bd:87:ASP:O	2.47	0.47
13:BI:102:VAL:HG11	13:BI:105:LEU:HD23	1.96	0.47
30:Bc:169:VAL:HG12	30:Bc:322:GLU:HB3	1.96	0.47
31:Bd:165:ASP:OD2	38:Bj:185:ARG:NH2	2.46	0.47
35:Bh:98:ILE:HG12	35:Bh:119:LEU:HD12	1.96	0.47
39:Bk:97:ALA:HB3	39:Bk:103:ALA:HB2	1.96	0.47
49:Bw:55:SER:HB2	53:BA:659:U:H5'	1.96	0.47
51:AA:198:C:H2'	51:AA:199:G:C8	2.49	0.47
53:BA:247:C:H2'	53:BA:248:A:H8	1.78	0.47
53:BA:713:A:H2'	53:BA:714:A:C8	2.48	0.47
53:BA:1411:G:O6	53:BA:1430:G:N1	2.47	0.47
54:AB:148:ARG:HH22	68:AU:82:ASP:HB2	1.79	0.47
57:AF:39:LEU:HD13	57:AF:66:VAL:HG22	1.95	0.47
65:AP:114:ARG:HG3	84:Ap:235:MET:HE3	1.96	0.47
1:B0:144:LEU:HD22	21:BS:44:VAL:HG11	1.96	0.47
4:B3:75:THR:HB	4:B3:83:LYS:HG2	1.95	0.47
4:B3:105:SER:HB3	53:BA:416:U:H1'	1.95	0.47
21:BS:116:LEU:HD13	29:Bb:130:ILE:HD11	1.94	0.47
27:BY:21:TYR:CZ	27:BY:82:GLN:HG2	2.49	0.47
36:B8:134:TRP:HE1	53:BA:1245:G:P	2.36	0.47
51:AA:88:C:H2'	51:AA:89:U:C6	2.49	0.47
53:BA:363:G:H2'	53:BA:364:A:C8	2.49	0.47
56:AE:136:ARG:N	78:Ai:67:PHE:O	2.46	0.47
56:AE:325:ARG:HH21	56:AE:430:THR:HG23	1.80	0.47
59:AI:218:ASP:OD1	59:AI:219:TYR:N	2.47	0.47
72:Ac:29:VAL:HB	72:Ac:79:TYR:HB2	1.96	0.47
74:Ae:321:ASP:O	74:Ae:325:ARG:HG2	2.14	0.47
76:Ag:205:GLU:HB3	76:Ag:207:TYR:CE2	2.49	0.47
83:Ao:435:ALA:HA	83:Ao:438:VAL:HG22	1.95	0.47
83:Ao:634:VAL:HG11	83:Ao:652:VAL:HG11	1.95	0.47
86:AV:22:U:C4	86:AV:23:U:C5	3.01	0.47
1:B0:78:GLY:HA2	21:BS:68:TRP:CE3	2.49	0.47
10:BD:290:LEU:HD12	10:BD:291:PRO:HD2	1.96	0.47
15:BK:156:VAL:HG11	15:BK:159:LEU:HB2	1.96	0.47
27:BY:15:LEU:HD11	27:BY:26:PRO:HB3	1.96	0.47
28:Ba:198:LEU:HD13	28:Ba:418:TYR:HE2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Bi:82:ALA:O	37:Bi:167:ASN:ND2	2.48	0.47
40:Bl:105:ARG:HD2	53:BA:388:A:H4'	1.97	0.47
49:Bw:195:ASP:HB2	49:Bw:234:GLN:HB2	1.96	0.47
51:AA:201:A:H2'	51:AA:202:A:C8	2.49	0.47
51:AA:892:A:C5	79:Aj:21:LEU:HD21	2.50	0.47
53:BA:565:A:N6	53:BA:1314:U:OP1	2.44	0.47
53:BA:744:A:OP1	53:BA:744:A:H4'	2.14	0.47
83:Ao:86:PRO:HG2	83:Ao:89:PHE:CD2	2.49	0.47
83:Ao:400:MET:HA	83:Ao:403:VAL:HG22	1.97	0.47
86:AY:50:U:N3	86:AY:54:U:C5	2.81	0.47
6:B5:136:GLU:HB3	6:B5:177:ARG:HH12	1.80	0.47
14:BJ:162:LYS:H	14:BJ:162:LYS:HD2	1.79	0.47
31:Bd:139:LEU:HD23	39:Bk:169:ILE:HG23	1.96	0.47
32:Be:28:ARG:HD2	53:BA:670:A:H5''	1.97	0.47
51:AA:572:A:OP2	51:AA:573:A:O2'	2.25	0.47
53:BA:1066:A:H2'	53:BA:1067:G:C8	2.47	0.47
90:BA:1792:SPM:H62	90:BA:1792:SPM:H91	1.69	0.47
76:Ag:211:LYS:HZ3	76:Ag:212:ARG:HE	1.62	0.47
86:AV:50:U:O4	86:AV:54:U:C5	2.58	0.47
7:B6:20:MET:HG2	7:B6:58:GLU:HA	1.95	0.47
10:BD:207:TYR:O	10:BD:209:ARG:HG3	2.14	0.47
12:BF:47:VAL:HG13	12:BF:78:GLY:HA3	1.95	0.47
22:BT:96:ARG:HA	22:BT:99:MET:SD	2.55	0.47
27:BY:184:GLU:OE1	27:BY:186:THR:OG1	2.32	0.47
30:Bc:289:LEU:HD23	30:Bc:289:LEU:H	1.78	0.47
53:BA:1357:C:H3'	53:BA:1358:G:H5''	1.97	0.47
56:AE:286:GLU:HB2	56:AE:288:HIS:CE1	2.50	0.47
58:AG:235:ALA:HB3	61:AK:123:LYS:HD2	1.97	0.47
74:Ae:89:HIS:HB3	74:Ae:92:ASP:OD2	2.14	0.47
76:Ag:290:HIS:HA	76:Ag:293:ARG:HD2	1.97	0.47
77:Ah:297:THR:HG22	83:Ao:67:LYS:HE2	1.96	0.47
80:Ak:268:LEU:HD12	80:Ak:285:LEU:HD22	1.95	0.47
4:B3:114:LYS:NZ	46:Bt:42:GLU:OE2	2.46	0.47
15:BK:35:LEU:HD12	15:BK:38:ILE:HD11	1.95	0.47
16:BN:15:ALA:HB1	35:Bh:269:VAL:HG21	1.97	0.47
29:Bb:197:GLU:OE1	29:Bb:197:GLU:N	2.48	0.47
29:Bb:374:GLU:HG3	47:Bu:140:ARG:HG2	1.96	0.47
38:Bj:162:ARG:HH21	38:Bj:164:LYS:HE2	1.79	0.47
51:AA:432:A:H4'	51:AA:433:U:H5''	1.97	0.47
51:AA:643:G:O2'	51:AA:651:G:OP2	2.22	0.47
53:BA:529:G:O2'	53:BA:548:A:N3	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:AE:188:LYS:H	56:AE:188:LYS:HG3	1.45	0.47
56:AE:245:VAL:HB	56:AE:271:ALA:HB1	1.96	0.47
56:AE:362:LEU:HA	56:AE:365:LYS:HG2	1.95	0.47
83:Ao:553:ASP:OD1	83:Ao:554:CYS:N	2.48	0.47
85:EL:72:ALA:HA	85:HL:76:LEU:CD2	2.44	0.47
6:B5:90:ASN:O	6:B5:94:ARG:HG2	2.14	0.47
8:BB:4:A:H3'	8:BB:5:A:H5''	1.95	0.47
18:BP:100:ARG:O	18:BP:104:LEU:HG	2.14	0.47
28:Ba:351:LEU:HD11	28:Ba:379:ASP:HA	1.95	0.47
29:Bb:136:ARG:NE	29:Bb:140:GLU:OE2	2.47	0.47
29:Bb:239:ASN:HD22	29:Bb:278:ARG:HH11	1.63	0.47
48:Bv:40:PRO:HG3	48:Bv:51:GLN:HB3	1.95	0.47
51:AA:114:A:N1	51:AA:136:C:O2'	2.45	0.47
51:AA:388:U:H2'	51:AA:389:A:H8	1.80	0.47
51:AA:562:A:H1'	51:AA:708:A:H61	1.79	0.47
51:AA:641:A:H2'	51:AA:642:G:H8	1.79	0.47
51:AA:703:U:H2'	51:AA:704:U:C6	2.49	0.47
51:AA:767:U:C2	51:AA:768:A:C8	3.02	0.47
51:AA:789:C:OP1	59:AI:389:ARG:NH1	2.46	0.47
53:BA:199:A:H2'	53:BA:200:A:H8	1.80	0.47
53:BA:319:G:H2'	53:BA:320:U:C6	2.50	0.47
53:BA:410:U:O2'	53:BA:1169:A:N7	2.44	0.47
53:BA:745:A:H3'	53:BA:746:U:H5''	1.96	0.47
53:BA:834:C:O2	53:BA:1431:G:O2'	2.30	0.47
56:AE:372:GLU:N	56:AE:382:ILE:O	2.34	0.47
60:Aj:81:LYS:HE2	60:Aj:140:TYR:HE1	1.80	0.47
68:AU:83:PRO:HG2	68:AU:84:TRP:CD1	2.49	0.47
75:Af:153:ARG:NH2	75:Af:157:ALA:O	2.48	0.47
75:Af:160:ASP:OD1	75:Af:160:ASP:N	2.45	0.47
79:Aj:192:ASN:OD1	79:Aj:193:LEU:N	2.48	0.47
86:AY:47:U:C4	86:AY:48:U:C4	3.02	0.47
3:B2:185:GLN:OE1	26:BX:9:LEU:N	2.42	0.47
5:B4:41:LEU:HD22	38:Bj:71:ALA:HB2	1.97	0.47
9:B7:85:ARG:HH12	32:Be:17:ARG:HH12	1.63	0.47
11:BE:69:ASN:HD21	11:BE:154:HIS:CE1	2.30	0.47
21:BS:122:VAL:HG22	21:BS:157:SER:HB3	1.97	0.47
31:Bd:77:LYS:NZ	86:AV:47:U:OP1	2.48	0.47
38:Bj:114:ILE:HG12	76:Ag:233:ARG:HE	1.79	0.47
41:Bm:74:HIS:HA	41:Bm:77:GLU:HG2	1.96	0.47
50:Bx:94:ARG:NE	53:BA:1518:A:H4'	2.30	0.47
51:AA:751:A:N7	51:AA:775:A:O2'	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:792:U:H4'	59:AI:389:ARG:HG3	1.96	0.47
53:BA:1006:U:H2'	53:BA:1007:G:O4'	2.14	0.47
53:BA:1146:G:H2'	53:BA:1147:G:C8	2.50	0.47
75:Af:109:VAL:HG12	75:Af:110:GLU:H	1.80	0.47
76:Ag:70:SER:HB3	76:Ag:73:GLU:HG3	1.96	0.47
76:Ag:325:GLN:NE2	80:Ak:306:ASP:OD1	2.41	0.47
2:B1:91:TYR:OH	53:BA:61:U:OP1	2.25	0.47
9:B7:84:ARG:NH1	53:BA:126:G:OP1	2.48	0.47
14:BJ:181:ILE:O	14:BJ:184:THR:OG1	2.24	0.47
17:BO:43:ASN:HD21	17:BO:118:ARG:HG2	1.80	0.47
28:Ba:115:GLU:HB2	28:Ba:119:GLN:HG3	1.97	0.47
29:Bb:217:LEU:HD13	29:Bb:236:LEU:HD13	1.96	0.47
29:Bb:257:PRO:HB3	29:Bb:268:PHE:CZ	2.50	0.47
39:Bk:137:LEU:HD21	39:Bk:141:GLY:HA2	1.95	0.47
51:AA:28:U:H2'	51:AA:29:A:C8	2.50	0.47
51:AA:900:A:H2	51:AA:901:A:H62	1.62	0.47
53:BA:1002:U:C2	53:BA:1003:C:C5	3.03	0.47
54:AB:213:LYS:HG2	71:Ab:5:ARG:HB3	1.97	0.47
59:AI:179:LEU:HD11	59:AI:184:LEU:HD22	1.96	0.47
71:Ab:106:LEU:HD23	71:Ab:109:LEU:HD12	1.97	0.47
72:Ac:32:VAL:HG22	72:Ac:76:LEU:HG	1.96	0.47
73:Ad:51:THR:HG21	84:Ap:228:SER:H	1.79	0.47
77:Ah:281:VAL:HG21	83:Ao:413:PRO:HA	1.96	0.47
20:BR:79:TRP:NE1	22:BT:269:MET:SD	2.88	0.47
28:Ba:301:PRO:HB3	53:BA:721:A:OP1	2.15	0.47
50:Bx:43:ASP:N	50:Bx:43:ASP:OD1	2.46	0.47
51:AA:27:U:H2'	51:AA:28:U:C6	2.50	0.47
52:B9:74:ARG:NH1	53:BA:545:U:O2'	2.48	0.47
53:BA:199:A:H2'	53:BA:200:A:C8	2.50	0.47
53:BA:372:U:H5''	53:BA:1253:G:P	2.55	0.47
66:AQ:50:PHE:HD2	66:AQ:76:HIS:HB3	1.80	0.47
79:Aj:58:VAL:HA	79:Aj:137:HIS:HD1	1.80	0.47
19:BQ:46:GLU:HG3	19:BQ:47:LYS:HG3	1.97	0.46
30:Bc:153:ARG:NH2	30:Bc:256:ASP:O	2.47	0.46
33:Bf:71:HIS:HA	34:Bg:141:GLY:H	1.80	0.46
49:Bw:399:ILE:HG22	49:Bw:404:VAL:HA	1.96	0.46
51:AA:9:U:H1'	51:AA:518:A:H5''	1.97	0.46
53:BA:869:G:H2'	53:BA:870:C:C6	2.49	0.46
56:AE:369:HIS:HA	56:AE:387:PRO:HD3	1.97	0.46
57:AF:24:ARG:NH2	57:AF:87:ASP:OD2	2.48	0.46
57:AF:49:TYR:OH	57:AF:90:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:Aj:158:GLU:HG3	83:Ao:70:ILE:HD13	1.97	0.46
74:Ae:196:ASN:ND2	74:Ae:199:ASP:OD2	2.48	0.46
6:B5:130:VAL:HG11	20:BR:134:LEU:HD23	1.97	0.46
11:BE:221:ARG:HA	11:BE:261:LEU:HD22	1.97	0.46
29:Bb:368:ARG:NH1	53:BA:1196:G:OP2	2.48	0.46
32:Be:21:TRP:O	32:Be:32:LYS:NZ	2.48	0.46
34:Bg:144:ARG:HB2	34:Bg:147:GLU:HB2	1.97	0.46
49:Bw:132:ASP:OD1	49:Bw:134:THR:OG1	2.24	0.46
49:Bw:278:ILE:HD11	49:Bw:333:GLN:HG2	1.97	0.46
51:AA:155:A:H2'	51:AA:156:C:C6	2.50	0.46
51:AA:883:C:H3'	74:Ae:433:ARG:HH12	1.79	0.46
51:AA:884:C:H5	74:Ae:143:TYR:HA	1.80	0.46
53:BA:193:U:H2'	53:BA:194:G:C8	2.50	0.46
53:BA:364:A:O2'	53:BA:385:U:OP1	2.33	0.46
53:BA:1246:A:C5	86:AY:70:C:C5	3.03	0.46
60:Aj:74:LYS:HG2	60:Aj:75:ARG:HG3	1.97	0.46
63:AN:34:MET:HE3	78:Ai:52:TYR:CD1	2.50	0.46
77:Ah:301:LYS:HE2	83:Ao:140:LEU:HD11	1.97	0.46
83:Ao:551:PHE:CG	83:Ao:585:LEU:HD22	2.50	0.46
85:CL:76:LEU:HB3	85:FL:72:ALA:HA	1.98	0.46
8:BB:40:U:H2'	8:BB:41:G:C8	2.50	0.46
24:BV:133:ARG:NH2	24:BV:155:LYS:O	2.48	0.46
28:Ba:140:ALA:HB1	28:Ba:412:ARG:HG2	1.97	0.46
38:Bj:151:ARG:HG2	38:Bj:152:LYS:HG3	1.96	0.46
38:Bj:187:THR:HG23	38:Bj:190:ARG:HH21	1.81	0.46
38:Bj:243:PHE:HZ	38:Bj:248:LYS:HE2	1.79	0.46
42:Bn:36:VAL:HG23	42:Bn:37:THR:HG23	1.97	0.46
51:AA:447:U:H2'	51:AA:448:A:H8	1.81	0.46
53:BA:421:U:H2'	53:BA:422:U:C6	2.51	0.46
56:AE:282:ILE:HG23	56:AE:353:LEU:HB3	1.97	0.46
61:AK:161:LEU:HD13	68:AU:23:TYR:CG	2.50	0.46
76:Ag:207:TYR:CZ	76:Ag:241:ILE:HG23	2.51	0.46
79:Aj:67:LEU:HD13	79:Aj:141:LEU:HB2	1.97	0.46
84:Ap:104:PRO:HB2	84:Ap:109:ARG:HB3	1.97	0.46
5:B4:59:LYS:HA	5:B4:78:MET:HB2	1.96	0.46
9:B7:66:LYS:NZ	53:BA:254:G:O5'	2.49	0.46
12:BF:279:ARG:H	40:Bl:90:ARG:HH21	1.63	0.46
28:Ba:139:LEU:HD22	28:Ba:416:ALA:HA	1.97	0.46
53:BA:1000:A:H2'	53:BA:1001:A:C8	2.51	0.46
53:BA:1000:A:H2'	53:BA:1001:A:H8	1.80	0.46
58:AG:61:GLU:HA	58:AG:64:TYR:CD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:AP:26:CYS:HB3	65:AP:29:ARG:HB3	1.96	0.46
83:Ao:294:VAL:HG21	83:Ao:334:ASN:H	1.80	0.46
86:AY:52:U:H5	86:AY:53:U:N3	2.10	0.46
14:BJ:64:CYS:HB3	50:Bx:70:CYS:HB2	1.97	0.46
30:Bc:52:GLN:HG3	30:Bc:216:LEU:HD11	1.97	0.46
32:Be:51:ILE:HG22	32:Be:53:GLU:H	1.79	0.46
34:Bg:45:GLU:OE2	34:Bg:49:ARG:NH2	2.49	0.46
51:AA:356:A:H2'	51:AA:357:G:H8	1.80	0.46
51:AA:713:A:O2'	86:AV:27:U:OP1	2.33	0.46
53:BA:342:C:H2'	53:BA:343:C:C6	2.51	0.46
53:BA:1017:U:HO2'	53:BA:1439:C:HO2'	1.62	0.46
80:Ak:168:PRO:O	80:Ak:171:ARG:NH1	2.48	0.46
6:B5:141:MET:O	6:B5:173:ARG:NH2	2.49	0.46
11:BE:329:PRO:HD2	11:BE:332:LEU:HD21	1.98	0.46
18:BP:43:ARG:NH1	53:BA:361:C:OP2	2.48	0.46
21:BS:54:ARG:HG3	21:BS:58:LEU:HG	1.97	0.46
27:BY:54:TRP:NE1	27:BY:56:LEU:O	2.49	0.46
29:Bb:138:GLU:HG2	29:Bb:141:ARG:HH12	1.81	0.46
38:Bj:152:LYS:HD2	38:Bj:157:LEU:HD21	1.96	0.46
43:Bo:91:TRP:CD2	46:Bt:58:GLN:HG2	2.51	0.46
46:Bt:37:ARG:NH1	53:BA:484:A:OP1	2.49	0.46
47:Bu:105:ALA:HA	47:Bu:115:ARG:HD3	1.96	0.46
53:BA:342:C:H2'	53:BA:343:C:H6	1.81	0.46
53:BA:860:G:H2'	53:BA:860:G:N3	2.30	0.46
53:BA:1060:C:H2'	53:BA:1061:U:H6	1.81	0.46
56:AE:186:LYS:HB3	56:AE:186:LYS:HE3	1.60	0.46
56:AE:230:ASN:O	56:AE:238:LYS:N	2.46	0.46
59:AI:228:ARG:NH1	68:AU:85:GLN:HB3	2.31	0.46
70:Aa:177:LYS:HB3	70:Aa:199:PRO:HD3	1.97	0.46
76:Ag:70:SER:OG	76:Ag:72:GLN:OE1	2.33	0.46
76:Ag:135:LEU:HG	92:Ag:500:GTP:C4	2.51	0.46
76:Ag:162:LYS:HD3	76:Ag:315:LEU:HD11	1.97	0.46
84:Ap:108:CYS:SG	84:Ap:146:GLN:HG3	2.56	0.46
3:B2:153:ASP:HA	3:B2:156:ARG:HG2	1.98	0.46
6:B5:93:ARG:HH12	53:BA:644:G:P	2.38	0.46
8:BB:9:A:H8	8:BB:11:C:H41	1.64	0.46
12:BF:59:ARG:NH2	12:BF:88:SER:O	2.48	0.46
18:BP:55:GLY:H	18:BP:59:ARG:NH1	2.12	0.46
19:BQ:172:VAL:HA	19:BQ:175:PHE:CD2	2.51	0.46
22:BT:117:LEU:HD22	22:BT:176:VAL:HG22	1.98	0.46
23:BU:14:VAL:HB	23:BU:17:ARG:HH21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BW:82:LYS:HD3	25:BW:147:ARG:HB3	1.96	0.46
27:BY:122:LEU:HD23	27:BY:133:VAL:HG21	1.98	0.46
30:Bc:75:VAL:HB	37:Bi:282:ILE:HB	1.96	0.46
40:Bl:96:VAL:O	40:Bl:158:LYS:NZ	2.36	0.46
43:Bo:48:ASP:OD1	43:Bo:48:ASP:N	2.49	0.46
49:Bw:145:LEU:HD22	49:Bw:402:ASN:HA	1.96	0.46
51:AA:226:G:H2'	51:AA:227:A:C8	2.50	0.46
53:BA:723:A:H3'	53:BA:724:A:H5''	1.96	0.46
56:AE:187:VAL:HG12	56:AE:188:LYS:HZ1	1.79	0.46
58:AG:192:ARG:HA	58:AG:201:MET:HE1	1.97	0.46
70:Aa:94:ASP:HB3	70:Aa:96:GLU:HG2	1.97	0.46
9:B7:81:VAL:HG22	9:B7:84:ARG:HH22	1.81	0.46
10:BD:128:ILE:HD12	10:BD:142:LEU:HG	1.97	0.46
14:BJ:143:LEU:HG	14:BJ:146:LEU:HD12	1.97	0.46
16:BN:169:VAL:HG13	50:Bx:75:TRP:CD1	2.50	0.46
18:BP:33:SER:O	53:BA:234:G:N2	2.43	0.46
18:BP:189:LYS:HB3	18:BP:192:PRO:HG2	1.98	0.46
27:BY:124:ASP:OD1	27:BY:124:ASP:N	2.49	0.46
28:Ba:125:LYS:NZ	28:Ba:366:SER:O	2.44	0.46
51:AA:385:C:H2'	51:AA:386:U:H6	1.81	0.46
53:BA:648:C:H2'	53:BA:649:A:C8	2.51	0.46
53:BA:742:U:H2'	53:BA:743:U:C6	2.50	0.46
53:BA:1146:G:H2'	53:BA:1147:G:H8	1.80	0.46
54:AB:141:ILE:O	54:AB:163:GLU:HB3	2.16	0.46
74:Ae:106:PRO:HB2	74:Ae:140:ASN:ND2	2.30	0.46
74:Ae:312:ASP:OD1	74:Ae:313:GLY:N	2.46	0.46
79:Aj:30:ASP:HA	79:Aj:33:ARG:HB3	1.97	0.46
12:BF:92:ARG:HD2	12:BF:92:ARG:HA	1.84	0.46
17:BO:41:VAL:HG12	17:BO:105:VAL:O	2.15	0.46
24:BV:162:ALA:HB2	24:BV:199:ILE:HG13	1.98	0.46
24:BV:165:ILE:HD11	24:BV:198:ARG:HB2	1.97	0.46
29:Bb:75:ARG:HB3	29:Bb:80:GLU:HB3	1.96	0.46
30:Bc:278:SER:H	30:Bc:295:GLY:HA2	1.81	0.46
39:Bk:90:VAL:HG23	39:Bk:189:HIS:HB3	1.97	0.46
49:Bw:264:LYS:NZ	53:BA:705:U:O4	2.36	0.46
51:AA:857:C:H2'	51:AA:858:C:H6	1.81	0.46
53:BA:188:C:O2'	53:BA:190:U:OP2	2.17	0.46
53:BA:1246:A:C4	86:AY:69:C:O2	2.68	0.46
53:BA:1513:U:H5''	53:BA:1525:C:H42	1.81	0.46
65:AP:91:LEU:HB3	65:AP:97:TYR:HB2	1.97	0.46
70:Aa:158:ALA:O	70:Aa:208:TRP:NE1	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Ab:128:GLU:OE1	71:Ab:128:GLU:N	2.46	0.46
83:Ao:461:TYR:CZ	83:Ao:488:VAL:HG11	2.51	0.46
83:Ao:608:ILE:HG13	83:Ao:640:PHE:HD2	1.80	0.46
84:Ap:119:ASN:OD1	84:Ap:119:ASN:N	2.47	0.46
23:BU:137:GLU:HB2	23:BU:138:PRO:HD3	1.98	0.46
27:BY:52:GLU:HB3	27:BY:143:ARG:HH22	1.81	0.46
30:Bc:61:LYS:HG2	37:Bi:275:PRO:HB3	1.96	0.46
30:Bc:223:ALA:HB1	30:Bc:237:ILE:HD13	1.97	0.46
31:Bd:173:ARG:HH21	39:Bk:175:HIS:HD2	1.63	0.46
49:Bw:99:ALA:HB3	49:Bw:102:ALA:HB2	1.98	0.46
51:AA:447:U:H2'	51:AA:448:A:C8	2.51	0.46
51:AA:674:A:H4'	55:AC:60:HIS:CE1	2.51	0.46
53:BA:50:A:H2'	53:BA:51:A:C8	2.51	0.46
53:BA:157:A:H2'	53:BA:158:A:C8	2.51	0.46
53:BA:1183:U:C6	53:BA:1230:U:H2'	2.51	0.46
57:AF:5:GLU:OE2	67:AR:75:TYR:OH	2.28	0.46
63:AN:41:ARG:NH1	78:Ai:48:THR:O	2.47	0.46
70:Aa:139:GLN:O	70:Aa:142:GLU:HG2	2.16	0.46
71:Ab:6:LEU:HD13	71:Ab:9:VAL:HG21	1.97	0.46
11:BE:231:HIS:CE1	53:BA:806:U:H1'	2.51	0.45
18:BP:80:LYS:HE3	36:B8:113:ARG:HH21	1.80	0.45
35:Bh:148:LEU:HD22	35:Bh:305:PHE:HB3	1.98	0.45
38:Bj:74:LEU:HD23	38:Bj:77:ILE:HD11	1.97	0.45
47:Bu:103:HIS:CE1	47:Bu:105:ALA:HB3	2.51	0.45
51:AA:217:U:H2'	51:AA:218:A:H8	1.82	0.45
53:BA:1315:U:H2'	53:BA:1316:U:C6	2.51	0.45
53:BA:1501:C:H2'	53:BA:1502:U:C6	2.51	0.45
80:Ak:188:ALA:O	80:Ak:235:SER:OG	2.34	0.45
83:Ao:581:TYR:O	83:Ao:585:LEU:HG	2.16	0.45
1:B0:102:GLU:OE2	1:B0:132:HIS:NE2	2.49	0.45
2:B1:81:GLY:O	2:B1:130:ARG:NH1	2.50	0.45
13:BI:133:SER:OG	13:BI:136:ASN:ND2	2.33	0.45
14:BJ:116:LEU:HG	14:BJ:164:MET:HE1	1.99	0.45
28:Ba:51:GLU:OE1	28:Ba:51:GLU:N	2.49	0.45
41:Bm:143:GLU:O	41:Bm:147:SER:OG	2.31	0.45
51:AA:189:A:H2'	51:AA:190:G:C8	2.52	0.45
53:BA:1246:A:C6	86:AY:70:C:C5	3.02	0.45
57:AF:96:HIS:CE1	57:AF:98:LEU:HD23	2.51	0.45
57:AF:108:ILE:HD11	67:AR:64:LYS:HB2	1.97	0.45
74:Ae:436:GLU:O	74:Ae:439:GLU:HG3	2.17	0.45
79:Aj:132:GLU:OE1	79:Aj:132:GLU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Ap:116:ASP:OD1	84:Ap:117:PHE:N	2.49	0.45
9:B7:85:ARG:HH22	32:Be:17:ARG:HH22	1.65	0.45
28:Ba:125:LYS:HZ2	28:Ba:364:LEU:HA	1.81	0.45
51:AA:340:A:H2'	86:AY:52:U:O4'	2.16	0.45
53:BA:108:A:O4'	53:BA:110:A:N6	2.50	0.45
53:BA:644:G:O2'	53:BA:1007:G:O6	2.31	0.45
53:BA:952:A:H2'	53:BA:953:G:H8	1.82	0.45
53:BA:1243:U:H2'	53:BA:1244:U:C6	2.50	0.45
53:BA:1274:A:H1'	86:AV:71:A:H2'	1.97	0.45
57:AF:115:GLU:HG2	75:Af:153:ARG:HH21	1.80	0.45
63:AN:36:ARG:O	63:AN:40:ARG:HG3	2.16	0.45
74:Ae:74:TYR:HE2	74:Ae:409:GLU:HB2	1.82	0.45
74:Ae:285:CYS:SG	74:Ae:286:ASN:N	2.88	0.45
74:Ae:433:ARG:O	74:Ae:436:GLU:HG3	2.16	0.45
77:Ah:309:ASN:N	77:Ah:309:ASN:OD1	2.49	0.45
78:Ai:27:ASP:OD1	78:Ai:30:SER:N	2.41	0.45
83:Ao:409:SER:H	83:Ao:411:ARG:HH21	1.64	0.45
29:Bb:360:ARG:NH2	53:BA:1203:C:OP2	2.31	0.45
37:Bi:278:LYS:HE3	37:Bi:280:VAL:HG22	1.99	0.45
38:Bj:162:ARG:HD3	38:Bj:171:TRP:HE3	1.81	0.45
51:AA:241:G:H2'	51:AA:242:U:H6	1.82	0.45
51:AA:836:G:O2'	51:AA:928:A:OP1	2.34	0.45
56:AE:285:TYR:N	56:AE:289:THR:O	2.49	0.45
74:Ae:269:ALA:HB3	74:Ae:320:LEU:HD23	1.98	0.45
76:Ag:182:GLU:OE1	76:Ag:182:GLU:N	2.47	0.45
76:Ag:272:THR:HG23	76:Ag:315:LEU:HD23	1.98	0.45
10:BD:85:ARG:HH12	53:BA:319:G:H21	1.65	0.45
18:BP:177:ALA:HA	18:BP:222:TYR:CD1	2.50	0.45
38:Bj:114:ILE:HG21	76:Ag:233:ARG:HH21	1.82	0.45
51:AA:185:A:H1'	51:AA:213:G:H22	1.81	0.45
51:AA:287:C:C2	72:Ac:2:PRO:HB3	2.51	0.45
53:BA:316:U:H2'	53:BA:317:A:C8	2.51	0.45
53:BA:993:U:H2'	53:BA:994:A:C8	2.51	0.45
53:BA:1246:A:H3'	86:AY:70:C:H5'	1.98	0.45
76:Ag:336:LEU:HD12	76:Ag:339:PHE:CD2	2.52	0.45
80:Ak:250:MET:HG3	80:Ak:252:GLU:H	1.81	0.45
4:B3:93:LYS:O	4:B3:96:THR:OG1	2.35	0.45
39:Bk:94:HIS:HB2	39:Bk:185:SER:HB3	1.98	0.45
46:Bt:14:GLY:H	53:BA:1279:G:H5''	1.82	0.45
50:Bx:77:LEU:HD13	50:Bx:88:LEU:HD22	1.98	0.45
51:AA:26:A:H2'	51:AA:27:U:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:194:U:O2	65:AP:43:ARG:NH1	2.47	0.45
51:AA:328:A:OP1	57:AF:90:ARG:NH2	2.41	0.45
51:AA:516:C:H2'	51:AA:517:A:C8	2.52	0.45
51:AA:526:G:H2'	51:AA:527:G:C8	2.51	0.45
53:BA:232:U:H2'	53:BA:233:A:H8	1.81	0.45
53:BA:339:G:N3	53:BA:1067:G:O2'	2.43	0.45
70:Aa:170:LEU:HD22	70:Aa:173:THR:HG21	1.97	0.45
75:Af:157:ALA:HB2	81:Am:113:ASN:HD21	1.81	0.45
78:Ai:5:SER:OG	80:Ak:249:ASP:OD2	2.35	0.45
81:Am:17:ARG:HH21	81:Am:20:ILE:HD11	1.81	0.45
83:Ao:442:LEU:HD12	83:Ao:450:LEU:HD12	1.99	0.45
8:BB:50:A:H2'	8:BB:51:G:C8	2.52	0.45
10:BD:213:THR:HG21	53:BA:862:A:H5''	1.98	0.45
11:BE:67:ASP:OD1	11:BE:68:GLU:N	2.50	0.45
17:BO:81:LYS:NZ	53:BA:1383:G:O3'	2.47	0.45
24:BV:115:GLU:HG2	34:Bg:19:LEU:HD11	1.98	0.45
30:Bc:101:ILE:HD12	30:Bc:126:THR:HA	1.97	0.45
30:Bc:206:LEU:HD12	30:Bc:209:LYS:HE3	1.99	0.45
51:AA:269:C:H2'	51:AA:270:C:C6	2.52	0.45
53:BA:290:A:O2'	53:BA:794:A:OP1	2.34	0.45
53:BA:1003:C:C2	53:BA:1004:A:C8	3.05	0.45
53:BA:1380:A:N6	53:BA:1381:A:N6	2.64	0.45
53:BA:1459:U:H2'	53:BA:1460:A:H8	1.81	0.45
74:Ae:325:ARG:HA	74:Ae:325:ARG:NH1	2.32	0.45
83:Ao:326:MET:HE2	83:Ao:331:VAL:HB	1.99	0.45
10:BD:156:GLU:N	10:BD:247:ARG:O	2.50	0.45
26:BX:50:ARG:NH1	26:BX:69:ARG:HA	2.32	0.45
50:Bx:121:MET:HE3	50:Bx:151:LEU:HA	1.98	0.45
53:BA:916:C:H2'	53:BA:917:G:C8	2.52	0.45
53:BA:1020:C:H2'	53:BA:1021:C:C6	2.52	0.45
72:Ac:90:VAL:HG21	72:Ac:98:ILE:HD11	1.98	0.45
74:Ae:114:ARG:NH2	74:Ae:434:GLU:OE2	2.49	0.45
76:Ag:122:ARG:NH1	76:Ag:336:LEU:HD13	2.32	0.45
83:Ao:86:PRO:HG2	83:Ao:89:PHE:HD2	1.82	0.45
11:BE:49:TRP:CD1	11:BE:155:PHE:HB3	2.52	0.45
48:Bv:34:SER:O	53:BA:96:U:N3	2.46	0.45
49:Bw:205:LEU:HG	49:Bw:224:ARG:HG2	1.99	0.45
51:AA:17:G:H2'	51:AA:18:G:H8	1.81	0.45
51:AA:300:G:N7	90:AA:3001:SPM:N10	2.65	0.45
51:AA:402:C:H2'	51:AA:403:A:C8	2.51	0.45
53:BA:454:U:C2	53:BA:455:A:C8	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:1248:C:C2	53:BA:1253:G:H1'	2.51	0.45
54:AB:140:ILE:HB	54:AB:189:PRO:HA	1.97	0.45
54:AB:193:ILE:HA	54:AB:219:VAL:O	2.16	0.45
79:Aj:68:LEU:HD12	79:Aj:71:LEU:HD12	1.97	0.45
80:Ak:211:THR:HG21	80:Ak:224:ALA:HB2	1.98	0.45
83:Ao:584:VAL:HA	83:Ao:587:LEU:HB2	1.98	0.45
10:BD:110:LEU:HD23	10:BD:113:ARG:HE	1.80	0.45
10:BD:208:ILE:H	10:BD:208:ILE:HG13	1.44	0.45
12:BF:283:LEU:HB2	18:BP:125:ARG:HH12	1.81	0.45
29:Bb:224:HIS:HA	29:Bb:232:TYR:CZ	2.52	0.45
29:Bb:307:HIS:HB2	29:Bb:311:MET:HE2	1.99	0.45
47:Bu:103:HIS:HB3	47:Bu:106:SER:HB2	1.98	0.45
49:Bw:188:VAL:HG21	49:Bw:423:PRO:HD2	1.99	0.45
51:AA:542:C:C2	51:AA:543:A:C8	3.05	0.45
51:AA:633:C:OP1	56:AE:269:ARG:NH1	2.50	0.45
53:BA:266:C:H5''	53:BA:267:A:H5'	1.98	0.45
53:BA:937:C:H3'	53:BA:938:U:H5''	1.99	0.45
58:AG:115:LEU:HD22	58:AG:141:PRO:HB2	1.98	0.45
70:Aa:197:ARG:CZ	70:Aa:203:LEU:HB2	2.47	0.45
79:Aj:125:GLU:HG3	79:Aj:127:GLU:H	1.82	0.45
6:B5:134:THR:HG23	20:BR:131:LEU:HD22	1.98	0.44
8:BB:50:A:H2'	8:BB:51:G:H8	1.82	0.44
13:BI:105:LEU:HD12	13:BI:112:VAL:HG21	2.00	0.44
16:BN:177:ARG:HB2	50:Bx:36:ARG:HE	1.82	0.44
18:BP:54:LYS:HE3	53:BA:184:U:H5''	1.98	0.44
23:BU:11:ARG:NH1	23:BU:13:ARG:HD2	2.32	0.44
31:Bd:149:GLU:CD	38:Bj:212:HIS:HB3	2.42	0.44
38:Bj:255:VAL:HG23	38:Bj:259:GLU:HB2	1.99	0.44
48:Bv:109:ALA:O	48:Bv:113:LYS:HG2	2.17	0.44
49:Bw:87:GLN:HG3	53:BA:773:C:O2'	2.17	0.44
51:AA:378:A:H2'	51:AA:379:A:C8	2.52	0.44
51:AA:601:A:N6	78:Ai:63:GLY:HA3	2.32	0.44
51:AA:734:A:H2'	51:AA:735:G:C8	2.52	0.44
51:AA:756:U:H2'	51:AA:757:U:C6	2.52	0.44
53:BA:666:G:O6	53:BA:774:A:N6	2.49	0.44
53:BA:1129:C:H3'	53:BA:1130:A:H8	1.82	0.44
53:BA:1246:A:H8	86:AY:69:C:O3'	1.99	0.44
53:BA:1252:G:H4'	53:BA:1253:G:C4	2.52	0.44
53:BA:1354:A:H61	53:BA:1465:A:N6	2.15	0.44
72:Ac:2:PRO:HB2	72:Ac:11:ARG:HH12	1.82	0.44
75:Af:151:THR:HG22	75:Af:162:THR:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:Ag:54:ASP:N	76:Ag:54:ASP:OD1	2.49	0.44
76:Ag:124:VAL:HG22	76:Ag:307:LEU:HB2	1.99	0.44
84:Ap:202:TRP:CD1	84:Ap:202:TRP:H	2.35	0.44
85:DL:75:THR:HG22	85:DL:78:GLU:HG2	2.00	0.44
19:BQ:76:SER:HB2	19:BQ:155:LYS:HB2	2.00	0.44
21:BS:117:TYR:CD1	29:Bb:114:ARG:HG2	2.53	0.44
22:BT:122:ALA:O	22:BT:170:ARG:NH2	2.50	0.44
25:BW:162:PHE:HB3	53:BA:762:A:N1	2.32	0.44
26:BX:86:ARG:HH12	32:Be:18:MET:HB2	1.82	0.44
30:Bc:187:ASP:HB3	30:Bc:289:LEU:HD11	1.99	0.44
53:BA:695:U:H3	53:BA:696:A:N6	2.15	0.44
53:BA:891:A:H3'	53:BA:892:G:H8	1.82	0.44
53:BA:1031:C:H2'	53:BA:1032:G:C8	2.52	0.44
53:BA:1323:U:H5'	53:BA:1324:C:OP2	2.17	0.44
53:BA:1336:A:H2'	53:BA:1337:G:C8	2.51	0.44
56:AE:103:LEU:HD11	56:AE:123:ARG:HB2	1.99	0.44
64:AO:87:ASP:OD1	64:AO:87:ASP:N	2.47	0.44
75:Af:140:ARG:HB2	75:Af:174:GLN:HG3	1.98	0.44
86:AV:52:U:H5	86:AV:53:U:N3	2.09	0.44
86:AY:3:U:O4	86:AY:4:U:O4	2.35	0.44
2:B1:163:ARG:HD3	2:B1:205:GLY:H	1.82	0.44
17:BO:119:ILE:HG21	17:BO:123:ILE:HD11	2.00	0.44
17:BO:131:GLU:O	17:BO:135:SER:OG	2.30	0.44
18:BP:191:VAL:HB	18:BP:192:PRO:HD3	2.00	0.44
20:BR:11:HIS:CG	53:BA:1558:U:H4'	2.52	0.44
27:BY:133:VAL:HG13	27:BY:145:ARG:HB3	1.99	0.44
31:Bd:164:ARG:HE	31:Bd:168:LEU:HD23	1.81	0.44
33:Bf:67:ILE:HG21	35:Bh:258:THR:HG23	1.98	0.44
34:Bg:35:ARG:HB2	46:Bt:101:TRP:HB2	2.00	0.44
35:Bh:216:ARG:HG3	35:Bh:220:ILE:HD12	1.99	0.44
37:Bi:192:PRO:HB3	37:Bi:216:MET:HG2	1.98	0.44
53:BA:144:A:H2'	53:BA:145:A:C8	2.52	0.44
53:BA:470:C:H2'	53:BA:471:U:H6	1.83	0.44
53:BA:1061:U:O4	53:BA:1062:A:N6	2.51	0.44
53:BA:1065:G:H2'	53:BA:1066:A:C8	2.53	0.44
79:Aj:88:GLN:O	84:Ap:215:ARG:NH1	2.51	0.44
85:EL:75:THR:HG22	85:EL:78:GLU:HG2	1.99	0.44
21:BS:104:SER:HG	29:Bb:150:ARG:HH22	1.58	0.44
28:Ba:50:TYR:OH	28:Ba:72:ARG:O	2.29	0.44
28:Ba:334:LYS:H	28:Ba:362:THR:HB	1.83	0.44
30:Bc:99:LYS:HE2	30:Bc:99:LYS:HB3	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Be:32:LYS:HG3	53:BA:36:A:C4	2.52	0.44
34:Bg:15:LEU:HD11	35:Bh:169:VAL:HA	1.99	0.44
36:B8:168:ARG:NH1	36:B8:170:ASN:OD1	2.47	0.44
51:AA:729:A:H2'	51:AA:730:C:O4'	2.18	0.44
53:BA:607:A:N1	53:BA:627:C:O2'	2.50	0.44
53:BA:611:U:H2'	53:BA:612:A:C8	2.52	0.44
53:BA:1021:C:H2'	53:BA:1022:G:H8	1.82	0.44
53:BA:1448:A:C8	53:BA:1503:C:H2'	2.52	0.44
53:BA:1502:U:H2'	53:BA:1503:C:C6	2.53	0.44
56:AE:187:VAL:HG12	56:AE:188:LYS:HZ2	1.81	0.44
56:AE:282:ILE:HD12	56:AE:353:LEU:HB3	1.98	0.44
60:AJ:74:LYS:HB2	60:AJ:177:LEU:HD21	1.98	0.44
72:Ac:89:ASP:OD2	73:Ad:120:ARG:NH2	2.50	0.44
72:Ac:91:GLU:HG2	73:Ad:123:ARG:HH12	1.83	0.44
76:Ag:206:LYS:HD2	76:Ag:216:GLU:HG3	1.99	0.44
77:Ah:334:PRO:HG2	77:Ah:339:ILE:HB	1.99	0.44
81:Am:114:LYS:HB3	81:Am:114:LYS:HE2	1.84	0.44
5:B4:58:VAL:HB	5:B4:64:THR:HG22	1.99	0.44
14:BJ:225:GLN:HB3	14:BJ:226:PRO:HD3	1.99	0.44
18:BP:51:ARG:HD3	42:Bn:126:LYS:HD2	1.99	0.44
39:Bk:122:GLU:N	39:Bk:158:GLN:O	2.51	0.44
48:Bv:129:PRO:HA	48:Bv:132:ILE:HG12	2.00	0.44
51:AA:418:C:O2'	61:AK:189:ARG:O	2.36	0.44
51:AA:761:U:O2'	51:AA:804:A:N3	2.38	0.44
53:BA:913:G:H21	53:BA:914:A:N6	2.16	0.44
53:BA:920:C:O2	53:BA:924:G:O6	2.35	0.44
53:BA:1050:C:N4	53:BA:1323:U:H1'	2.32	0.44
58:AG:78:PRO:HG2	58:AG:81:LYS:HB3	1.99	0.44
59:AI:201:LEU:O	59:AI:219:TYR:OH	2.32	0.44
61:AK:150:ARG:HG2	61:AK:175:ILE:HD11	1.99	0.44
76:Ag:264:VAL:HG21	76:Ag:307:LEU:HD13	1.99	0.44
3:B2:175:PHE:HA	9:B7:83:LEU:HD21	1.99	0.44
3:B2:212:ARG:HD3	42:Bn:104:ILE:HD11	1.99	0.44
11:BE:100:ILE:HD11	11:BE:177:LYS:HB2	2.00	0.44
11:BE:200:PRO:HG3	11:BE:332:LEU:HB3	2.00	0.44
16:BN:67:PHE:HB2	16:BN:72:TRP:CD1	2.52	0.44
16:BN:169:VAL:HG11	50:Bx:72:ILE:HD13	1.98	0.44
18:BP:180:ASP:OD1	18:BP:180:ASP:N	2.50	0.44
22:BT:114:GLY:HA3	22:BT:182:ARG:HG3	2.00	0.44
50:Bx:146:ARG:HH21	53:BA:1531:C:P	2.41	0.44
51:AA:368:A:H2'	51:AA:368:A:N3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:938:U:H2'	51:AA:939:A:H8	1.83	0.44
53:BA:411:U:H2'	53:BA:412:C:C6	2.52	0.44
53:BA:527:U:H2'	53:BA:529:G:N7	2.32	0.44
53:BA:838:A:H1'	53:BA:933:A:N6	2.33	0.44
53:BA:978:G:H4'	53:BA:1429:C:H4'	2.00	0.44
53:BA:1519:U:OP2	53:BA:1520:U:O2'	2.31	0.44
55:AC:130:HIS:NE2	56:AE:148:LEU:HB2	2.32	0.44
60:AJ:71:THR:O	60:AJ:150:GLY:N	2.49	0.44
70:Aa:193:PHE:CE2	79:Aj:173:MET:HG2	2.53	0.44
74:Ae:290:LEU:HB2	79:Aj:146:GLU:OE2	2.18	0.44
77:Ah:330:LEU:HD11	77:Ah:347:THR:HG21	2.00	0.44
86:AY:50:U:O4	86:AY:54:U:C5	2.58	0.44
20:BR:38:ARG:NH1	20:BR:82:GLU:OE1	2.51	0.44
20:BR:86:ILE:HB	20:BR:87:PRO:HD3	1.99	0.44
39:Bk:49:ARG:HA	39:Bk:54:HIS:CD2	2.53	0.44
46:Bt:82:PHE:CG	46:Bt:83:PRO:HD2	2.53	0.44
50:Bx:71:PRO:O	50:Bx:74:ARG:HG2	2.18	0.44
50:Bx:186:SER:HA	53:BA:575:C:H5	1.83	0.44
51:AA:388:U:H2'	51:AA:389:A:C8	2.53	0.44
53:BA:175:C:H2'	53:BA:176:U:C6	2.53	0.44
53:BA:354:U:H2'	53:BA:355:G:H8	1.82	0.44
53:BA:434:U:H2'	53:BA:435:C:C6	2.52	0.44
53:BA:1031:C:H2'	53:BA:1032:G:H8	1.81	0.44
76:Ag:283:PRO:HB2	76:Ag:293:ARG:HH21	1.81	0.44
10:BD:247:ARG:NH2	53:BA:863:U:O4	2.51	0.44
12:BF:230:VAL:HG12	12:BF:242:LEU:HD22	2.00	0.44
18:BP:47:ARG:NE	53:BA:183:U:OP1	2.46	0.44
28:Ba:201:ARG:NH1	28:Ba:418:TYR:O	2.37	0.44
29:Bb:213:LEU:HB2	29:Bb:275:GLN:HG3	2.00	0.44
37:Bi:107:GLN:OE1	37:Bi:107:GLN:N	2.51	0.44
51:AA:58:U:P	79:Aj:53:ARG:HD2	2.58	0.44
51:AA:62:C:N4	51:AA:63:G:O6	2.51	0.44
51:AA:204:U:H2'	51:AA:205:U:C6	2.52	0.44
51:AA:673:A:H1'	63:AN:127:MET:HE3	2.00	0.44
53:BA:1143:U:H2'	53:BA:1144:U:C6	2.53	0.44
53:BA:1308:A:H2'	53:BA:1309:U:C6	2.53	0.44
54:AB:205:HIS:O	54:AB:208:VAL:HG12	2.18	0.44
60:AJ:88:LEU:HB3	60:AJ:141:ARG:HG3	2.00	0.44
63:AN:31:ASP:OD1	63:AN:32:TRP:N	2.51	0.44
80:Ak:53:LYS:NZ	83:Ao:94:TYR:O	2.51	0.44
83:Ao:420:GLN:HG3	83:Ao:424:ARG:HH21	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Ao:423:MET:HB3	83:Ao:423:MET:HE3	1.78	0.44
83:Ao:600:GLY:HA2	83:Ao:603:ARG:HG2	1.99	0.44
85:GL:75:THR:HG22	85:GL:78:GLU:HG2	1.99	0.44
21:BS:176:ARG:HH12	53:BA:1211:A:P	2.41	0.44
28:Ba:389:LEU:H	53:BA:725:C:H5	1.66	0.44
31:Bd:67:ARG:HA	31:Bd:70:LYS:HE2	2.00	0.44
44:Bp:75:ILE:HG23	50:Bx:48:ILE:HG12	2.00	0.44
51:AA:562:A:H8	51:AA:708:A:H61	1.65	0.44
51:AA:568:G:H21	60:AJ:126:ILE:HD13	1.82	0.44
51:AA:836:G:H2'	51:AA:837:C:C6	2.53	0.44
51:AA:914:A:H2'	51:AA:915:G:C8	2.52	0.44
53:BA:84:G:H2'	53:BA:85:A:C8	2.53	0.44
53:BA:548:A:H2'	53:BA:549:C:C6	2.53	0.44
53:BA:871:A:OP2	53:BA:871:A:H8	2.01	0.44
53:BA:1021:C:H2'	53:BA:1022:G:C8	2.52	0.44
53:BA:1518:A:H2'	53:BA:1519:U:C6	2.53	0.44
56:AE:140:LEU:HD11	56:AE:160:ARG:HG3	2.00	0.44
56:AE:289:THR:HG22	56:AE:290:ILE:H	1.83	0.44
74:Ae:168:THR:HB	74:Ae:177:ILE:HD11	2.00	0.44
74:Ae:439:GLU:HA	74:Ae:442:ARG:NE	2.33	0.44
80:Ak:68:TRP:N	80:Ak:69:PRO:HD2	2.33	0.44
83:Ao:474:ILE:HG21	83:Ao:508:ARG:HG3	2.00	0.44
86:AV:3:U:O4	86:AV:4:U:O4	2.35	0.44
18:BP:115:PRO:HD3	18:BP:255:MET:HG2	2.00	0.43
23:BU:69:ILE:O	23:BU:73:THR:HG23	2.18	0.43
51:AA:332:U:H2'	51:AA:333:A:C8	2.52	0.43
51:AA:489:G:H2'	51:AA:490:A:H8	1.83	0.43
51:AA:816:U:H2'	51:AA:817:G:O4'	2.18	0.43
53:BA:948:A:O2'	53:BA:1382:C:O2	2.26	0.43
53:BA:1092:A:H61	53:BA:1122:A:N6	2.16	0.43
58:AG:176:ASP:HA	58:AG:179:ARG:HE	1.83	0.43
66:AQ:95:VAL:HG13	66:AQ:96:THR:HG23	2.00	0.43
72:Ac:141:CYS:HB3	72:Ac:149:CYS:N	2.33	0.43
80:Ak:315:LYS:HE2	80:Ak:315:LYS:HB3	1.84	0.43
83:Ao:375:TYR:O	83:Ao:379:ILE:HG12	2.18	0.43
83:Ao:579:LEU:HD22	83:Ao:602:PHE:HD2	1.81	0.43
85:HL:75:THR:HG22	85:HL:78:GLU:HG2	1.99	0.43
8:BB:63:C:H2'	8:BB:64:A:C8	2.52	0.43
12:BF:59:ARG:HH21	18:BP:10:PRO:HG3	1.82	0.43
12:BF:70:ARG:HA	12:BF:196:PRO:HD3	2.00	0.43
12:BF:190:VAL:O	12:BF:262:THR:HA	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BQ:96:TYR:HE1	19:BQ:153:PRO:HB3	1.83	0.43
24:BV:168:THR:OG1	24:BV:169:GLU:N	2.49	0.43
27:BY:36:PRO:O	27:BY:39:THR:HG22	2.18	0.43
38:Bj:114:ILE:H	38:Bj:114:ILE:HG13	1.72	0.43
48:Bv:48:PRO:HB2	48:Bv:50:TRP:CD1	2.53	0.43
51:AA:484:C:H2'	51:AA:485:G:H8	1.83	0.43
51:AA:616:C:H2'	51:AA:617:C:H6	1.83	0.43
51:AA:733:A:N7	76:Ag:319:ARG:NH2	2.66	0.43
51:AA:815:U:H2'	51:AA:816:U:C6	2.53	0.43
53:BA:181:C:H2'	53:BA:182:C:C6	2.54	0.43
53:BA:365:G:N1	53:BA:598:U:OP2	2.42	0.43
53:BA:1122:A:H2'	53:BA:1123:A:H8	1.83	0.43
53:BA:1390:G:H2'	53:BA:1391:U:C6	2.53	0.43
54:AB:194:PHE:HZ	54:AB:207:ALA:HB3	1.82	0.43
3:B2:119:GLN:HG2	26:BX:29:VAL:HG12	2.01	0.43
6:B5:125:TYR:O	6:B5:129:LYS:HG3	2.18	0.43
12:BF:287:ARG:HD2	48:Bv:33:ARG:NH1	2.33	0.43
13:BI:139:LEU:O	13:BI:142:GLU:HG3	2.18	0.43
14:BJ:121:ILE:HD11	14:BJ:154:LEU:HB3	2.01	0.43
14:BJ:142:ASN:ND2	85:CL:49:ALA:O	2.51	0.43
14:BJ:204:GLN:HB3	85:CL:90:LEU:HD21	1.99	0.43
15:BK:61:LYS:HE3	45:Bq:79:LYS:HG3	2.00	0.43
19:BQ:154:VAL:HG13	19:BQ:158:ARG:HD3	2.00	0.43
26:BX:59:ARG:HB3	32:Be:60:VAL:HG11	2.01	0.43
27:BY:64:ILE:HD11	27:BY:88:VAL:HG21	2.00	0.43
28:Ba:350:ARG:NH1	28:Ba:383:TYR:O	2.50	0.43
30:Bc:63:GLU:O	30:Bc:119:SER:OG	2.34	0.43
31:Bd:164:ARG:HD2	39:Bk:88:TYR:CE2	2.53	0.43
31:Bd:173:ARG:HB3	39:Bk:184:LEU:HD23	2.01	0.43
37:Bi:240:ARG:NH1	37:Bi:274:GLN:OE1	2.51	0.43
51:AA:217:U:H2'	51:AA:218:A:C8	2.53	0.43
51:AA:296:G:O2'	51:AA:461:A:OP2	2.34	0.43
51:AA:341:G:H2'	51:AA:342:C:C6	2.53	0.43
51:AA:912:A:H2'	51:AA:913:G:C8	2.53	0.43
51:AA:928:A:O2'	51:AA:929:A:H5'	2.18	0.43
53:BA:446:C:H2'	53:BA:447:A:C8	2.53	0.43
53:BA:645:U:H2'	53:BA:646:A:C8	2.50	0.43
53:BA:709:A:H2'	53:BA:710:A:H8	1.82	0.43
53:BA:1380:A:C6	53:BA:1381:A:N6	2.86	0.43
55:AC:154:HIS:CD2	80:Ak:77:PRO:HG3	2.52	0.43
76:Ag:129:LYS:HD2	76:Ag:319:ARG:HH21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:EL:77:LEU:HD11	85:HL:72:ALA:HB1	2.01	0.43
2:B1:91:TYR:CZ	13:BI:79:VAL:HG11	2.53	0.43
18:BP:260:LYS:HE3	18:BP:267:PHE:CZ	2.53	0.43
22:BT:96:ARG:O	22:BT:99:MET:HG2	2.19	0.43
24:BV:181:ARG:HH21	53:BA:188:C:P	2.41	0.43
29:Bb:175:VAL:HB	29:Bb:187:VAL:HB	1.99	0.43
37:Bi:176:ILE:HD12	37:Bi:176:ILE:HA	1.90	0.43
38:Bj:147:THR:HG22	38:Bj:253:VAL:HG22	1.98	0.43
51:AA:789:C:H4'	51:AA:790:A:H5'	2.00	0.43
53:BA:942:U:H2'	53:BA:943:C:H6	1.83	0.43
56:AE:305:MET:HE1	56:AE:353:LEU:HD21	2.00	0.43
57:AF:2:PRO:HB3	57:AF:37:ARG:HD2	2.00	0.43
57:AF:36:VAL:HB	73:Ad:168:ILE:HB	1.99	0.43
58:AG:161:ILE:HD12	58:AG:170:VAL:HG21	2.01	0.43
63:AN:53:ARG:HH21	77:Ah:364:HIS:CE1	2.36	0.43
85:FL:75:THR:HG22	85:FL:78:GLU:HG2	1.99	0.43
12:BF:291:CYS:HB3	40:Bl:54:PRO:HA	2.00	0.43
19:BQ:79:ALA:HA	19:BQ:123:ARG:HH21	1.82	0.43
24:BV:120:ILE:HG22	24:BV:122:ASN:H	1.83	0.43
31:Bd:67:ARG:NH1	86:AV:10:U:OP2	2.51	0.43
34:Bg:35:ARG:HD3	41:Bm:157:TRP:CH2	2.54	0.43
37:Bi:124:LYS:O	37:Bi:127:GLU:HG3	2.18	0.43
44:Bp:72:HIS:CD2	44:Bp:97:ARG:HD3	2.53	0.43
47:Bu:75:ARG:NH1	47:Bu:108:ASP:OD1	2.51	0.43
51:AA:50:U:H2'	51:AA:51:G:C8	2.42	0.43
51:AA:285:C:N4	62:AL:43:LYS:O	2.49	0.43
51:AA:543:A:H4'	58:AG:159:VAL:HG23	2.00	0.43
51:AA:622:U:H2'	51:AA:623:C:C6	2.54	0.43
51:AA:787:A:H2'	51:AA:788:G:H8	1.83	0.43
53:BA:143:A:H2'	53:BA:144:A:C8	2.53	0.43
53:BA:440:A:H2'	53:BA:441:A:H8	1.83	0.43
53:BA:1248:C:N4	53:BA:1253:G:N3	2.67	0.43
53:BA:1459:U:H2'	53:BA:1460:A:C8	2.53	0.43
74:Ae:203:VAL:O	74:Ae:206:GLU:HG3	2.17	0.43
76:Ag:209:TRP:HD1	76:Ag:234:ASN:HB3	1.82	0.43
79:Aj:82:ARG:NH1	79:Aj:133:GLN:OE1	2.51	0.43
83:Ao:485:ILE:HG23	83:Ao:491:PRO:HD3	1.99	0.43
15:BK:140:VAL:O	15:BK:144:ILE:HG12	2.18	0.43
16:BN:111:MET:HG2	53:BA:571:A:N3	2.33	0.43
27:BY:108:MET:HE1	37:Bi:169:PHE:HB3	2.00	0.43
31:Bd:164:ARG:HH12	39:Bk:91:LEU:HD21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Bk:195:LYS:HD2	39:Bk:198:PHE:HD2	1.84	0.43
40:Bl:128:LEU:HB2	40:Bl:136:PRO:HG3	2.00	0.43
50:Bx:70:CYS:HB3	50:Bx:73:CYS:SG	2.59	0.43
51:AA:210:U:H2'	51:AA:211:A:C8	2.54	0.43
51:AA:335:A:H2'	51:AA:336:A:H8	1.83	0.43
53:BA:32:C:O2'	53:BA:36:A:N6	2.52	0.43
53:BA:513:A:N1	53:BA:514:A:N6	2.67	0.43
53:BA:653:A:H2'	53:BA:654:G:O4'	2.18	0.43
53:BA:1420:A:H8	53:BA:1420:A:OP2	2.02	0.43
55:AC:88:GLU:HG2	55:AC:147:TYR:CZ	2.54	0.43
58:AG:82:THR:HG23	58:AG:84:SER:H	1.84	0.43
58:AG:157:GLY:HA2	58:AG:226:MET:HE2	2.00	0.43
77:Ah:339:ILE:HG12	77:Ah:386:LEU:HD22	2.00	0.43
12:BF:92:ARG:HH12	40:Bl:144:THR:HG23	1.83	0.43
17:BO:75:LEU:HD23	17:BO:77:ILE:HD11	1.99	0.43
25:BW:204:ARG:HA	53:BA:170:U:N3	2.34	0.43
27:BY:180:GLU:O	27:BY:184:GLU:HB2	2.18	0.43
37:Bi:189:LEU:HB2	37:Bi:217:HIS:HD2	1.84	0.43
51:AA:265:U:H2'	51:AA:266:U:H6	1.83	0.43
51:AA:515:U:H2'	51:AA:516:C:C6	2.54	0.43
51:AA:578:G:H3'	51:AA:579:A:H8	1.84	0.43
53:BA:335:U:OP1	53:BA:338:C:N4	2.40	0.43
53:BA:1050:C:O5'	53:BA:1051:G:H5''	2.19	0.43
59:AI:105:ASP:OD1	59:AI:106:ARG:N	2.50	0.43
67:AR:66:CYS:HB2	67:AR:100:LEU:HA	2.00	0.43
67:AR:125:TYR:HE2	68:Au:4:HIS:HB3	1.84	0.43
74:Ae:181:ASN:HD21	74:Ae:419:ARG:HD3	1.84	0.43
83:Ao:551:PHE:HB3	83:Ao:585:LEU:HD13	2.01	0.43
85:CL:80:SER:HA	85:CL:83:ASN:HD21	1.83	0.43
8:BB:65:U:H2'	8:BB:66:A:H8	1.82	0.43
21:BS:68:TRP:C	21:BS:70:THR:H	2.27	0.43
31:Bd:193:GLN:HG3	39:Bk:133:GLU:HB3	2.01	0.43
33:Bf:46:LYS:O	33:Bf:63:PRO:HD2	2.18	0.43
37:Bi:226:ASP:OD1	37:Bi:227:ARG:N	2.51	0.43
47:Bu:103:HIS:HE1	47:Bu:105:ALA:HB3	1.83	0.43
51:AA:900:A:N3	51:AA:902:C:N4	2.66	0.43
56:AE:296:LEU:HG	56:AE:303:ILE:HB	2.00	0.43
59:AI:263:TYR:HD1	59:AI:268:MET:HA	1.84	0.43
74:Ae:157:LEU:HA	74:Ae:161:ALA:HB2	2.01	0.43
80:Ak:304:GLU:OE1	80:Ak:304:GLU:N	2.51	0.43
84:Ap:215:ARG:HG3	84:Ap:218:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B2:221:ILE:HG12	3:B2:224:ARG:NH2	2.33	0.43
8:BB:28:A:H4'	31:Bd:133:ARG:HH12	1.83	0.43
11:BE:148:GLY:HA3	11:BE:173:LYS:HG3	1.99	0.43
18:BP:57:ARG:HH21	53:BA:378:U:H5''	1.84	0.43
21:BS:173:ARG:NH1	21:BS:174:GLU:O	2.52	0.43
22:BT:192:ASP:CG	22:BT:230:SER:H	2.26	0.43
24:BV:76:GLU:OE1	24:BV:80:HIS:NE2	2.52	0.43
26:BX:5:VAL:HG21	32:Be:135:ARG:HD2	2.01	0.43
28:Ba:161:ALA:O	28:Ba:165:HIS:ND1	2.52	0.43
49:Bw:267:LEU:HD23	49:Bw:267:LEU:HA	1.89	0.43
51:AA:357:G:H2'	51:AA:358:U:C6	2.54	0.43
51:AA:638:A:H1'	51:AA:639:A:H2'	1.99	0.43
51:AA:849:G:H2'	51:AA:850:U:H6	1.84	0.43
53:BA:792:G:H2'	53:BA:793:A:H8	1.83	0.43
53:BA:1083:C:H2'	53:BA:1084:C:C6	2.54	0.43
63:AN:91:CYS:HB3	63:AN:96:ARG:H	1.84	0.43
74:Ae:76:ASP:HB2	74:Ae:154:ARG:NH1	2.34	0.43
2:B1:163:ARG:NH1	28:Ba:55:LEU:HD11	2.33	0.43
3:B2:92:LEU:HD12	3:B2:100:LEU:HD22	2.00	0.43
21:BS:103:VAL:HG13	29:Bb:151:LEU:HD21	1.99	0.43
28:Ba:85:PRO:HB3	53:BA:744:A:OP2	2.19	0.43
42:Bn:57:TYR:OH	48:Bv:28:ARG:O	2.21	0.43
46:Bt:100:LYS:NZ	53:BA:614:U:O3'	2.51	0.43
51:AA:355:U:H2'	51:AA:356:A:C8	2.53	0.43
51:AA:812:U:H2'	51:AA:813:G:H8	1.83	0.43
53:BA:1060:C:H2'	53:BA:1061:U:C6	2.54	0.43
56:AE:192:GLY:H	56:AE:201:VAL:HG12	1.83	0.43
59:AI:139:GLN:HB2	59:AI:140:TRP:CE3	2.54	0.43
76:Ag:317:LYS:NZ	76:Ag:327:LEU:O	2.52	0.43
77:Ah:303:TRP:CZ2	80:Ak:165:ILE:HG12	2.53	0.43
77:Ah:304:GLU:HG2	83:Ao:67:LYS:HE3	2.01	0.43
78:Ai:14:LEU:HD23	78:Ai:18:LEU:HD23	2.00	0.43
2:B1:6:VAL:HG12	53:BA:21:C:H41	1.84	0.42
4:B3:66:LEU:HD12	4:B3:122:LEU:HD23	2.01	0.42
5:B4:74:ARG:HB2	38:Bj:128:PHE:HB2	2.01	0.42
8:BB:40:U:H2'	8:BB:41:G:H8	1.84	0.42
11:BE:96:ARG:NH1	11:BE:301:ASP:OD2	2.52	0.42
16:BN:109:TYR:HD1	16:BN:122:MET:HE3	1.84	0.42
16:BN:152:PRO:HB3	50:Bx:84:GLU:HG3	2.01	0.42
18:BP:127:VAL:HG21	18:BP:138:VAL:HG21	1.99	0.42
32:Be:126:PHE:HD1	32:Be:133:PHE:HB3	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Bf:75:ILE:HG23	35:Bh:289:VAL:HG11	2.01	0.42
34:Bg:4:ARG:NH2	53:BA:167:G:O6	2.52	0.42
37:Bi:137:PHE:N	37:Bi:138:PRO:HD2	2.34	0.42
37:Bi:165:THR:HG23	37:Bi:167:ASN:H	1.84	0.42
37:Bi:215:ARG:HH21	37:Bi:243:LEU:HD11	1.84	0.42
39:Bk:125:TYR:CE2	39:Bk:197:ARG:HD3	2.54	0.42
45:Bq:95:TRP:HA	45:Bq:98:GLU:HG3	2.01	0.42
51:AA:308:A:C2	72:Ac:36:THR:HG21	2.55	0.42
51:AA:408:A:H4'	51:AA:949:G:N2	2.34	0.42
51:AA:903:C:H2'	51:AA:904:A:C8	2.54	0.42
53:BA:1185:A:H2'	53:BA:1186:U:C6	2.54	0.42
59:AI:316:PHE:HB3	59:AI:317:PRO:HD3	2.01	0.42
67:AR:50:ASP:HA	75:Af:86:ARG:HH11	1.83	0.42
70:Aa:298:VAL:HA	70:Aa:303:ILE:HD11	2.01	0.42
70:Aa:345:GLU:HG3	70:Aa:346:GLY:H	1.83	0.42
79:Aj:16:ARG:HD3	79:Aj:19:ARG:HH22	1.84	0.42
83:Ao:458:ASN:HB3	83:Ao:492:HIS:HE2	1.83	0.42
17:BO:58:ILE:HD11	17:BO:76:ALA:HB2	2.01	0.42
17:BO:69:VAL:HG12	17:BO:127:LEU:HD21	2.01	0.42
28:Ba:233:LYS:HA	28:Ba:286:PRO:HD2	2.00	0.42
42:Bn:32:PHE:CD1	53:BA:199:A:H5''	2.51	0.42
49:Bw:242:PRO:HB3	49:Bw:424:LYS:HG2	2.00	0.42
49:Bw:251:ILE:HG22	49:Bw:253:ILE:H	1.84	0.42
51:AA:406:A:C2	51:AA:407:U:H1'	2.54	0.42
51:AA:740:U:H2'	51:AA:741:C:C6	2.54	0.42
53:BA:1023:U:H2'	53:BA:1024:G:C8	2.54	0.42
70:Aa:135:GLU:HA	70:Aa:138:LYS:HG2	2.02	0.42
76:Ag:239:VAL:HA	76:Ag:242:VAL:HG12	2.01	0.42
84:Ap:59:LEU:HD13	84:Ap:121:LYS:HB2	2.01	0.42
84:Ap:115:VAL:HG13	84:Ap:150:LEU:HD23	2.01	0.42
10:BD:281:GLY:O	53:BA:885:G:N2	2.42	0.42
13:BI:59:TRP:CD1	13:BI:79:VAL:HG12	2.54	0.42
16:BN:21:LEU:HB3	16:BN:59:ILE:HG12	2.01	0.42
16:BN:67:PHE:HB2	16:BN:72:TRP:NE1	2.34	0.42
25:BW:46:SER:N	53:BA:3:C:OP2	2.52	0.42
37:Bi:180:THR:HB	37:Bi:225:TYR:HB2	2.01	0.42
51:AA:23:U:H2'	51:AA:24:C:H6	1.84	0.42
51:AA:663:A:H2'	51:AA:664:U:C6	2.54	0.42
51:AA:956:G:H2'	51:AA:957:A:H8	1.83	0.42
53:BA:51:A:H2'	53:BA:52:A:N3	2.35	0.42
53:BA:119:A:C4	53:BA:129:A:N6	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:619:C:H2'	53:BA:620:A:C8	2.54	0.42
53:BA:698:U:H2'	53:BA:699:G:C8	2.54	0.42
53:BA:1531:C:H3'	53:BA:1532:U:H5''	2.02	0.42
65:AP:101:PRO:HB3	73:Ad:59:ARG:HB3	2.01	0.42
66:AQ:69:LEU:HD12	66:AQ:70:PRO:HD2	2.02	0.42
83:Ao:134:GLU:N	83:Ao:135:PRO:HD2	2.35	0.42
2:B1:133:ASP:OD1	13:Bl:120:ARG:NH2	2.52	0.42
12:BF:92:ARG:NH2	53:BA:214:A:H5''	2.35	0.42
12:BF:284:TYR:HB2	12:BF:288:LEU:HD12	2.00	0.42
16:BN:80:HIS:CD2	16:BN:82:GLY:H	2.37	0.42
18:BP:51:ARG:HB3	18:BP:58:GLN:HA	2.02	0.42
29:Bb:362:PRO:HB2	29:Bb:364:ARG:HG2	2.01	0.42
31:Bd:83:ILE:HG12	39:Bk:199:LYS:HB3	2.01	0.42
35:Bh:188:PRO:N	35:Bh:189:PRO:HD2	2.34	0.42
49:Bw:81:ARG:O	49:Bw:85:LYS:HB3	2.18	0.42
51:AA:116:G:OP1	64:AO:207:LYS:NZ	2.33	0.42
51:AA:238:C:H2'	51:AA:239:U:C6	2.54	0.42
51:AA:389:A:H5''	64:AO:101:GLN:HB2	2.01	0.42
51:AA:513:A:N3	51:AA:857:C:O2'	2.49	0.42
51:AA:770:A:H2'	51:AA:771:A:C8	2.54	0.42
53:BA:191:A:N6	53:BA:1029:G:OP1	2.52	0.42
53:BA:457:A:H2'	53:BA:458:A:C8	2.53	0.42
53:BA:523:U:O2'	53:BA:532:A:OP1	2.37	0.42
58:AG:48:LYS:HD3	59:AI:320:PHE:HA	2.02	0.42
59:AI:100:THR:HG23	59:AI:102:GLU:HG3	2.01	0.42
59:AI:294:ILE:HG12	59:AI:329:MET:HG3	2.00	0.42
61:AK:120:ARG:HD3	61:AK:120:ARG:HA	1.85	0.42
72:Ac:7:PHE:O	72:Ac:10:ARG:HG2	2.20	0.42
72:Ac:97:GLU:HA	72:Ac:100:GLU:HG2	2.01	0.42
74:Ae:164:LYS:HB2	74:Ae:164:LYS:HE3	1.86	0.42
85:CL:74:LEU:HD13	85:CL:78:GLU:CD	2.44	0.42
86:AV:50:U:C4	86:AV:54:U:C5	3.04	0.42
86:AY:22:U:C2	86:AY:23:U:C6	3.07	0.42
86:AY:52:U:C5	86:AY:53:U:N3	2.86	0.42
4:B3:109:LYS:O	4:B3:113:VAL:HG22	2.17	0.42
5:B4:50:ALA:HB2	31:Bd:94:PHE:HE2	1.84	0.42
5:B4:64:THR:HG21	38:Bj:133:LEU:HD22	2.00	0.42
11:BE:275:ARG:NH1	22:BT:98:ASP:OD2	2.48	0.42
12:BF:184:GLN:NE2	18:BP:20:PRO:O	2.52	0.42
19:BQ:109:ILE:O	19:BQ:113:MET:HB3	2.20	0.42
19:BQ:224:LEU:N	46:Bt:42:GLU:OE1	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BX:131:GLN:HA	26:BX:134:LYS:HG2	2.01	0.42
27:BY:96:ARG:HB3	53:BA:140:A:H4'	2.01	0.42
29:Bb:44:ASP:HB3	29:Bb:47:ARG:HG2	2.01	0.42
36:B8:126:LYS:HG2	36:B8:144:LEU:HA	2.00	0.42
51:AA:30:A:H2'	51:AA:31:U:C6	2.53	0.42
51:AA:174:C:H1'	51:AA:207:G:H1'	2.02	0.42
51:AA:441:U:H2'	51:AA:442:A:C8	2.52	0.42
51:AA:857:C:H2'	51:AA:858:C:C6	2.54	0.42
53:BA:118:U:O4	53:BA:129:A:N7	2.53	0.42
53:BA:952:A:H2'	53:BA:953:G:C8	2.53	0.42
53:BA:1543:U:H2'	53:BA:1544:A:H8	1.85	0.42
76:Ag:339:PHE:HE1	76:Ag:341:PRO:HB3	1.84	0.42
77:Ah:319:GLU:HB2	77:Ah:321:HIS:CE1	2.54	0.42
80:Ak:214:CYS:HB2	80:Ak:220:ASN:CG	2.44	0.42
86:AV:52:U:C5	86:AV:53:U:N3	2.85	0.42
4:B3:73:LYS:HA	53:BA:472:U:OP1	2.19	0.42
11:BE:277:ASN:HB3	11:BE:282:ILE:HB	2.00	0.42
12:BF:83:HIS:CG	12:BF:274:LEU:HD11	2.55	0.42
14:BJ:33:VAL:HB	19:BQ:69:LEU:HD13	2.01	0.42
14:BJ:63:ARG:NH2	50:Bx:102:ARG:HH21	2.18	0.42
18:BP:40:PRO:HG3	53:BA:204:G:H2'	2.00	0.42
33:Bf:134:ARG:NH2	53:BA:171:A:O2'	2.52	0.42
38:Bj:126:GLN:HG3	38:Bj:130:HIS:CE1	2.54	0.42
51:AA:88:C:H4'	65:AP:82:HIS:CE1	2.54	0.42
51:AA:282:A:H2	56:AE:421:VAL:HG21	1.84	0.42
51:AA:531:U:O2'	51:AA:929:A:N7	2.53	0.42
51:AA:772:A:H2'	51:AA:773:C:C6	2.54	0.42
53:BA:562:A:H3'	53:BA:562:A:N3	2.34	0.42
53:BA:1165:U:OP2	53:BA:1166:A:O2'	2.29	0.42
53:BA:1479:G:H2'	53:BA:1480:G:H8	1.85	0.42
54:AB:83:LEU:HD23	54:AB:247:LEU:HD21	2.01	0.42
56:AE:136:ARG:HG3	78:Ai:67:PHE:CD1	2.54	0.42
61:AK:135:ILE:HD11	61:AK:169:MET:HE2	2.01	0.42
76:Ag:322:TYR:HA	76:Ag:327:LEU:HD11	2.01	0.42
2:B1:222:ASP:N	2:B1:222:ASP:OD1	2.48	0.42
22:BT:189:TYR:CD1	22:BT:243:ILE:HD11	2.55	0.42
23:BU:31:PHE:CD1	53:BA:165:A:H5''	2.55	0.42
24:BV:105:PHE:HE2	24:BV:120:ILE:HG12	1.85	0.42
29:Bb:354:GLN:NE2	36:B8:183:ARG:HD2	2.35	0.42
47:Bu:109:TRP:CD1	47:Bu:110:ILE:HG23	2.55	0.42
51:AA:386:U:H2'	51:AA:387:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:810:C:H2'	51:AA:811:U:C6	2.55	0.42
53:BA:48:U:O2'	53:BA:49:A:H4'	2.20	0.42
53:BA:838:A:H1'	53:BA:933:A:H61	1.83	0.42
53:BA:919:G:H2'	53:BA:920:C:C6	2.54	0.42
53:BA:1336:A:H2'	53:BA:1337:G:H8	1.85	0.42
55:AC:87:VAL:HA	55:AC:90:VAL:HG12	2.00	0.42
64:AO:133:LEU:HD12	64:AO:167:MET:HE2	2.02	0.42
76:Ag:154:ILE:HB	76:Ag:261:VAL:HG12	2.01	0.42
8:BB:1:G:O6	8:BB:70:A:N6	2.53	0.42
11:BE:66:SER:HA	53:BA:1569:A:H2	1.83	0.42
12:BF:108:ARG:HD3	12:BF:161:TYR:CD1	2.55	0.42
20:BR:15:PHE:HB2	53:BA:1492:C:N4	2.35	0.42
22:BT:182:ARG:HD3	22:BT:187:LEU:HD22	2.01	0.42
30:Bc:199:PHE:HB3	30:Bc:277:VAL:HG21	2.01	0.42
39:Bk:172:GLU:HA	39:Bk:175:HIS:ND1	2.33	0.42
46:Bt:97:VAL:HG23	46:Bt:98:THR:HG23	2.01	0.42
47:Bu:71:ILE:HG21	47:Bu:150:LEU:HD22	2.01	0.42
49:Bw:90:LYS:HD2	49:Bw:226:GLN:HB2	2.02	0.42
51:AA:294:A:H3'	51:AA:294:A:OP2	2.20	0.42
51:AA:343:U:H2'	51:AA:344:G:O4'	2.20	0.42
53:BA:293:U:O2'	53:BA:1434:U:O2'	2.28	0.42
53:BA:636:U:O4	53:BA:637:A:N6	2.52	0.42
53:BA:1246:A:C8	86:AY:69:C:O3'	2.72	0.42
61:AK:77:TRP:HB2	61:AK:85:ILE:HD11	2.01	0.42
64:AO:115:LYS:HG3	64:AO:116:VAL:HG23	2.01	0.42
65:AP:54:TYR:HD1	65:AP:66:VAL:HG22	1.85	0.42
83:Ao:81:ASP:HB3	83:Ao:84:ALA:HB3	2.02	0.42
16:BN:78:SER:HB2	53:BA:568:C:C2	2.55	0.42
17:BO:33:GLN:H	17:BO:36:THR:HG21	1.85	0.42
17:BO:58:ILE:HG23	53:BA:947:A:N1	2.34	0.42
17:BO:128:ARG:HG2	17:BO:138:LEU:HD13	2.02	0.42
20:BR:149:LEU:HD23	30:Bc:312:LEU:HD13	2.02	0.42
23:BU:34:ARG:NH2	53:BA:1014:A:H5''	2.35	0.42
30:Bc:172:ILE:H	30:Bc:172:ILE:HD12	1.83	0.42
33:Bf:126:ARG:HD3	33:Bf:126:ARG:HA	1.94	0.42
34:Bg:146:ARG:HD3	34:Bg:146:ARG:HA	1.84	0.42
42:Bn:118:TYR:OH	53:BA:87:A:OP1	2.25	0.42
45:Bq:93:PRO:HB2	45:Bq:95:TRP:CD1	2.55	0.42
51:AA:94:G:C1'	73:Ad:79:ARG:HH22	2.33	0.42
51:AA:358:U:H2'	51:AA:359:U:C6	2.55	0.42
51:AA:364:U:C2	51:AA:365:A:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:542:C:C2	51:AA:824:G:N2	2.87	0.42
51:AA:617:C:O2'	56:AE:97:GLU:OE1	2.38	0.42
53:BA:731:U:O2'	53:BA:732:A:O5'	2.35	0.42
53:BA:1059:C:H2'	53:BA:1060:C:C6	2.55	0.42
59:AI:251:ILE:H	59:AI:251:ILE:HG13	1.32	0.42
59:AI:319:HIS:NE2	76:Ag:378:GLU:OE2	2.52	0.42
67:AR:86:SER:OG	67:AR:90:GLY:N	2.53	0.42
70:Aa:254:VAL:HA	70:Aa:264:TYR:HE2	1.85	0.42
72:Ac:101:HIS:O	72:Ac:105:ILE:HG12	2.20	0.42
74:Ae:169:LEU:HD22	74:Ae:177:ILE:HD13	2.02	0.42
74:Ae:367:LYS:HG2	74:Ae:370:GLN:HB3	2.02	0.42
83:Ao:421:SER:HA	83:Ao:424:ARG:HG2	2.02	0.42
3:B2:128:MET:HE3	3:B2:131:PRO:HA	2.02	0.42
11:BE:257:MET:HE2	11:BE:257:MET:HB3	1.83	0.42
21:BS:51:ARG:HG3	29:Bb:267:ARG:HH21	1.84	0.42
23:BU:111:LYS:NZ	33:Bf:64:SER:HB2	2.34	0.42
28:Ba:337:GLU:HG2	28:Ba:338:GLN:HG2	2.02	0.42
37:Bi:251:HIS:HD2	37:Bi:254:ASP:HB2	1.85	0.42
51:AA:380:A:O2'	51:AA:406:A:O4'	2.32	0.42
51:AA:397:U:H5''	51:AA:462:A:O2'	2.20	0.42
51:AA:786:U:H2'	51:AA:787:A:C8	2.55	0.42
54:AB:161:CYS:SG	54:AB:253:GLN:HA	2.59	0.42
73:Ad:54:PHE:HB2	84:Ap:216:LEU:HD11	2.02	0.42
74:Ae:189:ASP:OD1	74:Ae:193:LYS:NZ	2.53	0.42
74:Ae:227:TYR:CD1	74:Ae:394:LEU:HD11	2.55	0.42
79:Aj:64:LEU:HD13	79:Aj:80:VAL:HG21	2.01	0.42
86:AV:22:U:C2	86:AV:23:U:C6	3.07	0.42
86:AV:41:U:H2'	86:AV:42:U:O4'	2.20	0.42
86:AY:58:U:O2	86:AY:58:U:H2'	2.20	0.42
4:B3:101:LYS:HB3	43:Bo:84:MET:HE1	2.02	0.41
7:B6:50:VAL:HG23	7:B6:52:LYS:HB2	2.02	0.41
10:BD:275:LEU:HB2	53:BA:329:A:C5	2.55	0.41
11:BE:62:LYS:HE2	53:BA:1569:A:H5'	2.00	0.41
11:BE:202:GLN:NE2	11:BE:301:ASP:OD1	2.53	0.41
12:BF:48:LEU:HA	12:BF:79:LEU:O	2.20	0.41
18:BP:231:GLU:O	18:BP:235:GLU:HG2	2.20	0.41
20:BR:65:LEU:HB3	20:BR:69:ASN:HD22	1.85	0.41
21:BS:152:GLU:HB3	21:BS:158:ILE:HD12	2.02	0.41
24:BV:88:ASN:HD22	24:BV:208:LEU:HB3	1.85	0.41
28:Ba:153:ARG:HH22	49:Bw:191:ALA:HA	1.85	0.41
30:Bc:164:VAL:HG13	30:Bc:232:TYR:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Bg:15:LEU:HD11	35:Bh:169:VAL:HG22	2.02	0.41
35:Bh:91:ALA:O	35:Bh:122:ASN:ND2	2.53	0.41
46:Bt:18:ILE:HD11	53:BA:468:A:C2	2.54	0.41
46:Bt:71:PHE:CE2	46:Bt:75:LYS:HD2	2.54	0.41
51:AA:437:C:OP1	61:AK:191:ARG:NH2	2.49	0.41
53:BA:443:G:O2'	53:BA:446:C:N4	2.35	0.41
53:BA:868:G:H2'	53:BA:869:G:H8	1.85	0.41
53:BA:1019:C:H2'	53:BA:1020:C:H6	1.85	0.41
53:BA:1246:A:H5''	86:AY:70:C:C5'	2.50	0.41
53:BA:1343:C:H2'	53:BA:1344:C:C6	2.55	0.41
53:BA:1345:A:H2	53:BA:1366:A:H61	1.67	0.41
80:Ak:216:LEU:HD13	80:Ak:218:ARG:HE	1.84	0.41
8:BB:43:C:H2'	8:BB:44:U:H5'	2.02	0.41
11:BE:334:ASP:HB3	11:BE:337:VAL:HG23	2.02	0.41
18:BP:14:ASP:OD1	18:BP:17:ARG:NH1	2.52	0.41
18:BP:38:ARG:HD3	18:BP:45:ARG:HH21	1.84	0.41
24:BV:146:THR:HB	33:Bf:60:CYS:SG	2.60	0.41
28:Ba:43:PRO:HA	28:Ba:44:PRO:HD3	1.94	0.41
28:Ba:122:TRP:HE3	28:Ba:123:LEU:HD23	1.84	0.41
29:Bb:258:PHE:HA	29:Bb:327:VAL:HG13	2.02	0.41
38:Bj:189:GLU:O	38:Bj:192:LEU:HG	2.20	0.41
39:Bk:162:LEU:HD11	39:Bk:166:PHE:HD2	1.86	0.41
40:Bl:139:GLN:HA	46:Bt:85:HIS:CD2	2.56	0.41
51:AA:616:C:H2'	51:AA:617:C:C6	2.55	0.41
51:AA:724:U:H5	58:AG:201:MET:HE3	1.85	0.41
53:BA:1083:C:H2'	53:BA:1084:C:H6	1.85	0.41
53:BA:1156:A:H2'	53:BA:1157:C:C6	2.54	0.41
72:Ac:74:PRO:HB2	72:Ac:90:VAL:HG13	2.03	0.41
84:Ap:67:ARG:NH1	84:Ap:110:ASP:OD2	2.53	0.41
10:BD:168:ASP:HA	10:BD:184:PRO:HD3	2.01	0.41
11:BE:183:GLU:H	11:BE:183:GLU:CD	2.28	0.41
16:BN:16:ARG:O	35:Bh:261:SER:OG	2.26	0.41
19:BQ:204:GLU:HA	19:BQ:207:ARG:HG2	2.02	0.41
21:BS:114:LYS:HE3	21:BS:115:HIS:NE2	2.34	0.41
31:Bd:138:SER:O	31:Bd:141:GLU:HG2	2.21	0.41
31:Bd:146:ALA:HA	38:Bj:212:HIS:HB2	2.03	0.41
37:Bi:72:LEU:HD22	53:BA:139:G:C6	2.54	0.41
49:Bw:201:HIS:CD2	49:Bw:228:ASN:HD22	2.38	0.41
51:AA:242:U:O4	51:AA:259:A:N7	2.54	0.41
51:AA:765:A:H1'	51:AA:767:U:C5	2.56	0.41
53:BA:415:A:H2'	53:BA:416:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BA:477:A:N6	53:BA:478:G:O6	2.54	0.41
53:BA:1239:A:H5'	53:BA:1240:A:C2	2.55	0.41
59:AI:241:PHE:O	59:AI:244:ARG:HG2	2.20	0.41
73:Ad:114:GLN:O	73:Ad:118:GLU:HG2	2.20	0.41
86:AV:25:U:C2	86:AV:26:U:C5	3.08	0.41
2:B1:202:GLU:HG3	2:B1:203:TRP:CD1	2.55	0.41
11:BE:274:TRP:NE1	11:BE:286:ASN:HB2	2.35	0.41
16:BN:28:PRO:HG3	16:BN:67:PHE:CZ	2.56	0.41
28:Ba:233:LYS:HG2	28:Ba:284:PRO:O	2.20	0.41
31:Bd:101:ARG:HD2	31:Bd:102:PRO:HD2	2.02	0.41
39:Bk:86:TYR:HD1	39:Bk:88:TYR:HD2	1.67	0.41
41:Bm:78:VAL:HA	41:Bm:104:ARG:HH21	1.85	0.41
43:Bo:34:ALA:HB2	43:Bo:40:TYR:CE2	2.55	0.41
51:AA:55:G:O6	51:AA:63:G:N1	2.54	0.41
51:AA:143:C:H2'	51:AA:144:C:C6	2.55	0.41
51:AA:164:C:H3'	51:AA:165:G:H8	1.85	0.41
51:AA:189:A:H2'	51:AA:190:G:H8	1.84	0.41
51:AA:279:U:O2'	62:AL:54:GLY:O	2.39	0.41
51:AA:578:G:H3'	51:AA:579:A:C8	2.55	0.41
51:AA:750:G:N1	51:AA:776:A:OP2	2.52	0.41
51:AA:855:C:H2'	51:AA:856:U:H6	1.82	0.41
53:BA:306:A:H2'	53:BA:307:G:C8	2.54	0.41
53:BA:1001:A:C4	53:BA:1002:U:C5	3.09	0.41
53:BA:1303:C:H2'	53:BA:1304:G:O4'	2.20	0.41
53:BA:1373:U:H2'	53:BA:1374:U:C6	2.56	0.41
54:AB:79:SER:N	54:AB:82:SER:OG	2.36	0.41
59:AI:75:LYS:O	59:AI:79:GLU:HG2	2.20	0.41
62:AL:109:LEU:HB3	62:AL:129:LYS:HG3	2.03	0.41
66:AQ:72:PRO:HB3	66:AQ:78:LYS:HG2	2.02	0.41
72:Ac:34:TYR:CZ	72:Ac:68:LYS:HG2	2.56	0.41
73:Ad:90:GLN:O	73:Ad:94:LYS:HG2	2.21	0.41
74:Ae:147:TRP:CD1	74:Ae:147:TRP:H	2.38	0.41
86:AY:25:U:C2	86:AY:26:U:C5	3.08	0.41
3:B2:156:ARG:HA	32:Be:128:LEU:HD13	2.02	0.41
4:B3:38:ARG:O	53:BA:409:A:H5'	2.21	0.41
6:B5:84:ARG:HG3	53:BA:641:U:H1'	2.03	0.41
12:BF:117:ARG:NH1	53:BA:241:C:OP1	2.47	0.41
24:BV:167:LYS:HB2	34:Bg:106:ASP:HB3	2.01	0.41
27:BY:161:ARG:NE	27:BY:163:ASP:HB2	2.36	0.41
51:AA:11:G:O6	51:AA:524:U:O4	2.37	0.41
51:AA:159:C:P	51:AA:172:A:H61	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AA:480:U:O4	51:AA:481:A:N6	2.53	0.41
53:BA:215:A:N6	53:BA:231:C:H42	2.17	0.41
53:BA:353:C:O2	53:BA:1267:A:O2'	2.38	0.41
53:BA:657:U:H1'	53:BA:658:U:H5	1.85	0.41
53:BA:672:G:H2'	53:BA:673:C:C6	2.55	0.41
53:BA:738:U:H2'	53:BA:739:U:C6	2.55	0.41
53:BA:743:U:H3'	53:BA:744:A:C5'	2.50	0.41
53:BA:1273:A:O2'	86:AV:71:A:N1	2.52	0.41
53:BA:1448:A:H2'	53:BA:1449:U:C6	2.56	0.41
58:AG:149:LEU:O	58:AG:153:GLU:HG3	2.21	0.41
58:AG:152:CYS:SG	58:AG:183:ALA:HB1	2.60	0.41
64:AO:66:ASP:N	64:AO:66:ASP:OD1	2.54	0.41
72:Ac:139:CYS:O	72:Ac:142:GLU:HG2	2.21	0.41
74:Ae:74:TYR:OH	74:Ae:409:GLU:O	2.28	0.41
76:Ag:129:LYS:NZ	76:Ag:319:ARG:HE	2.18	0.41
79:Aj:102:PRO:HA	79:Aj:112:GLY:HA3	2.01	0.41
3:B2:120:GLU:HG2	26:BX:110:LEU:HD12	2.02	0.41
11:BE:303:LYS:HG3	53:BA:1544:A:H5'	2.03	0.41
12:BF:184:GLN:NE2	18:BP:22:VAL:HG23	2.36	0.41
14:BJ:46:LYS:HE2	46:Bt:35:MET:HE3	2.01	0.41
22:BT:87:THR:HG21	22:BT:91:LYS:HD3	2.03	0.41
34:Bg:92:LYS:HB2	34:Bg:97:ILE:HD11	2.03	0.41
41:Bm:157:TRP:NE1	41:Bm:159:TYR:HB2	2.35	0.41
49:Bw:289:GLY:HA3	49:Bw:329:TRP:CZ2	2.56	0.41
51:AA:143:C:H2'	51:AA:144:C:H6	1.86	0.41
51:AA:243:G:O2'	51:AA:256:G:H4'	2.20	0.41
51:AA:364:U:H2'	51:AA:365:A:H8	1.85	0.41
51:AA:911:A:H2'	51:AA:912:A:C8	2.56	0.41
53:BA:115:U:H2'	53:BA:131:A:H61	1.86	0.41
53:BA:124:A:N3	53:BA:251:C:O2'	2.47	0.41
53:BA:516:G:H1'	53:BA:533:A:H2'	2.01	0.41
53:BA:668:A:H2'	53:BA:669:C:C6	2.55	0.41
53:BA:1405:A:H2'	53:BA:1406:G:H8	1.83	0.41
56:AE:225:VAL:HG22	56:AE:243:VAL:HG22	2.02	0.41
64:AO:203:ARG:HG3	82:An:169:PHE:CE1	2.54	0.41
74:Ae:103:ARG:HB3	74:Ae:105:LEU:HD23	2.01	0.41
74:Ae:229:CYS:SG	74:Ae:230:LEU:N	2.93	0.41
86:AV:33:U:C2	86:AV:34:U:C6	3.09	0.41
86:AY:33:U:C2	86:AY:34:U:C6	3.09	0.41
1:B0:122:GLN:HA	29:Bb:51:TYR:CD2	2.55	0.41
6:B5:155:GLU:HB3	6:B5:172:LYS:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:BF:231:VAL:HG13	48:Bv:26:ARG:HD2	2.03	0.41
18:BP:111:ASP:OD1	18:BP:111:ASP:N	2.48	0.41
25:BW:110:LYS:HB2	53:BA:1005:G:H5''	2.02	0.41
26:BX:144:VAL:HG21	37:Bi:276:ILE:HD12	2.03	0.41
31:Bd:187:PRO:HA	31:Bd:188:PRO:HD3	1.90	0.41
40:Bl:117:ILE:HD12	40:Bl:142:GLU:HA	2.02	0.41
49:Bw:420:LEU:O	49:Bw:422:ARG:HG3	2.19	0.41
50:Bx:99:MET:O	53:BA:1518:A:O2'	2.38	0.41
51:AA:638:A:H2	56:AE:258:ILE:HD12	1.86	0.41
51:AA:947:G:H2'	51:AA:948:U:C6	2.55	0.41
53:BA:229:A:H1'	53:BA:230:G:C8	2.55	0.41
53:BA:230:G:H2'	53:BA:231:C:H6	1.85	0.41
53:BA:1381:A:H2'	53:BA:1382:C:C6	2.56	0.41
65:AP:31:PHE:HE1	65:AP:53:SER:HB2	1.85	0.41
68:AU:82:ASP:N	68:AU:82:ASP:OD1	2.53	0.41
73:Ad:55:VAL:O	73:Ad:58:GLU:HG3	2.21	0.41
76:Ag:111:LEU:O	76:Ag:114:THR:OG1	2.32	0.41
83:Ao:603:ARG:HD3	83:Ao:636:LEU:HD23	2.02	0.41
85:EL:72:ALA:HA	85:HL:76:LEU:HD22	2.02	0.41
86:AY:24:U:H2'	86:AY:25:U:C6	2.56	0.41
12:BF:62:VAL:HG23	41:Bm:119:HIS:HB3	2.03	0.41
12:BF:195:LEU:HD23	12:BF:195:LEU:HA	1.90	0.41
12:BF:217:LEU:HB2	12:BF:256:HIS:CD2	2.56	0.41
12:BF:249:ASN:OD1	12:BF:249:ASN:N	2.53	0.41
15:BK:62:GLU:OE2	45:Bq:76:ASN:ND2	2.54	0.41
18:BP:78:ILE:O	36:B8:113:ARG:HD3	2.20	0.41
22:BT:148:THR:HG22	22:BT:165:GLU:HG2	2.02	0.41
28:Ba:88:ARG:NH2	53:BA:743:U:O3'	2.54	0.41
37:Bi:160:LEU:O	37:Bi:164:VAL:HG22	2.21	0.41
42:Bn:68:LYS:HG2	42:Bn:72:GLU:HG3	2.02	0.41
50:Bx:65:ASN:O	50:Bx:74:ARG:HB2	2.21	0.41
51:AA:483:U:H2'	51:AA:484:C:H6	1.86	0.41
53:BA:102:G:H2'	53:BA:103:A:C8	2.55	0.41
53:BA:453:U:C2	53:BA:454:U:C5	3.08	0.41
53:BA:642:G:H3'	53:BA:643:A:H8	1.86	0.41
53:BA:688:A:H3'	53:BA:689:A:H4'	2.02	0.41
53:BA:1527:U:O2	53:BA:1527:U:H2'	2.20	0.41
54:AB:87:ARG:HB3	54:AB:90:LEU:HD12	2.03	0.41
59:AI:91:MET:HE2	59:AI:91:MET:HB3	1.95	0.41
63:AN:81:ASP:OD1	63:AN:86:ARG:NE	2.54	0.41
65:AP:21:LEU:HD22	65:AP:34:ILE:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Aa:282:ASP:OD1	70:Aa:282:ASP:N	2.53	0.41
73:Ad:128:ALA:O	73:Ad:132:GLU:HG2	2.21	0.41
79:Aj:90:ASP:OD2	84:Ap:215:ARG:NH2	2.53	0.41
83:Ao:358:GLN:O	83:Ao:362:GLU:HG2	2.21	0.41
86:AV:24:U:H2'	86:AV:25:U:C6	2.56	0.41
86:AV:54:U:H2'	86:AV:55:U:H5''	2.03	0.41
2:B1:42:HIS:CE1	2:B1:83:GLU:HB2	2.56	0.41
2:B1:46:HIS:CE1	2:B1:62:VAL:HG22	2.55	0.41
3:B2:96:SER:O	3:B2:100:LEU:HG	2.21	0.41
6:B5:86:SER:OG	53:BA:1016:C:OP1	2.33	0.41
8:BB:8:U:O2	8:BB:14:A:N6	2.54	0.41
11:BE:79:PRO:HG3	11:BE:192:PRO:HD2	2.03	0.41
11:BE:211:ILE:HG12	11:BE:292:HIS:HB3	2.02	0.41
11:BE:275:ARG:HB3	11:BE:284:TYR:CG	2.56	0.41
14:BJ:96:ILE:HB	14:BJ:180:CYS:SG	2.60	0.41
14:BJ:219:TYR:OH	85:EL:90:LEU:HB2	2.21	0.41
15:BK:84:GLN:HG3	15:BK:124:LYS:HA	2.02	0.41
20:BR:33:LEU:HB2	20:BR:52:LEU:HD11	2.03	0.41
21:BS:85:ARG:HB3	21:BS:120:ARG:HH12	1.86	0.41
23:BU:52:LYS:HD3	53:BA:165:A:N3	2.35	0.41
23:BU:55:ARG:NH1	53:BA:177:U:O2'	2.54	0.41
23:BU:116:LEU:HD21	24:BV:148:LEU:HD21	2.03	0.41
27:BY:189:PRO:O	32:Be:93:THR:OG1	2.27	0.41
28:Ba:113:LEU:HD22	28:Ba:311:ALA:HB1	2.03	0.41
30:Bc:212:PRO:HG3	30:Bc:268:ARG:NH1	2.36	0.41
35:Bh:60:ARG:NH1	35:Bh:63:LYS:HB2	2.36	0.41
35:Bh:240:LEU:HD23	35:Bh:301:LEU:HD21	2.03	0.41
38:Bj:44:PRO:HG2	38:Bj:227:LEU:HA	2.03	0.41
41:Bm:157:TRP:CE2	41:Bm:159:TYR:HB2	2.56	0.41
51:AA:40:A:H2'	51:AA:41:A:H8	1.85	0.41
51:AA:722:A:N6	51:AA:738:U:O2'	2.54	0.41
53:BA:1155:G:C6	53:BA:1156:A:C5	3.08	0.41
53:BA:1248:C:C4	53:BA:1253:G:H1'	2.55	0.41
53:BA:1477:A:H2'	53:BA:1478:U:C6	2.56	0.41
54:AB:166:HIS:CE1	59:AI:153:THR:HA	2.56	0.41
54:AB:187:ARG:NH2	54:AB:190:ASP:OD2	2.54	0.41
55:AC:144:SER:OG	55:AC:151:VAL:HG22	2.21	0.41
57:AF:105:CYS:HB2	67:AR:70:GLU:H	1.85	0.41
65:AP:114:ARG:NH2	84:Ap:237:GLU:HA	2.36	0.41
66:AQ:59:THR:OG1	66:AQ:60:VAL:N	2.53	0.41
67:AR:67:ILE:H	67:AR:67:ILE:HD12	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Aa:276:ASP:OD1	70:Aa:277:LYS:N	2.54	0.41
73:Ad:176:ARG:HA	73:Ad:179:GLU:HG2	2.03	0.41
76:Ag:204:GLN:HA	76:Ag:217:LYS:HG2	2.03	0.41
79:Aj:87:TRP:O	84:Ap:218:ARG:NH2	2.54	0.41
81:Am:102:LYS:HE3	81:Am:102:LYS:HB3	1.97	0.41
85:EL:82:LEU:HD22	85:FL:67:LEU:HD13	2.02	0.41
86:AV:50:U:C2	86:AV:54:U:O4	2.74	0.41
86:AY:41:U:H2'	86:AY:42:U:O4'	2.20	0.41
1:B0:78:GLY:HA3	1:B0:132:HIS:ND1	2.36	0.41
9:B7:60:ASN:ND2	32:Be:25:ARG:O	2.54	0.41
10:BD:198:GLU:HB3	10:BD:241:CYS:HB3	2.02	0.41
11:BE:230:THR:HG21	53:BA:811:A:N3	2.35	0.41
11:BE:244:SER:HB2	11:BE:251:VAL:HG12	2.02	0.41
16:BN:67:PHE:HD1	16:BN:71:LYS:HE2	1.87	0.41
20:BR:94:ALA:HB3	20:BR:95:PRO:HD3	2.02	0.41
28:Ba:236:LEU:HD12	28:Ba:237:PRO:HD2	2.03	0.41
30:Bc:61:LYS:HD3	30:Bc:61:LYS:HA	1.95	0.41
37:Bi:138:PRO:HB2	37:Bi:192:PRO:HG2	2.03	0.41
38:Bj:203:LYS:HB2	38:Bj:239:LEU:HD11	2.03	0.41
39:Bk:199:LYS:H	39:Bk:199:LYS:HG2	1.69	0.41
45:Bq:119:ARG:NE	53:BA:529:G:OP1	2.54	0.41
48:Bv:111:GLU:O	48:Bv:115:GLN:HG2	2.20	0.41
49:Bw:128:GLU:O	49:Bw:130:THR:N	2.53	0.41
51:AA:335:A:H2'	51:AA:336:A:C8	2.55	0.41
51:AA:386:U:O2'	57:AF:93:ILE:O	2.38	0.41
60:AJ:145:LEU:HB3	60:AJ:148:LEU:HD21	2.03	0.41
70:Aa:113:PHE:HE1	70:Aa:147:ARG:HG3	1.86	0.41
74:Ae:170:LYS:HD3	74:Ae:202:SER:HB2	2.03	0.41
76:Ag:265:ASN:OD1	76:Ag:265:ASN:N	2.53	0.41
77:Ah:322:GLU:OE1	77:Ah:322:GLU:N	2.53	0.41
83:Ao:240:THR:O	83:Ao:243:THR:OG1	2.26	0.41
86:AV:67:U:C4	86:AV:68:U:C5	3.09	0.41
86:AY:31:U:C2	86:AY:32:U:C5	3.09	0.41
86:AY:50:U:C2	86:AY:54:U:O4	2.74	0.41
1:B0:144:LEU:HB3	21:BS:46:PRO:HB3	2.03	0.40
8:BB:67:A:H2'	8:BB:68:A:C8	2.56	0.40
12:BF:62:VAL:HG13	12:BF:82:LEU:HB2	2.03	0.40
16:BN:75:LYS:HB2	50:Bx:174:MET:HE1	2.02	0.40
18:BP:38:ARG:HD3	18:BP:45:ARG:NH2	2.36	0.40
24:BV:186:ARG:NE	53:BA:362:C:OP1	2.39	0.40
28:Ba:166:SER:HB3	28:Ba:171:PRO:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Ba:244:GLU:O	28:Ba:248:THR:OG1	2.39	0.40
28:Ba:313:MET:HE1	28:Ba:353:GLN:HB2	2.03	0.40
29:Bb:155:CYS:O	29:Bb:267:ARG:NH1	2.54	0.40
30:Bc:230:ASN:O	30:Bc:234:LEU:HG	2.21	0.40
48:Bv:29:PRO:HA	48:Bv:30:PRO:HD3	1.94	0.40
50:Bx:60:SER:HB2	50:Bx:75:TRP:CH2	2.56	0.40
51:AA:108:G:H2'	51:AA:109:G:H8	1.86	0.40
51:AA:689:G:H2'	51:AA:690:U:O4'	2.22	0.40
51:AA:915:G:H2'	51:AA:916:A:C8	2.56	0.40
53:BA:341:G:H2'	53:BA:342:C:C6	2.55	0.40
53:BA:1001:A:H2'	53:BA:1002:U:H6	1.85	0.40
53:BA:1056:G:H2'	53:BA:1324:C:O2'	2.21	0.40
53:BA:1497:G:C4	53:BA:1499:G:C8	3.09	0.40
56:AE:220:THR:HB	56:AE:247:VAL:HG12	2.03	0.40
56:AE:232:THR:N	56:AE:236:GLY:O	2.39	0.40
60:AJ:101:GLU:OE1	80:Ak:122:LYS:HA	2.21	0.40
70:Aa:104:MET:HE2	70:Aa:290:PHE:HE2	1.86	0.40
76:Ag:117:ALA:O	76:Ag:301:GLN:NE2	2.48	0.40
76:Ag:144:CYS:SG	76:Ag:258:LEU:HD22	2.62	0.40
86:AY:3:U:H2'	86:AY:4:U:H6	1.85	0.40
9:B7:85:ARG:HH12	32:Be:17:ARG:NH1	2.19	0.40
14:BJ:107:GLU:H	14:BJ:107:GLU:CD	2.29	0.40
15:BK:66:LEU:HD13	15:BK:82:ILE:HG23	2.02	0.40
17:BO:43:ASN:OD1	17:BO:43:ASN:N	2.54	0.40
31:Bd:72:ILE:HG12	39:Bk:207:LEU:HD23	2.02	0.40
47:Bu:118:LEU:HD11	47:Bu:157:ILE:HD13	2.03	0.40
51:AA:13:U:H2'	51:AA:14:C:H6	1.86	0.40
51:AA:123:U:H2'	51:AA:124:A:C4	2.57	0.40
51:AA:209:C:H2'	51:AA:210:U:C6	2.57	0.40
51:AA:446:C:C2	51:AA:447:U:C5	3.09	0.40
51:AA:619:C:H1'	60:AJ:124:VAL:HG23	2.02	0.40
51:AA:856:U:H2'	51:AA:857:C:C6	2.56	0.40
53:BA:302:A:H2'	53:BA:303:G:C8	2.56	0.40
53:BA:713:A:H2'	53:BA:714:A:H8	1.86	0.40
53:BA:1059:C:H2'	53:BA:1060:C:H6	1.86	0.40
53:BA:1127:A:H2'	53:BA:1128:A:C8	2.55	0.40
54:AB:145:SER:HB3	54:AB:154:ILE:HD13	2.03	0.40
59:AI:123:PRO:HG3	80:Ak:89:MET:SD	2.60	0.40
60:AJ:76:LEU:HB3	60:AJ:145:LEU:HB2	2.04	0.40
61:AK:65:TYR:CG	67:AR:131:LEU:HD21	2.55	0.40
66:AQ:13:VAL:O	66:AQ:65:LEU:HD12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Ab:115:GLU:O	71:Ab:119:VAL:HG22	2.20	0.40
74:Ae:172:LYS:NZ	74:Ae:209:MET:HB2	2.37	0.40
76:Ag:55:PRO:HD2	76:Ag:146:LYS:NZ	2.37	0.40
77:Ah:273:GLU:O	77:Ah:276:LYS:HG3	2.21	0.40
84:Ap:126:PHE:HD1	84:Ap:140:THR:HG21	1.86	0.40
86:AV:58:U:O2	86:AV:58:U:H2'	2.20	0.40
1:B0:71:ARG:NH1	53:BA:1162:G:H5''	2.36	0.40
6:B5:109:VAL:HG12	6:B5:116:LEU:HD23	2.02	0.40
6:B5:148:PRO:O	20:BR:38:ARG:NH2	2.54	0.40
11:BE:58:VAL:HB	11:BE:59:PRO:HD3	2.02	0.40
14:BJ:81:LEU:HD21	45:Bq:115:ARG:HH21	1.86	0.40
14:BJ:104:LEU:HB2	44:Bp:43:ARG:HH12	1.86	0.40
28:Ba:209:LEU:O	28:Ba:223:HIS:HA	2.22	0.40
38:Bj:191:THR:HG23	38:Bj:195:LEU:HD13	2.03	0.40
42:Bn:95:LYS:NZ	53:BA:64:C:O3'	2.54	0.40
49:Bw:89:MET:HG3	49:Bw:269:LYS:HB3	2.02	0.40
49:Bw:247:LEU:HD11	49:Bw:383:ARG:HH11	1.86	0.40
51:AA:434:A:H2'	51:AA:435:C:C6	2.56	0.40
51:AA:584:C:O2	63:AN:86:ARG:HG2	2.21	0.40
51:AA:849:G:H2'	51:AA:850:U:C6	2.57	0.40
51:AA:923:G:H1'	51:AA:944:A:C2	2.54	0.40
51:AA:937:A:H2'	51:AA:938:U:O4'	2.20	0.40
53:BA:253:A:N1	53:BA:334:C:H1'	2.36	0.40
53:BA:447:A:N6	53:BA:449:C:O2	2.55	0.40
53:BA:1534:A:H2'	53:BA:1535:U:O4'	2.21	0.40
59:AI:314:LEU:O	59:AI:317:PRO:HD2	2.21	0.40
68:AU:78:LYS:HD3	75:Af:163:ILE:HG12	2.03	0.40
72:Ac:102:ILE:HD13	72:Ac:105:ILE:HD11	2.03	0.40
76:Ag:211:LYS:NZ	76:Ag:212:ARG:HE	2.20	0.40
77:Ah:321:HIS:HA	77:Ah:325:PHE:HD2	1.87	0.40
79:Aj:120:PHE:CD2	79:Aj:121:LYS:HG2	2.56	0.40
86:AY:67:U:C4	86:AY:68:U:C5	3.09	0.40
8:BB:30:G:H2'	8:BB:31:C:C6	2.56	0.40
10:BD:85:ARG:HH12	53:BA:319:G:N2	2.20	0.40
11:BE:248:VAL:HG12	11:BE:250:ARG:HG2	2.04	0.40
12:BF:65:TRP:CD1	41:Bm:118:LEU:HD11	2.56	0.40
16:BN:11:TRP:NE1	35:Bh:269:VAL:HG22	2.36	0.40
19:BQ:75:PRO:HB3	19:BQ:241:TYR:CZ	2.57	0.40
30:Bc:153:ARG:HH22	30:Bc:256:ASP:C	2.28	0.40
31:Bd:128:GLU:HA	31:Bd:131:MET:HG2	2.02	0.40
34:Bg:35:ARG:HA	34:Bg:44:ARG:HD3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Bh:45:LEU:HD22	53:BA:147:U:H4'	2.03	0.40
39:Bk:136:GLN:NE2	39:Bk:147:ASP:OD2	2.54	0.40
40:Bl:111:ARG:HD2	53:BA:217:A:H62	1.86	0.40
49:Bw:356:THR:HG22	49:Bw:357:ASP:O	2.21	0.40
51:AA:168:A:O2'	51:AA:169:A:O4'	2.23	0.40
51:AA:203:G:H2'	51:AA:204:U:C6	2.56	0.40
51:AA:299:U:O2'	51:AA:378:A:N3	2.42	0.40
51:AA:365:A:H5''	51:AA:445:C:O2'	2.20	0.40
51:AA:814:A:H2'	51:AA:815:U:C6	2.56	0.40
51:AA:957:A:OP2	81:Am:24:ASN:ND2	2.54	0.40
53:BA:75:A:N1	53:BA:89:A:H5''	2.36	0.40
53:BA:77:U:H2'	53:BA:78:A:C8	2.56	0.40
53:BA:147:U:H2'	53:BA:148:A:O4'	2.21	0.40
53:BA:322:G:C5	53:BA:341:G:C8	3.09	0.40
53:BA:417:G:H2'	53:BA:418:U:C6	2.57	0.40
53:BA:635:U:H2'	53:BA:636:U:C6	2.57	0.40
56:AE:316:CYS:HB3	56:AE:334:ALA:HB3	2.03	0.40
59:AI:362:VAL:HA	59:AI:365:MET:HE2	2.02	0.40
76:Ag:75:LYS:HE2	76:Ag:75:LYS:HB3	1.96	0.40
79:Aj:169:LEU:O	79:Aj:173:MET:HG3	2.21	0.40
80:Ak:94:LYS:HE2	80:Ak:94:LYS:HB2	1.96	0.40
12:BF:280:TYR:CE1	40:Bl:57:ILE:HG12	2.56	0.40
22:BT:57:PRO:HA	22:BT:58:PRO:HD3	1.93	0.40
23:BU:68:TRP:CZ3	23:BU:100:LYS:HB2	2.57	0.40
45:Bq:100:ASN:HD21	45:Bq:103:PRO:HG2	1.86	0.40
51:AA:125:U:H1'	51:AA:127:A:N6	2.37	0.40
51:AA:388:U:C2	51:AA:389:A:C8	3.09	0.40
51:AA:697:U:H5	78:Ai:97:GLY:HA2	1.86	0.40
53:BA:219:A:H2'	53:BA:220:G:H8	1.86	0.40
53:BA:640:A:C6	53:BA:641:U:C4	3.10	0.40
55:AC:48:ASP:OD1	55:AC:48:ASP:N	2.55	0.40
70:Aa:151:PRO:HA	70:Aa:152:PRO:HD3	1.92	0.40
73:Ad:200:PRO:O	73:Ad:203:LYS:HG2	2.21	0.40
76:Ag:66:HIS:CD2	76:Ag:99:MET:HB2	2.57	0.40
78:Ai:86:LYS:HG3	78:Ai:89:ARG:NH2	2.36	0.40
83:Ao:92:ASP:O	83:Ao:96:ILE:HG13	2.22	0.40
86:AV:31:U:C2	86:AV:32:U:C5	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	B0	108/148 (73%)	108 (100%)	0	0	100	100
2	B1	242/256 (94%)	241 (100%)	1 (0%)	0	100	100
3	B2	177/252 (70%)	176 (99%)	1 (1%)	0	100	100
4	B3	116/161 (72%)	113 (97%)	3 (3%)	0	100	100
5	B4	60/126 (48%)	54 (90%)	6 (10%)	0	100	100
6	B5	108/188 (57%)	107 (99%)	1 (1%)	0	100	100
7	B6	50/65 (77%)	49 (98%)	1 (2%)	0	100	100
9	B7	44/95 (46%)	44 (100%)	0	0	100	100
10	BD	238/306 (78%)	231 (97%)	7 (3%)	0	100	100
11	BE	305/399 (76%)	293 (96%)	12 (4%)	0	100	100
12	BF	248/294 (84%)	245 (99%)	3 (1%)	0	100	100
13	BI	96/268 (36%)	96 (100%)	0	0	100	100
14	BJ	210/262 (80%)	200 (95%)	10 (5%)	0	100	100
15	BK	174/192 (91%)	171 (98%)	3 (2%)	0	100	100
16	BN	175/178 (98%)	169 (97%)	6 (3%)	0	100	100
17	BO	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
18	BP	286/296 (97%)	276 (96%)	10 (4%)	0	100	100
19	BQ	220/251 (88%)	218 (99%)	2 (1%)	0	100	100
20	BR	151/169 (89%)	146 (97%)	5 (3%)	0	100	100
21	BS	141/180 (78%)	132 (94%)	9 (6%)	0	100	100
22	BT	226/292 (77%)	221 (98%)	5 (2%)	0	100	100
23	BU	138/149 (93%)	138 (100%)	0	0	100	100
24	BV	153/209 (73%)	150 (98%)	3 (2%)	0	100	100
25	BW	164/210 (78%)	160 (98%)	4 (2%)	0	100	100
26	BX	147/150 (98%)	144 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	BY	204/216 (94%)	199 (98%)	5 (2%)	0	100	100
28	Ba	391/423 (92%)	375 (96%)	16 (4%)	0	100	100
29	Bb	352/380 (93%)	339 (96%)	13 (4%)	0	100	100
30	Bc	293/334 (88%)	279 (95%)	14 (5%)	0	100	100
31	Bd	139/206 (68%)	134 (96%)	5 (4%)	0	100	100
32	Be	120/135 (89%)	114 (95%)	6 (5%)	0	100	100
33	Bf	106/142 (75%)	102 (96%)	2 (2%)	2 (2%)	6	33
34	Bg	146/159 (92%)	137 (94%)	9 (6%)	0	100	100
35	Bh	287/332 (86%)	276 (96%)	11 (4%)	0	100	100
36	B8	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
37	Bi	258/306 (84%)	253 (98%)	5 (2%)	0	100	100
38	Bj	224/279 (80%)	213 (95%)	11 (5%)	0	100	100
39	Bk	163/269 (61%)	156 (96%)	7 (4%)	0	100	100
40	Bl	131/166 (79%)	128 (98%)	3 (2%)	0	100	100
41	Bm	107/198 (54%)	105 (98%)	2 (2%)	0	100	100
42	Bn	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
43	Bo	95/124 (77%)	94 (99%)	1 (1%)	0	100	100
44	Bp	95/112 (85%)	91 (96%)	4 (4%)	0	100	100
45	Bq	78/138 (56%)	72 (92%)	5 (6%)	1 (1%)	9	40
46	Bt	92/102 (90%)	88 (96%)	4 (4%)	0	100	100
47	Bu	147/205 (72%)	142 (97%)	3 (2%)	2 (1%)	9	38
48	Bv	133/222 (60%)	133 (100%)	0	0	100	100
49	Bw	385/433 (89%)	367 (95%)	18 (5%)	0	100	100
50	Bx	160/196 (82%)	154 (96%)	6 (4%)	0	100	100
52	B9	36/100 (36%)	36 (100%)	0	0	100	100
54	AB	218/289 (75%)	211 (97%)	7 (3%)	0	100	100
55	AC	130/167 (78%)	125 (96%)	5 (4%)	0	100	100
56	AE	341/430 (79%)	329 (96%)	12 (4%)	0	100	100
57	AF	120/276 (44%)	117 (98%)	3 (2%)	0	100	100
58	AG	206/242 (85%)	205 (100%)	1 (0%)	0	100	100
59	AI	326/397 (82%)	315 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	AJ	138/200 (69%)	130 (94%)	8 (6%)	0	100	100
61	AK	135/196 (69%)	128 (95%)	7 (5%)	0	100	100
62	AL	107/139 (77%)	102 (95%)	5 (5%)	0	100	100
63	AN	99/128 (77%)	98 (99%)	1 (1%)	0	100	100
64	AO	173/239 (72%)	168 (97%)	5 (3%)	0	100	100
65	AP	115/135 (85%)	112 (97%)	3 (3%)	0	100	100
66	AQ	110/130 (85%)	109 (99%)	1 (1%)	0	100	100
67	AR	95/143 (66%)	93 (98%)	2 (2%)	0	100	100
68	AU	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
70	Aa	290/382 (76%)	283 (98%)	7 (2%)	0	100	100
71	Ab	133/190 (70%)	131 (98%)	2 (2%)	0	100	100
72	Ac	167/173 (96%)	167 (100%)	0	0	100	100
73	Ad	175/205 (85%)	174 (99%)	1 (1%)	0	100	100
74	Ae	386/455 (85%)	364 (94%)	20 (5%)	2 (0%)	24	59
75	Af	97/188 (52%)	94 (97%)	3 (3%)	0	100	100
76	Ag	351/410 (86%)	336 (96%)	15 (4%)	0	100	100
77	Ah	118/387 (30%)	117 (99%)	1 (1%)	0	100	100
78	Ai	97/106 (92%)	95 (98%)	2 (2%)	0	100	100
79	Aj	211/218 (97%)	207 (98%)	4 (2%)	0	100	100
80	Ak	273/325 (84%)	269 (98%)	4 (2%)	0	100	100
81	Am	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
82	An	70/199 (35%)	69 (99%)	1 (1%)	0	100	100
83	Ao	532/690 (77%)	518 (97%)	14 (3%)	0	100	100
84	Ap	188/258 (73%)	183 (97%)	5 (3%)	0	100	100
85	CL	43/198 (22%)	42 (98%)	1 (2%)	0	100	100
85	DL	25/198 (13%)	25 (100%)	0	0	100	100
85	EL	26/198 (13%)	26 (100%)	0	0	100	100
85	FL	25/198 (13%)	25 (100%)	0	0	100	100
85	GL	25/198 (13%)	25 (100%)	0	0	100	100
85	HL	24/198 (12%)	24 (100%)	0	0	100	100
All	All	14187/19424 (73%)	13772 (97%)	408 (3%)	7 (0%)	100	100

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	Bf	78	PRO
33	Bf	80	PRO
47	Bu	167	PRO
45	Bq	64	ASP
74	Ae	342	PRO
74	Ae	341	GLN
47	Bu	166	GLU

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	B0	90/115 (78%)	86 (96%)	4 (4%)	25	49
2	B1	219/229 (96%)	217 (99%)	2 (1%)	70	75
3	B2	164/228 (72%)	163 (99%)	1 (1%)	78	80
4	B3	110/150 (73%)	109 (99%)	1 (1%)	70	75
5	B4	45/114 (40%)	43 (96%)	2 (4%)	25	49
6	B5	99/163 (61%)	97 (98%)	2 (2%)	48	65
7	B6	49/60 (82%)	48 (98%)	1 (2%)	48	65
9	B7	41/78 (53%)	41 (100%)	0	100	100
10	BD	193/248 (78%)	189 (98%)	4 (2%)	47	65
11	BE	263/320 (82%)	261 (99%)	2 (1%)	73	77
12	BF	217/251 (86%)	214 (99%)	3 (1%)	59	71
13	BI	88/228 (39%)	87 (99%)	1 (1%)	65	74
14	BJ	192/230 (84%)	191 (100%)	1 (0%)	81	82
15	BK	129/151 (85%)	129 (100%)	0	100	100
16	BN	156/157 (99%)	156 (100%)	0	100	100
17	BO	99/123 (80%)	99 (100%)	0	100	100
18	BP	245/249 (98%)	243 (99%)	2 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	BQ	190/210 (90%)	189 (100%)	1 (0%)	81	82
20	BR	132/143 (92%)	131 (99%)	1 (1%)	73	77
21	BS	123/153 (80%)	122 (99%)	1 (1%)	73	77
22	BT	208/258 (81%)	206 (99%)	2 (1%)	68	75
23	BU	118/127 (93%)	118 (100%)	0	100	100
24	BV	136/178 (76%)	133 (98%)	3 (2%)	45	64
25	BW	144/180 (80%)	144 (100%)	0	100	100
26	BX	116/134 (87%)	116 (100%)	0	100	100
27	BY	185/192 (96%)	182 (98%)	3 (2%)	55	69
28	Ba	348/365 (95%)	342 (98%)	6 (2%)	53	68
29	Bb	310/328 (94%)	307 (99%)	3 (1%)	68	75
30	Bc	271/299 (91%)	268 (99%)	3 (1%)	65	74
31	Bd	130/181 (72%)	128 (98%)	2 (2%)	57	70
32	Be	100/108 (93%)	99 (99%)	1 (1%)	68	75
33	Bf	80/133 (60%)	80 (100%)	0	100	100
34	Bg	128/136 (94%)	122 (95%)	6 (5%)	23	48
35	Bh	251/284 (88%)	250 (100%)	1 (0%)	84	83
36	B8	87/162 (54%)	85 (98%)	2 (2%)	44	63
37	Bi	236/275 (86%)	231 (98%)	5 (2%)	47	65
38	Bj	201/242 (83%)	194 (96%)	7 (4%)	32	54
39	Bk	144/226 (64%)	140 (97%)	4 (3%)	38	59
40	Bl	122/147 (83%)	121 (99%)	1 (1%)	73	77
41	Bm	103/178 (58%)	103 (100%)	0	100	100
42	Bn	88/113 (78%)	86 (98%)	2 (2%)	44	63
43	Bo	77/97 (79%)	77 (100%)	0	100	100
44	Bp	79/88 (90%)	77 (98%)	2 (2%)	42	62
45	Bq	70/114 (61%)	66 (94%)	4 (6%)	18	44
46	Bt	75/82 (92%)	75 (100%)	0	100	100
47	Bu	126/177 (71%)	126 (100%)	0	100	100
48	Bv	115/183 (63%)	115 (100%)	0	100	100
49	Bw	340/373 (91%)	336 (99%)	4 (1%)	63	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	Bx	149/173 (86%)	146 (98%)	3 (2%)	48	65
52	B9	36/77 (47%)	35 (97%)	1 (3%)	38	59
54	AB	187/233 (80%)	185 (99%)	2 (1%)	65	74
55	AC	115/142 (81%)	112 (97%)	3 (3%)	40	60
56	AE	282/351 (80%)	271 (96%)	11 (4%)	28	52
57	AF	107/210 (51%)	105 (98%)	2 (2%)	50	66
58	AG	181/205 (88%)	178 (98%)	3 (2%)	53	68
59	AI	273/333 (82%)	269 (98%)	4 (2%)	57	70
60	AJ	130/180 (72%)	128 (98%)	2 (2%)	57	70
61	AK	103/151 (68%)	102 (99%)	1 (1%)	68	75
62	AL	92/116 (79%)	92 (100%)	0	100	100
63	AN	92/114 (81%)	92 (100%)	0	100	100
64	AO	159/205 (78%)	156 (98%)	3 (2%)	50	66
65	AP	97/113 (86%)	96 (99%)	1 (1%)	68	75
66	AQ	97/114 (85%)	96 (99%)	1 (1%)	68	75
67	AR	89/127 (70%)	88 (99%)	1 (1%)	65	74
68	AU	77/78 (99%)	77 (100%)	0	100	100
70	Aa	258/330 (78%)	254 (98%)	4 (2%)	55	69
71	Ab	113/162 (70%)	112 (99%)	1 (1%)	70	75
72	Ac	152/155 (98%)	147 (97%)	5 (3%)	33	56
73	Ad	149/168 (89%)	146 (98%)	3 (2%)	48	65
74	Ae	325/393 (83%)	320 (98%)	5 (2%)	57	70
75	Af	86/160 (54%)	83 (96%)	3 (4%)	32	54
76	Ag	312/361 (86%)	307 (98%)	5 (2%)	55	69
77	Ah	109/346 (32%)	107 (98%)	2 (2%)	51	67
78	Ai	86/93 (92%)	86 (100%)	0	100	100
79	Aj	188/190 (99%)	188 (100%)	0	100	100
80	Ak	249/289 (86%)	247 (99%)	2 (1%)	73	77
81	Am	100/102 (98%)	99 (99%)	1 (1%)	68	75
82	An	66/174 (38%)	66 (100%)	0	100	100
83	Ao	478/541 (88%)	468 (98%)	10 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
84	Ap	170/225 (76%)	170 (100%)	0	100	100
85	CL	30/157 (19%)	30 (100%)	0	100	100
85	DL	26/157 (17%)	26 (100%)	0	100	100
85	EL	27/157 (17%)	27 (100%)	0	100	100
85	FL	26/157 (17%)	26 (100%)	0	100	100
85	GL	26/157 (17%)	25 (96%)	1 (4%)	29	52
85	HL	24/157 (15%)	24 (100%)	0	100	100
All	All	12498/16513 (76%)	12328 (99%)	170 (1%)	57	71

All (170) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B0	42	LEU
1	B0	53	ILE
1	B0	117	VAL
1	B0	131	VAL
2	B1	6	VAL
2	B1	126	THR
3	B2	92	LEU
4	B3	86	ILE
5	B4	48	THR
5	B4	58	VAL
6	B5	153	THR
6	B5	158	VAL
7	B6	16	ILE
10	BD	125	GLU
10	BD	208	ILE
10	BD	216	VAL
10	BD	240	THR
11	BE	236	THR
11	BE	245	THR
12	BF	47	VAL
12	BF	120	VAL
12	BF	262	THR
13	BI	107	VAL
14	BJ	161	VAL
18	BP	61	THR
18	BP	286	THR
19	BQ	56	VAL
20	BR	144	THR

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Mol	Chain	Res	Type
21	BS	141	ILE
22	BT	187	LEU
22	BT	217	VAL
24	BV	55	VAL
24	BV	103	VAL
24	BV	113	THR
27	BY	86	VAL
27	BY	98	VAL
27	BY	186	THR
28	Ba	74	VAL
28	Ba	270	VAL
28	Ba	273	VAL
28	Ba	341	VAL
28	Ba	342	VAL
28	Ba	391	VAL
29	Bb	179	VAL
29	Bb	189	HIS
29	Bb	233	VAL
30	Bc	56	THR
30	Bc	260	VAL
30	Bc	283	LEU
31	Bd	136	ILE
31	Bd	150	LEU
32	Be	60	VAL
34	Bg	14	VAL
34	Bg	61	VAL
34	Bg	75	VAL
34	Bg	112	VAL
34	Bg	127	GLN
34	Bg	148	VAL
35	Bh	267	LEU
36	B8	137	THR
36	B8	163	THR
37	Bi	56	PHE
37	Bi	153	ASN
37	Bi	186	VAL
37	Bi	221	THR
37	Bi	238	VAL
38	Bj	47	LEU
38	Bj	84	TYR
38	Bj	101	LYS
38	Bj	105	LEU

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Mol	Chain	Res	Type
38	Bj	111	GLU
38	Bj	120	LEU
38	Bj	126	GLN
39	Bk	71	LYS
39	Bk	74	LYS
39	Bk	78	ARG
39	Bk	84	THR
40	Bl	42	VAL
42	Bn	43	VAL
42	Bn	44	VAL
44	Bp	27	VAL
44	Bp	75	ILE
45	Bq	66	PHE
45	Bq	73	MET
45	Bq	77	ILE
45	Bq	101	VAL
49	Bw	47	ILE
49	Bw	131	LEU
49	Bw	255	VAL
49	Bw	370	THR
50	Bx	70	CYS
50	Bx	152	THR
50	Bx	159	VAL
52	B9	65	THR
54	AB	201	VAL
54	AB	206	VAL
55	AC	42	VAL
55	AC	44	VAL
55	AC	52	THR
56	AE	156	THR
56	AE	177	GLU
56	AE	186	LYS
56	AE	187	VAL
56	AE	188	LYS
56	AE	189	ARG
56	AE	190	GLU
56	AE	191	ARG
56	AE	336	VAL
56	AE	340	VAL
56	AE	405	THR
57	AF	105	CYS
57	AF	111	VAL

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Mol	Chain	Res	Type
58	AG	64	TYR
58	AG	176	ASP
58	AG	205	LEU
59	AI	100	THR
59	AI	251	ILE
59	AI	252	GLN
59	AI	296	VAL
60	AJ	54	VAL
60	AJ	108	VAL
61	AK	183	ILE
64	AO	67	ASP
64	AO	74	LEU
64	AO	86	VAL
65	AP	26	CYS
66	AQ	71	VAL
67	AR	69	CYS
70	Aa	153	VAL
70	Aa	196	VAL
70	Aa	228	THR
70	Aa	303	ILE
71	Ab	125	LEU
72	Ac	33	ASN
72	Ac	90	VAL
72	Ac	106	LEU
72	Ac	139	CYS
72	Ac	149	CYS
73	Ad	44	THR
73	Ad	137	GLU
73	Ad	198	VAL
74	Ae	132	LEU
74	Ae	280	LEU
74	Ae	355	VAL
74	Ae	388	VAL
74	Ae	393	LEU
75	Af	109	VAL
75	Af	160	ASP
75	Af	173	LEU
76	Ag	74	LEU
76	Ag	208	VAL
76	Ag	236	THR
76	Ag	306	VAL
76	Ag	336	LEU

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Mol	Chain	Res	Type
77	Ah	302	LEU
77	Ah	309	ASN
80	Ak	93	VAL
80	Ak	290	GLU
81	Am	66	CYS
83	Ao	74	LEU
83	Ao	78	VAL
83	Ao	307	VAL
83	Ao	326	MET
83	Ao	425	VAL
83	Ao	489	PHE
83	Ao	587	LEU
83	Ao	613	LEU
83	Ao	644	VAL
83	Ao	659	THR
85	GL	90	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (102) such sidechains are listed below:

Mol	Chain	Res	Type
3	B2	197	ASN
5	B4	37	ASN
6	B5	115	HIS
6	B5	188	ASN
7	B6	31	ASN
9	B7	87	HIS
10	BD	166	ASN
10	BD	169	HIS
10	BD	222	ASN
11	BE	69	ASN
11	BE	154	HIS
11	BE	156	HIS
11	BE	202	GLN
12	BF	83	HIS
12	BF	97	HIS
12	BF	138	HIS
12	BF	153	HIS
13	BI	126	GLN
14	BJ	101	HIS
14	BJ	151	ASN
14	BJ	223	GLN
16	BN	26	GLN

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Mol	Chain	Res	Type
16	BN	40	GLN
16	BN	89	GLN
16	BN	147	GLN
17	BO	59	HIS
17	BO	142	GLN
20	BR	100	GLN
20	BR	109	GLN
21	BS	55	ASN
22	BT	172	GLN
23	BU	89	ASN
28	Ba	149	ASN
28	Ba	156	ASN
28	Ba	360	ASN
29	Bb	220	ASN
29	Bb	243	ASN
29	Bb	354	GLN
32	Be	42	HIS
34	Bg	107	GLN
34	Bg	127	GLN
35	Bh	94	ASN
36	B8	154	GLN
37	Bi	167	ASN
37	Bi	196	GLN
39	Bk	81	ASN
39	Bk	158	GLN
40	Bl	93	ASN
41	Bm	120	GLN
42	Bn	59	ASN
45	Bq	135	ASN
46	Bt	21	HIS
48	Bv	81	GLN
49	Bw	60	GLN
49	Bw	67	GLN
49	Bw	87	GLN
49	Bw	104	ASN
49	Bw	228	ASN
49	Bw	234	GLN
49	Bw	352	GLN
49	Bw	376	GLN
50	Bx	69	GLN
50	Bx	76	ASN
50	Bx	109	GLN

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Mol	Chain	Res	Type
54	AB	119	GLN
54	AB	200	ASN
55	AC	60	HIS
55	AC	154	HIS
56	AE	277	HIS
59	AI	139	GLN
59	AI	156	GLN
59	AI	297	ASN
59	AI	327	HIS
59	AI	385	GLN
60	AJ	163	ASN
61	AK	111	HIS
62	AL	100	HIS
70	Aa	270	HIS
70	Aa	330	HIS
71	Ab	107	GLN
72	Ac	51	ASN
72	Ac	95	ASN
72	Ac	101	HIS
74	Ae	140	ASN
75	Af	104	GLN
76	Ag	65	GLN
76	Ag	109	HIS
76	Ag	142	HIS
76	Ag	147	GLN
76	Ag	148	ASN
76	Ag	265	ASN
77	Ah	341	HIS
80	Ak	66	GLN
80	Ak	187	HIS
80	Ak	263	ASN
81	Am	113	ASN
83	Ao	104	HIS
83	Ao	115	ASN
83	Ao	439	HIS
83	Ao	507	ASN
84	Ap	98	ASN
85	GL	83	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	AA	959/962 (99%)	169 (17%)	0
53	BA	1542/1571 (98%)	411 (26%)	2 (0%)
8	BB	64/73 (87%)	17 (26%)	0
86	AV	70/71 (98%)	24 (34%)	3 (4%)
86	AY	70/71 (98%)	24 (34%)	3 (4%)
87	AX	5/6 (83%)	5 (100%)	0
All	All	2710/2754 (98%)	650 (23%)	8 (0%)

All (650) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	BB	3	U
8	BB	5	A
8	BB	7	G
8	BB	8	U
8	BB	9	A
8	BB	13	U
8	BB	21	C
8	BB	23	A
8	BB	29	G
8	BB	34	U
8	BB	43	C
8	BB	44	U
8	BB	46	G
8	BB	47	A
8	BB	48	U
8	BB	69	C
8	BB	70	A
51	AA	5	A
51	AA	10	U
51	AA	27	U
51	AA	34	U
51	AA	41	A
51	AA	42	A
51	AA	43	U
51	AA	54	A
51	AA	58	U
51	AA	65	C
51	AA	67	C
51	AA	81	U
51	AA	83	C
51	AA	115	A
51	AA	119	C

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Mol	Chain	Res	Type
51	AA	120	A
51	AA	127	A
51	AA	147	G
51	AA	152	A
51	AA	161	C
51	AA	164	C
51	AA	168	A
51	AA	170	A
51	AA	171	C
51	AA	173	G
51	AA	175	A
51	AA	186	U
51	AA	190	G
51	AA	191	C
51	AA	212	A
51	AA	216	A
51	AA	222	A
51	AA	223	U
51	AA	224	U
51	AA	231	G
51	AA	235	A
51	AA	238	C
51	AA	244	C
51	AA	247	G
51	AA	253	G
51	AA	256	G
51	AA	258	C
51	AA	259	A
51	AA	273	A
51	AA	281	G
51	AA	287	C
51	AA	288	G
51	AA	294	A
51	AA	296	G
51	AA	297	A
51	AA	308	A
51	AA	309	A
51	AA	310	A
51	AA	314	A
51	AA	315	U
51	AA	317	A
51	AA	320	A

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Mol	Chain	Res	Type
51	AA	328	A
51	AA	337	C
51	AA	341	G
51	AA	345	U
51	AA	354	C
51	AA	355	U
51	AA	362	A
51	AA	368	A
51	AA	372	C
51	AA	395	C
51	AA	399	A
51	AA	417	C
51	AA	421	A
51	AA	433	U
51	AA	450	C
51	AA	455	A
51	AA	457	C
51	AA	458	C
51	AA	461	A
51	AA	464	A
51	AA	471	U
51	AA	472	A
51	AA	477	A
51	AA	479	C
51	AA	502	A
51	AA	503	A
51	AA	518	A
51	AA	531	U
51	AA	532	G
51	AA	538	C
51	AA	540	U
51	AA	561	U
51	AA	566	U
51	AA	571	A
51	AA	574	C
51	AA	576	C
51	AA	589	C
51	AA	592	A
51	AA	593	C
51	AA	596	U
51	AA	597	U
51	AA	604	U

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Mol	Chain	Res	Type
51	AA	616	C
51	AA	618	G
51	AA	619	C
51	AA	620	C
51	AA	625	U
51	AA	628	G
51	AA	633	C
51	AA	639	A
51	AA	644	A
51	AA	645	A
51	AA	646	C
51	AA	649	U
51	AA	652	U
51	AA	665	A
51	AA	681	A
51	AA	682	G
51	AA	685	C
51	AA	691	G
51	AA	698	A
51	AA	699	U
51	AA	707	A
51	AA	708	A
51	AA	709	A
51	AA	711	A
51	AA	720	A
51	AA	722	A
51	AA	731	A
51	AA	732	U
51	AA	739	A
51	AA	741	C
51	AA	743	A
51	AA	744	C
51	AA	746	A
51	AA	748	A
51	AA	775	A
51	AA	790	A
51	AA	791	G
51	AA	802	A
51	AA	803	U
51	AA	808	U
51	AA	823	G
51	AA	825	C

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Mol	Chain	Res	Type
51	AA	838	A
51	AA	841	C
51	AA	842	A
51	AA	863	G
51	AA	869	A
51	AA	876	A
51	AA	877	A
51	AA	883	C
51	AA	885	U
51	AA	886	A
51	AA	893	A
51	AA	894	U
51	AA	899	C
51	AA	902	C
51	AA	910	G
51	AA	918	A
51	AA	920	G
51	AA	923	G
51	AA	925	A
51	AA	928	A
51	AA	930	G
51	AA	932	U
51	AA	943	G
51	AA	946	A
51	AA	955	G
51	AA	956	G
51	AA	959	U
51	AA	960	A
53	BA	4	A
53	BA	7	G
53	BA	11	G
53	BA	15	A
53	BA	19	U
53	BA	20	A
53	BA	21	C
53	BA	22	U
53	BA	26	C
53	BA	27	A
53	BA	31	A
53	BA	32	C
53	BA	36	A
53	BA	37	A

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Mol	Chain	Res	Type
53	BA	40	C
53	BA	41	A
53	BA	44	A
53	BA	45	A
53	BA	46	A
53	BA	49	A
53	BA	56	A
53	BA	57	A
53	BA	59	A
53	BA	60	U
53	BA	63	A
53	BA	66	U
53	BA	67	A
53	BA	68	A
53	BA	82	G
53	BA	83	A
53	BA	96	U
53	BA	97	A
53	BA	105	G
53	BA	109	U
53	BA	118	U
53	BA	119	A
53	BA	122	G
53	BA	129	A
53	BA	130	A
53	BA	132	G
53	BA	139	G
53	BA	140	A
53	BA	141	A
53	BA	142	U
53	BA	143	A
53	BA	146	A
53	BA	147	U
53	BA	163	C
53	BA	164	A
53	BA	168	A
53	BA	172	C
53	BA	178	C
53	BA	180	A
53	BA	182	C
53	BA	190	U
53	BA	192	A

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Mol	Chain	Res	Type
53	BA	205	A
53	BA	218	A
53	BA	219	A
53	BA	223	A
53	BA	225	C
53	BA	229	A
53	BA	231	C
53	BA	237	A
53	BA	238	C
53	BA	239	C
53	BA	243	A
53	BA	245	A
53	BA	254	G
53	BA	263	G
53	BA	271	U
53	BA	272	A
53	BA	273	A
53	BA	275	A
53	BA	277	A
53	BA	295	G
53	BA	309	A
53	BA	311	A
53	BA	312	C
53	BA	322	G
53	BA	324	G
53	BA	329	A
53	BA	330	A
53	BA	331	A
53	BA	336	A
53	BA	337	A
53	BA	338	C
53	BA	340	A
53	BA	351	A
53	BA	352	G
53	BA	359	G
53	BA	366	A
53	BA	368	A
53	BA	369	G
53	BA	372	U
53	BA	373	U
53	BA	374	U
53	BA	376	A

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Mol	Chain	Res	Type
53	BA	389	A
53	BA	390	A
53	BA	393	A
53	BA	394	C
53	BA	398	A
53	BA	409	A
53	BA	413	C
53	BA	414	A
53	BA	417	G
53	BA	427	G
53	BA	428	A
53	BA	432	A
53	BA	433	G
53	BA	446	C
53	BA	447	A
53	BA	448	G
53	BA	459	A
53	BA	460	C
53	BA	467	A
53	BA	468	A
53	BA	472	U
53	BA	473	G
53	BA	474	A
53	BA	479	A
53	BA	480	G
53	BA	488	U
53	BA	490	U
53	BA	491	U
53	BA	492	A
53	BA	493	A
53	BA	494	U
53	BA	497	U
53	BA	498	A
53	BA	499	C
53	BA	500	C
53	BA	501	A
53	BA	503	A
53	BA	505	U
53	BA	509	C
53	BA	514	A
53	BA	515	A
53	BA	516	G

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Mol	Chain	Res	Type
53	BA	517	C
53	BA	518	A
53	BA	526	A
53	BA	527	U
53	BA	530	A
53	BA	532	A
53	BA	533	A
53	BA	547	A
53	BA	548	A
53	BA	549	C
53	BA	550	A
53	BA	551	A
53	BA	553	U
53	BA	554	U
53	BA	557	C
53	BA	560	A
53	BA	561	C
53	BA	562	A
53	BA	563	U
53	BA	570	A
53	BA	574	A
53	BA	576	U
53	BA	578	A
53	BA	579	U
53	BA	584	A
53	BA	586	C
53	BA	592	G
53	BA	593	C
53	BA	595	C
53	BA	596	A
53	BA	617	A
53	BA	618	A
53	BA	625	A
53	BA	626	G
53	BA	631	A
53	BA	633	U
53	BA	634	G
53	BA	640	A
53	BA	648	C
53	BA	654	G
53	BA	660	C
53	BA	665	C

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Mol	Chain	Res	Type
53	BA	673	C
53	BA	674	U
53	BA	675	U
53	BA	683	U
53	BA	684	A
53	BA	689	A
53	BA	694	A
53	BA	695	U
53	BA	697	C
53	BA	704	U
53	BA	707	A
53	BA	713	A
53	BA	719	C
53	BA	720	C
53	BA	721	A
53	BA	722	A
53	BA	723	A
53	BA	724	A
53	BA	725	C
53	BA	727	A
53	BA	728	C
53	BA	744	A
53	BA	745	A
53	BA	746	U
53	BA	748	A
53	BA	763	C
53	BA	764	A
53	BA	774	A
53	BA	777	A
53	BA	778	A
53	BA	780	G
53	BA	782	A
53	BA	783	A
53	BA	784	G
53	BA	814	C
53	BA	819	A
53	BA	825	C
53	BA	835	A
53	BA	847	U
53	BA	848	C
53	BA	852	C
53	BA	853	A

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Mol	Chain	Res	Type
53	BA	854	U
53	BA	855	U
53	BA	856	A
53	BA	859	A
53	BA	864	U
53	BA	872	A
53	BA	883	G
53	BA	889	C
53	BA	892	G
53	BA	894	U
53	BA	895	U
53	BA	896	A
53	BA	897	A
53	BA	899	G
53	BA	900	G
53	BA	902	C
53	BA	903	G
53	BA	909	U
53	BA	910	U
53	BA	922	A
53	BA	923	A
53	BA	924	G
53	BA	925	G
53	BA	926	U
53	BA	931	U
53	BA	933	A
53	BA	935	C
53	BA	938	U
53	BA	939	U
53	BA	947	A
53	BA	948	A
53	BA	950	U
53	BA	958	U
53	BA	959	G
53	BA	960	U
53	BA	962	U
53	BA	964	A
53	BA	965	A
53	BA	967	G
53	BA	970	C
53	BA	977	G
53	BA	983	U

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Mol	Chain	Res	Type
53	BA	986	U
53	BA	992	U
53	BA	1015	C
53	BA	1016	C
53	BA	1018	U
53	BA	1026	A
53	BA	1027	G
53	BA	1028	A
53	BA	1038	A
53	BA	1041	A
53	BA	1045	U
53	BA	1050	C
53	BA	1051	G
53	BA	1055	A
53	BA	1056	G
53	BA	1057	A
53	BA	1063	U
53	BA	1064	G
53	BA	1071	U
53	BA	1072	A
53	BA	1074	U
53	BA	1075	U
53	BA	1081	U
53	BA	1089	G
53	BA	1091	U
53	BA	1092	A
53	BA	1093	A
53	BA	1127	A
53	BA	1129	C
53	BA	1138	G
53	BA	1140	A
53	BA	1146	G
53	BA	1152	G
53	BA	1167	C
53	BA	1168	A
53	BA	1169	A
53	BA	1180	G
53	BA	1183	U
53	BA	1188	U
53	BA	1194	U
53	BA	1195	A
53	BA	1204	A

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Mol	Chain	Res	Type
53	BA	1206	U
53	BA	1207	C
53	BA	1217	A
53	BA	1218	U
53	BA	1219	A
53	BA	1220	A
53	BA	1221	C
53	BA	1222	A
53	BA	1226	C
53	BA	1231	U
53	BA	1233	A
53	BA	1237	A
53	BA	1238	A
53	BA	1239	A
53	BA	1240	A
53	BA	1241	U
53	BA	1242	U
53	BA	1245	G
53	BA	1246	A
53	BA	1247	U
53	BA	1248	C
53	BA	1249	A
53	BA	1251	C
53	BA	1252	G
53	BA	1253	G
53	BA	1254	A
53	BA	1258	A
53	BA	1264	C
53	BA	1270	G
53	BA	1271	A
53	BA	1287	G
53	BA	1288	U
53	BA	1291	U
53	BA	1294	A
53	BA	1298	C
53	BA	1299	C
53	BA	1314	U
53	BA	1321	C
53	BA	1323	U
53	BA	1325	G
53	BA	1326	A
53	BA	1328	G

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Mol	Chain	Res	Type
53	BA	1332	G
53	BA	1336	A
53	BA	1341	A
53	BA	1342	C
53	BA	1352	G
53	BA	1357	C
53	BA	1358	G
53	BA	1385	U
53	BA	1386	U
53	BA	1387	A
53	BA	1388	A
53	BA	1389	A
53	BA	1390	G
53	BA	1395	A
53	BA	1396	C
53	BA	1405	A
53	BA	1407	U
53	BA	1408	U
53	BA	1409	C
53	BA	1420	A
53	BA	1425	A
53	BA	1426	G
53	BA	1429	C
53	BA	1432	U
53	BA	1433	U
53	BA	1436	U
53	BA	1445	U
53	BA	1448	A
53	BA	1451	U
53	BA	1455	C
53	BA	1457	A
53	BA	1458	G
53	BA	1468	A
53	BA	1474	G
53	BA	1475	A
53	BA	1476	A
53	BA	1493	A
53	BA	1494	A
53	BA	1498	C
53	BA	1504	A
53	BA	1505	G
53	BA	1509	U

Continued on next page...

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Mol	Chain	Res	Type
53	BA	1514	A
53	BA	1518	A
53	BA	1521	U
53	BA	1522	A
53	BA	1526	U
53	BA	1527	U
53	BA	1528	A
53	BA	1531	C
53	BA	1532	U
53	BA	1533	A
53	BA	1536	U
53	BA	1548	A
53	BA	1549	A
53	BA	1551	C
53	BA	1552	C
53	BA	1553	A
53	BA	1558	U
53	BA	1559	A
53	BA	1571	A
86	AV	6	U
86	AV	9	U
86	AV	10	U
86	AV	14	U
86	AV	16	U
86	AV	17	U
86	AV	18	U
86	AV	43	U
86	AV	44	U
86	AV	45	U
86	AV	50	U
86	AV	52	U
86	AV	53	U
86	AV	54	U
86	AV	55	U
86	AV	56	U
86	AV	58	U
86	AV	62	U
86	AV	63	U
86	AV	64	U
86	AV	65	U
86	AV	69	C
86	AV	70	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
86	AV	71	A
87	AX	2	U
87	AX	3	U
87	AX	4	U
87	AX	5	U
87	AX	6	U
86	AY	6	U
86	AY	9	U
86	AY	10	U
86	AY	14	U
86	AY	16	U
86	AY	17	U
86	AY	18	U
86	AY	43	U
86	AY	44	U
86	AY	45	U
86	AY	50	U
86	AY	52	U
86	AY	53	U
86	AY	54	U
86	AY	55	U
86	AY	56	U
86	AY	58	U
86	AY	62	U
86	AY	63	U
86	AY	64	U
86	AY	65	U
86	AY	69	C
86	AY	70	C
86	AY	71	A

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	BA	48	U
53	BA	1241	U
86	AV	43	U
86	AV	69	C
86	AV	70	C
86	AY	43	U
86	AY	69	C
86	AY	70	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 335 ligands modelled in this entry, 330 are monoatomic - leaving 5 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	$\# Z > 2$
90	SPM	BA	1793	-	13,13,13	0.34	0	12,12,12	0.79	0
91	5GP	BA	1791	88	26,26,26	0.99	2 (7%)	40,40,40	1.67	8 (20%)
90	SPM	AA	3001	-	13,13,13	0.34	0	12,12,12	0.79	0
90	SPM	BA	1792	-	13,13,13	0.33	0	12,12,12	0.79	0
92	GTP	Ag	500	88	30,34,34	0.83	1 (3%)	46,54,54	1.82	11 (23%)

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
90	SPM	BA	1793	-	-	4/11/11/11	-
91	5GP	BA	1791	88	-	0/10/26/26	0/3/3/3
90	SPM	AA	3001	-	-	2/11/11/11	-
90	SPM	BA	1792	-	-	3/11/11/11	-
92	GTP	Ag	500	88	-	0/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	BA	1791	5GP	C6-N1	-2.51	1.34	1.38
92	Ag	500	GTP	C2-N3	2.23	1.38	1.33
91	BA	1791	5GP	C5-N7	-2.05	1.35	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	BA	1791	5GP	C5-C4-N3	-5.60	119.38	128.46
92	Ag	500	GTP	C5-C4-N3	-5.31	119.84	128.46
92	Ag	500	GTP	C2-N3-C4	4.67	120.63	112.30
91	BA	1791	5GP	C2-N3-C4	4.33	120.01	112.30
92	Ag	500	GTP	PA-O3A-PB	-4.07	118.85	132.83
92	Ag	500	GTP	PB-O3B-PG	-3.78	119.85	132.83
92	Ag	500	GTP	N9-C4-N3	3.51	132.99	125.94
91	BA	1791	5GP	N9-C4-N3	3.50	132.97	125.94
92	Ag	500	GTP	C2-N1-C6	-2.95	119.73	125.10
92	Ag	500	GTP	C5-C6-N1	2.58	119.74	113.19
92	Ag	500	GTP	C8-N7-C5	2.44	108.66	104.24
91	BA	1791	5GP	C5-C6-N1	2.44	119.38	113.19
92	Ag	500	GTP	N9-C8-N7	-2.43	108.81	113.39
92	Ag	500	GTP	O6-C6-C5	-2.43	120.16	126.60
91	BA	1791	5GP	O6-C6-C5	-2.39	120.25	126.60
92	Ag	500	GTP	C3'-C2'-C1'	2.35	105.89	101.43
91	BA	1791	5GP	C2-N1-C6	-2.28	120.94	125.10
91	BA	1791	5GP	N9-C8-N7	-2.27	109.12	113.39
91	BA	1791	5GP	C4-C5-N7	-2.02	107.52	110.72

There are no chirality outliers.

All (9) torsion outliers are listed below:

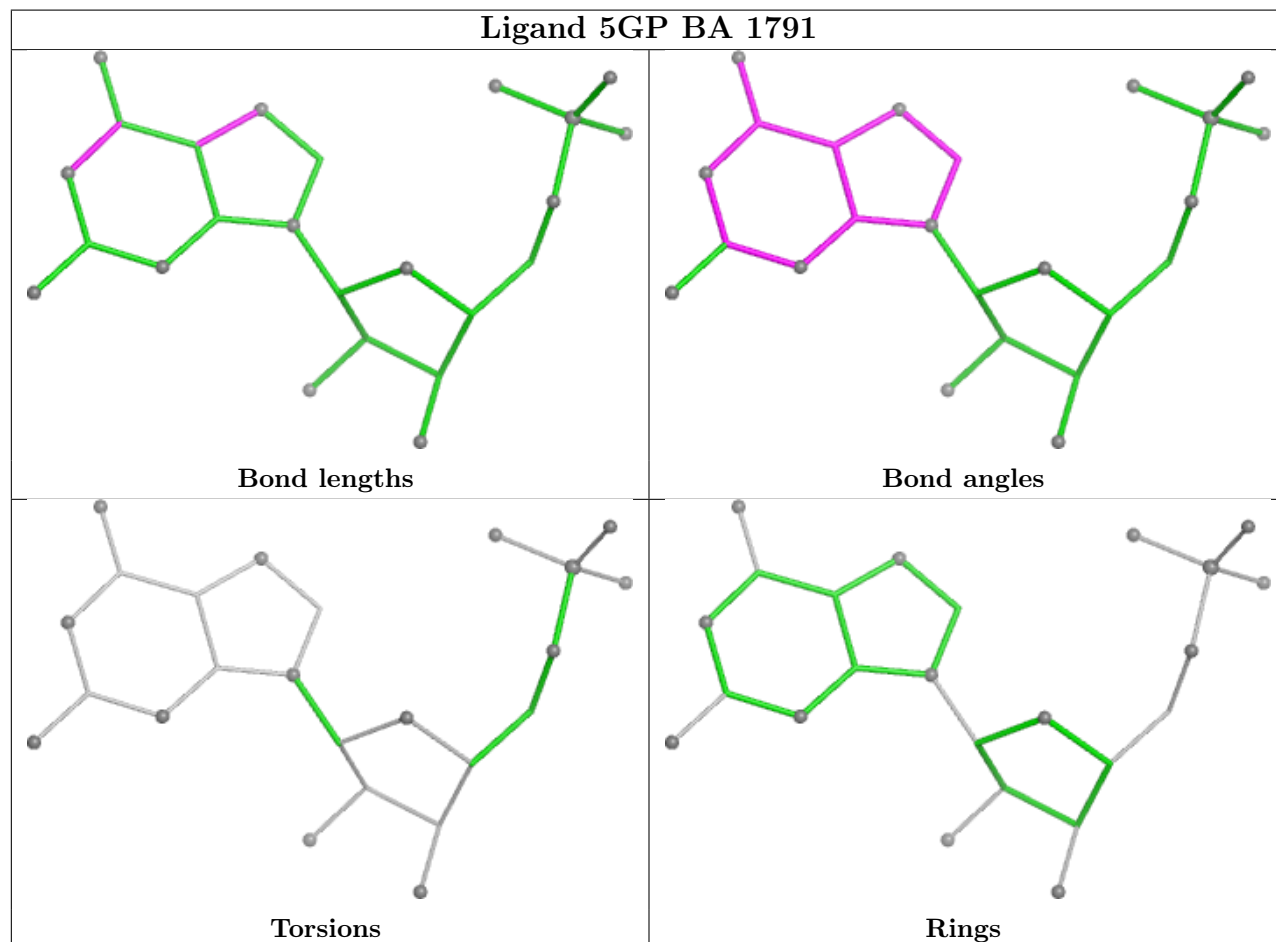
Mol	Chain	Res	Type	Atoms
90	BA	1793	SPM	N5-C6-C7-C8
90	AA	3001	SPM	C8-C9-N10-C11
90	BA	1792	SPM	C7-C8-C9-N10
90	BA	1793	SPM	C8-C9-N10-C11
90	BA	1793	SPM	C7-C8-C9-N10
90	BA	1793	SPM	C6-C7-C8-C9
90	BA	1792	SPM	C6-C7-C8-C9
90	AA	3001	SPM	C7-C6-N5-C4
90	BA	1792	SPM	C7-C6-N5-C4

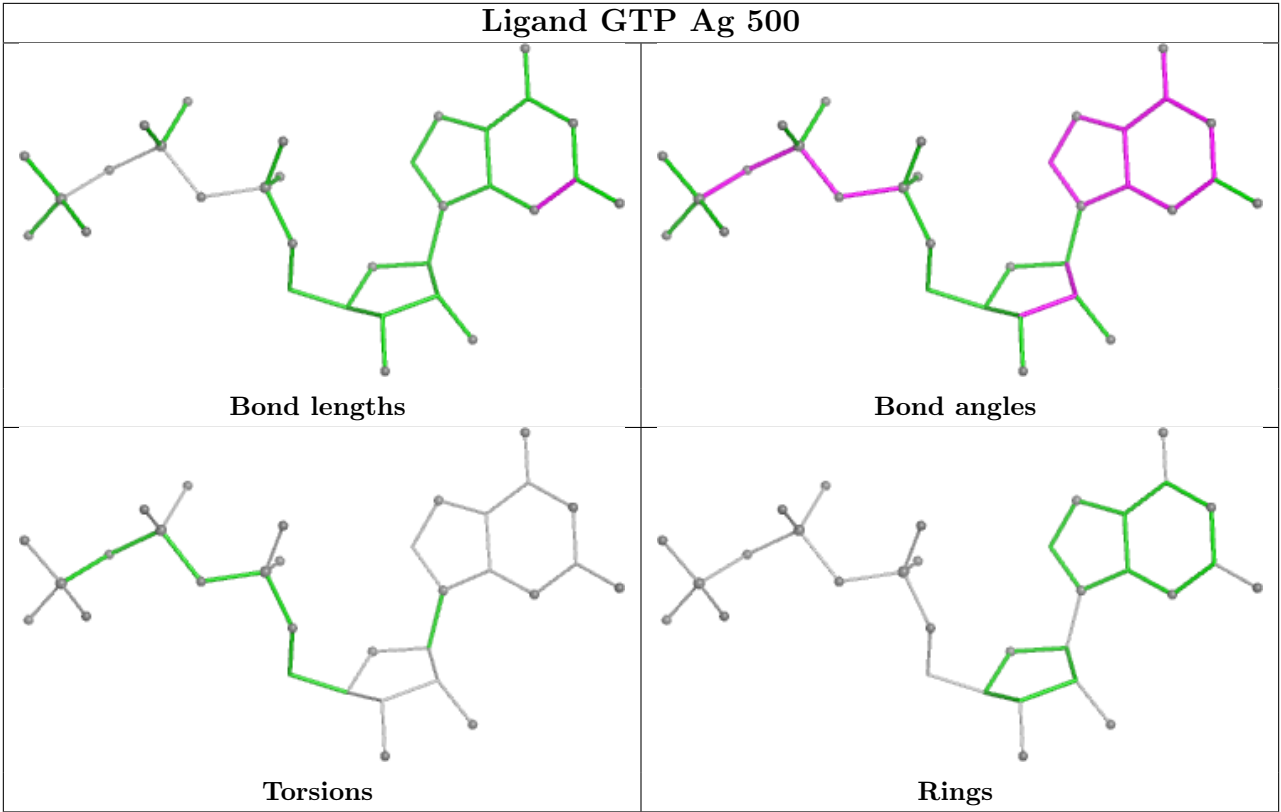
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
90	AA	3001	SPM	1	0
90	BA	1792	SPM	2	0
92	Ag	500	GTP	1	0

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
83	Ao	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Ao	234:UNK	C	240:THR	N	8.00

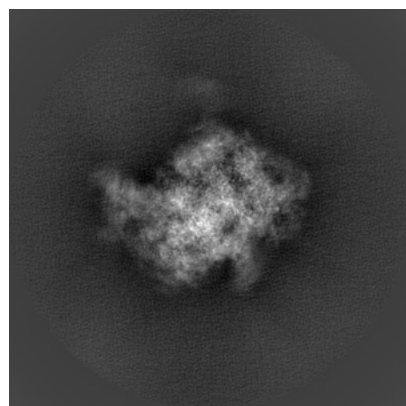
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12569. These allow visual inspection of the internal detail of the map and identification of artifacts.

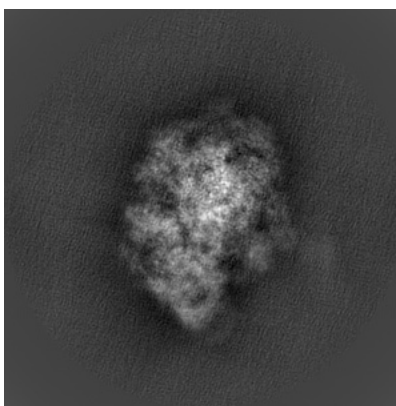
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

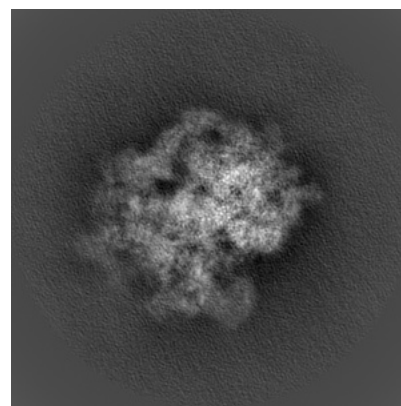
6.1.1 Primary map



X

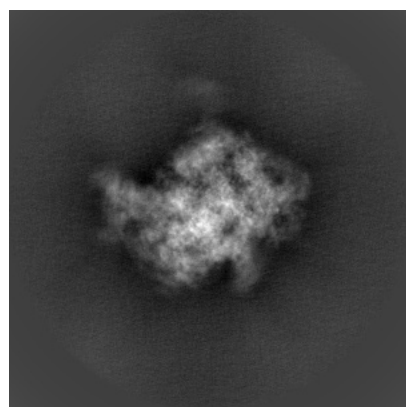


Y

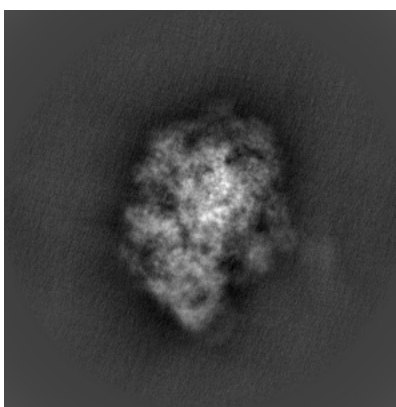


Z

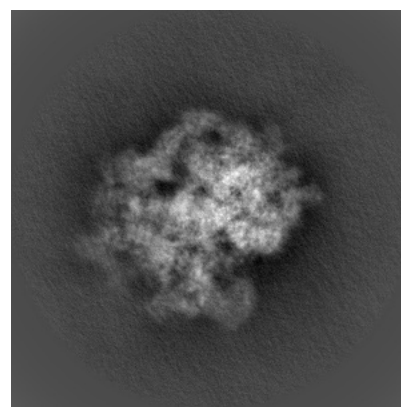
6.1.2 Raw map



X



Y

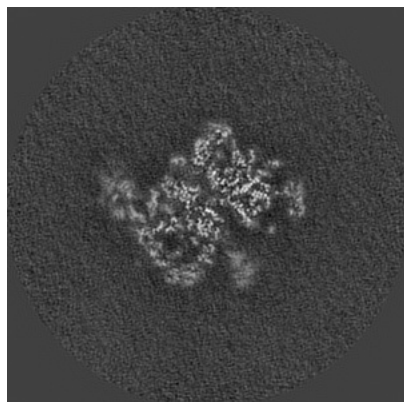


Z

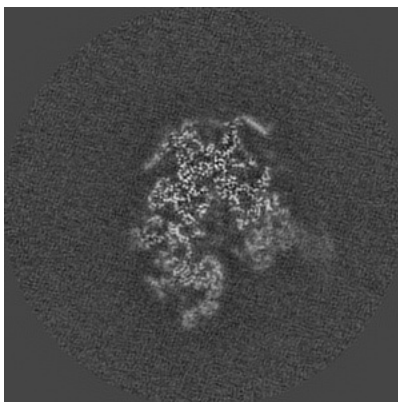
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

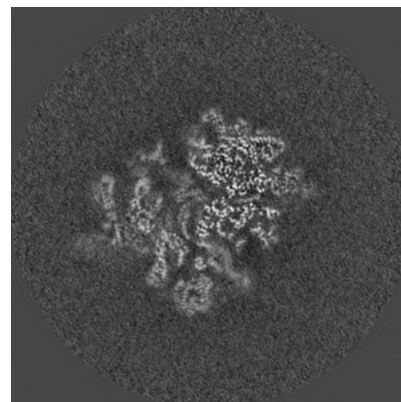
6.2.1 Primary map



X Index: 240

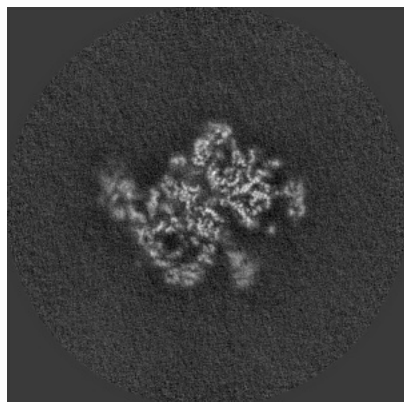


Y Index: 240

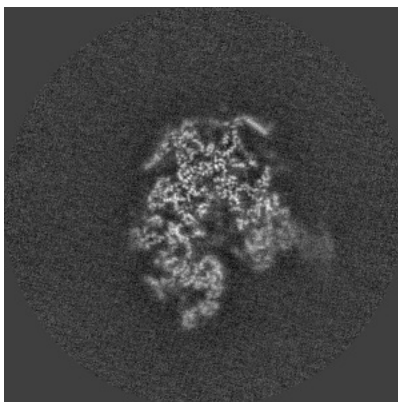


Z Index: 240

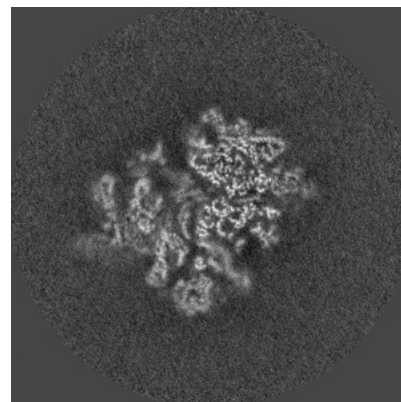
6.2.2 Raw map



X Index: 240



Y Index: 240

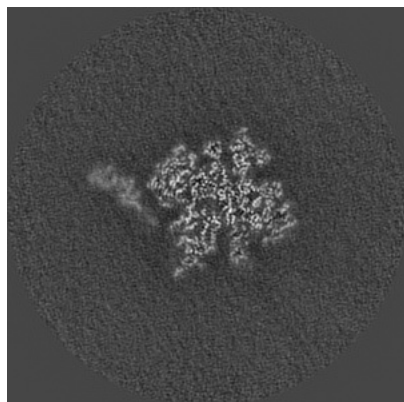


Z Index: 240

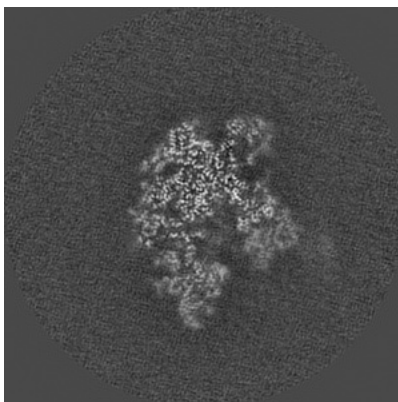
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

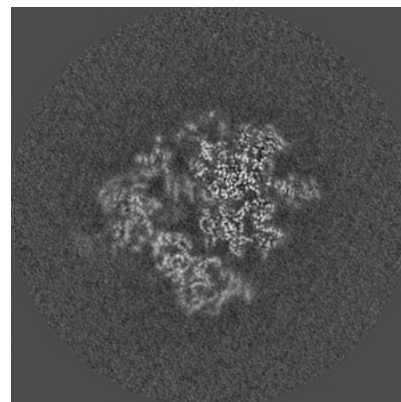
6.3.1 Primary map



X Index: 270

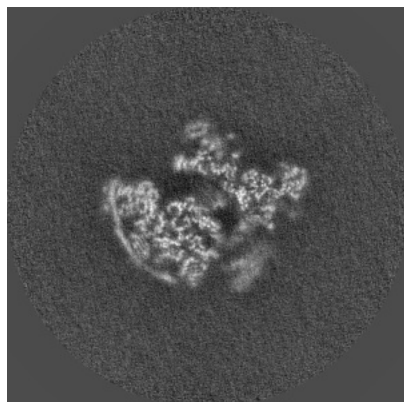


Y Index: 235

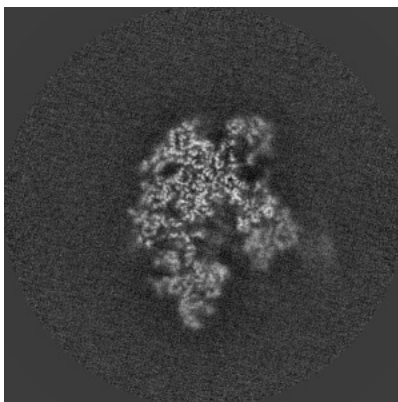


Z Index: 249

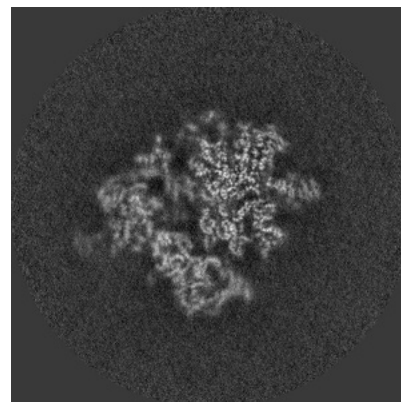
6.3.2 Raw map



X Index: 227



Y Index: 235

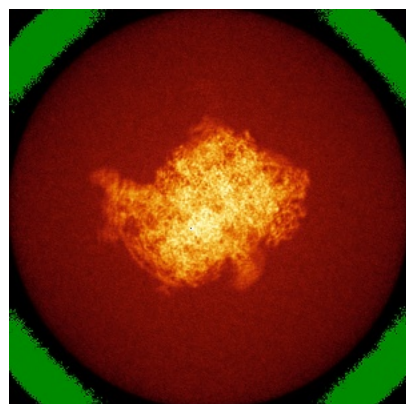


Z Index: 248

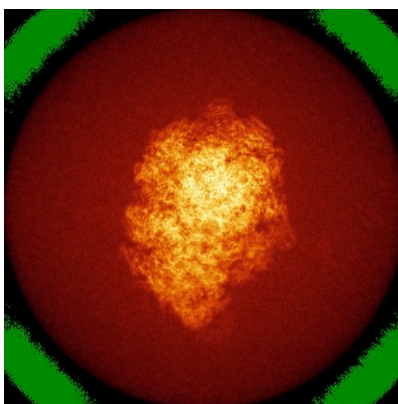
The images above show the largest variance slices of the map in three orthogonal directions.

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

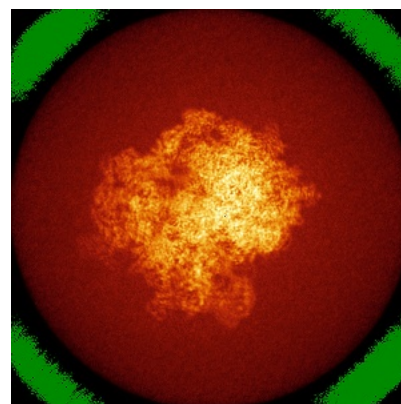
6.4.1 Primary map



X

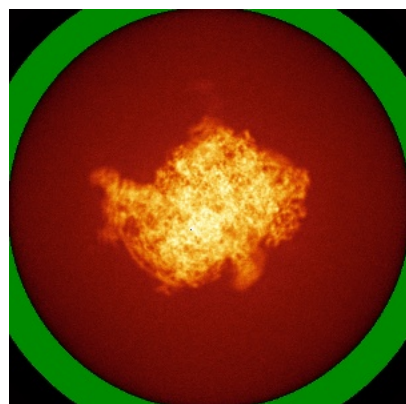


Y

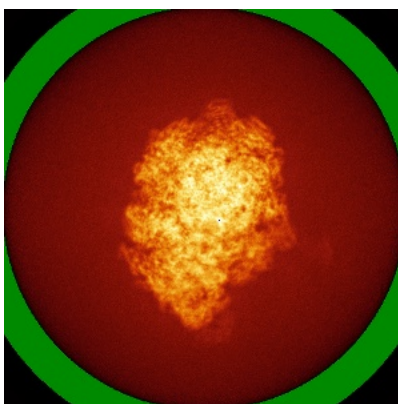


Z

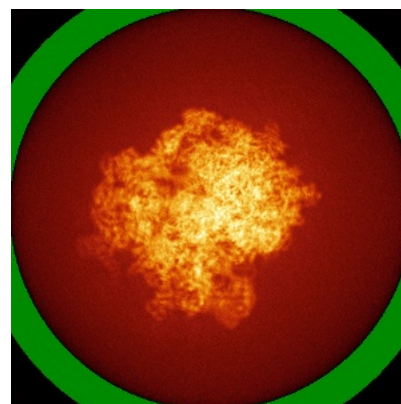
6.4.2 Raw map



X



Y

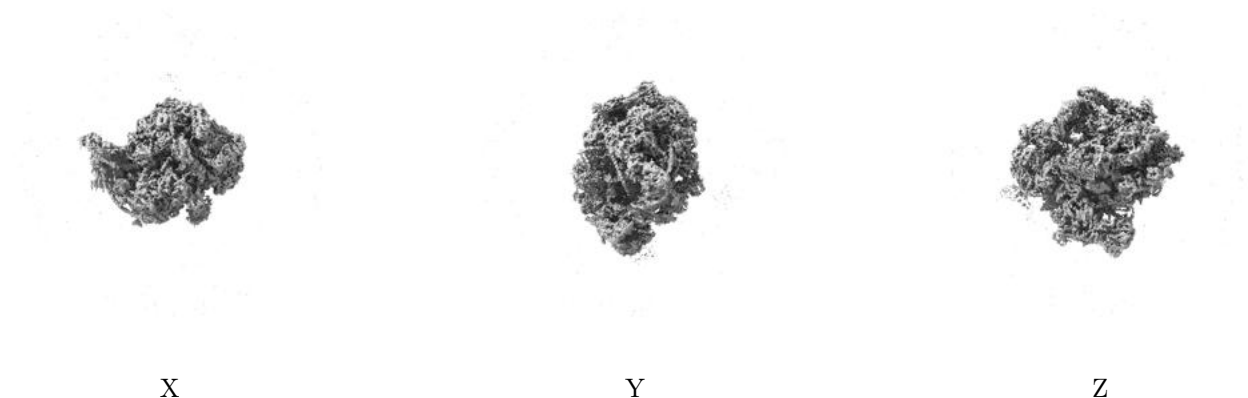


Z

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

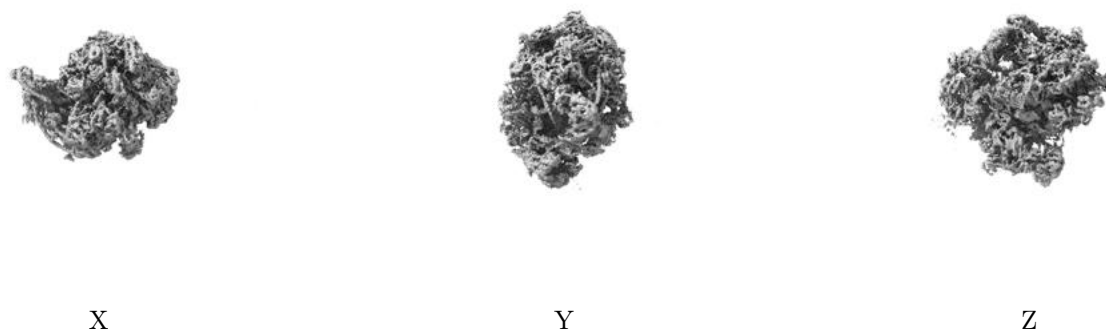
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

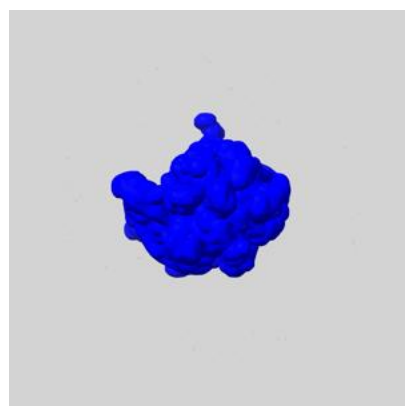
6.6 Mask visualisation [i](#)

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

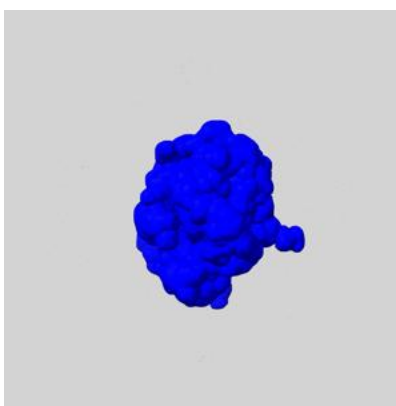
A mask typically either:

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

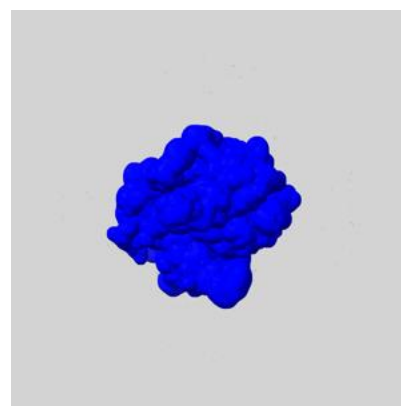
6.6.1 emd_12569_msk_1.map [i](#)



X



Y

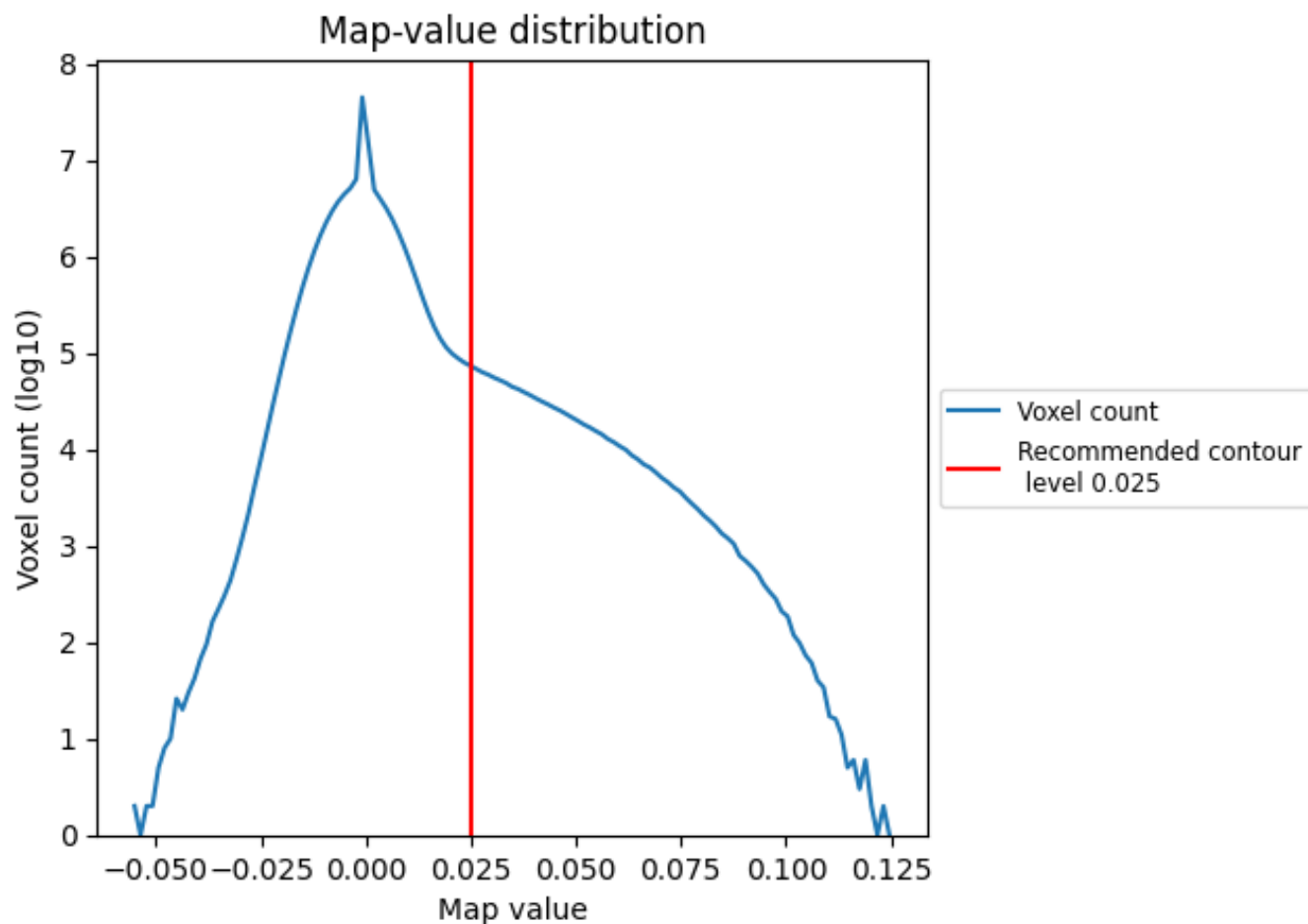


Z

7 Map analysis [i](#)

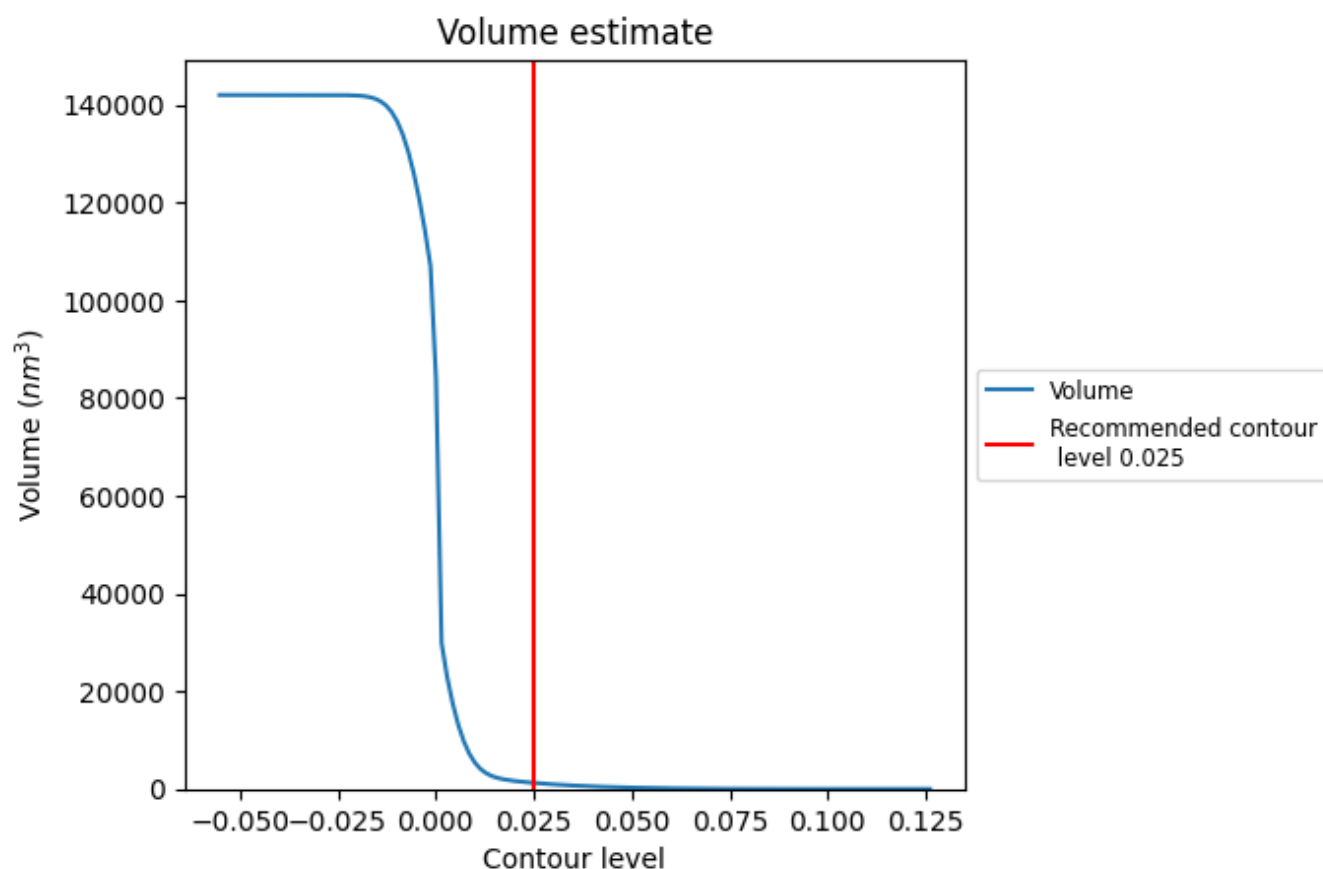
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

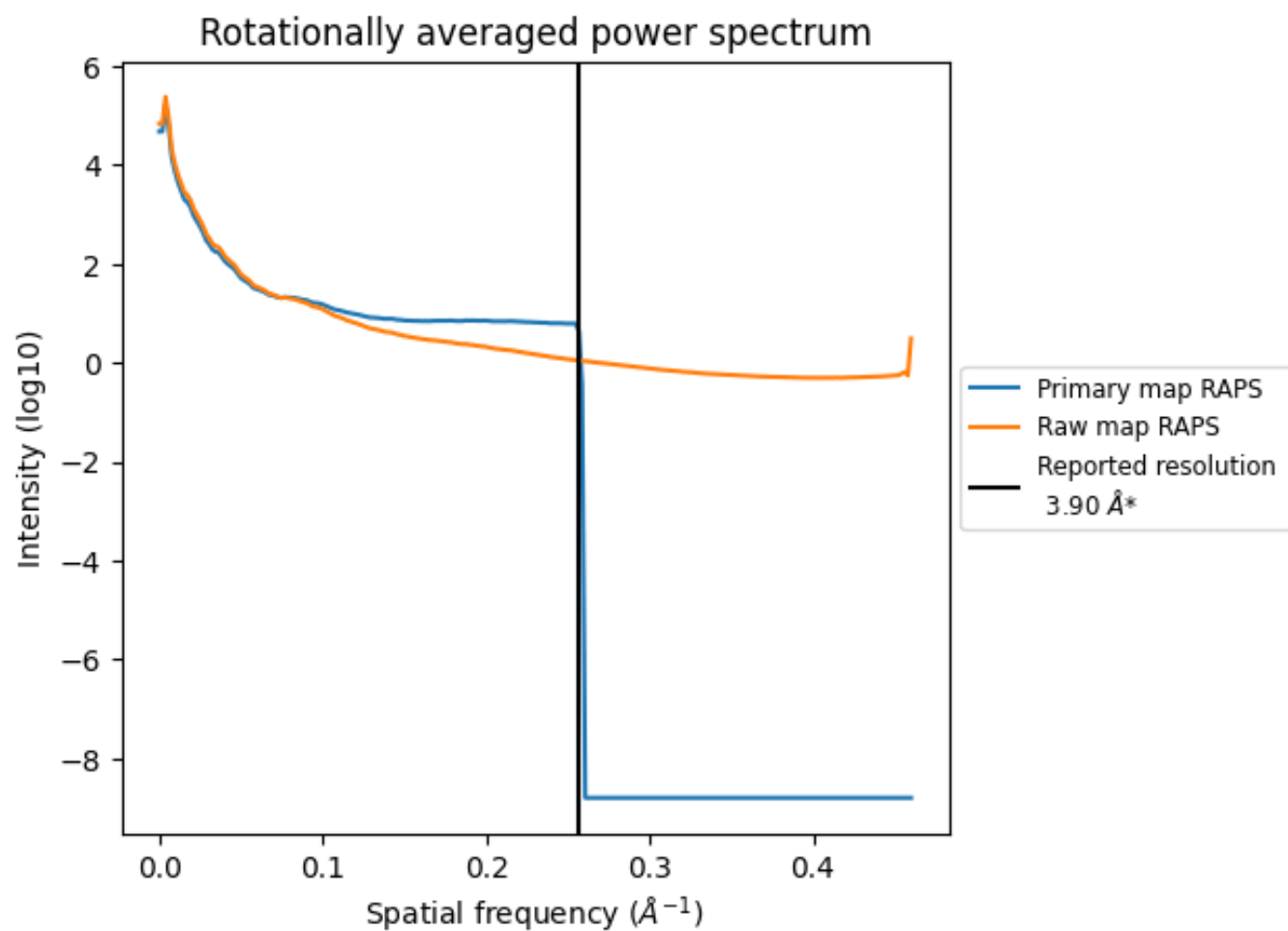
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1243 nm³; this corresponds to an approximate mass of 1123 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

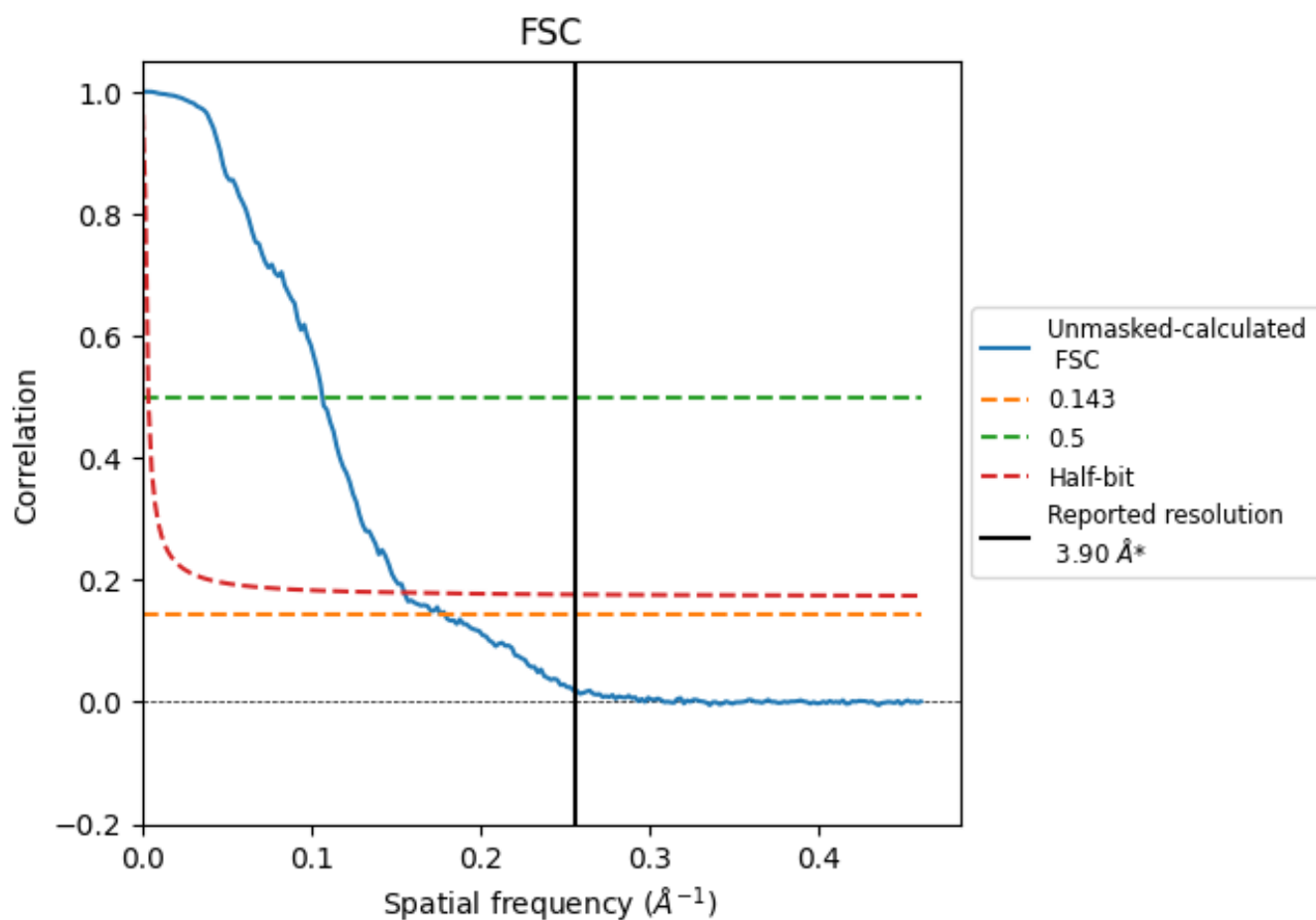


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

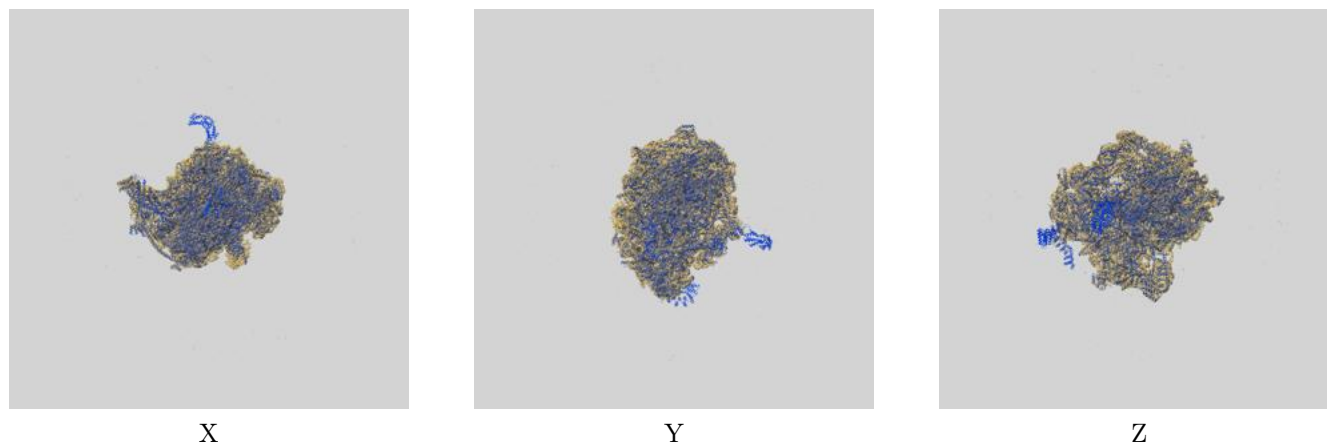
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.59	9.38	6.45

*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 5.59 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

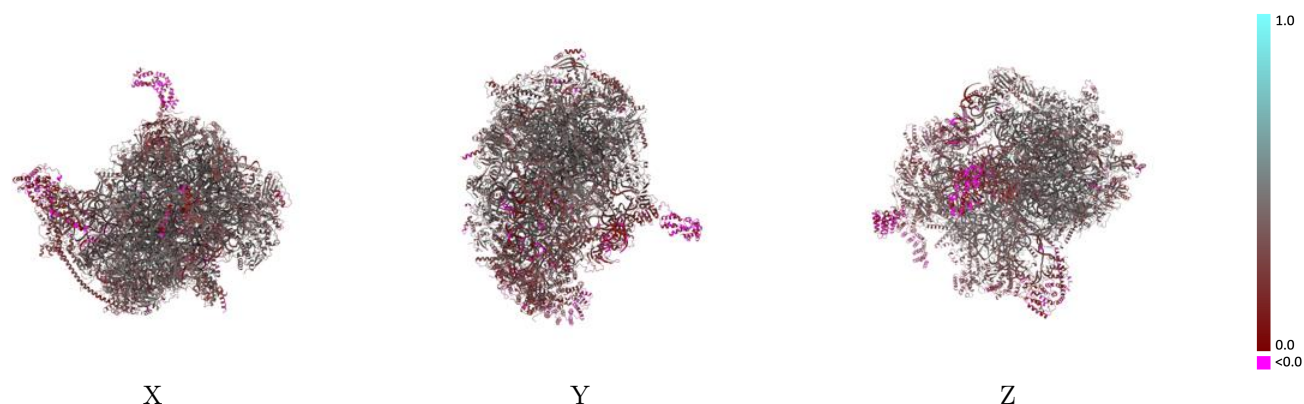
This section contains information regarding the fit between EMDB map EMD-12569 and PDB model 7NSJ. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



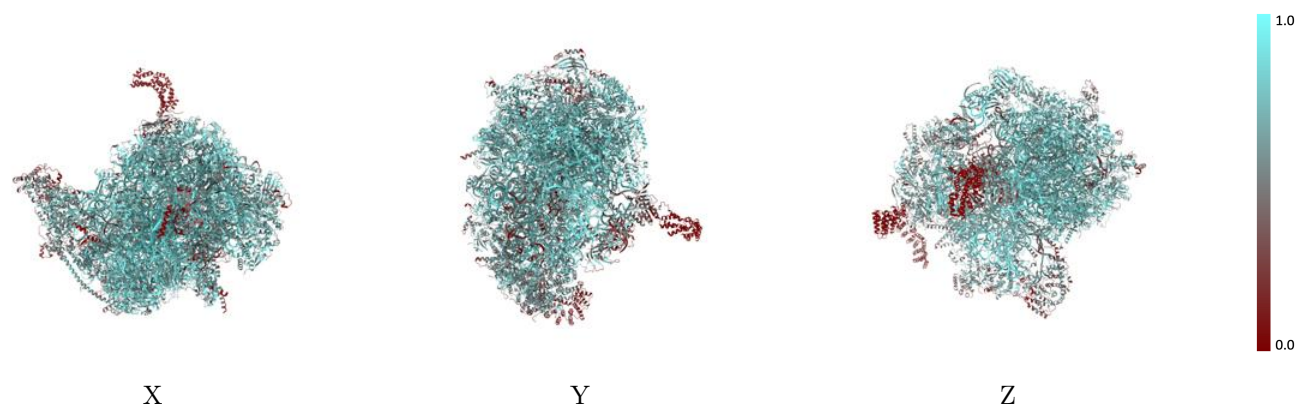
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



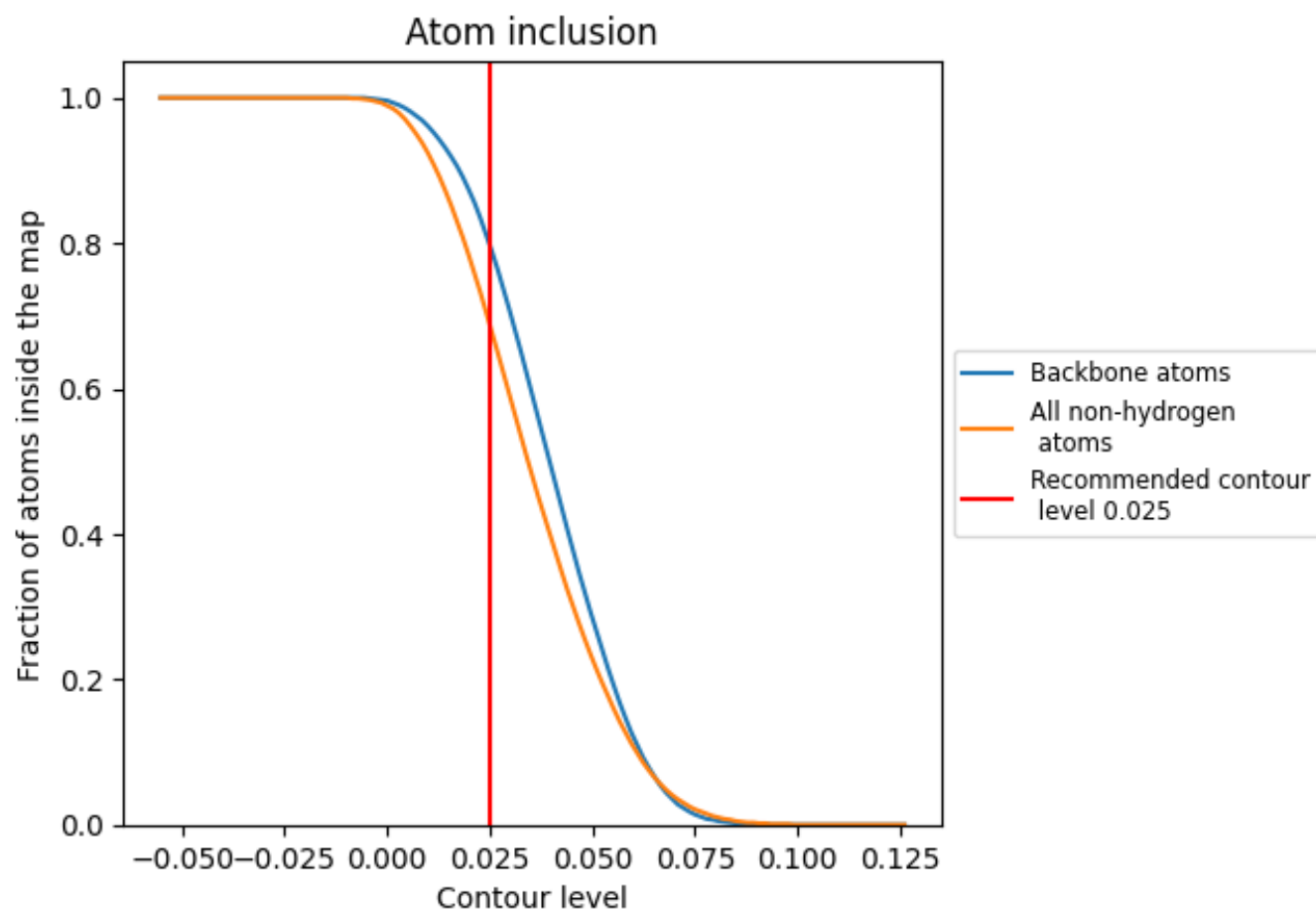
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6890	 0.3450
AA	 0.8720	 0.3700
AB	 0.6740	 0.3490
AC	 0.5700	 0.3490
AE	 0.5580	 0.3480
AF	 0.6910	 0.3910
AG	 0.5900	 0.3050
AI	 0.5980	 0.3020
AJ	 0.5890	 0.3180
AK	 0.6920	 0.3760
AL	 0.6560	 0.3840
AN	 0.6670	 0.3370
AO	 0.6170	 0.3420
AP	 0.5960	 0.2780
AQ	 0.6780	 0.3780
AR	 0.6750	 0.3800
AU	 0.6920	 0.3870
AV	 0.5960	 0.2780
AX	 0.6920	 0.3360
AY	 0.3010	 0.0800
AZ	 0.6330	 0.2350
Aa	 0.4910	 0.2570
Ab	 0.5430	 0.2920
Ac	 0.6630	 0.3500
Ad	 0.6400	 0.2650
Ae	 0.4210	 0.1380
Af	 0.6030	 0.3480
Ag	 0.5990	 0.2610
Ah	 0.4850	 0.2420
Ai	 0.5760	 0.3020
Aj	 0.5250	 0.2310
Ak	 0.5650	 0.2670
Am	 0.5710	 0.3140
An	 0.6590	 0.3810
Ao	 0.1080	 0.1160



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Chain	Atom inclusion	Q-score
Ap	 0.5980	 0.2810
B0	 0.8010	 0.4490
B1	 0.6800	 0.3780
B2	 0.7470	 0.3850
B3	 0.7580	 0.4190
B4	 0.6790	 0.3270
B5	 0.7430	 0.4090
B6	 0.6030	 0.3360
B7	 0.7940	 0.4530
B8	 0.7570	 0.4400
B9	 0.8070	 0.4330
BA	 0.8720	 0.4050
BB	 0.7130	 0.2380
BD	 0.7530	 0.4320
BE	 0.7400	 0.4130
BF	 0.7290	 0.4150
BI	 0.6210	 0.3400
BJ	 0.3270	 0.2160
BK	 0.2280	 0.1670
BN	 0.7520	 0.4200
BO	 0.7150	 0.4180
BP	 0.7570	 0.4140
BQ	 0.7290	 0.4130
BR	 0.7520	 0.4250
BS	 0.7430	 0.3870
BT	 0.7060	 0.3910
BU	 0.7200	 0.4140
BV	 0.7190	 0.4110
BW	 0.7250	 0.4400
BX	 0.6990	 0.3970
BY	 0.5530	 0.3520
Ba	 0.7680	 0.3960
Bb	 0.7550	 0.3640
Bc	 0.6910	 0.3480
Bd	 0.5480	 0.2540
Be	 0.6650	 0.3550
Bf	 0.6670	 0.3660
Bg	 0.7490	 0.4200
Bh	 0.6990	 0.3630
Bi	 0.4960	 0.2980
Bj	 0.5420	 0.1900
Bk	 0.5420	 0.2950

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Chain	Atom inclusion	Q-score
Bl	 0.7830	 0.4140
Bm	 0.3810	 0.3000
Bn	 0.7520	 0.4350
Bo	 0.7320	 0.3810
Bp	 0.3740	 0.2330
Bq	 0.3100	 0.2450
Bt	 0.7880	 0.4190
Bu	 0.5900	 0.3200
Bv	 0.6160	 0.3020
Bw	 0.7520	 0.3930
Bx	 0.7190	 0.3730
CL	 0.0000	 0.0240
DL	 0.0000	 0.0300
EL	 0.0000	 0.0390
FL	 0.0050	 0.0480
GL	 0.0000	 0.0060
HL	 0.0000	 0.0140