



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 08:39 am BST

PDB ID : 7NSI / pdb_00007nsi
EMDB ID : EMD-12568
Title : 55S mammalian mitochondrial ribosome with mtRRF (pre) and tRNA(P/E)
Authors : Kummer, E.; Schubert, K.; Ban, N.
Deposited on : 2021-03-07
Resolution : 4.60 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:

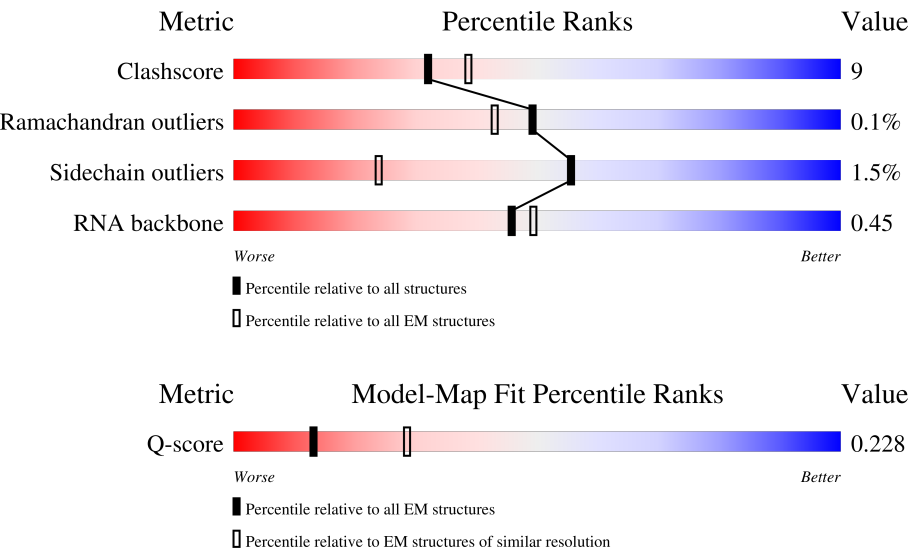
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 4.60 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	2407 (4.10 - 5.10)

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

Mol	Chain	Length	Quality of chain
1	B0	148	5% 61% 13% 26%
2	B1	256	29% 86% 9% 5%
3	B2	252	10% 60% 12% 29%

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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	BG	257	
14	BI	268	
15	BJ	262	
16	BK	192	
17	BN	178	
18	BO	145	
19	BP	296	
20	BQ	251	
21	BR	169	
22	BS	180	
23	BT	292	
24	BU	149	
25	BV	209	
26	BW	210	
27	BX	150	
28	BY	216	

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Mol	Chain	Length	Quality of chain
29	Ba	423	
30	Bb	380	
31	Bc	334	
32	Bd	206	
33	Be	135	
34	Bf	142	
35	Bg	159	
36	B8	188	
37	Bh	332	
38	Bi	306	
39	Bj	279	
40	Bk	269	
41	Bl	166	
42	Bm	198	
43	Bn	128	
44	Bo	124	
45	Bp	112	
46	Bq	138	
47	Bt	102	
48	Bu	205	
49	Bv	222	
50	Bw	433	
51	Bx	196	
52	AA	962	
53	B9	100	

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Mol	Chain	Length	Quality of chain
54	AV	71	
55	AX	5	
56	BA	1571	
57	AB	289	
58	AC	167	
59	AE	430	
60	AF	276	
61	AG	242	
62	AI	397	
63	AJ	200	
64	AK	196	
65	AL	139	
66	AN	128	
67	AO	239	
68	AP	135	
69	AQ	130	
70	AR	143	
71	AU	87	
72	AZ	18	
73	Aa	382	
74	Ab	190	
75	Ac	173	
76	Ad	205	
77	Ae	455	
78	Af	188	

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Mol	Chain	Length	Quality of chain
79	Ag	410	
80	Ah	387	
81	Ai	106	
82	Aj	218	
83	Ak	325	
84	Am	118	
85	An	199	
86	Ao	690	
87	Ap	258	
88	CL	198	
88	DL	198	
88	EL	198	
88	FL	198	
88	GL	198	
88	HL	198	

2 Entry composition

There are 94 unique types of molecules in this entry. The entry contains 174700 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 39S ribosomal protein L27, mitochondrial.

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 39S ribosomal protein L28, mitochondrial.

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 39S ribosomal protein L30, mitochondrial.

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 Mitochondrial ribosomal protein L55.

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 39S ribosomal protein L33, mitochondrial.

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 are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	72	C	A	conflict	GB 45826169
BB	73	A	C	conflict	GB 45826169

- Molecule 9 is a protein called 39S ribosomal protein L34, mitochondrial.

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 Ribosomal_L2_C domain-containing protein.

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 Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BG	193	Total	C	N	O	S	0	0
			1501	930	269	294	8		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BG	6	MET	-	initiating methionine	UNP Q96E11
BG	7	HIS	-	expression tag	UNP Q96E11
BG	8	HIS	-	expression tag	UNP Q96E11
BG	9	HIS	-	expression tag	UNP Q96E11
BG	10	HIS	-	expression tag	UNP Q96E11
BG	11	HIS	-	expression tag	UNP Q96E11
BG	12	HIS	-	expression tag	UNP Q96E11
BG	13	GLU	-	expression tag	UNP Q96E11
BG	14	ASN	-	expression tag	UNP Q96E11
BG	15	LEU	-	expression tag	UNP Q96E11
BG	16	TYR	-	expression tag	UNP Q96E11
BG	17	PHE	-	expression tag	UNP Q96E11
BG	18	GLN	-	expression tag	UNP Q96E11
BG	19	SER	-	expression tag	UNP Q96E11
BG	20	GLY	-	expression tag	UNP Q96E11
BG	21	GLY	-	expression tag	UNP Q96E11
BG	22	SER	-	expression tag	UNP Q96E11
BG	23	GLY	-	expression tag	UNP Q96E11
BG	24	SER	-	expression tag	UNP Q96E11
BG	25	GLY	-	expression tag	UNP Q96E11

- Molecule 14 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L10, mitochondrial isoform a.

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

- Molecule 16 is a protein called 39S ribosomal protein L11, mitochondrial isoform a.

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

- Molecule 17 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 18 is a protein called uL14m.

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

- Molecule 19 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 21 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L18, mitochondrial isoform 1.

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

- Molecule 23 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L20, mitochondrial isoform 1.

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

- Molecule 25 is a protein called 39S ribosomal protein L21, mitochondrial isoform d.

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

- Molecule 26 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 28 is a protein called 39S ribosomal protein L24, mitochondrial isoform X1.

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

- Molecule 29 is a protein called 39S ribosomal protein L37, mitochondrial.

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

- Molecule 30 is a protein called 39S ribosomal protein L38, mitochondrial.

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

- Molecule 31 is a protein called TGS domain-containing protein.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bc	328	THR	SER	conflict	UNP A0A4X1UDR3

- Molecule 32 is a protein called Mitochondrial ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bd	138	Total	C	N	O	S	0	0
			1158	729	211	217	1		

- Molecule 33 is a protein called Mitochondrial ribosomal protein L41.

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

- Molecule 34 is a protein called mL42.

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

- Molecule 35 is a protein called 39S ribosomal protein L43, mitochondrial isoform X2.

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

- Molecule 36 is a protein called 39S ribosomal protein L35, mitochondrial.

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 39S ribosomal protein L44, mitochondrial.

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

- Molecule 38 is a protein called Mitochondrial ribosomal protein L45.

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

- Molecule 39 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bj	217	Total	C	N	O	S	0	0
			1775	1137	311	321	6		

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bk	155	Total	C	N	O	S	0	0
			1246	796	214	231	5		

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	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 A0A4X1V1G7

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 45 is a protein called mL53.

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

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 47 is a protein called Mitochondrial ribosomal protein L57.

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

- Molecule 48 is a protein called Mitochondrial ribosomal protein L58.

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

- Molecule 49 is a protein called 39S ribosomal protein L59, mitochondrial.

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

- Molecule 50 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 51 is a protein called Mitochondrial ribosomal protein S18A.

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

- Molecule 52 is a RNA chain called 12S rRNA.

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

- Molecule 53 is a protein called Ribosomal protein.

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

- Molecule 54 is a RNA chain called tRNA (P/E).

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

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AX	5	Total	C	N	O	P	0	0
			100	45	10	40	5		

- Molecule 56 is a RNA chain called 16S rRNA.

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

- Molecule 57 is a protein called 28S ribosomal protein S2, mitochondrial.

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

- Molecule 58 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 59 is a protein called 28S ribosomal protein S5, mitochondrial isoform X2.

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

- Molecule 60 is a protein called Mitochondrial ribosomal protein S6.

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

- Molecule 61 is a protein called 28S ribosomal protein S7, mitochondrial.

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

- Molecule 62 is a protein called 28S ribosomal protein S9, mitochondrial.

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

- Molecule 63 is a protein called 28S ribosomal protein S10, mitochondrial.

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

- Molecule 64 is a protein called Mitochondrial ribosomal protein S11.

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

- Molecule 65 is a protein called Mitoribosomal protein us12m, mrps12.

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

- Molecule 66 is a protein called 28S ribosomal protein S14, mitochondrial.

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

- Molecule 67 is a protein called 28S ribosomal protein S15, mitochondrial.

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

- Molecule 68 is a protein called 28S ribosomal protein S16, mitochondrial.

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

- Molecule 69 is a protein called uS17m.

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

- Molecule 70 is a protein called 28S ribosomal protein S18c, mitochondrial isoform 1.

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

- Molecule 71 is a protein called 28S ribosomal protein S21, mitochondrial.

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

- Molecule 72 is a protein called unknown.

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

- Molecule 73 is a protein called Mitochondrial ribosomal protein S22.

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

- Molecule 74 is a protein called Mitochondrial ribosomal protein S23.

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

- Molecule 75 is a protein called Interferon alpha-inducible protein 6.

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

- Molecule 76 is a protein called 28S ribosomal protein S26, mitochondrial.

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

- Molecule 77 is a protein called Mitochondrial ribosomal protein S27.

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

- Molecule 78 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 79 is a protein called Death associated protein 3.

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

- Molecule 80 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	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 81 is a protein called Mitochondrial ribosomal protein S33.

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

- Molecule 82 is a protein called Mitochondrial ribosomal protein S34.

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

- Molecule 83 is a protein called 28S ribosomal protein S35, mitochondrial isoform 1.

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

- Molecule 84 is a protein called Coiled-coil-helix-coiled-coil-helix domain containing 1.

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

- Molecule 85 is a protein called Aurora kinase A interacting protein 1.

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

- Molecule 86 is a protein called Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,mS39,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3.

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

- Molecule 87 is a protein called 28S ribosomal protein S18b, mitochondrial.

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

- Molecule 88 is a protein called Mitochondrial ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	CL	45	Total	C	N	O		0	0
			317	203	52	62			
88	DL	27	Total	C	N	O		0	0
			213	137	33	43			
88	EL	28	Total	C	N	O		0	0
			222	143	35	44			
88	FL	27	Total	C	N	O		0	0
			213	137	33	43			
88	GL	27	Total	C	N	O		0	0
			213	137	33	43			
88	HL	26	Total	C	N	O		0	0
			205	131	32	42			

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	B3	1	Total 1	Mg 1	0
89	BB	1	Total 1	Mg 1	0
89	BD	3	Total 3	Mg 3	0
89	BE	1	Total 1	Mg 1	0
89	BJ	1	Total 1	Mg 1	0
89	BP	2	Total 2	Mg 2	0
89	BQ	1	Total 1	Mg 1	0
89	Be	1	Total 1	Mg 1	0
89	Bl	1	Total 1	Mg 1	0
89	Bt	1	Total 1	Mg 1	0
89	AA	105	Total 105	Mg 105	0
89	AX	1	Total 1	Mg 1	0
89	BA	204	Total 204	Mg 204	0
89	AB	1	Total 1	Mg 1	0
89	Ag	1	Total 1	Mg 1	0
89	Am	1	Total 1	Mg 1	0
89	An	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

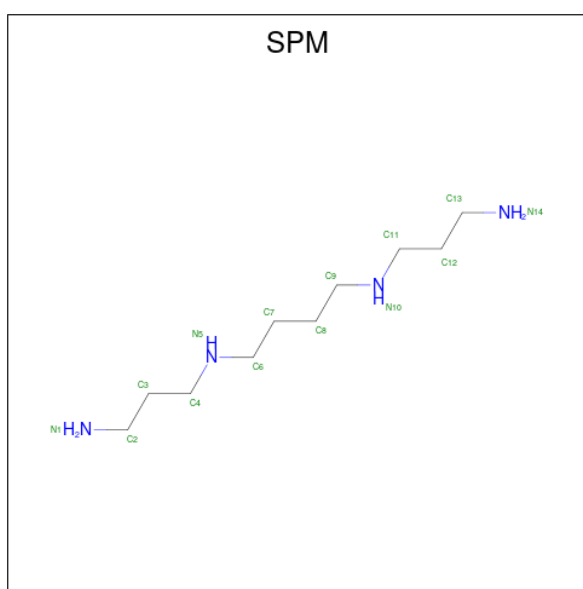
Mol	Chain	Residues	Atoms		AltConf
90	B5	1	Total 1	Zn 1	0
90	Bx	1	Total 1	Zn 1	0

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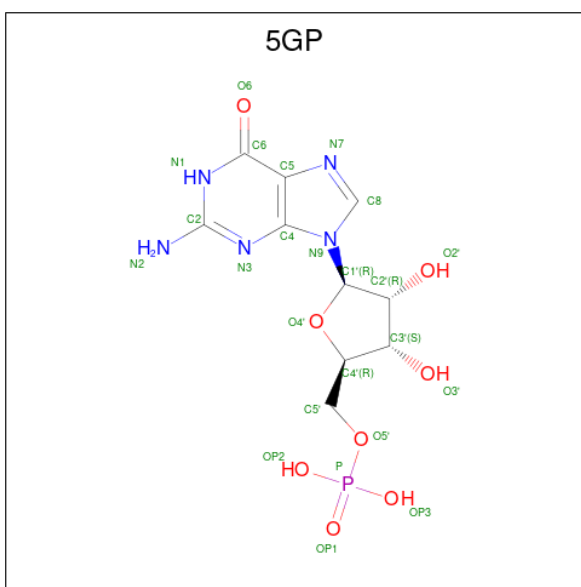
Mol	Chain	Residues	Atoms		AltConf
90	B9	1	Total	Zn	0
			1	1	
90	AR	1	Total	Zn	0
			1	1	
90	Ac	1	Total	Zn	0
			1	1	
90	Ap	1	Total	Zn	0
			1	1	

- Molecule 91 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



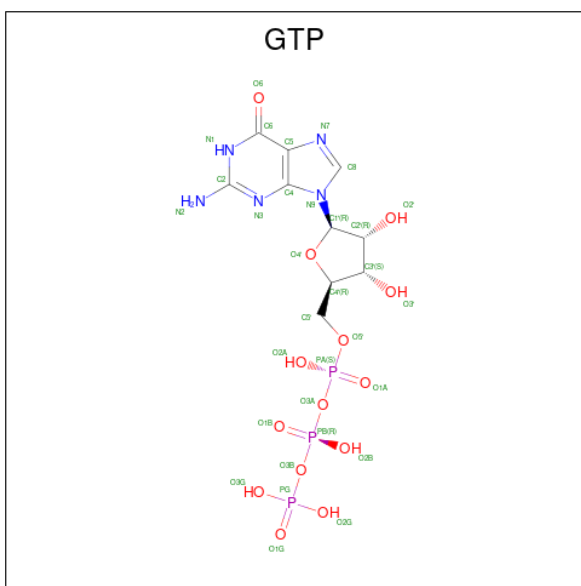
Mol	Chain	Residues	Atoms			AltConf
91	AA	1	Total	C	N	0
			14	10	4	
91	BA	1	Total	C	N	0
			14	10	4	
91	BA	1	Total	C	N	0
			14	10	4	

- Molecule 92 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



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

- Molecule 93 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

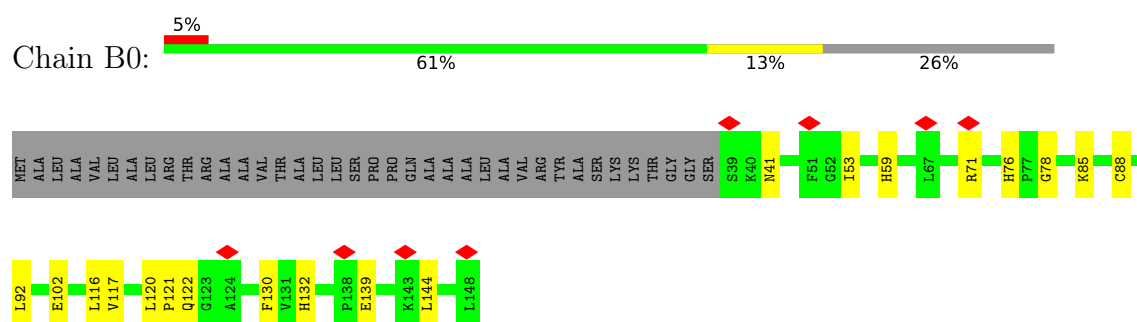
- Molecule 94 is water.

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

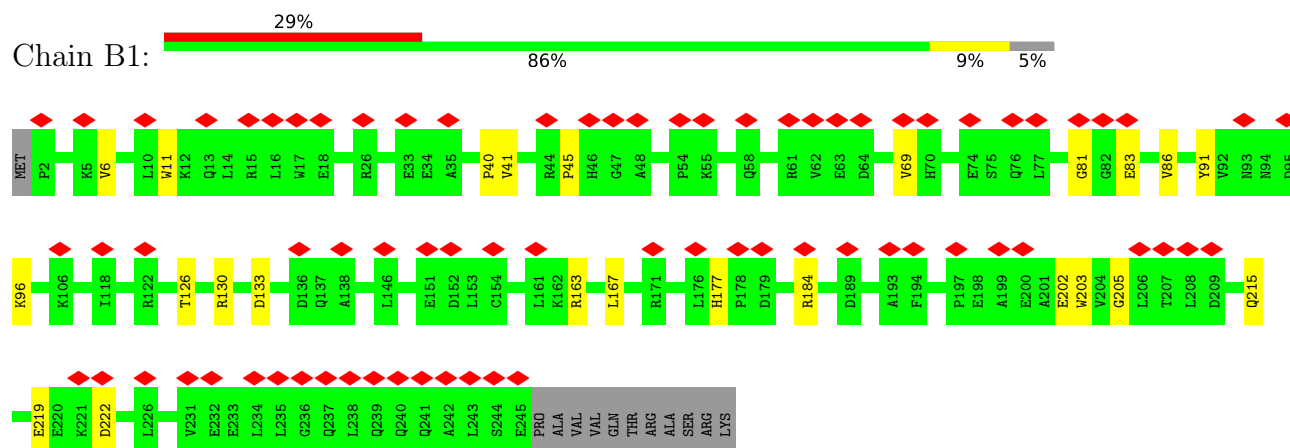
3 Residue-property plots

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

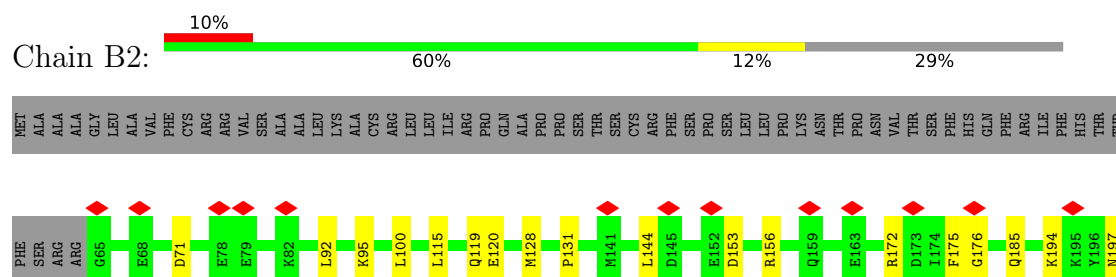
- Molecule 1: 39S ribosomal protein L27, mitochondrial

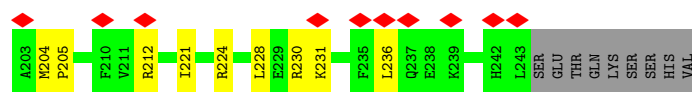


- Molecule 2: 39S ribosomal protein L28, mitochondrial

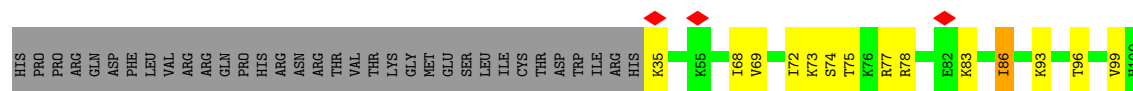


- Molecule 3: Mitochondrial ribosomal protein L47

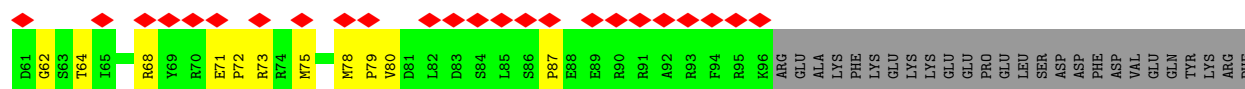
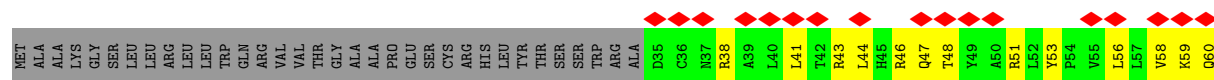
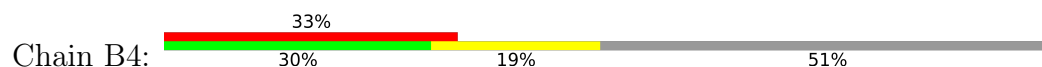




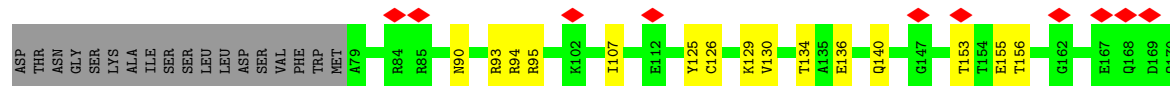
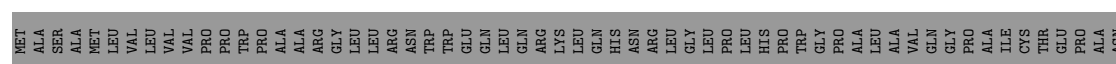
- Molecule 4: 39S ribosomal protein L30, mitochondrial



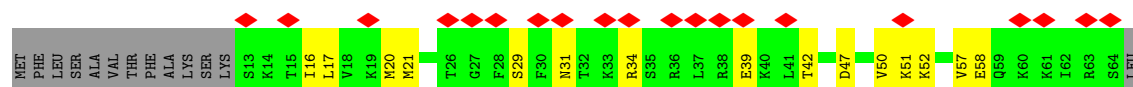
- Molecule 5: Mitochondrial ribosomal protein L55



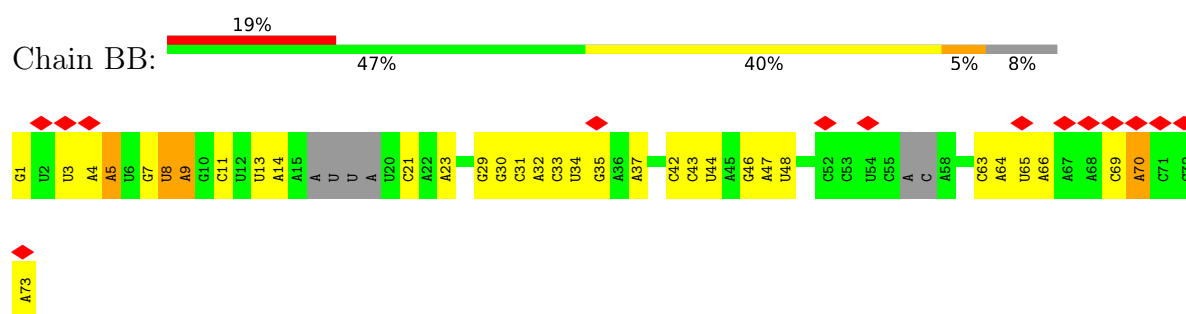
- Molecule 6: bL32m



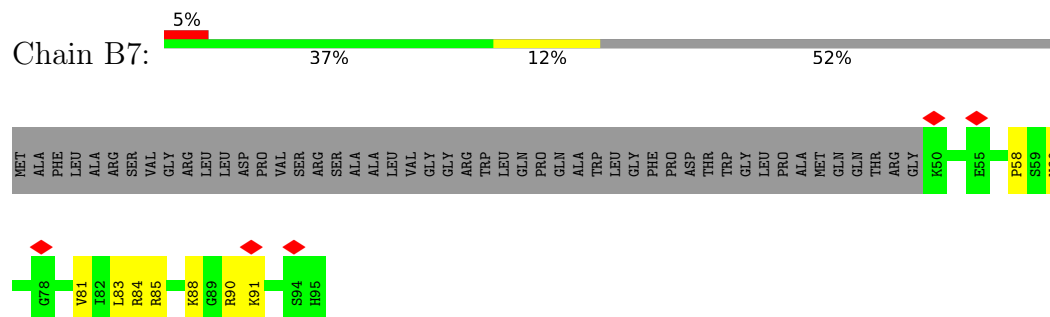
- Molecule 7: 39S ribosomal protein L33, mitochondrial



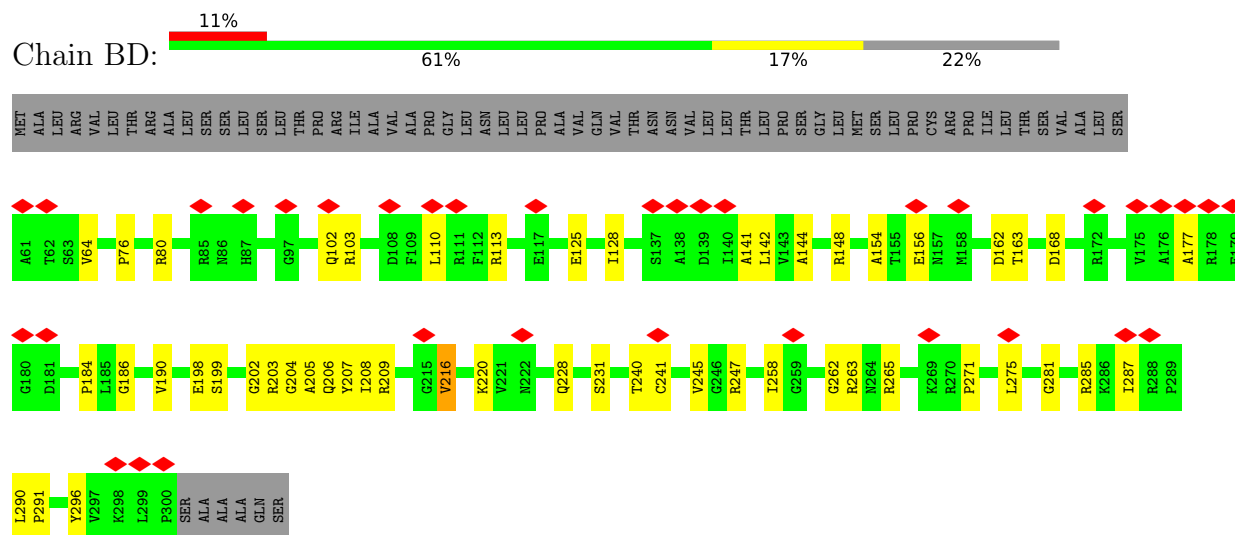
- Molecule 8: CP tRNA^{Phe}



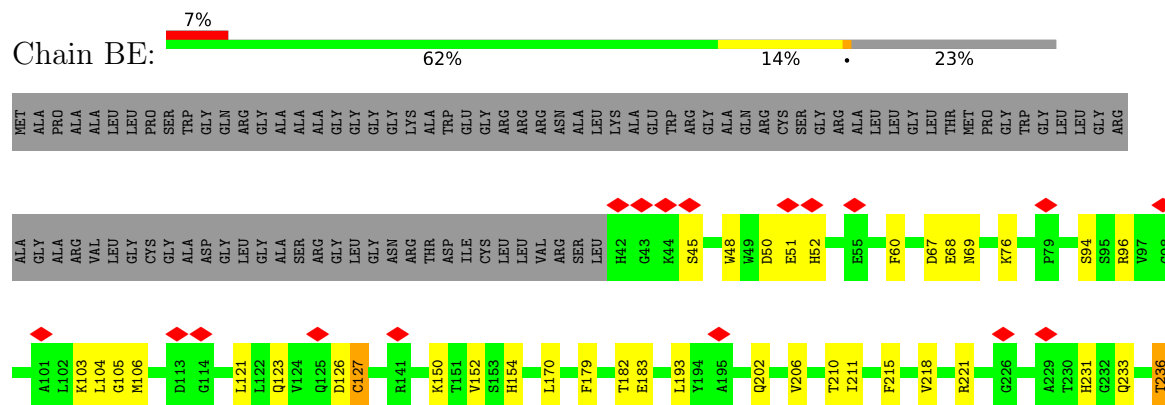
- Molecule 9: 39S ribosomal protein L34, mitochondrial



- Molecule 10: Ribosomal_L2_C domain-containing protein

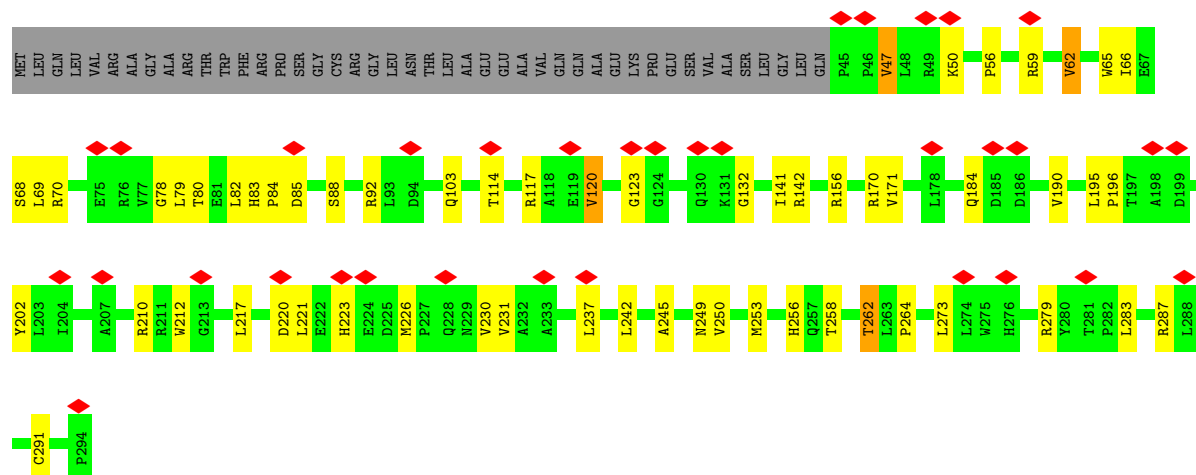


- Molecule 11: ICT1

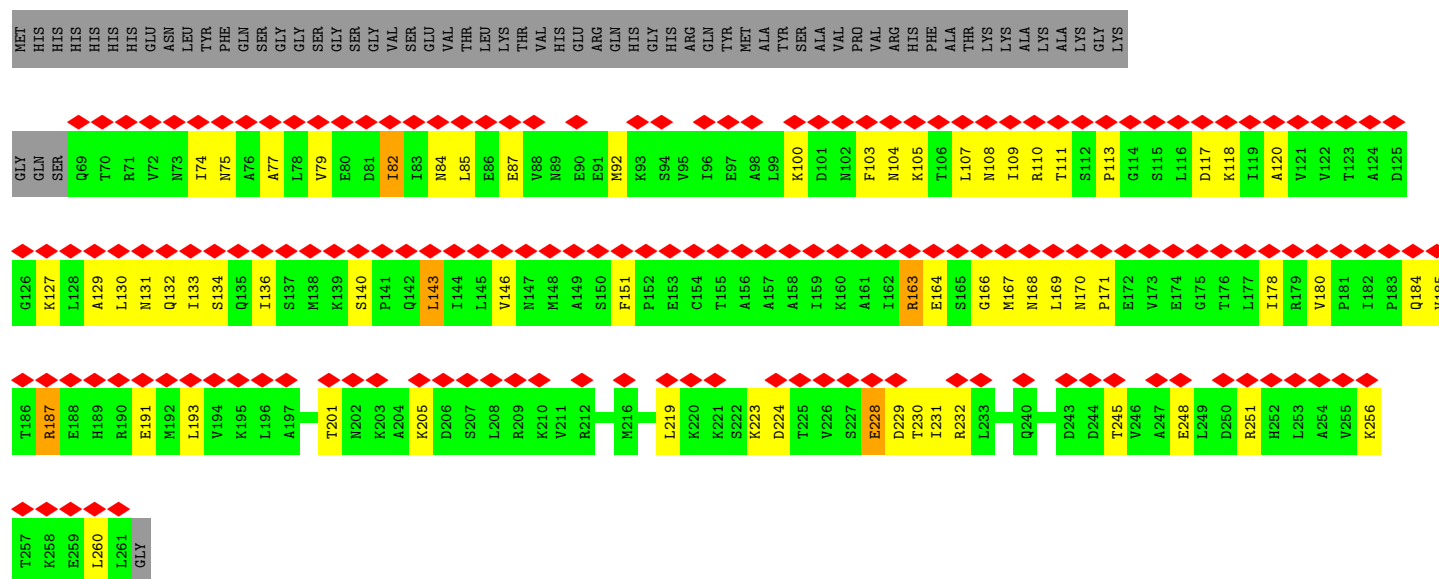




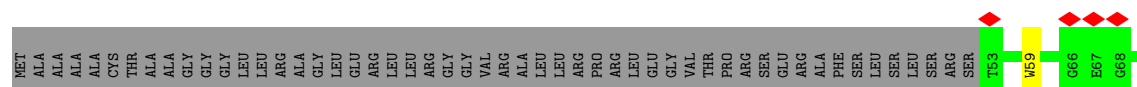
• Molecule 12: Mitochondrial ribosomal protein L4

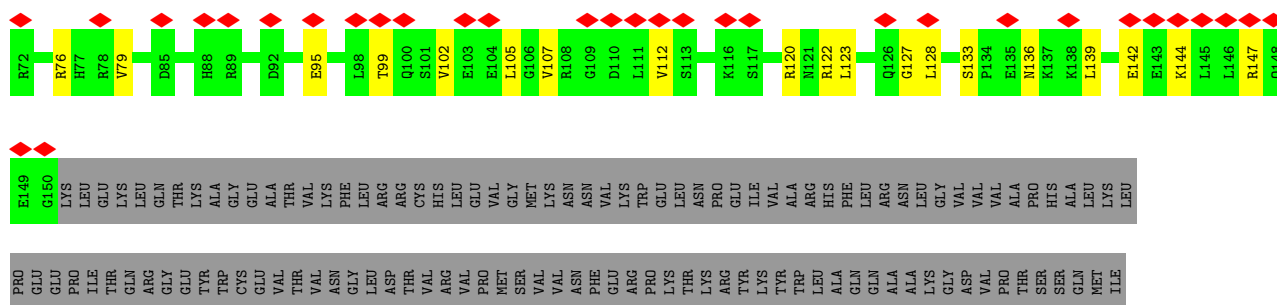


• Molecule 13: Ribosome-recycling factor, mitochondrial



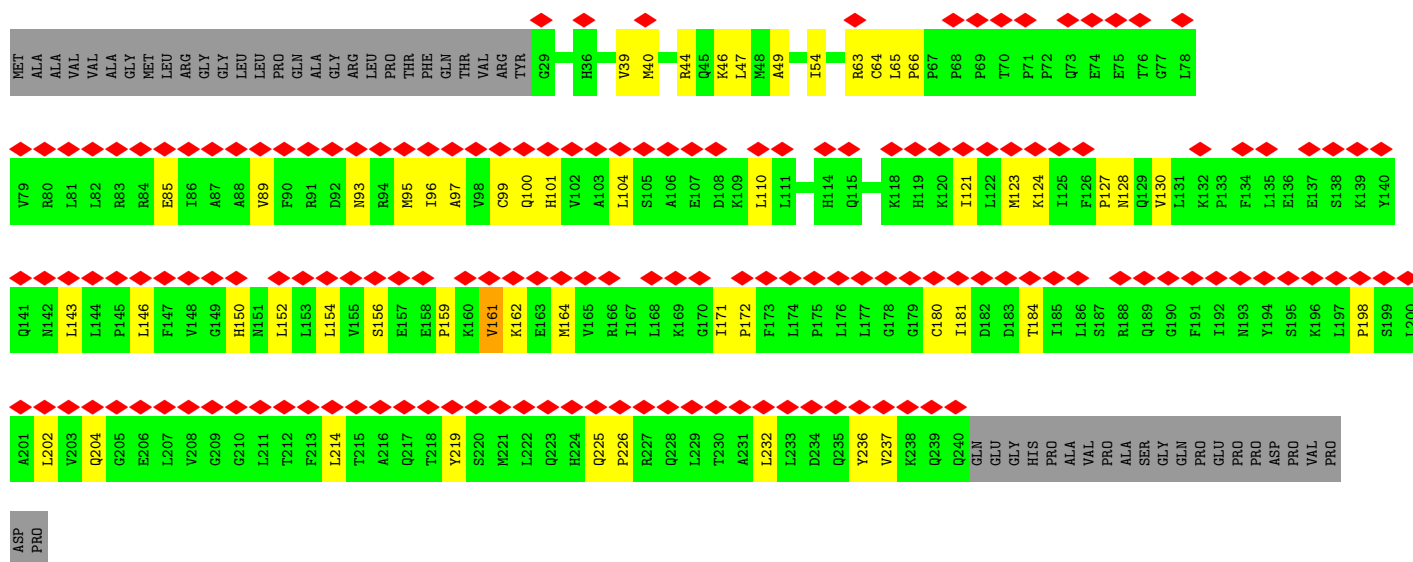
• Molecule 14: 39S ribosomal protein L9, mitochondrial





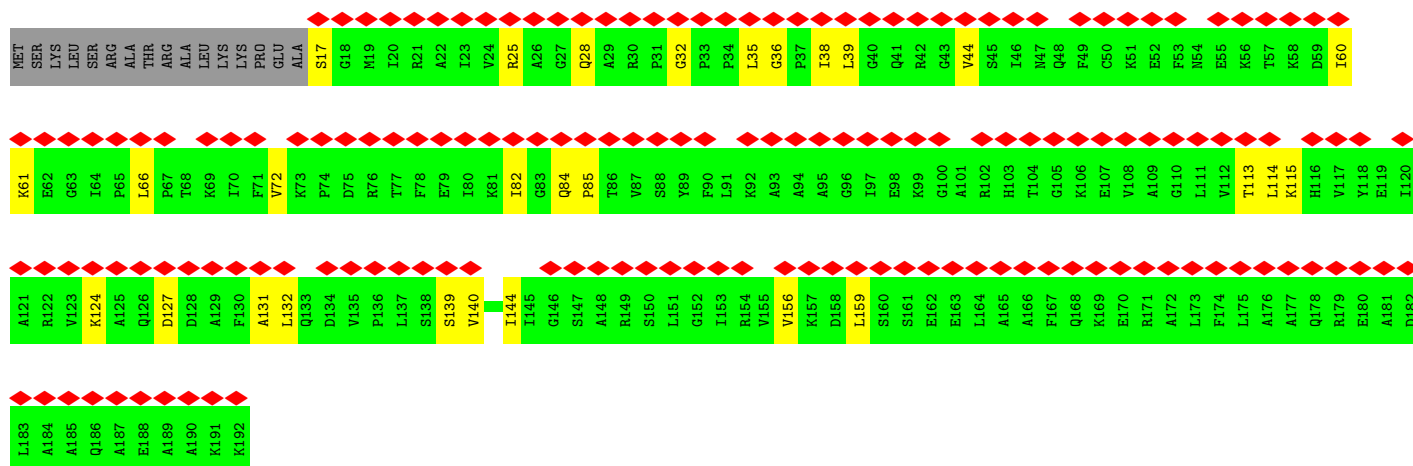
- Molecule 15: 39S ribosomal protein L10, mitochondrial isoform a

Chain BJ:

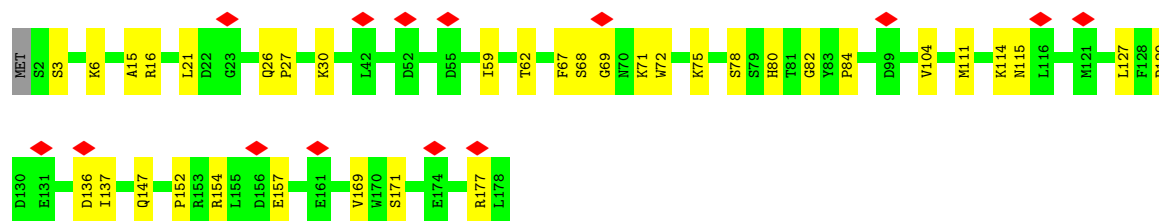
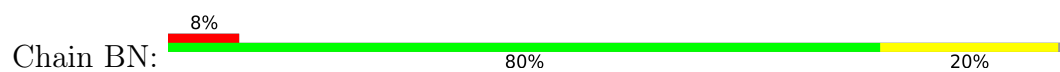


- Molecule 16: 39S ribosomal protein L11, mitochondrial isoform a

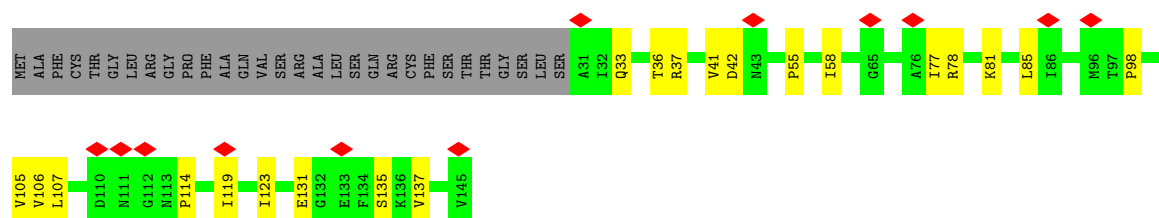
Chain BK:



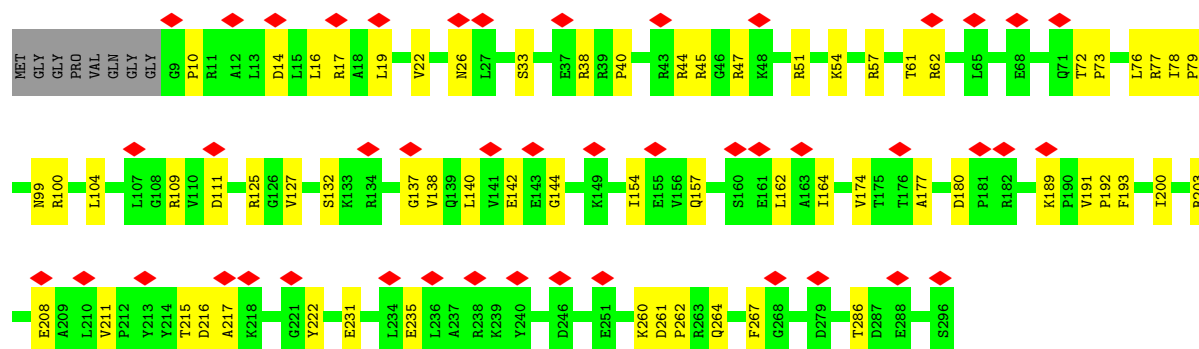
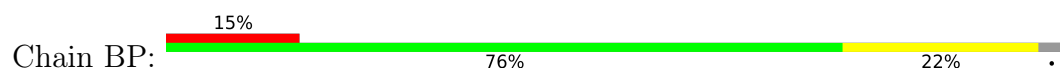
- Molecule 17: 39S ribosomal protein L13, mitochondrial



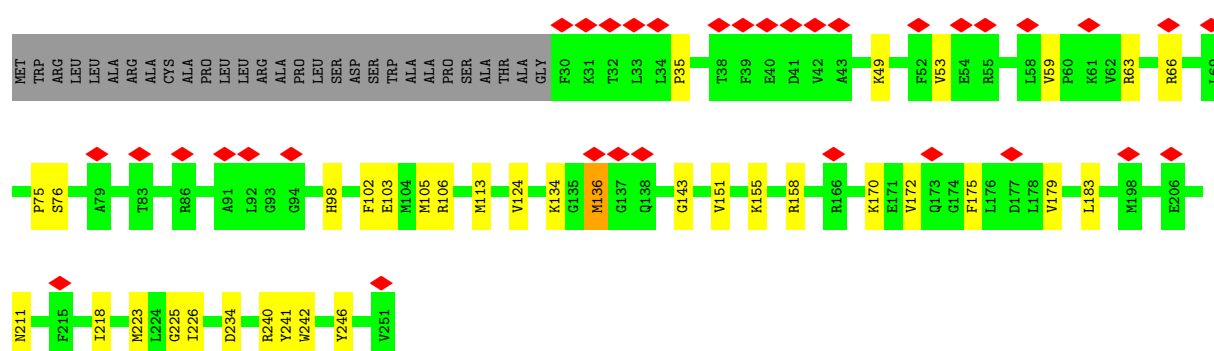
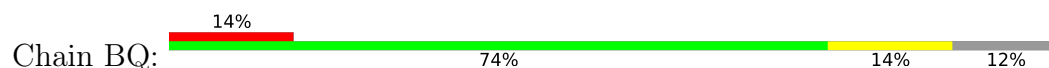
• Molecule 18: uL14m

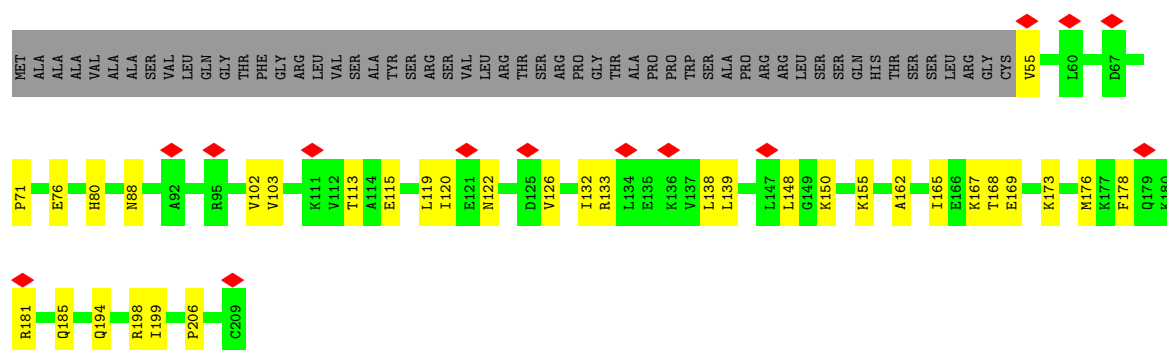


• Molecule 19: 39S ribosomal protein L15, mitochondrial

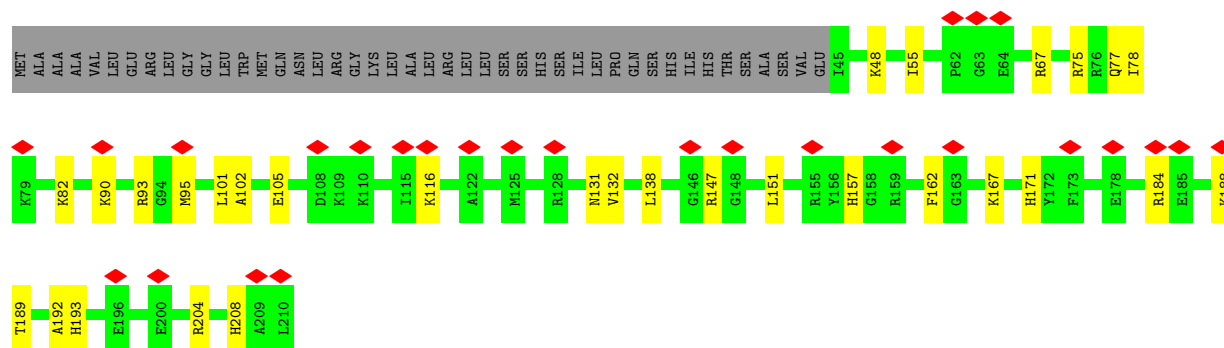


• Molecule 20: 39S ribosomal protein L16, mitochondrial

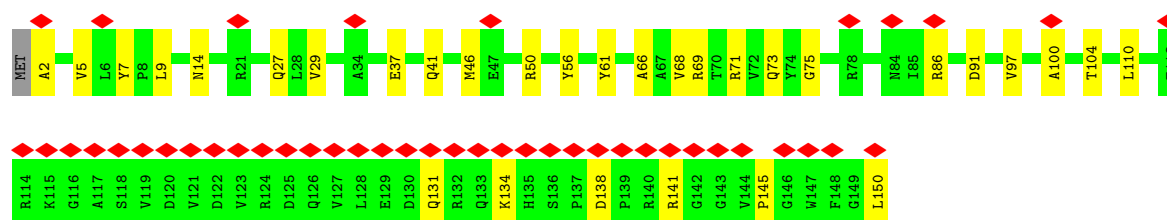
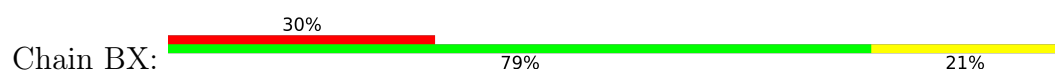




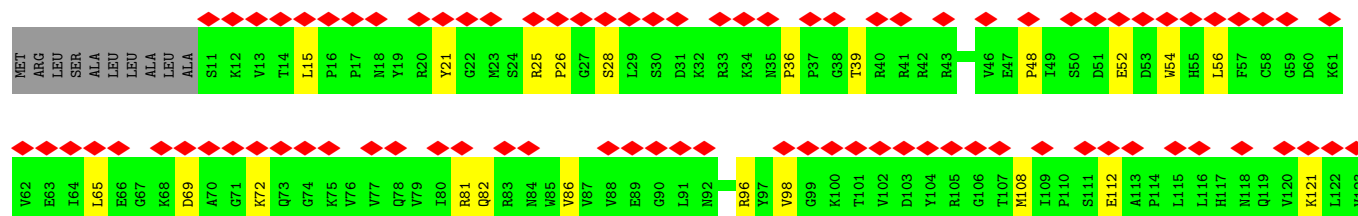
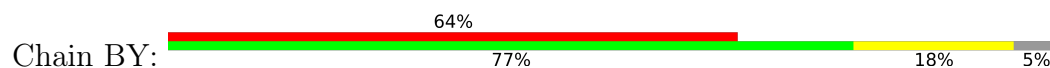
- Molecule 26: 39S ribosomal protein L22, mitochondrial

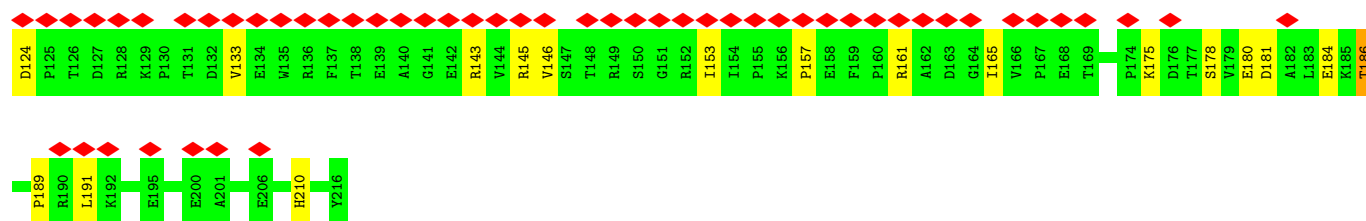


- Molecule 27: 39S ribosomal protein L23, mitochondrial

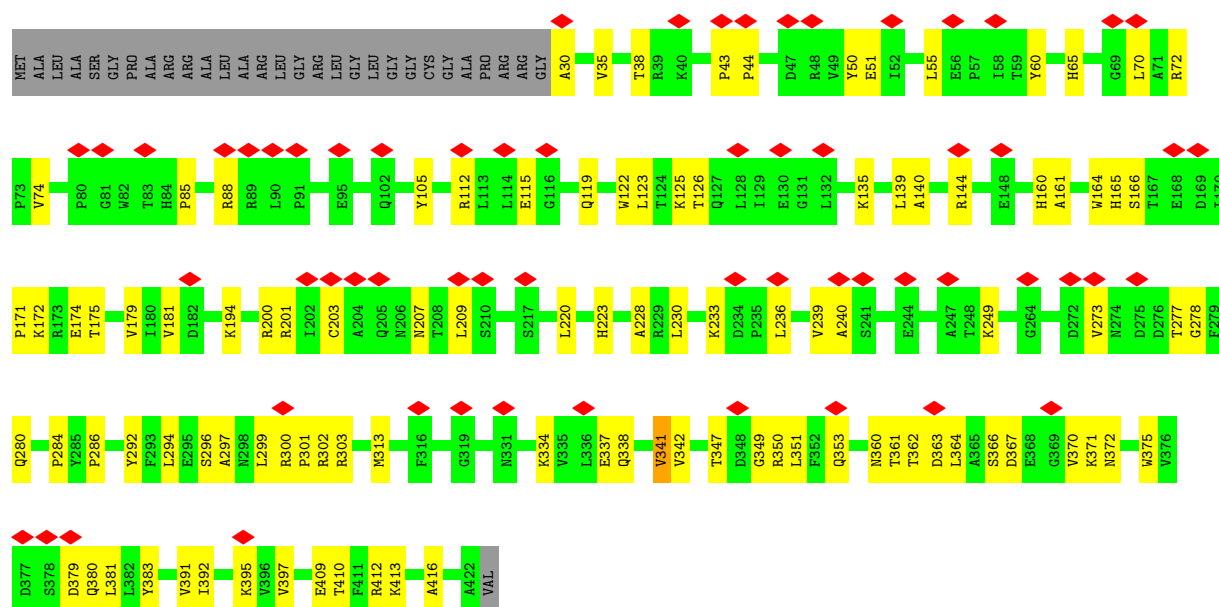


- Molecule 28: 39S ribosomal protein L24, mitochondrial isoform X1

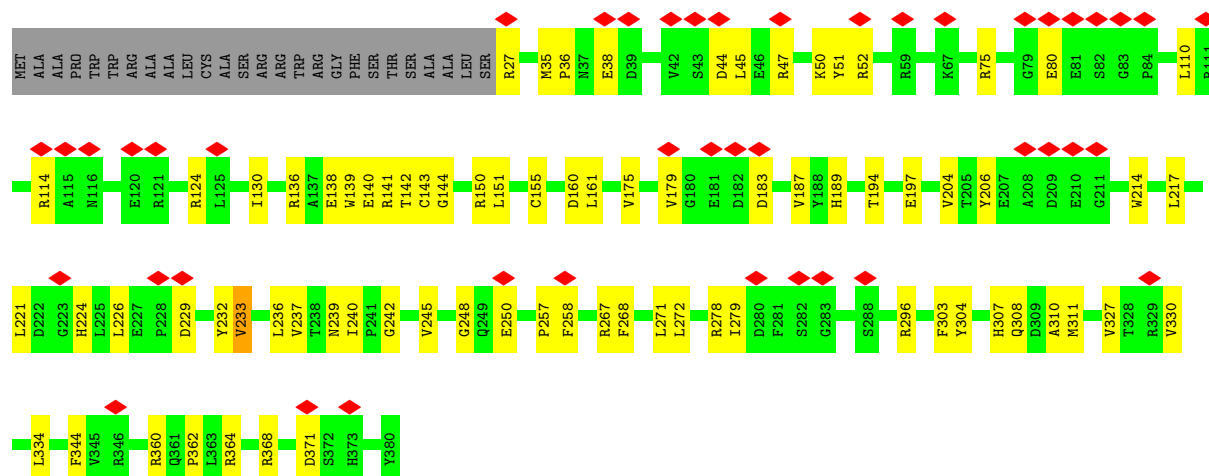
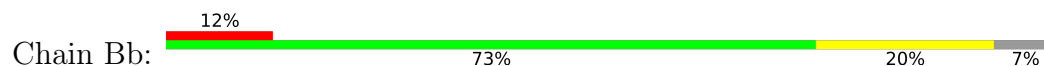




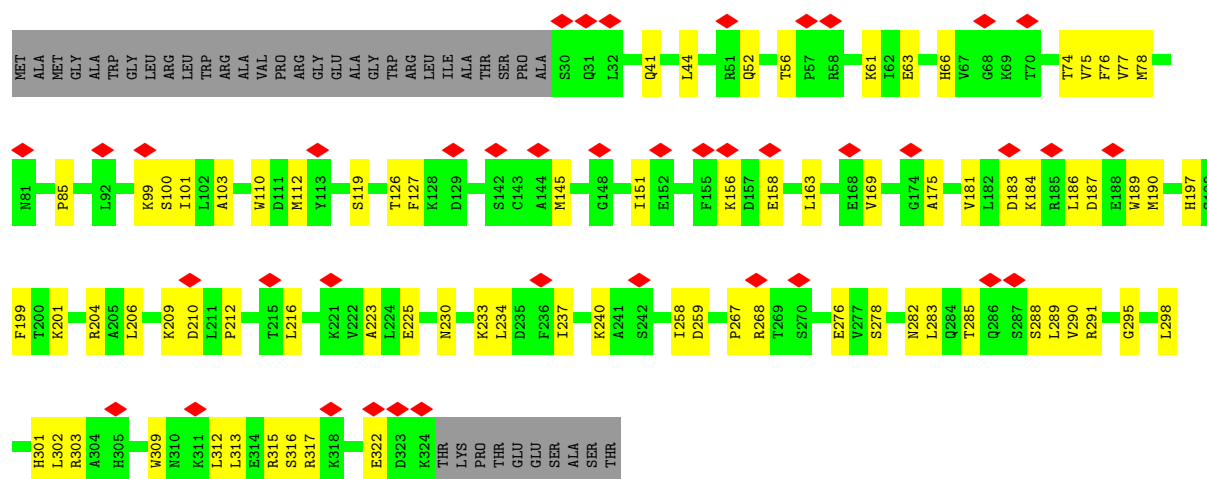
- Molecule 29: 39S ribosomal protein L37, mitochondrial



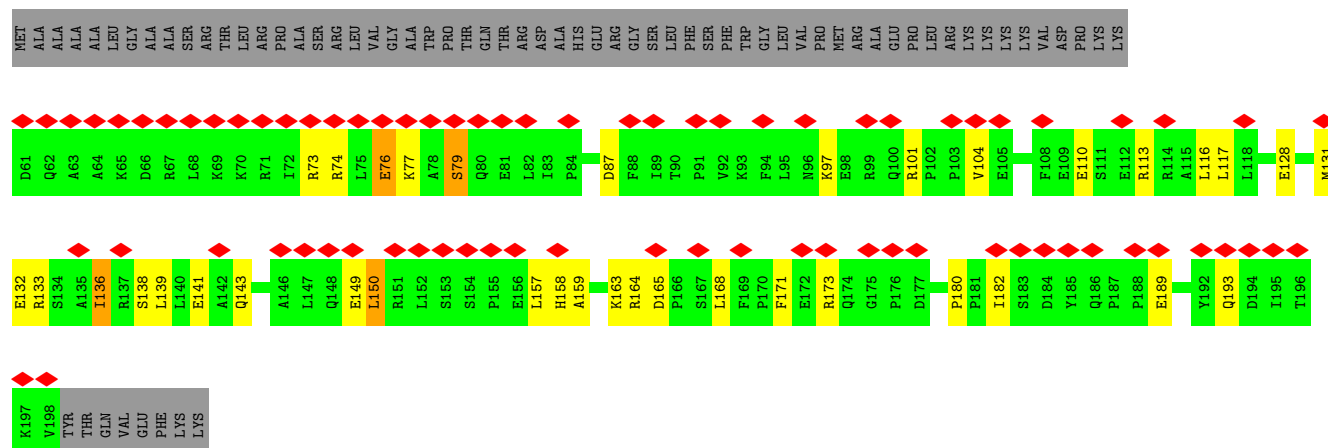
- Molecule 30: 39S ribosomal protein L38, mitochondrial



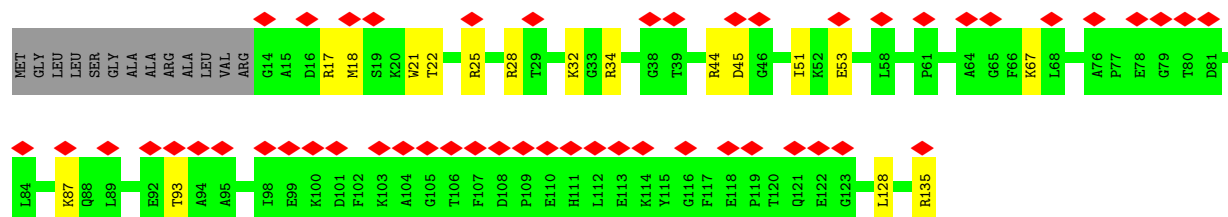
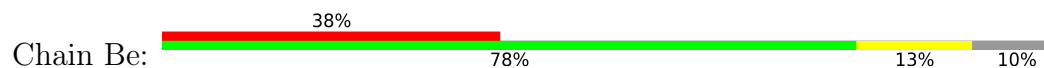
- Molecule 31: TGS domain-containing protein



• Molecule 32: Mitochondrial ribosomal protein L40

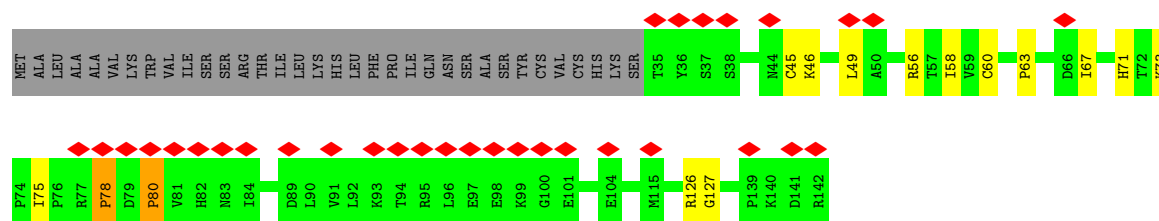


• Molecule 33: Mitochondrial ribosomal protein L41

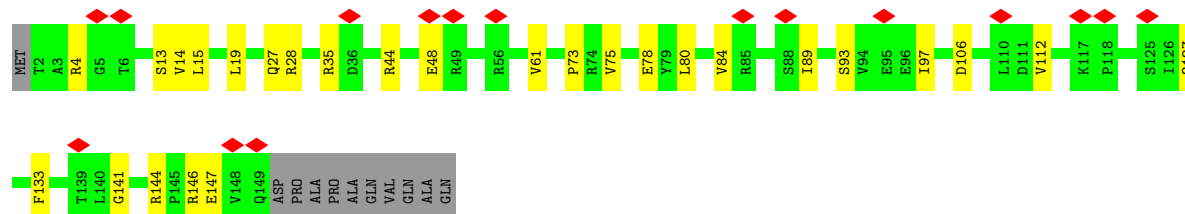
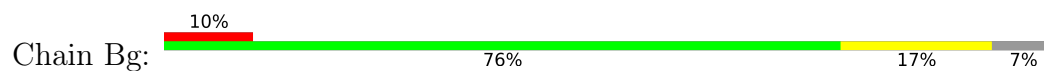


• Molecule 34: mL42

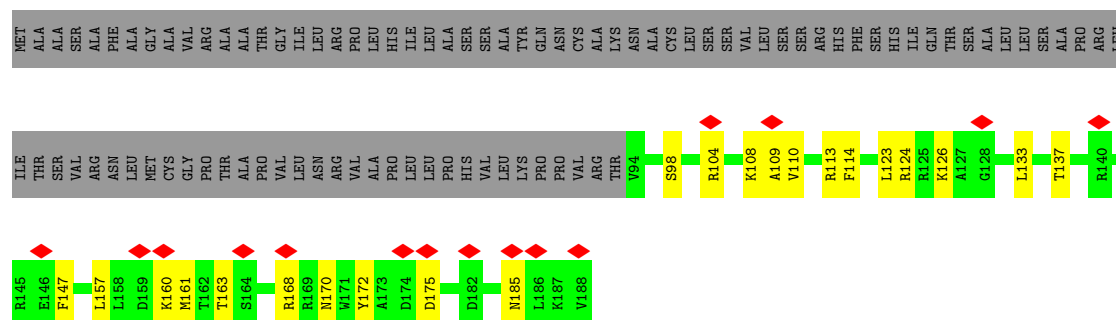
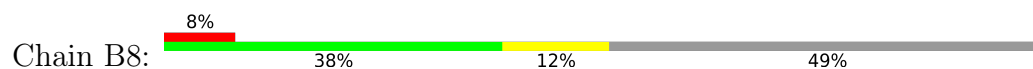




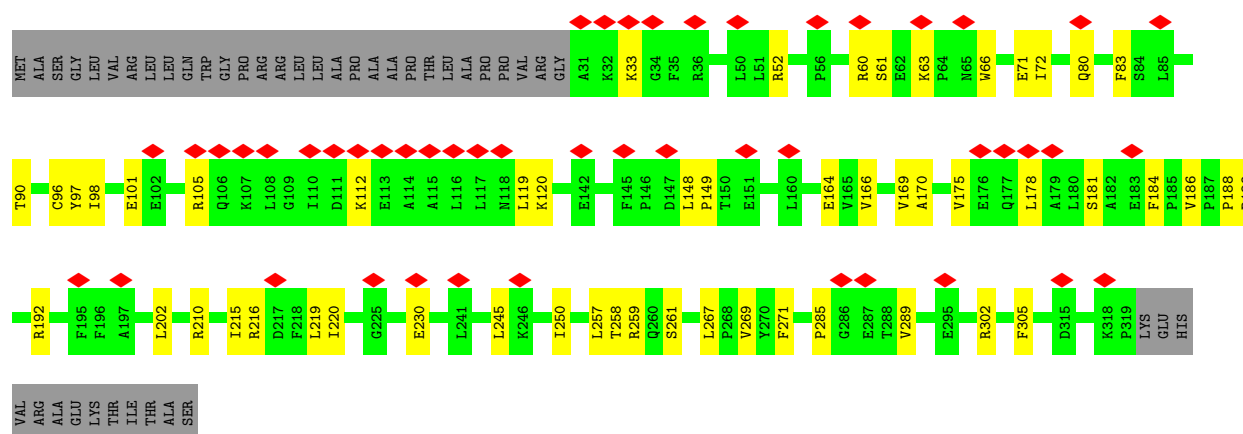
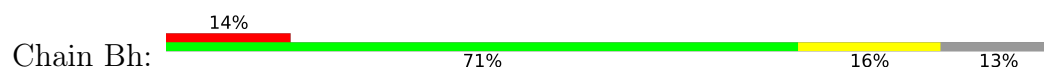
- Molecule 35: 39S ribosomal protein L43, mitochondrial isoform X2



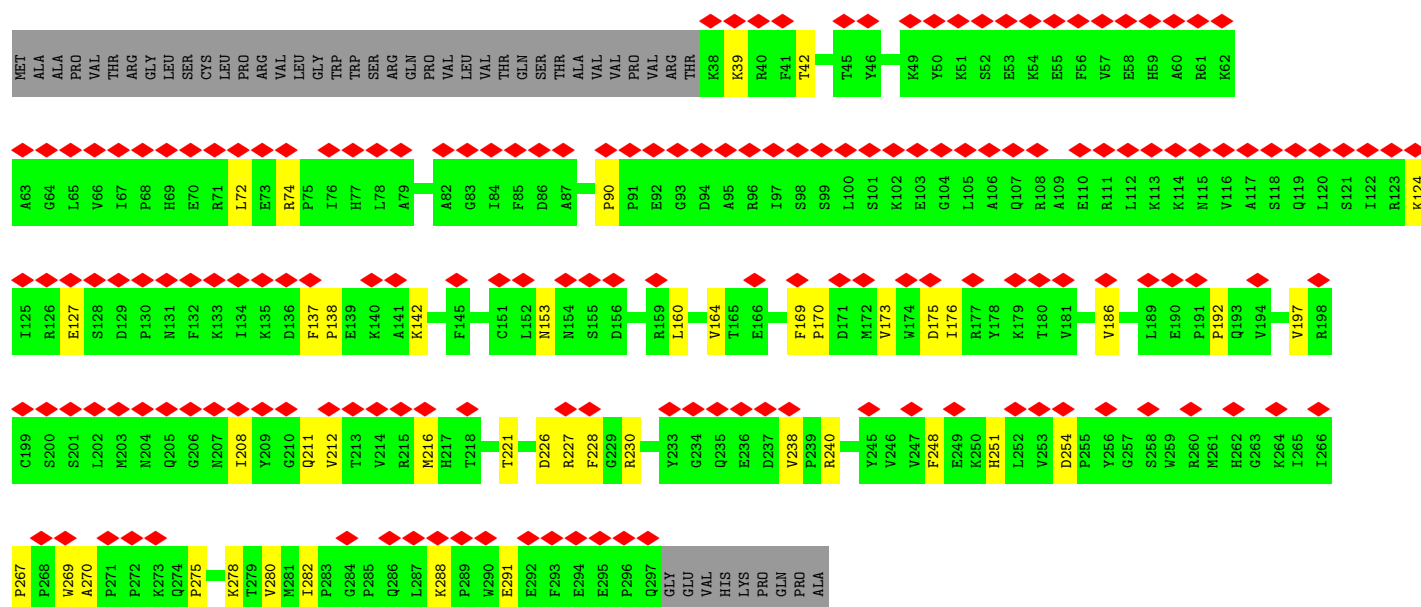
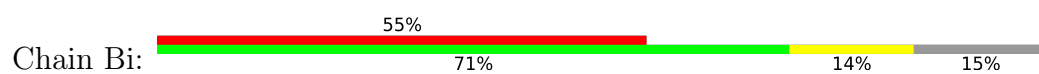
- Molecule 36: 39S ribosomal protein L35, mitochondrial



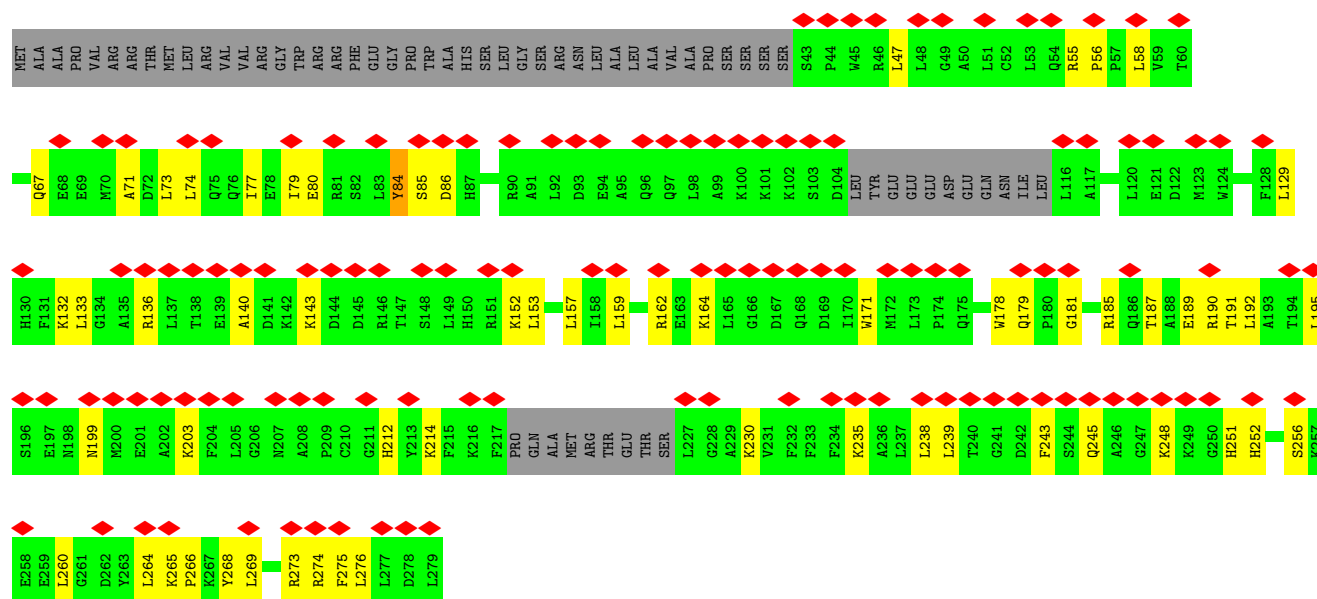
- Molecule 37: 39S ribosomal protein L44, mitochondrial



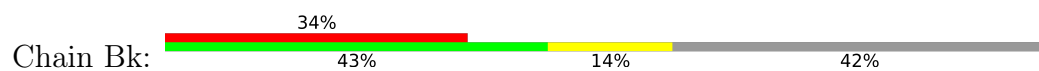
- Molecule 38: Mitochondrial ribosomal protein L45



- Molecule 39: 39S ribosomal protein L46, mitochondrial

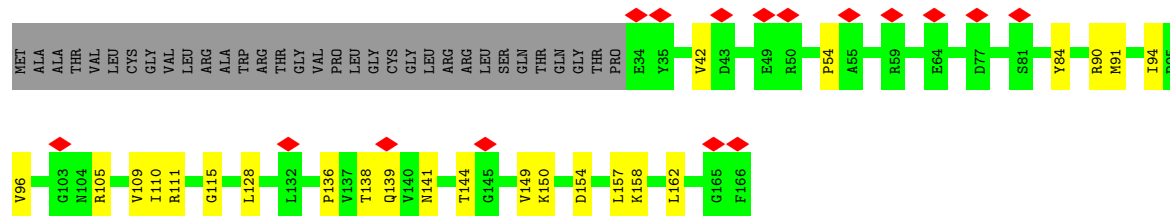


- Molecule 40: 39S ribosomal protein L48, mitochondrial

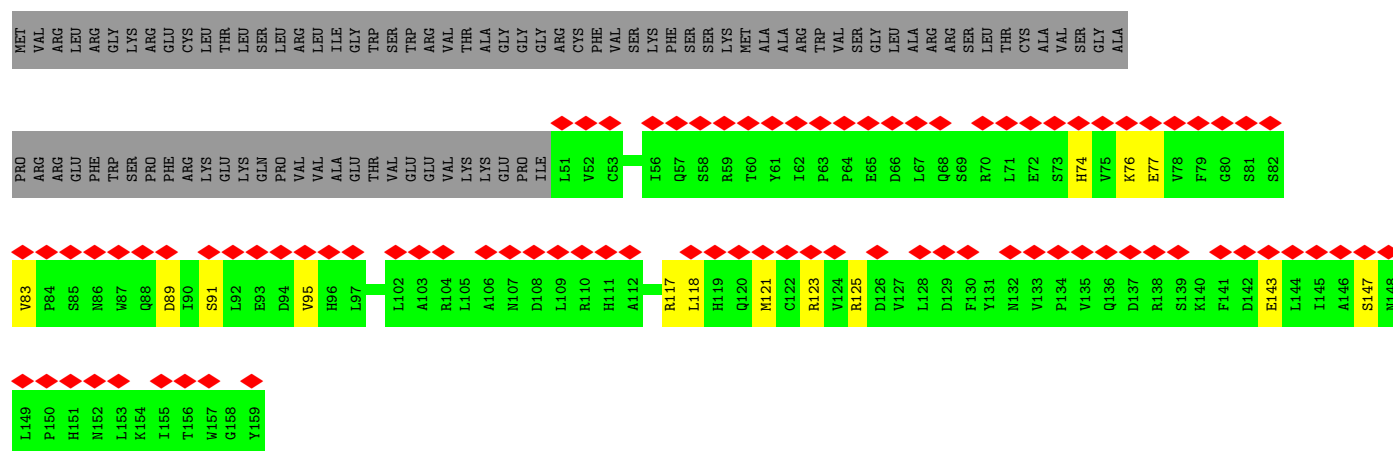




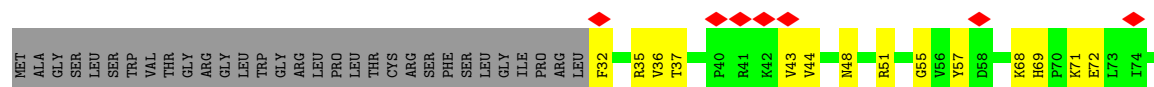
- Molecule 41: 39S ribosomal protein L49, mitochondrial



- Molecule 42: 39S ribosomal protein L50, mitochondrial

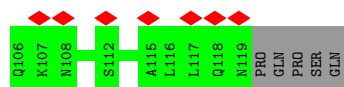


- Molecule 43: 39S ribosomal protein L51, mitochondrial

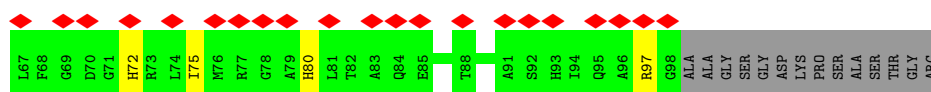
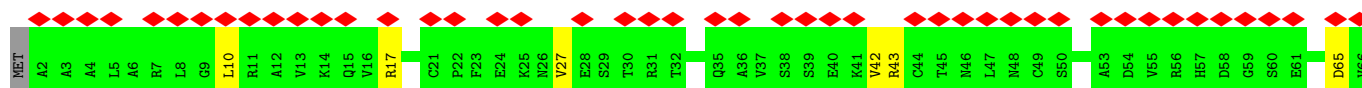
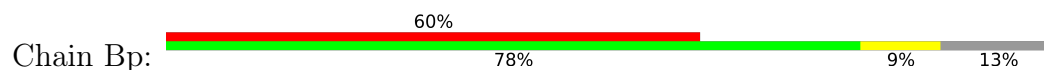




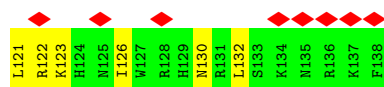
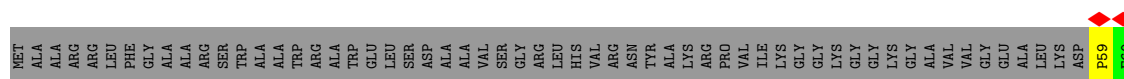
- Molecule 44: 39S ribosomal protein L52, mitochondrial



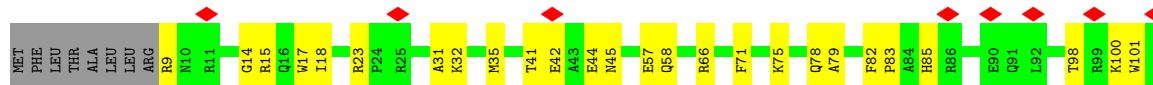
- Molecule 45: mL53



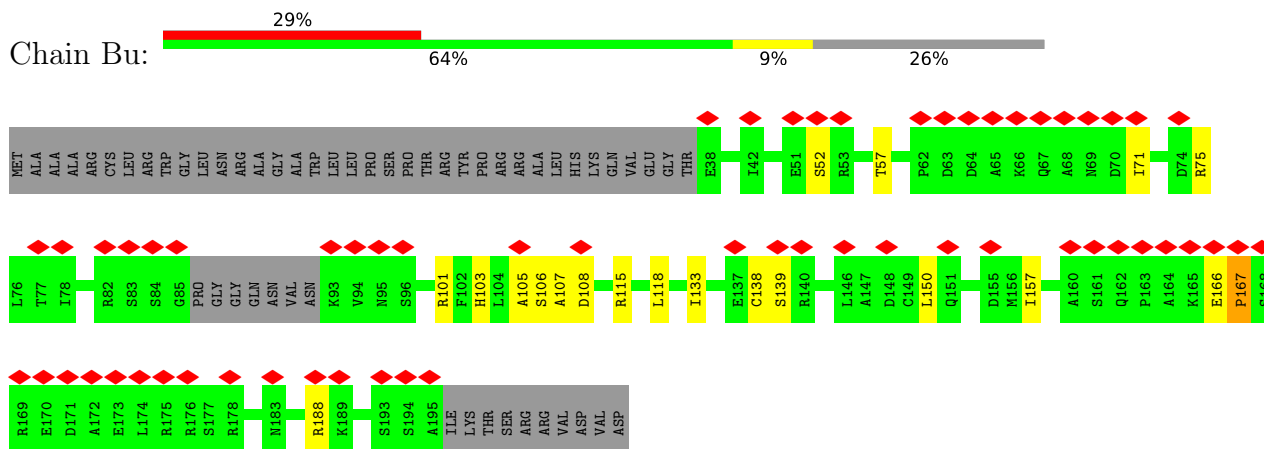
- Molecule 46: 39S ribosomal protein L54, mitochondrial



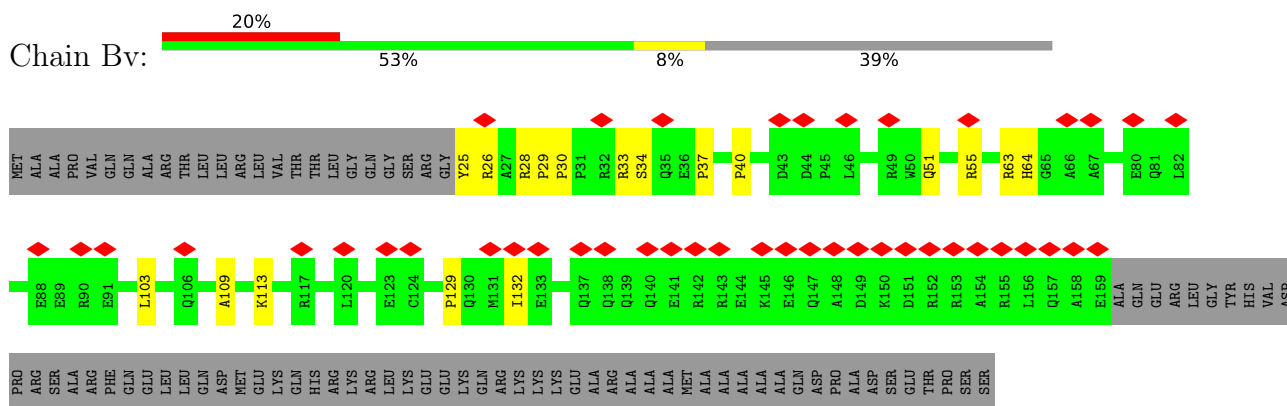
- Molecule 47: Mitochondrial ribosomal protein L57



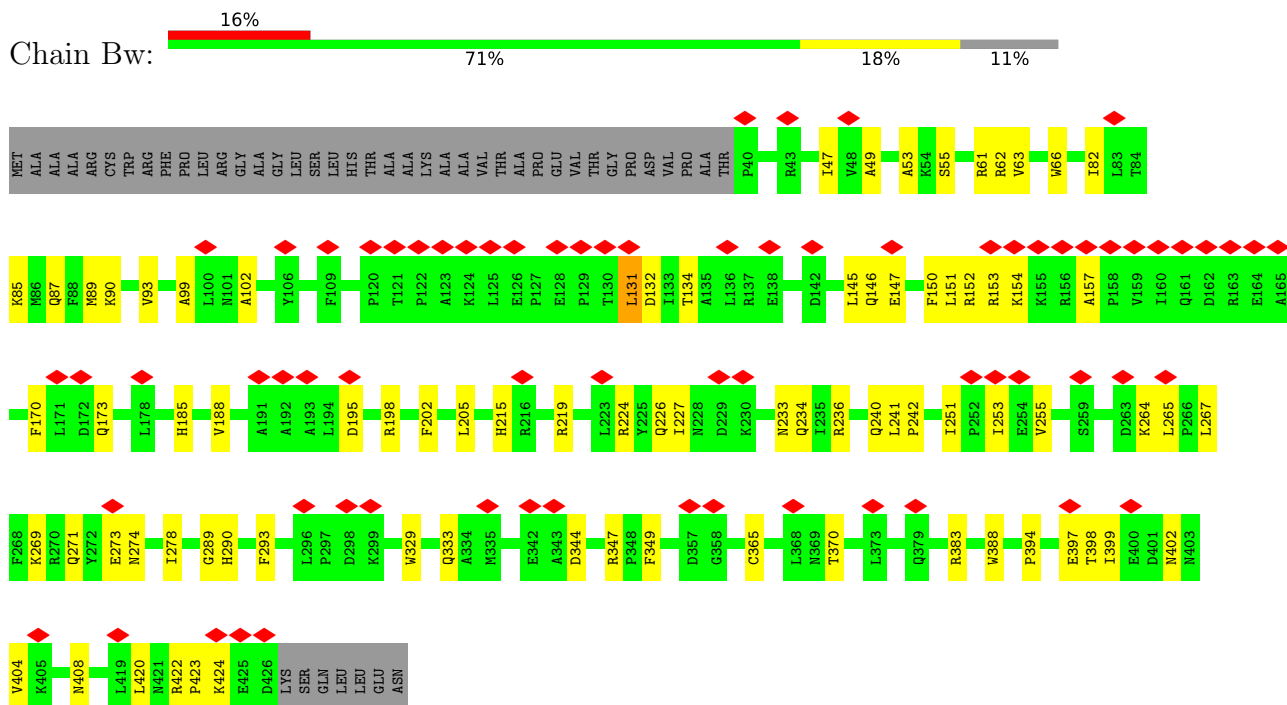
- Molecule 48: Mitochondrial ribosomal protein L58



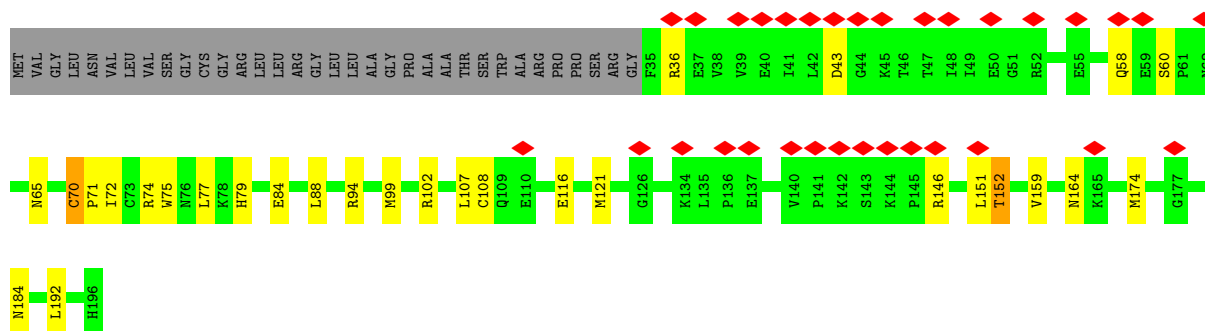
- Molecule 49: 39S ribosomal protein L59, mitochondrial



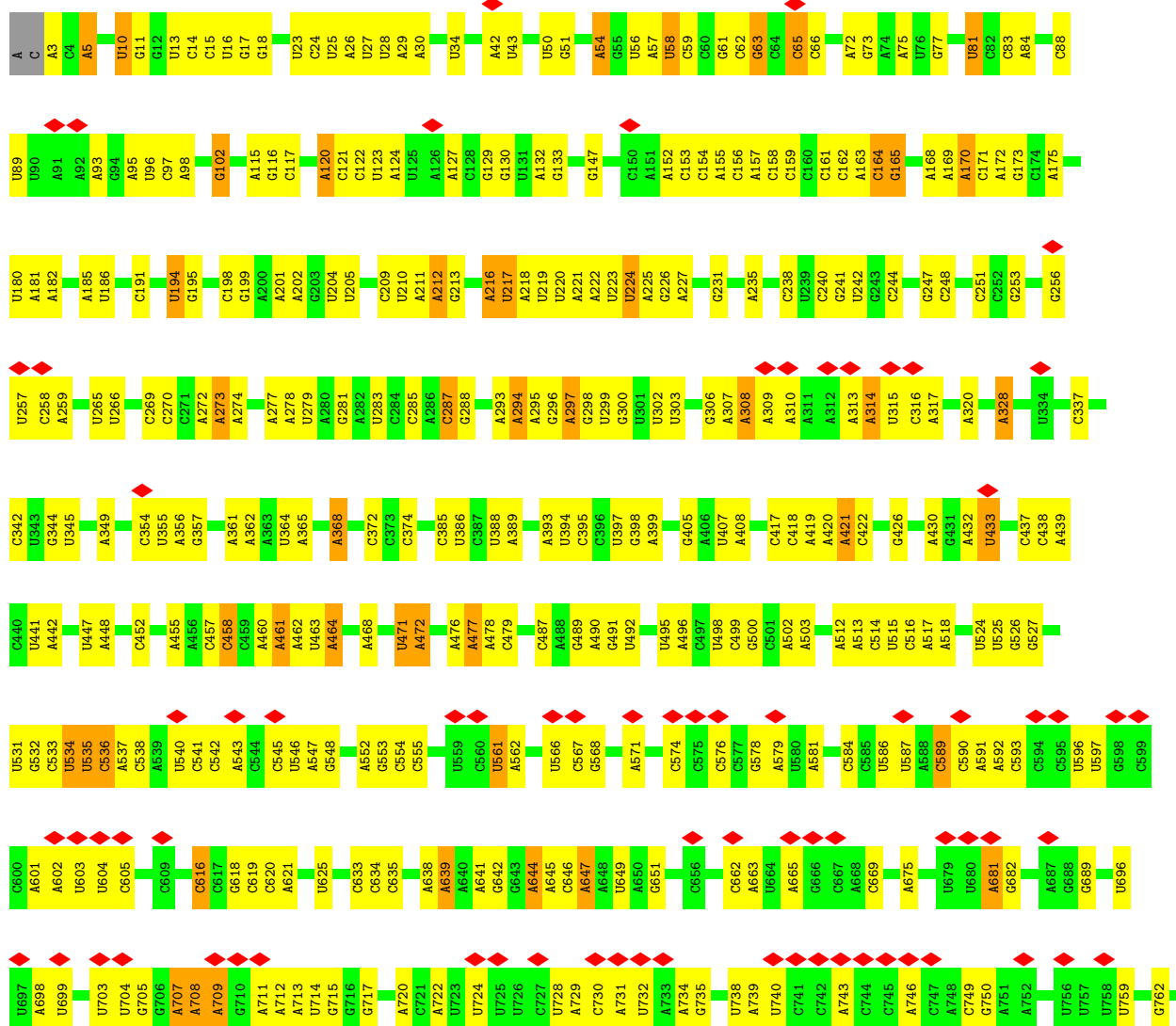
- Molecule 50: 39S ribosomal protein S30, mitochondrial

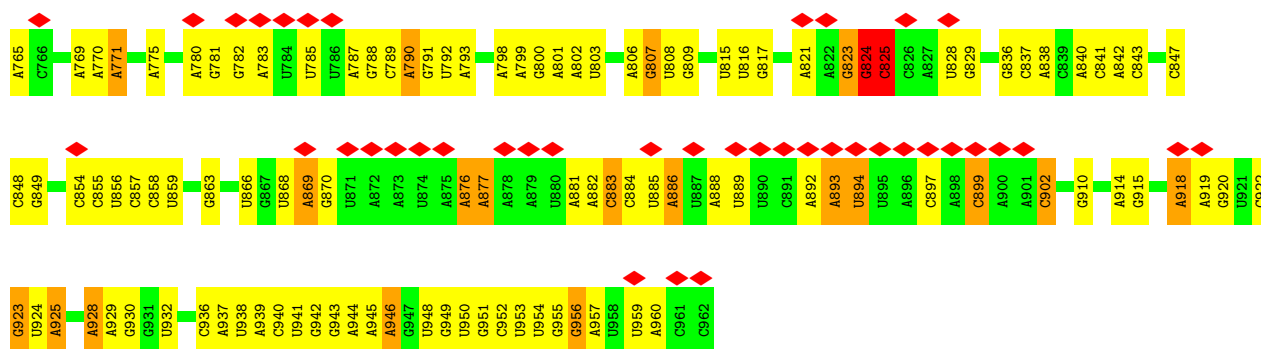


- Molecule 51: Mitochondrial ribosomal protein S18A

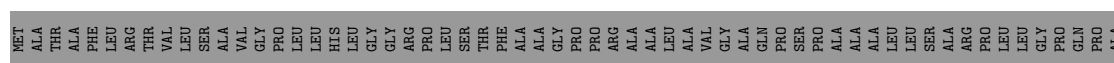


• Molecule 52: 12S rRNA

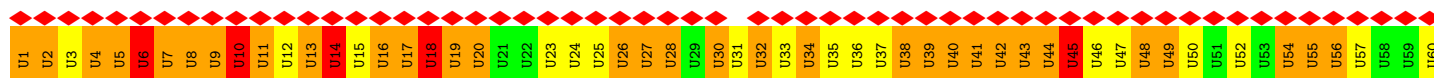




• Molecule 53: Ribosomal protein



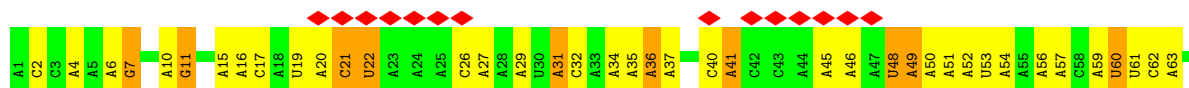
• Molecule 54: tRNA (P/E)

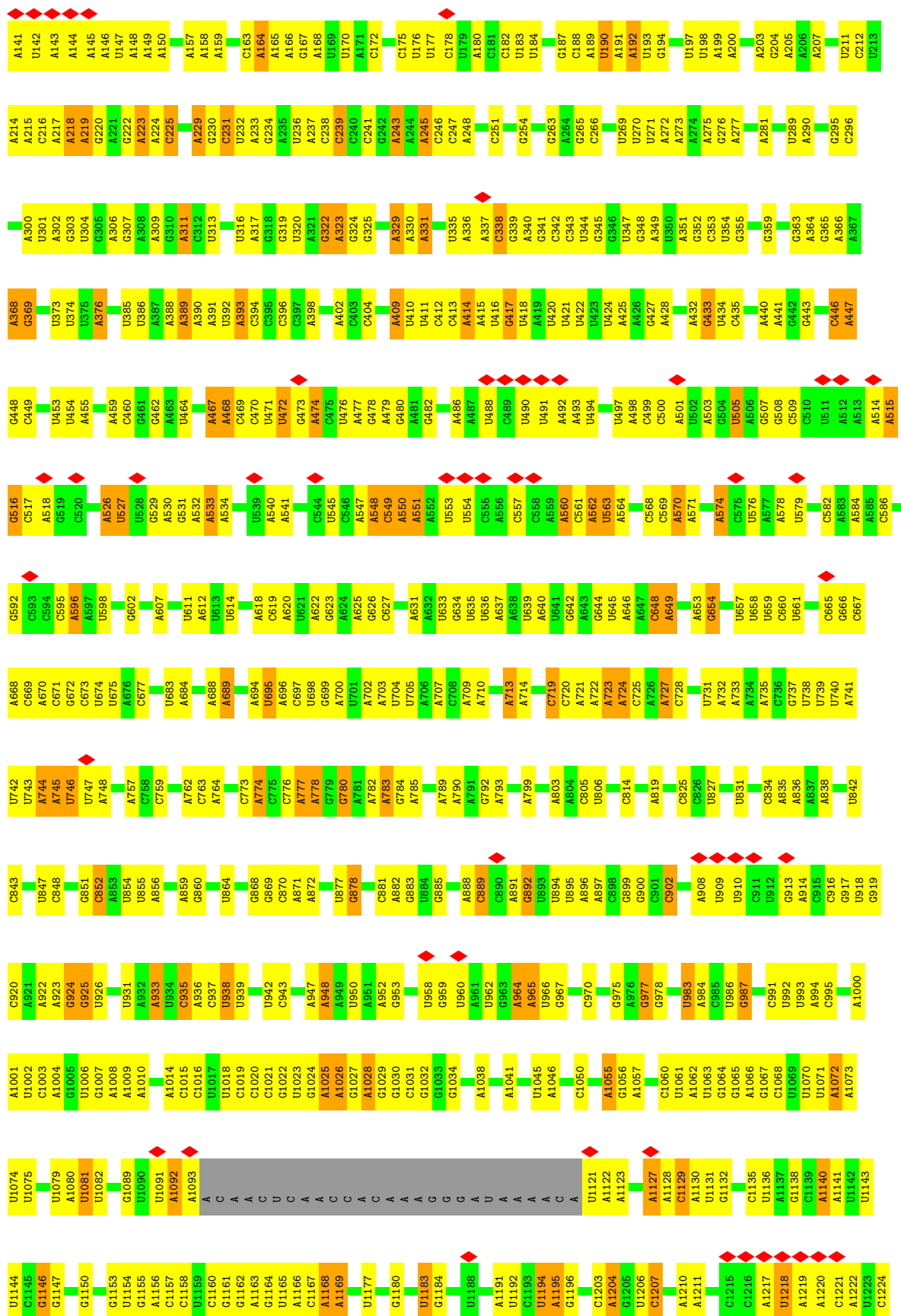


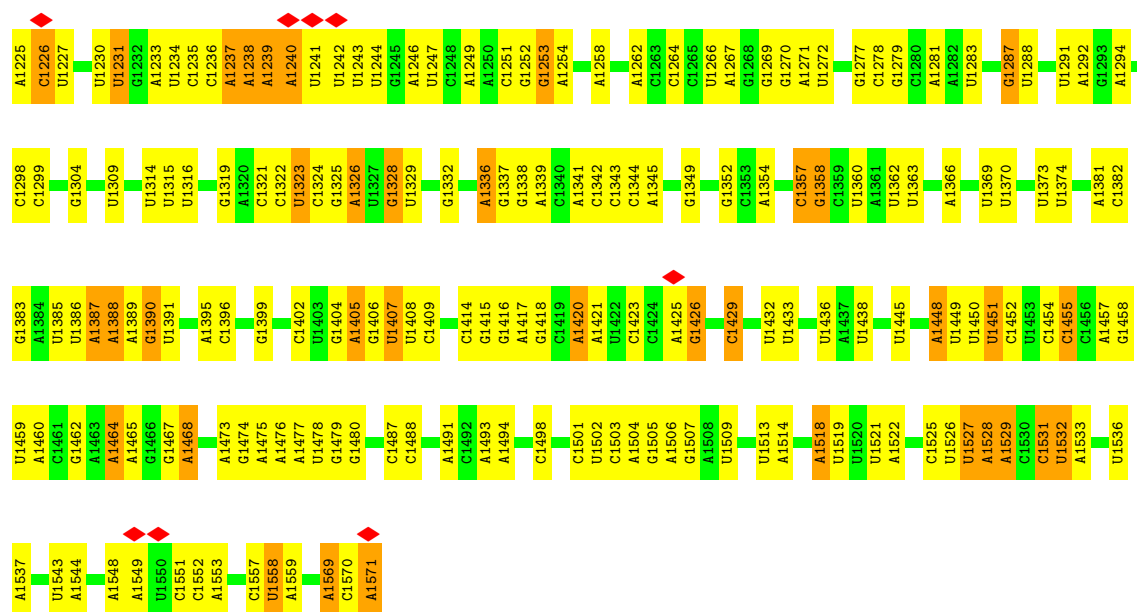
• Molecule 55: mRNA



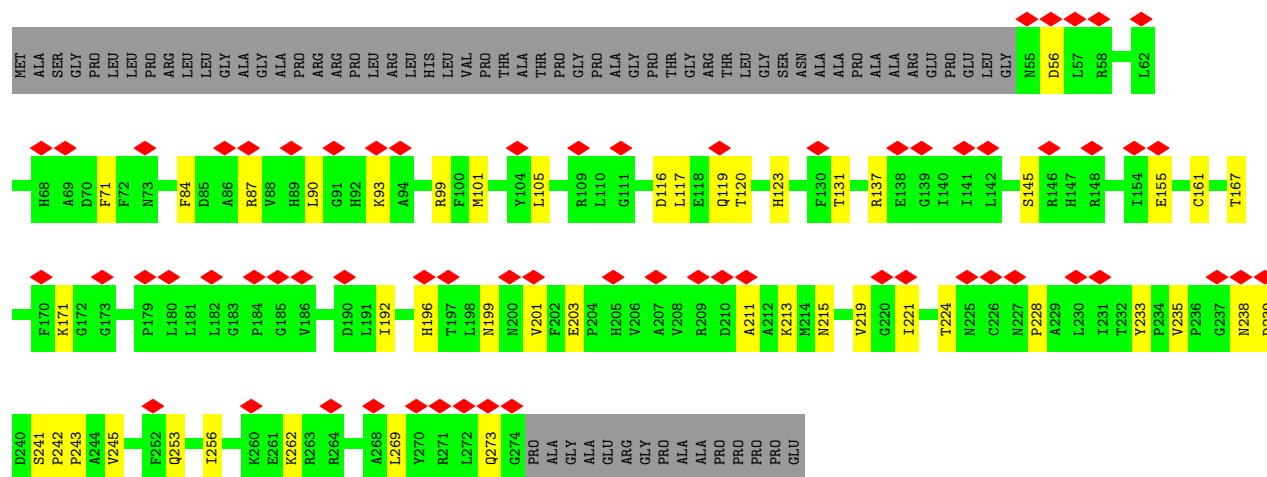
• Molecule 56: 16S rRNA



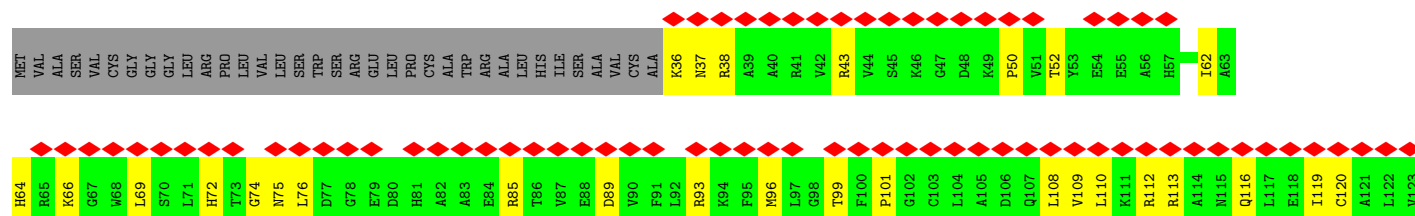




• Molecule 57: 28S ribosomal protein S2, mitochondrial



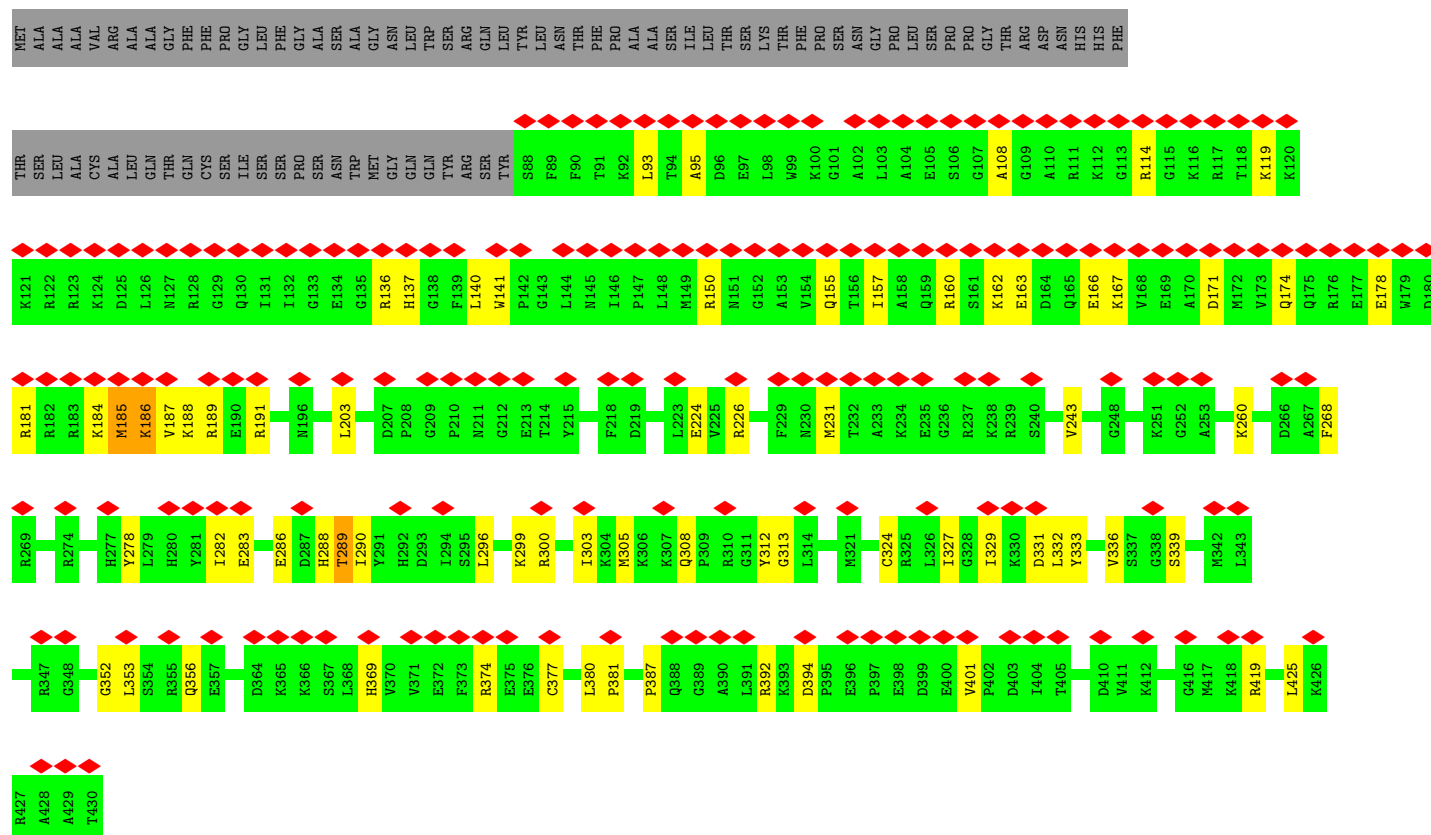
• Molecule 58: 28S ribosomal protein S24, mitochondrial





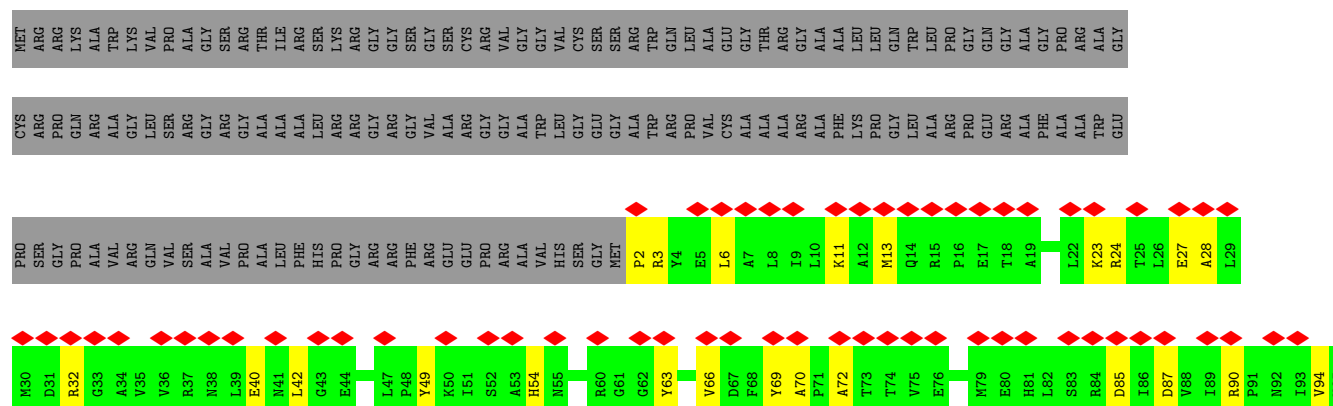
- Molecule 59: 28S ribosomal protein S5, mitochondrial isoform X2

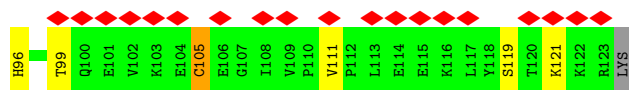
Chain AE: 45% 63% 16% 20%



- Molecule 60: Mitochondrial ribosomal protein S6

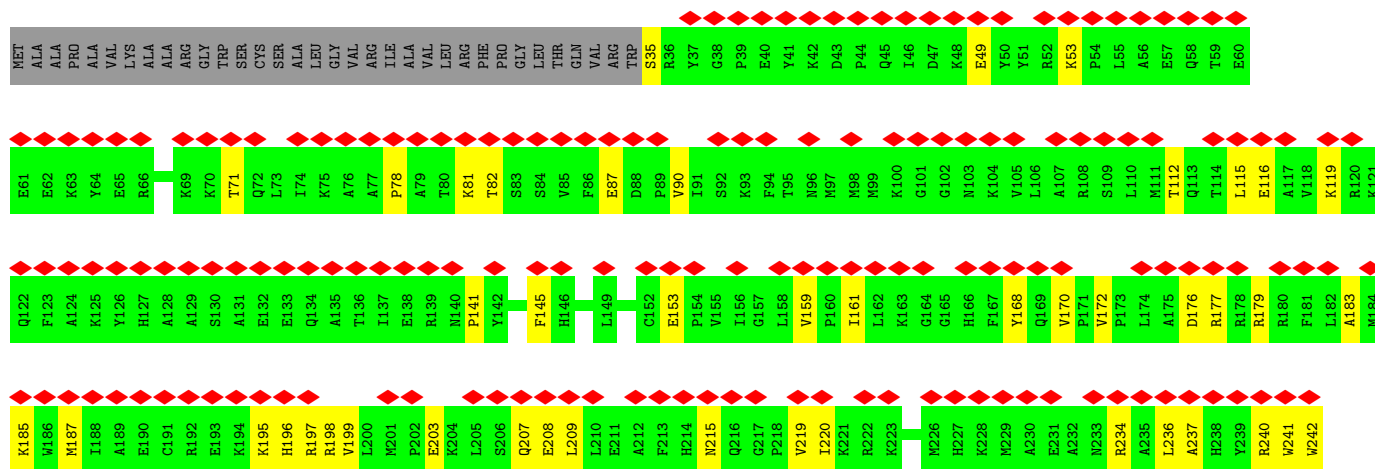
Chain AF: 29% 34% 10% 56%





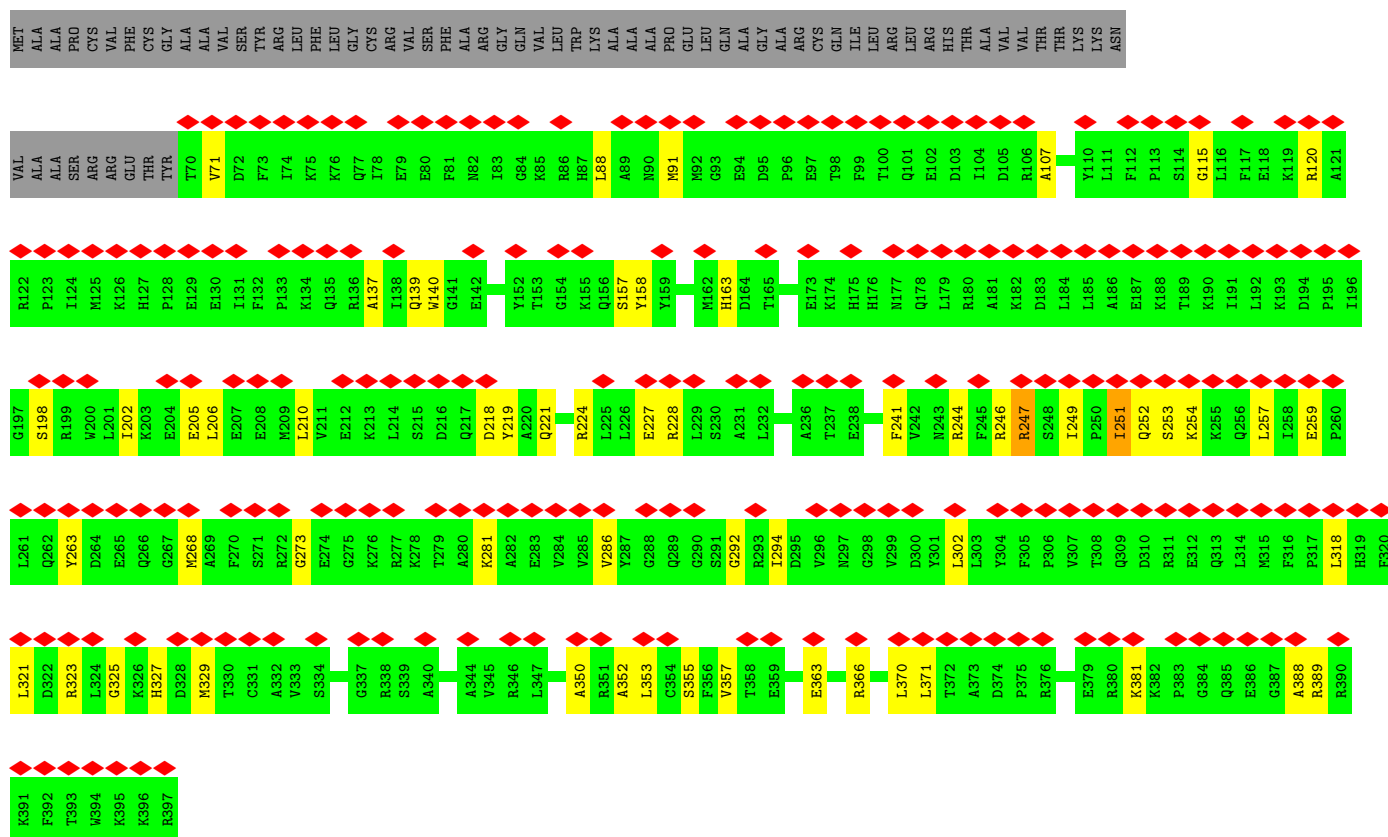
- Molecule 61: 28S ribosomal protein S7, mitochondrial

Chain AG:



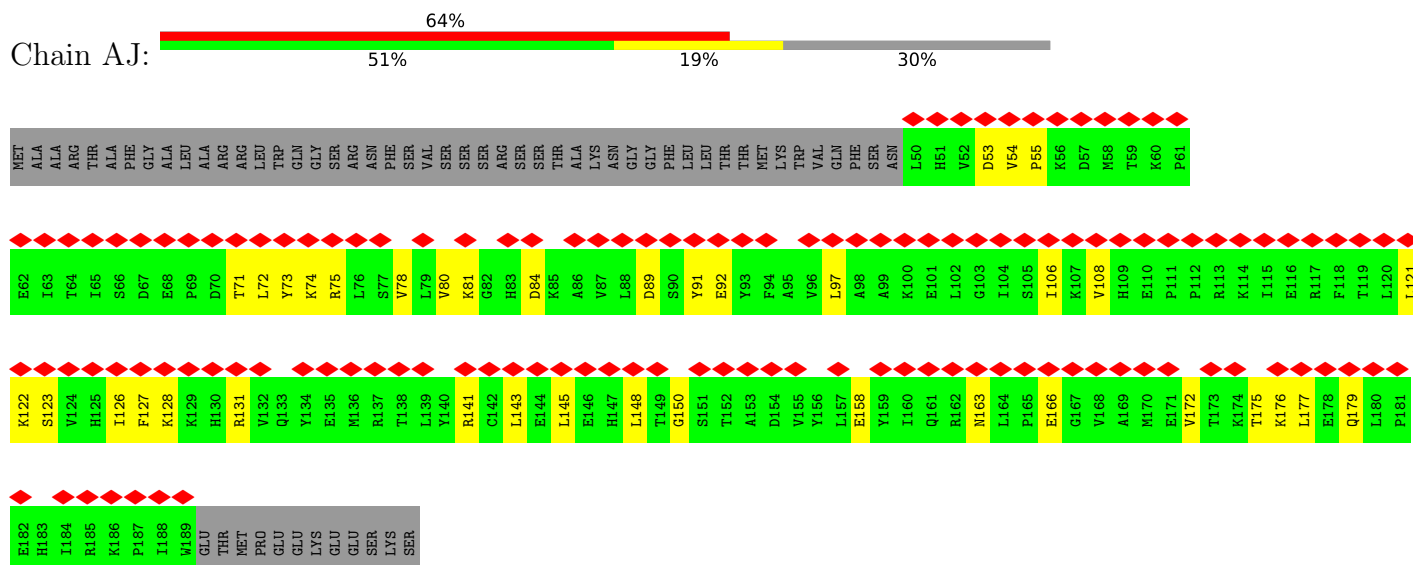
- Molecule 62: 28S ribosomal protein S9, mitochondrial

Chain AI:



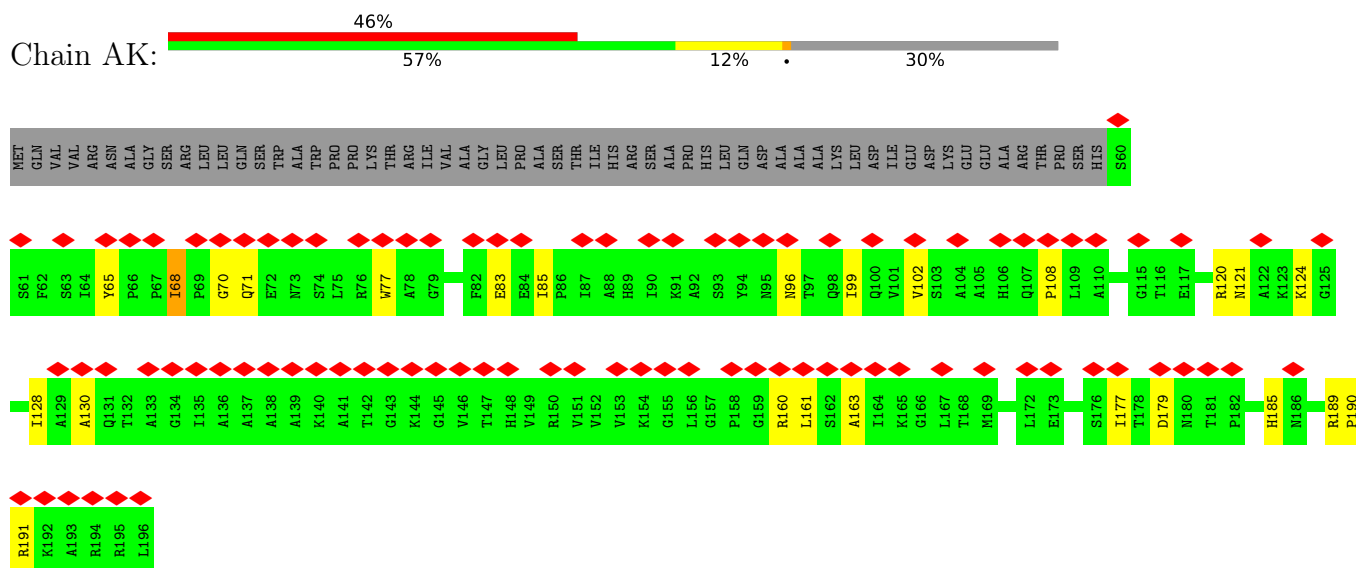
- Molecule 63: 28S ribosomal protein S10, mitochondrial

Chain AJ:



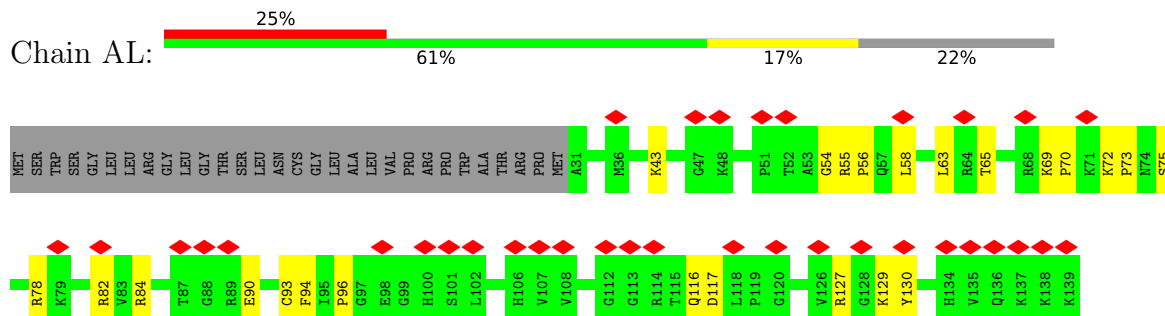
- Molecule 64: Mitochondrial ribosomal protein S11

Chain AK:

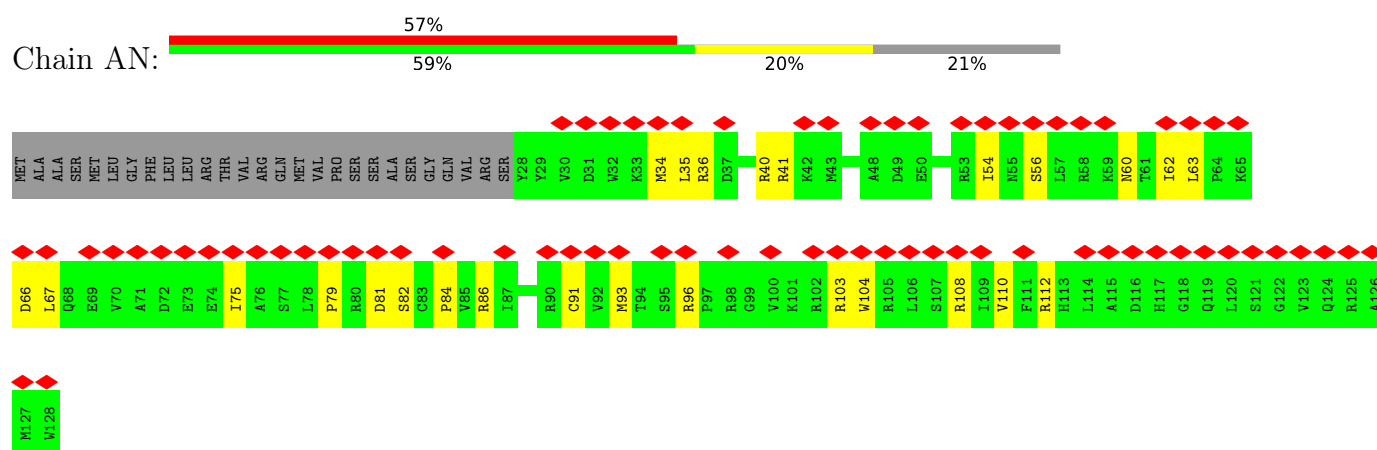


- Molecule 65: Mitoribosomal protein us12m, mrps12

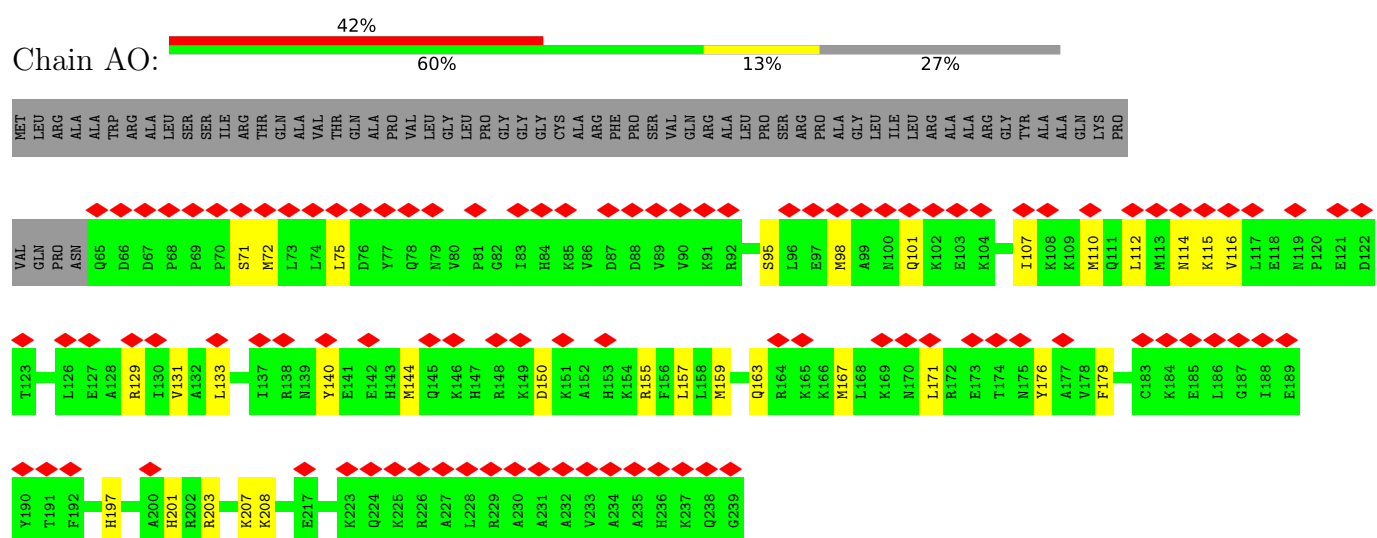
Chain AL:



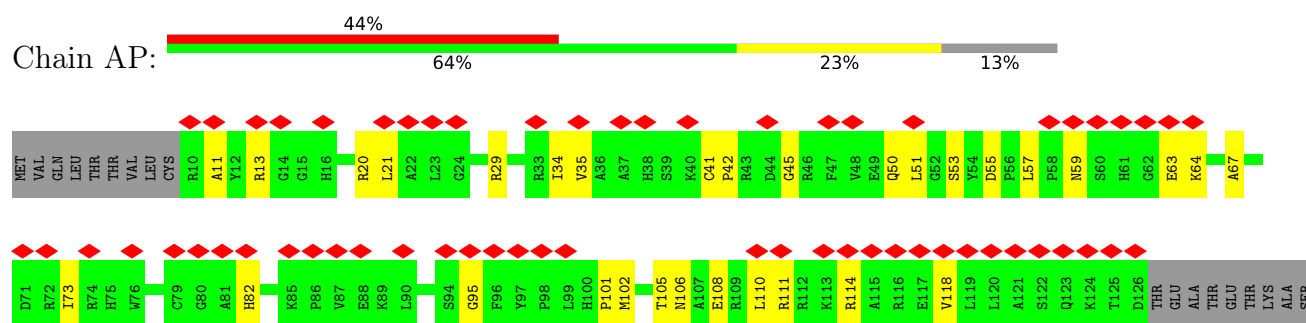
- Molecule 66: 28S ribosomal protein S14, mitochondrial



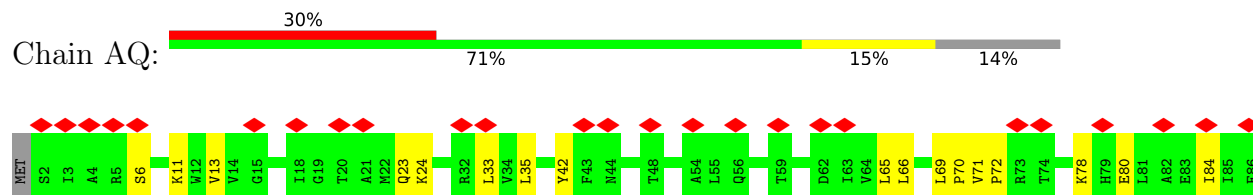
- Molecule 67: 28S ribosomal protein S15, mitochondrial

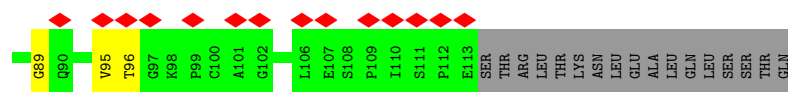


- Molecule 68: 28S ribosomal protein S16, mitochondrial



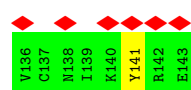
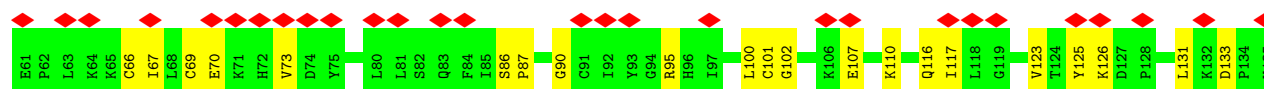
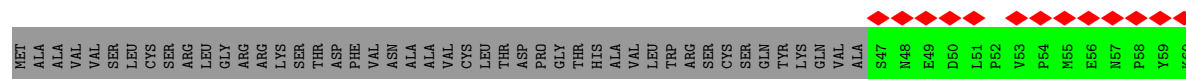
- Molecule 69: uS17m





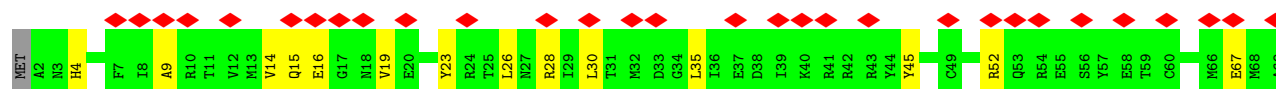
- Molecule 70: 28S ribosomal protein S18c, mitochondrial isoform 1

Chain AR:



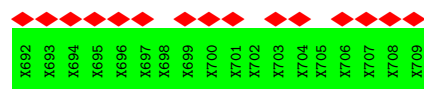
- Molecule 71: 28S ribosomal protein S21, mitochondrial

Chain AU:



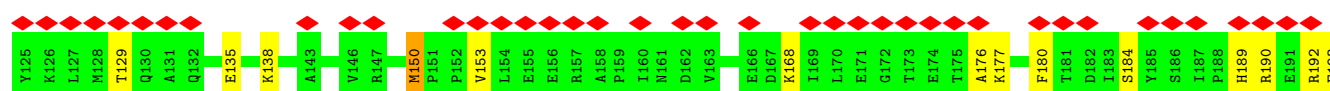
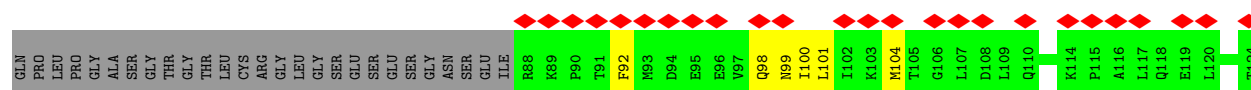
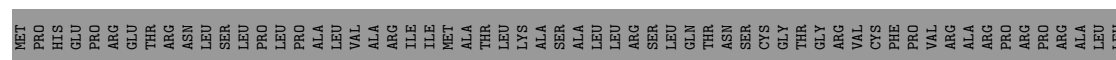
- Molecule 72: unknown

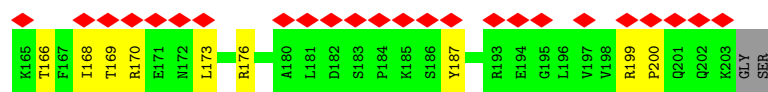
Chain AZ:



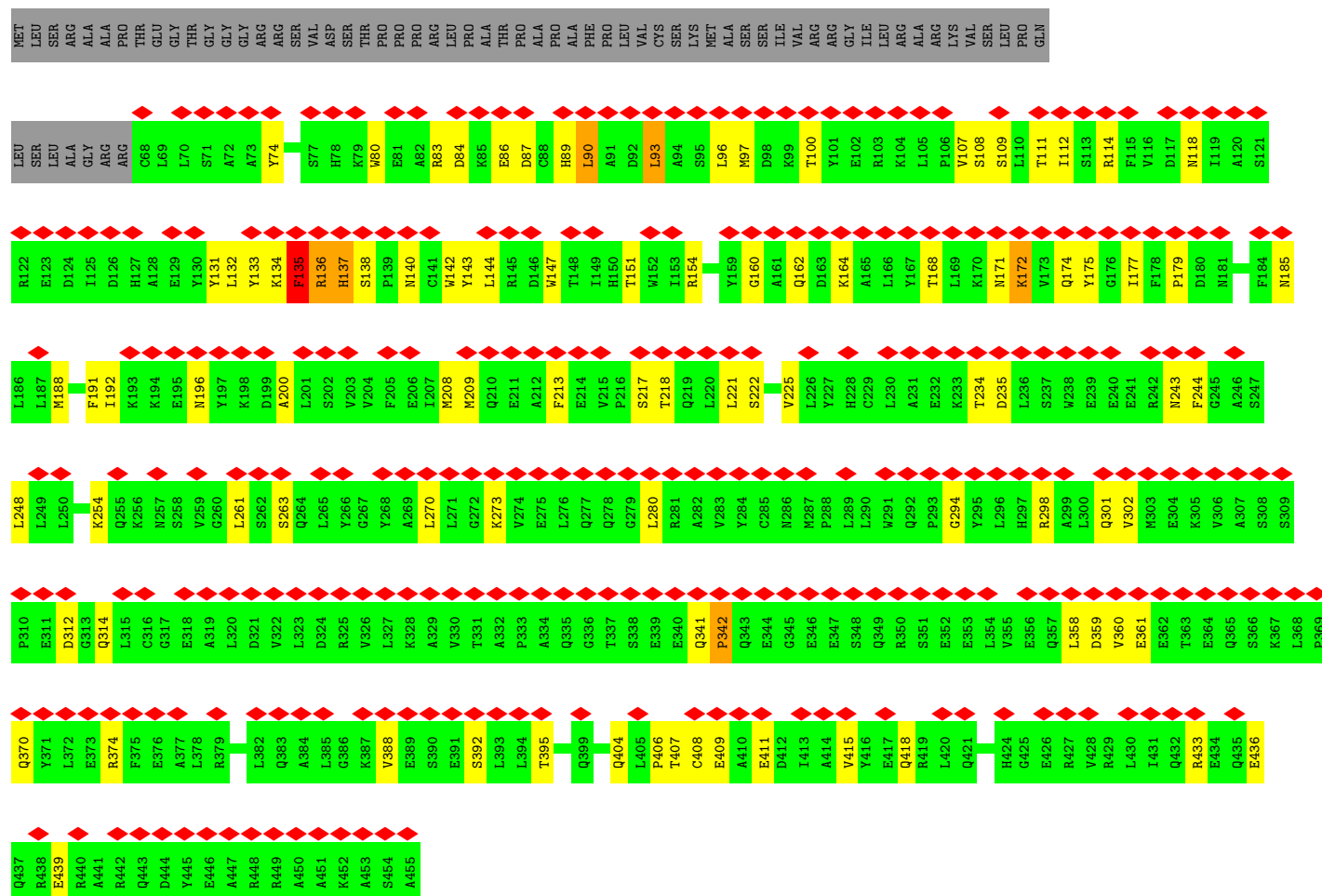
- Molecule 73: Mitochondrial ribosomal protein S22

Chain Aa:

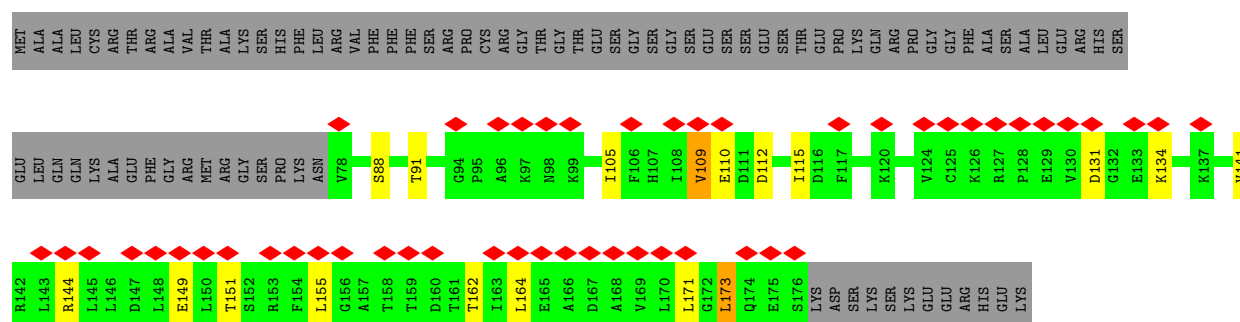
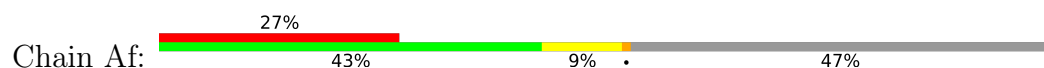




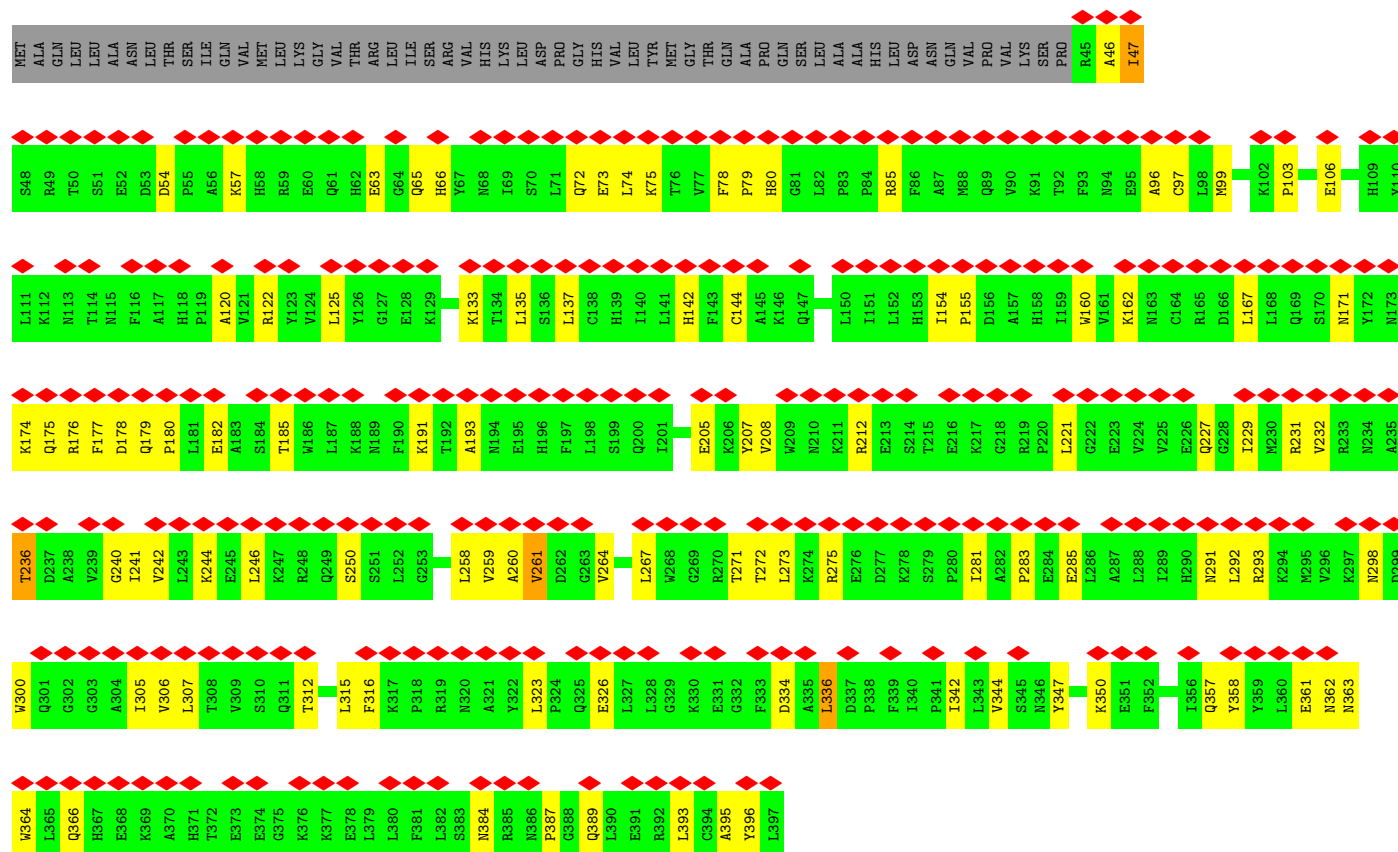
• Molecule 77: Mitochondrial ribosomal protein S27



• Molecule 78: 28S ribosomal protein S28, mitochondrial

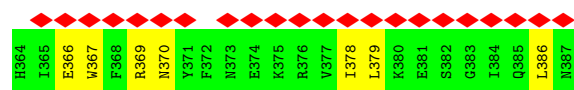


• Molecule 79: Death associated protein 3

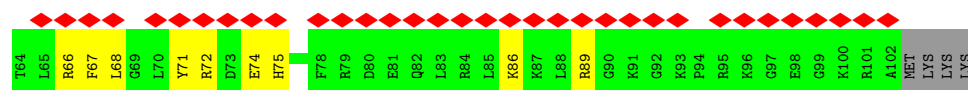
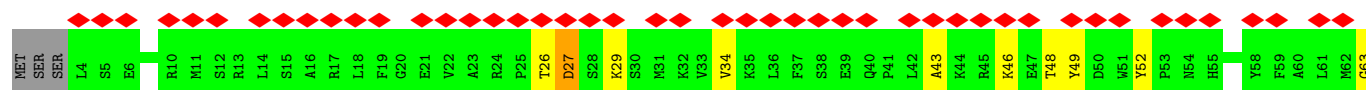
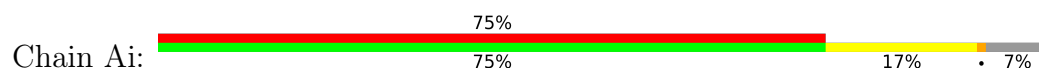


Chain Ah:

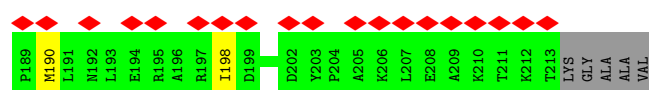
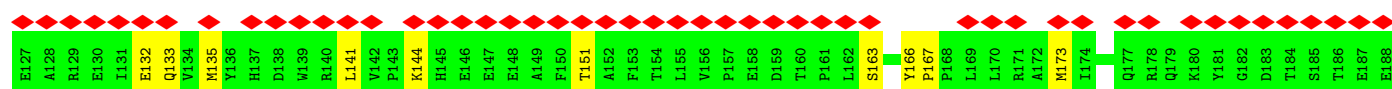
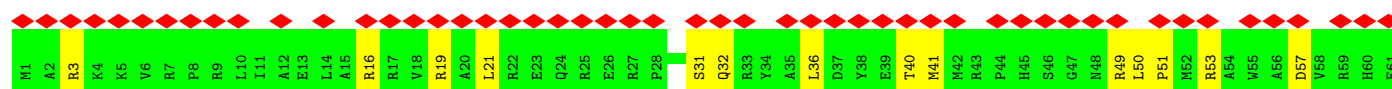
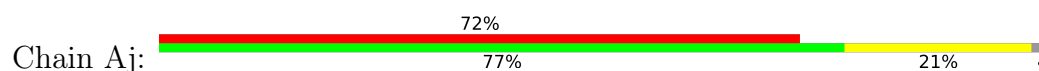




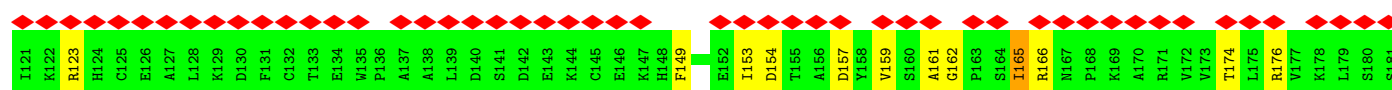
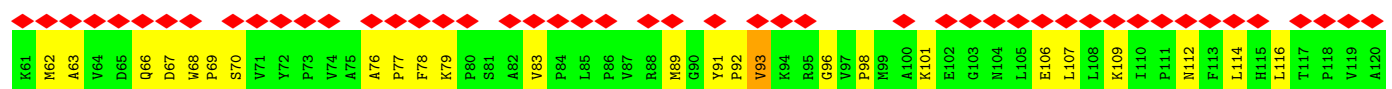
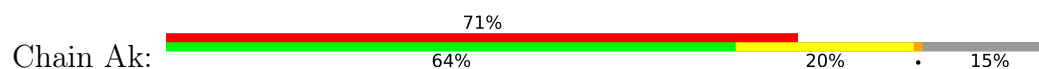
• Molecule 81: Mitochondrial ribosomal protein S33



• Molecule 82: Mitochondrial ribosomal protein S34

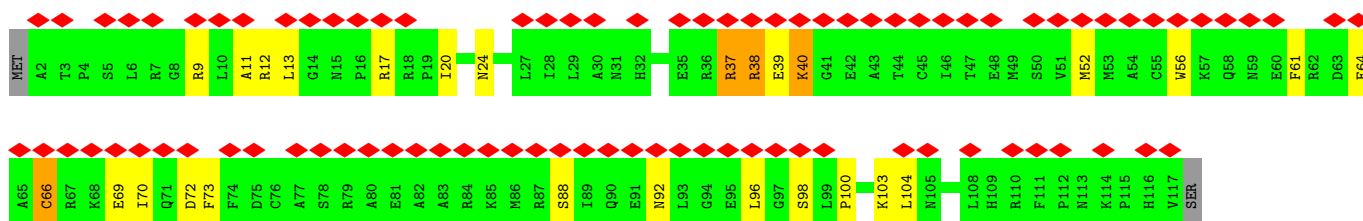
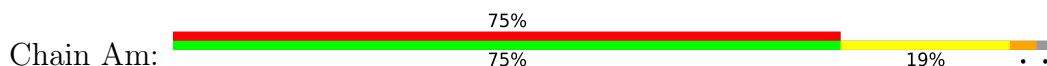


• Molecule 83: 28S ribosomal protein S35, mitochondrial isoform 1

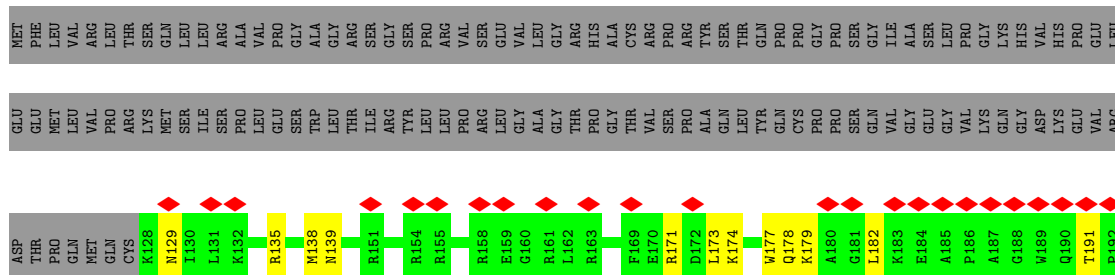




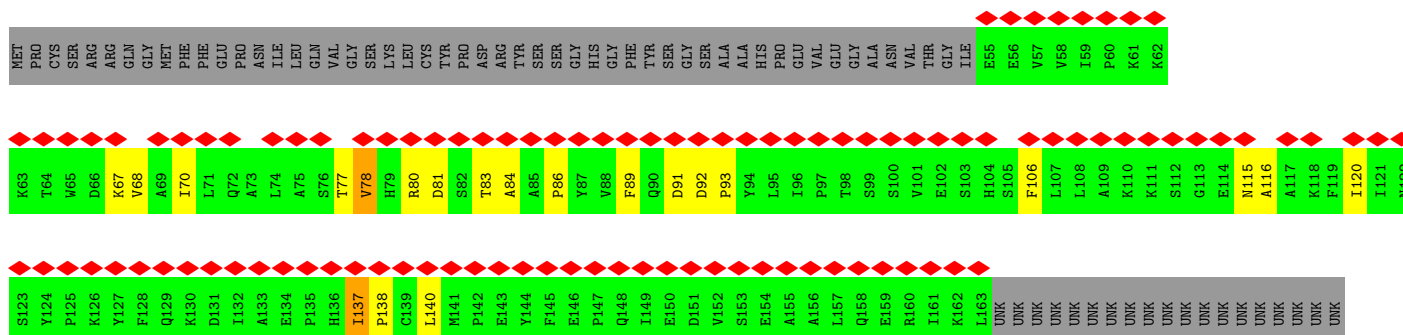
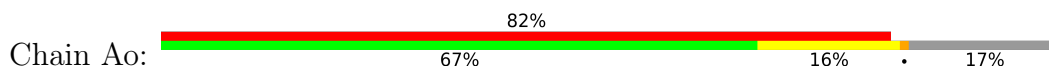
- Molecule 84: Coiled-coil-helix-coiled-coil-helix domain containing 1

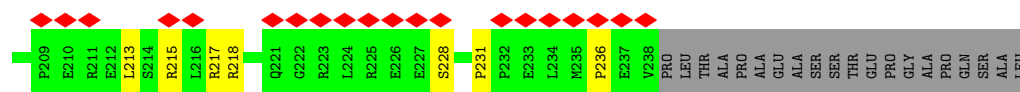


- Molecule 85: Aurora kinase A interacting protein 1

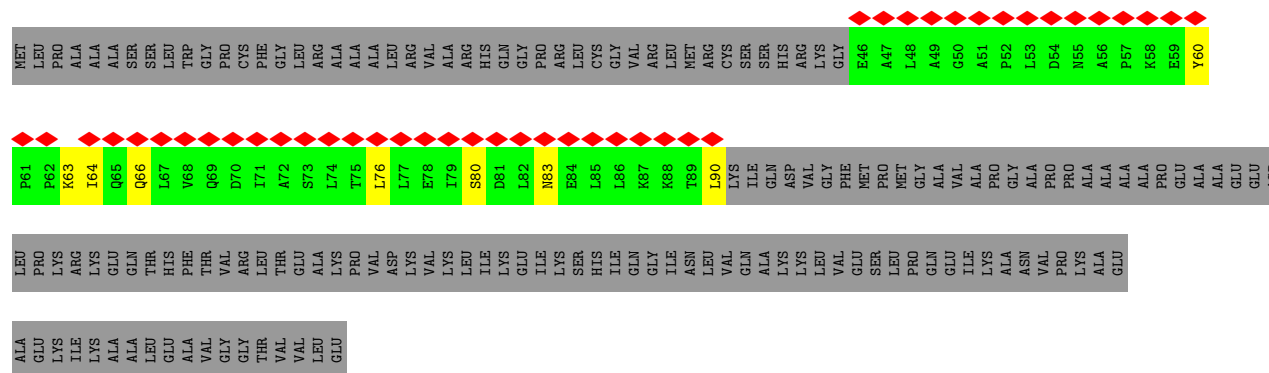


- Molecule 86: Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3,mS39,Pentatricopeptide repeat domain 3,Pentatricopeptide repeat domain 3

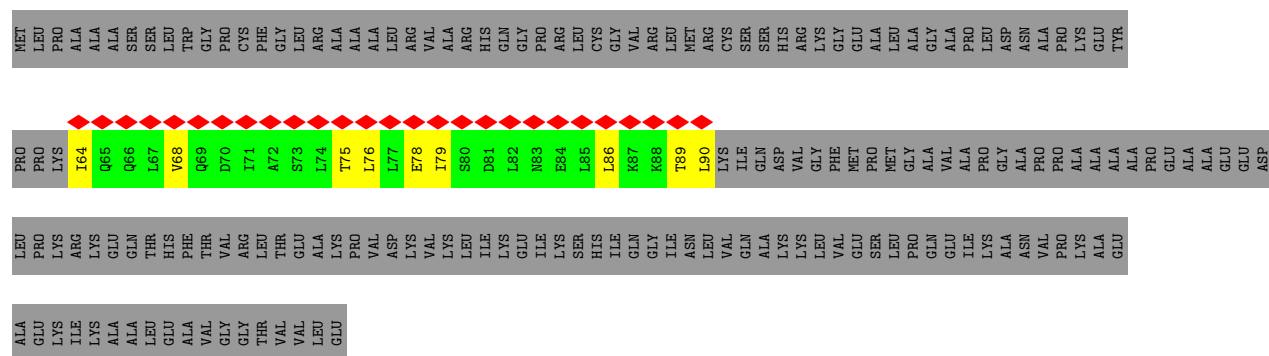




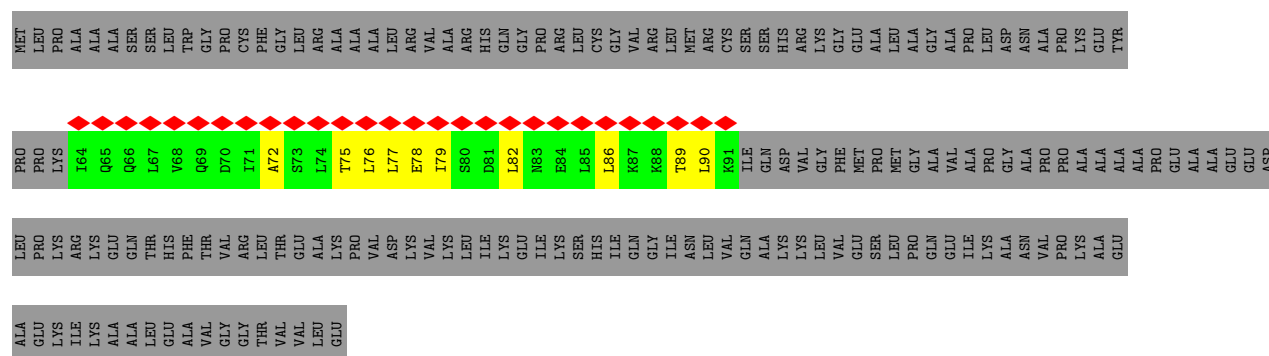
- Molecule 88: Mitochondrial ribosomal protein L12



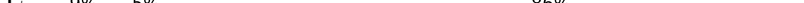
- Molecule 88: Mitochondrial ribosomal protein L12

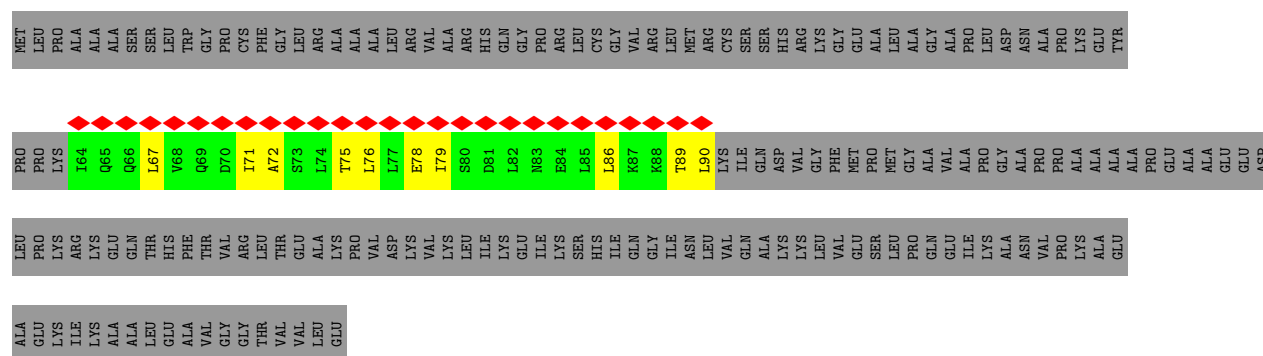


- Molecule 88: Mitochondrial ribosomal protein L12

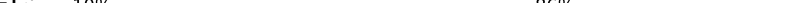


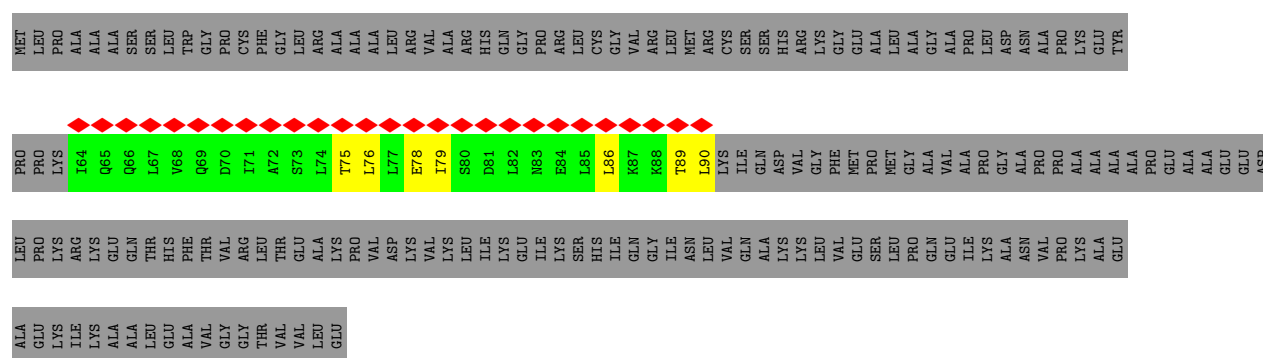
- Molecule 88: Mitochondrial ribosomal protein L12

Chain FL: 

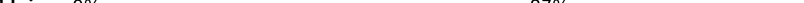


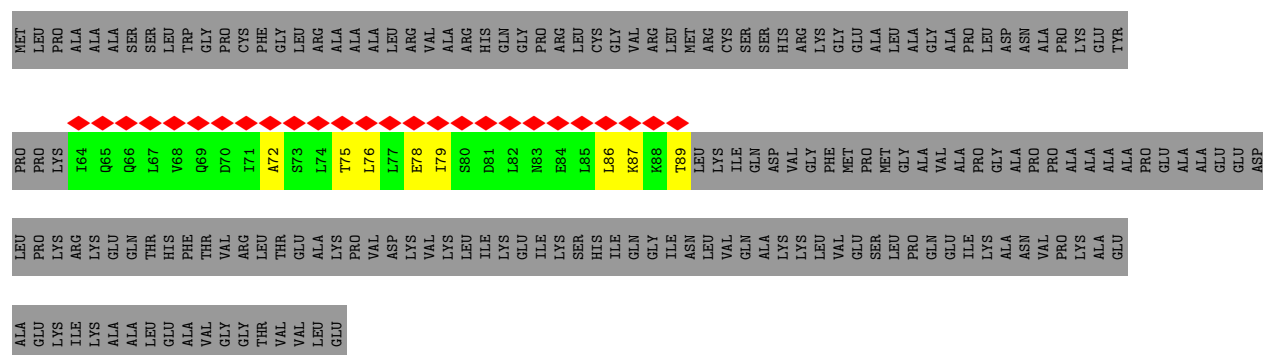
- Molecule 88: Mitochondrial ribosomal protein L12

Chain GL:  14% 10% 86%



- Molecule 88: Mitochondrial ribosomal protein L12

Chain HL:  13% 9% 87%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15545	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	0.108	Depositor
Minimum map value	-0.049	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: ZN, MG, 5GP, GTP, SPM

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	0.09	0/880	0.28	0/1189
2	B1	0.08	0/2093	0.22	0/2835
3	B2	0.08	0/1586	0.22	0/2123
4	B3	0.09	0/993	0.27	0/1341
5	B4	0.15	0/481	0.40	1/653 (0.2%)
6	B5	0.08	0/917	0.24	0/1227
7	B6	0.09	0/430	0.27	0/570
8	BB	0.07	0/1595	0.19	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	BG	0.12	0/1510	0.37	0/2033
14	BI	0.09	0/819	0.26	0/1101
15	BJ	0.10	0/1742	0.29	0/2358
16	BK	0.11	0/1323	0.30	0/1785
17	BN	0.10	0/1487	0.25	0/2017
18	BO	0.07	0/912	0.24	0/1231
19	BP	0.10	0/2368	0.27	0/3198
20	BQ	0.08	0/1850	0.24	0/2491
21	BR	0.09	0/1262	0.27	0/1700
22	BS	0.10	0/1197	0.30	0/1624
23	BT	0.22	1/1936 (0.1%)	0.38	3/2615 (0.1%)
24	BU	0.09	0/1179	0.23	0/1578
25	BV	0.11	0/1256	0.29	0/1706
26	BW	0.08	0/1407	0.23	0/1891
27	BX	0.12	0/1211	0.28	0/1646
28	BY	0.09	0/1719	0.26	0/2329
29	Ba	0.10	0/3267	0.27	0/4455
30	Bb	0.10	0/3047	0.27	0/4139
31	Bc	0.09	0/2464	0.26	0/3330
32	Bd	0.23	0/1183	0.37	0/1594

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Be	0.09	0/1000	0.26	0/1345
34	Bf	0.11	0/851	0.45	2/1159 (0.2%)
35	Bg	0.10	0/1191	0.30	0/1614
36	B8	0.07	0/853	0.22	0/1136
37	Bh	0.09	0/2372	0.26	0/3211
38	Bi	0.09	0/2199	0.28	0/2980
39	Bj	0.09	0/1811	0.27	0/2436
40	Bk	0.09	0/1270	0.26	0/1714
41	Bl	0.11	0/1135	0.28	0/1549
42	Bm	0.10	0/917	0.25	0/1248
43	Bn	0.08	0/860	0.25	0/1150
44	Bo	0.10	0/787	0.26	0/1056
45	Bp	0.10	0/752	0.32	0/1013
46	Bq	0.13	0/692	0.43	1/936 (0.1%)
47	Bt	0.10	0/798	0.26	0/1073
48	Bu	0.09	0/1214	0.33	1/1630 (0.1%)
49	Bv	0.08	0/1157	0.21	0/1560
50	Bw	0.10	0/3206	0.27	0/4354
51	Bx	0.11	0/1364	0.29	0/1849
52	AA	0.09	0/22852	0.21	3/35580 (0.0%)
53	B9	0.08	0/342	0.22	0/450
54	AV	0.92	33/1561 (2.1%)	0.37	0/2411
55	AX	1.17	4/109 (3.7%)	0.35	0/166
56	BA	0.09	0/36784	0.23	0/57270
57	AB	0.12	0/1804	0.32	0/2445
58	AC	0.10	0/1105	0.30	0/1496
59	AE	0.16	0/2785	0.32	0/3735
60	AF	0.09	0/999	0.27	0/1347
61	AG	0.10	0/1763	0.29	0/2368
62	AI	0.16	0/2707	0.32	0/3636
63	AJ	0.11	0/1181	0.29	0/1597
64	AK	0.10	0/1027	0.27	0/1389
65	AL	0.12	0/858	0.28	0/1152
66	AN	0.08	0/874	0.25	0/1171
67	AO	0.09	0/1473	0.30	0/1970
68	AP	0.09	0/954	0.29	0/1284
69	AQ	0.10	0/894	0.25	0/1213
70	AR	0.10	0/802	0.31	0/1079
71	AU	0.07	0/745	0.26	0/993
73	Aa	0.09	0/2428	0.29	0/3279
74	Ab	0.09	0/1126	0.28	0/1514
75	Ac	0.09	0/1399	0.29	0/1881
76	Ad	0.10	0/1490	0.28	0/2005

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	Ae	0.24	1/3171 (0.0%)	0.46	1/4292 (0.0%)
78	Af	0.09	0/790	0.29	0/1064
79	Ag	0.10	0/2945	0.31	0/3984
80	Ah	0.09	0/1045	0.26	0/1409
81	Ai	0.09	0/841	0.29	0/1121
82	Aj	0.10	0/1835	0.29	0/2484
83	Ak	0.10	0/2268	0.29	0/3069
84	Am	0.30	0/947	0.44	0/1268
85	An	0.09	0/650	0.30	0/858
86	Ao	0.10	0/4458	0.31	0/6036
87	Ap	0.10	0/1616	0.32	0/2195
88	CL	0.11	0/319	0.34	0/435
88	DL	0.10	0/212	0.32	0/286
88	EL	0.11	0/221	0.34	0/297
88	FL	0.10	0/212	0.31	0/286
88	GL	0.10	0/212	0.31	0/286
88	HL	0.10	0/204	0.32	0/275
All	All	0.14	39/183406 (0.0%)	0.27	12/260605 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
23	BT	0	1
77	Ae	0	1
All	All	0	2

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	AV	43	U	C1'-N1	6.60	1.58	1.48
54	AV	23	U	C1'-N1	6.58	1.58	1.48
55	AX	2	U	C1'-N1	6.58	1.58	1.48
54	AV	16	U	C1'-N1	6.54	1.57	1.47
54	AV	18	U	C1'-N1	6.40	1.58	1.48
54	AV	41	U	C1'-N1	6.32	1.57	1.48
54	AV	40	U	C1'-N1	6.30	1.57	1.48
54	AV	10	U	C1'-N1	6.30	1.57	1.48
54	AV	65	U	C1'-N1	6.28	1.57	1.48
54	AV	1	U	C1'-N1	6.26	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	AV	5	U	C1'-N1	6.26	1.57	1.48
55	AX	3	U	C1'-N1	6.26	1.57	1.48
54	AV	52	U	C1'-N1	6.25	1.57	1.48
54	AV	42	U	C1'-N1	6.24	1.57	1.48
54	AV	11	U	C1'-N1	6.23	1.57	1.48
54	AV	68	U	C1'-N1	6.19	1.56	1.47
54	AV	54	U	C1'-N1	6.17	1.57	1.48
54	AV	45	U	C1'-N1	6.17	1.57	1.48
54	AV	4	U	C1'-N1	6.17	1.57	1.48
54	AV	19	U	C1'-N1	6.16	1.57	1.48
54	AV	34	U	C1'-N1	6.14	1.57	1.48
54	AV	15	U	C1'-N1	6.14	1.56	1.47
54	AV	48	U	C1'-N1	6.11	1.57	1.48
54	AV	63	U	C1'-N1	6.10	1.57	1.48
54	AV	14	U	C1'-N1	6.09	1.57	1.48
54	AV	6	U	C1'-N1	6.06	1.57	1.48
54	AV	32	U	C1'-N1	6.01	1.57	1.48
55	AX	4	U	C1'-N1	5.98	1.57	1.48
54	AV	27	U	C1'-N1	5.90	1.57	1.48
54	AV	20	U	C1'-N1	5.89	1.57	1.48
54	AV	49	U	C1'-N1	5.87	1.57	1.48
54	AV	2	U	C1'-N1	5.86	1.57	1.48
54	AV	39	U	C1'-N1	5.83	1.57	1.48
54	AV	28	U	C1'-N1	5.78	1.57	1.48
54	AV	26	U	C1'-N1	5.75	1.57	1.48
23	BT	57	PRO	N-CA	5.66	1.58	1.46
54	AV	7	U	C1'-N1	5.57	1.55	1.47
77	Ae	135	PHE	N-CA	5.07	1.52	1.46
55	AX	6	U	C1'-N1	5.04	1.55	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	AA	824	G	OP2-P-O3'	-8.61	82.19	108.00
23	BT	57	PRO	N-CA-C	7.98	120.44	110.70
52	AA	824	G	OP1-P-O3'	-7.86	84.41	108.00
34	Bf	80	PRO	N-CA-CB	7.65	111.28	103.25
77	Ae	342	PRO	N-CA-CB	7.54	111.17	103.25
34	Bf	78	PRO	N-CA-CB	7.39	111.01	103.25
48	Bu	167	PRO	N-CA-CB	7.38	111.00	103.25
23	BT	58	PRO	CA-N-CD	-6.80	102.48	112.00
46	Bq	59	PRO	N-CA-CB	6.72	110.40	103.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B4	87	PRO	N-CA-CB	6.43	110.11	103.23
52	AA	825	C	OP1-P-OP2	5.71	136.73	119.60
23	BT	61	VAL	N-CA-C	-5.62	106.83	112.17

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
77	Ae	90	LEU	Peptide
23	BT	59	LYS	Peptide

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	18	0
2	B1	2036	0	2058	16	0
3	B2	1548	0	1583	24	0
4	B3	968	0	1018	28	0
5	B4	474	0	454	18	0
6	B5	902	0	916	17	0
7	B6	425	0	471	7	0
8	BB	1427	0	726	15	0
9	B7	387	0	413	11	0
10	BD	1860	0	1923	34	0
11	BE	2420	0	2418	44	0
12	BF	2011	0	2049	52	0
13	BG	1501	0	1587	42	0
14	BI	805	0	845	12	0
15	BJ	1705	0	1804	40	0
16	BK	1303	0	1343	19	0
17	BN	1444	0	1437	30	0
18	BO	896	0	946	14	0
19	BP	2312	0	2373	45	0
20	BQ	1803	0	1841	24	0
21	BR	1240	0	1260	23	0
22	BS	1168	0	1159	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	BT	1890	0	1898	86	0
24	BU	1159	0	1228	17	0
25	BV	1231	0	1278	23	0
26	BW	1374	0	1405	23	0
27	BX	1181	0	1139	23	0
28	BY	1678	0	1683	28	0
29	Ba	3173	0	3153	63	0
30	Bb	2952	0	2840	58	0
31	Bc	2408	0	2415	51	0
32	Bd	1158	0	1166	54	0
33	Be	972	0	971	20	0
34	Bf	827	0	736	12	0
35	Bg	1167	0	1173	21	0
36	B8	833	0	883	15	0
37	Bh	2319	0	2332	39	0
38	Bi	2138	0	2139	29	0
39	Bj	1775	0	1797	43	0
40	Bk	1246	0	1250	47	0
41	Bl	1097	0	1080	21	0
42	Bm	893	0	878	8	0
43	Bn	837	0	860	18	0
44	Bo	772	0	773	13	0
45	Bp	742	0	749	6	0
46	Bq	672	0	647	18	0
47	Bt	780	0	792	25	0
48	Bu	1198	0	1192	11	0
49	Bv	1131	0	1093	16	0
50	Bw	3126	0	3153	55	0
51	Bx	1325	0	1354	26	0
52	AA	20411	0	10345	347	0
53	B9	335	0	359	6	0
54	AV	1419	0	715	65	0
55	AX	100	0	51	6	0
56	BA	32844	0	16617	554	0
57	AB	1762	0	1774	29	0
58	AC	1075	0	1087	33	0
59	AE	2732	0	2774	50	0
60	AF	981	0	1012	20	0
61	AG	1721	0	1747	38	0
62	AI	2650	0	2613	46	0
63	AJ	1155	0	1193	28	0
64	AK	1007	0	1042	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	AL	840	0	890	21	0
66	AN	858	0	883	22	0
67	AO	1448	0	1536	22	0
68	AP	932	0	951	28	0
69	AQ	875	0	931	12	0
70	AR	784	0	813	16	0
71	AU	734	0	745	17	0
72	AZ	90	0	20	0	0
73	Aa	2378	0	2392	40	0
74	Ab	1101	0	1118	11	0
75	Ac	1367	0	1385	20	0
76	Ad	1467	0	1466	21	0
77	Ae	3109	0	3029	123	0
78	Af	778	0	791	13	0
79	Ag	2875	0	2886	70	0
80	Ah	1015	0	969	21	0
81	Ai	824	0	842	19	0
82	Aj	1788	0	1799	35	0
83	Ak	2222	0	2270	47	0
84	Am	930	0	959	23	0
85	An	639	0	709	9	0
86	Ao	4527	0	4391	72	0
87	Ap	1564	0	1531	33	0
88	CL	317	0	309	7	0
88	DL	213	0	234	5	0
88	EL	222	0	247	11	0
88	FL	213	0	234	7	0
88	GL	213	0	234	5	0
88	HL	205	0	223	8	0
89	AA	105	0	0	0	0
89	AB	1	0	0	0	0
89	AX	1	0	0	0	0
89	Ag	1	0	0	0	0
89	Am	1	0	0	0	0
89	An	1	0	0	0	0
89	B3	1	0	0	0	0
89	BA	204	0	0	0	0
89	BB	1	0	0	0	0
89	BD	3	0	0	0	0
89	BE	1	0	0	0	0
89	BJ	1	0	0	0	0
89	BP	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	BQ	1	0	0	0	0
89	Be	1	0	0	0	0
89	Bl	1	0	0	0	0
89	Bt	1	0	0	0	0
90	AR	1	0	0	0	0
90	Ac	1	0	0	0	0
90	Ap	1	0	0	0	0
90	B5	1	0	0	0	0
90	B9	1	0	0	0	0
90	Bx	1	0	0	0	0
91	AA	14	0	26	0	0
91	BA	28	0	52	5	0
92	BA	24	0	11	0	0
93	Ag	32	0	12	3	0
94	Ag	3	0	0	0	0
All	All	174700	0	147776	2719	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 9.

All (2719) 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)
32:Bd:76:GLU:CD	40:Bk:204:LEU:CD1	1.77	1.53
32:Bd:76:GLU:CD	40:Bk:204:LEU:HD13	1.04	1.44
32:Bd:76:GLU:CG	40:Bk:204:LEU:HD13	1.47	1.41
52:AA:533:C:O2'	84:Am:37:ARG:CZ	1.77	1.32
32:Bd:76:GLU:OE1	40:Bk:204:LEU:CD1	1.80	1.29
54:AV:9:U:O4	54:AV:20:U:O4	1.54	1.21
61:AG:71:THR:CG2	62:AI:252:GLN:HA	1.70	1.20
32:Bd:79:SER:CB	40:Bk:201:ARG:HH12	1.60	1.14
32:Bd:73:ARG:O	32:Bd:77:LYS:HD2	1.55	1.06
32:Bd:76:GLU:OE1	40:Bk:204:LEU:HD11	1.57	1.01
61:AG:71:THR:HG21	62:AI:252:GLN:CA	1.91	0.99
23:BT:56:PRO:O	77:Ae:134:LYS:N	1.96	0.98
52:AA:405:G:H1	52:AA:452:C:HO2'	1.10	0.97
32:Bd:76:GLU:HG2	40:Bk:204:LEU:HD13	1.43	0.96
61:AG:71:THR:HG22	62:AI:252:GLN:O	1.65	0.95
23:BT:57:PRO:C	77:Ae:135:PHE:HB3	1.92	0.95
61:AG:71:THR:HG21	62:AI:252:GLN:HA	0.95	0.94
13:BG:117:ASP:HB3	13:BG:131:ASN:HB2	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:533:C:O2'	84:Am:37:ARG:NH1	2.02	0.92
32:Bd:79:SER:OG	40:Bk:201:ARG:NH1	2.04	0.91
56:BA:118:U:H3	56:BA:129:A:H62	1.18	0.90
32:Bd:79:SER:CB	40:Bk:201:ARG:NH1	2.35	0.89
54:AV:10:U:H5	54:AV:42:U:O2'	1.54	0.89
23:BT:58:PRO:HD2	77:Ae:131:TYR:HA	1.55	0.89
23:BT:56:PRO:C	77:Ae:132:LEU:O	2.14	0.89
52:AA:11:G:H1	52:AA:524:U:H3	1.21	0.88
32:Bd:76:GLU:CD	40:Bk:204:LEU:HD12	1.98	0.87
23:BT:56:PRO:O	77:Ae:135:PHE:N	2.07	0.87
23:BT:57:PRO:N	77:Ae:136:ARG:H	1.72	0.87
23:BT:57:PRO:HA	77:Ae:131:TYR:O	1.75	0.86
23:BT:58:PRO:HG3	77:Ae:134:LYS:HB3	1.57	0.86
61:AG:71:THR:CG2	62:Al:252:GLN:CA	2.53	0.86
32:Bd:79:SER:HB2	40:Bk:201:ARG:NH1	1.93	0.83
52:AA:533:C:H4'	84:Am:37:ARG:HD2	1.61	0.83
23:BT:56:PRO:HB3	77:Ae:137:HIS:H	1.44	0.82
77:Ae:135:PHE:O	77:Ae:137:HIS:N	2.13	0.82
54:AV:50:U:H3	54:AV:54:U:H5	1.28	0.80
23:BT:56:PRO:HA	77:Ae:136:ARG:N	1.97	0.79
53:B9:76:CYS:SG	53:B9:89:CYS:HB2	2.22	0.79
75:Ac:33:ASN:HD21	75:Ac:70:MET:HB2	1.45	0.79
52:AA:548:G:H1	52:AA:785:U:H3	1.30	0.78
23:BT:56:PRO:C	77:Ae:135:PHE:H	1.91	0.77
29:Ba:126:THR:HG22	29:Ba:372:ASN:HB2	1.66	0.77
52:AA:537:A:N6	52:AA:825:C:C4	2.52	0.77
38:Bi:39:LYS:HE2	56:BA:834:C:H41	1.48	0.76
56:BA:920:C:H42	56:BA:924:G:H22	1.33	0.76
54:AV:25:U:C4	54:AV:26:U:O4	2.37	0.76
32:Bd:173:ARG:HH22	39:Bj:56:PRO:HB3	1.51	0.76
52:AA:66:C:H42	76:Ad:27:ARG:HB2	1.52	0.75
23:BT:56:PRO:C	77:Ae:135:PHE:N	2.44	0.75
32:Bd:76:GLU:CG	40:Bk:204:LEU:CD1	2.41	0.75
68:AP:53:SER:H	68:AP:67:ALA:HB3	1.51	0.74
52:AA:50:U:H2'	52:AA:51:G:H8	1.50	0.74
52:AA:533:C:HO2'	84:Am:37:ARG:CZ	1.95	0.74
52:AA:16:U:O2'	52:AA:294:A:N6	2.19	0.74
23:BT:57:PRO:CD	77:Ae:136:ARG:H	2.01	0.74
54:AV:26:U:H2'	54:AV:27:U:C6	2.23	0.74
32:Bd:76:GLU:HG2	40:Bk:204:LEU:CD1	2.14	0.73
32:Bd:76:GLU:HG2	40:Bk:204:LEU:HD22	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BE:69:ASN:ND2	56:BA:1569:A:N1	2.35	0.73
28:BY:161:ARG:HH21	28:BY:165:ILE:HB	1.53	0.73
23:BT:56:PRO:CA	77:Ae:136:ARG:N	2.51	0.73
86:Ao:543:HIS:HB2	86:Ao:588:ARG:HD2	1.71	0.72
56:BA:392:U:H2'	56:BA:393:A:H8	1.54	0.72
73:Aa:100:ILE:HG23	73:Aa:321:SER:HB3	1.71	0.72
15:BJ:101:HIS:HB3	15:BJ:150:HIS:HB3	1.72	0.72
54:AV:26:U:H2'	54:AV:27:U:H6	1.53	0.72
56:BA:486:A:H61	56:BA:582:C:H42	1.35	0.72
46:Bq:126:ILE:HD11	56:BA:548:A:H5''	1.71	0.72
37:Bh:97:TYR:HB2	37:Bh:181:SER:HA	1.72	0.72
54:AV:50:U:N3	54:AV:54:U:H5	1.88	0.72
23:BT:57:PRO:CD	77:Ae:136:ARG:HB2	2.20	0.71
52:AA:536:C:H2'	52:AA:537:A:H8	1.55	0.71
4:B3:134:MET:HG3	44:Bo:75:ARG:HE	1.56	0.71
52:AA:227:A:H61	52:AA:270:C:H42	1.38	0.71
52:AA:537:A:N6	52:AA:825:C:N4	2.39	0.71
39:Bj:264:LEU:HD13	39:Bj:269:LEU:HB3	1.71	0.71
23:BT:56:PRO:C	77:Ae:136:ARG:H	1.98	0.70
23:BT:58:PRO:N	77:Ae:135:PHE:HB3	2.06	0.70
77:Ae:172:LYS:HE2	77:Ae:209:MET:HB2	1.72	0.70
23:BT:57:PRO:HD2	77:Ae:136:ARG:HB2	1.73	0.70
52:AA:957:A:OP2	84:Am:24:ASN:ND2	2.24	0.70
54:AV:62:U:H2'	54:AV:63:U:H6	1.55	0.70
56:BA:529:G:H1'	56:BA:549:C:H1'	1.73	0.70
54:AV:62:U:H2'	54:AV:63:U:C6	2.27	0.70
54:AV:70:C:O2'	54:AV:71:A:N7	2.24	0.70
5:B4:38:ARG:NH1	32:Bd:132:GLU:OE1	2.25	0.70
12:BF:283:LEU:HB2	19:BP:125:ARG:HH12	1.57	0.70
56:BA:1026:A:O2'	56:BA:1277:G:N2	2.24	0.69
63:AJ:176:LYS:HB3	83:Ak:153:ILE:HB	1.74	0.69
73:Aa:287:THR:HG23	73:Aa:289:HIS:H	1.56	0.69
52:AA:194:U:H2'	52:AA:195:G:H8	1.57	0.69
86:Ao:485:ILE:HD12	86:Ao:491:PRO:HG3	1.72	0.69
4:B3:74:SER:HB3	56:BA:472:U:H5''	1.74	0.69
4:B3:78:ARG:HH12	20:BQ:225:GLY:HA3	1.57	0.69
52:AA:88:C:HO2'	68:AP:82:HIS:HE2	1.41	0.69
29:Ba:160:HIS:HA	29:Ba:164:TRP:HB2	1.75	0.69
31:Bc:175:ALA:HB2	31:Bc:316:SER:HB2	1.74	0.69
52:AA:84:A:N6	52:AA:98:A:O2'	2.26	0.69
58:AC:128:PRO:HD2	58:AC:131:LYS:HD3	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BU:33:GLY:O	24:BU:36:ASN:ND2	2.25	0.69
54:AV:38:U:C4	54:AV:39:U:O4	2.46	0.69
28:BY:146:VAL:HG22	28:BY:153:ILE:HG22	1.75	0.69
52:AA:533:C:O2'	84:Am:37:ARG:NE	2.26	0.69
5:B4:46:ARG:HH22	32:Bd:87:ASP:HB3	1.57	0.69
30:Bb:221:LEU:HB2	30:Bb:267:ARG:HG3	1.74	0.69
23:BT:56:PRO:HA	77:Ae:136:ARG:H	1.56	0.69
52:AA:724:U:OP1	61:AG:195:LYS:NZ	2.26	0.68
86:Ao:231:UNK:O	86:Ao:271:LYS:NZ	2.24	0.68
54:AV:10:U:C5	54:AV:42:U:O2'	2.36	0.68
83:Ak:63:ALA:HB3	83:Ak:66:GLN:HB2	1.73	0.68
17:BN:27:PRO:HG2	17:BN:30:LYS:HB2	1.75	0.68
12:BF:170:ARG:NH2	56:BA:222:G:N7	2.38	0.68
49:Bv:63:ARG:NH2	56:BA:95:U:OP1	2.27	0.68
50:Bw:236:ARG:HA	50:Bw:289:GLY:HA2	1.76	0.68
56:BA:803:A:N3	56:BA:805:C:N4	2.42	0.68
63:AJ:158:GLU:HG2	86:Ao:70:ILE:HD13	1.74	0.68
73:Aa:184:SER:H	73:Aa:192:ARG:HH12	1.41	0.68
50:Bw:146:GLN:HA	50:Bw:150:PHE:HB2	1.75	0.68
78:Af:162:THR:HG22	78:Af:164:LEU:H	1.59	0.68
4:B3:69:VAL:HG12	4:B3:119:ILE:HG12	1.75	0.68
8:BB:35:G:N2	40:Bk:124:SER:O	2.26	0.68
56:BA:1158:C:O2'	56:BA:1251:C:OP2	2.12	0.68
23:BT:55:GLN:N	77:Ae:174:GLN:O	2.27	0.68
50:Bw:53:ALA:O	50:Bw:62:ARG:NH2	2.27	0.68
88:CL:60:TYR:HB3	88:CL:64:ILE:HD11	1.76	0.68
56:BA:789:A:N6	56:BA:1000:A:O2'	2.28	0.68
38:Bi:211:GLN:HA	38:Bi:248:PHE:O	1.94	0.67
52:AA:344:G:O6	64:AK:124:LYS:NZ	2.26	0.67
52:AA:942:G:N2	52:AA:945:A:OP2	2.25	0.67
66:AN:81:ASP:HA	66:AN:86:ARG:HD3	1.75	0.67
39:Bj:256:SER:O	39:Bj:260:LEU:HB2	1.93	0.67
1:B0:121:PRO:HA	30:Bb:50:LYS:HG3	1.75	0.67
15:BJ:47:LEU:HD22	20:BQ:226:ILE:HG12	1.76	0.67
56:BA:112:A:N6	56:BA:115:U:OP2	2.28	0.67
56:BA:198:U:H2'	56:BA:199:A:H8	1.60	0.67
1:B0:41:ASN:HD21	56:BA:1177:U:H3'	1.57	0.67
13:BG:109:ILE:HA	13:BG:113:PRO:HB3	1.75	0.67
41:Bl:110:ILE:HD11	41:Bl:157:LEU:HD13	1.76	0.67
43:Bn:69:HIS:HD2	43:Bn:71:LYS:HG3	1.59	0.67
86:Ao:268:GLY:HA2	86:Ao:271:LYS:HE2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BS:122:VAL:HG13	22:BS:157:SER:HA	1.77	0.67
28:BY:191:LEU:HG	33:Be:93:THR:HG21	1.76	0.67
78:Af:105:ILE:HG12	78:Af:115:ILE:HG12	1.77	0.67
23:BT:56:PRO:CA	77:Ae:136:ARG:H	2.07	0.67
27:BX:41:GLN:NE2	56:BA:703:A:OP1	2.28	0.67
35:Bg:133:PHE:HZ	37:Bh:261:SER:HB2	1.58	0.67
56:BA:569:C:N4	56:BA:1020:C:O2	2.28	0.67
13:BG:229:ASP:OD1	13:BG:232:ARG:NH2	2.28	0.67
36:B8:113:ARG:NH2	56:BA:84:G:OP2	2.28	0.66
54:AV:9:U:C4	54:AV:20:U:O4	2.47	0.66
56:BA:889:C:H41	56:BA:1082:U:H4'	1.60	0.66
30:Bb:371:ASP:OD1	36:B8:185:ASN:ND2	2.28	0.66
52:AA:463:U:O4	52:AA:464:A:N6	2.28	0.66
55:AX:3:U:HO2'	55:AX:4:U:H5	1.43	0.66
56:BA:743:U:H3'	56:BA:744:A:H5''	1.77	0.66
25:BV:150:LYS:HE3	34:Bf:58:ILE:HD11	1.77	0.66
35:Bg:28:ARG:HG2	35:Bg:78:GLU:HB2	1.78	0.66
52:AA:923:G:H1'	52:AA:944:A:H2	1.59	0.66
5:B4:73:ARG:NH1	40:Bk:147:ASP:OD1	2.26	0.66
12:BF:142:ARG:NH2	56:BA:129:A:OP1	2.29	0.66
52:AA:57:A:C8	82:Aj:51:PRO:HB3	2.31	0.66
54:AV:10:U:H5	54:AV:42:U:HO2'	0.74	0.66
30:Bb:27:ARG:N	56:BA:1168:A:N1	2.42	0.66
13:BG:140:SER:HB2	13:BG:143:LEU:HB2	1.77	0.66
38:Bi:267:PRO:HG2	38:Bi:270:ALA:HB2	1.78	0.66
47:Bt:78:GLN:NE2	56:BA:420:U:O4	2.29	0.66
52:AA:248:C:N4	65:AL:117:ASP:OD2	2.29	0.66
52:AA:349:A:N3	52:AA:426:G:O2'	2.29	0.66
23:BT:57:PRO:HA	77:Ae:131:TYR:C	2.21	0.66
74:Ab:71:ARG:HH12	78:Af:91:THR:HG22	1.61	0.66
54:AV:38:U:C2	54:AV:39:U:C5	2.84	0.65
68:AP:20:ARG:NH2	68:AP:41:CYS:SG	2.69	0.65
52:AA:492:U:OP1	85:An:139:ASN:ND2	2.30	0.65
88:HL:76:LEU:HD12	88:HL:79:ILE:HD11	1.78	0.65
16:BK:25:ARG:HB3	16:BK:28:GLN:HB2	1.78	0.65
19:BP:142:GLU:HG3	19:BP:162:LEU:HD23	1.78	0.65
57:AB:215:ASN:OD1	74:Ab:15:ARG:NH1	2.29	0.65
68:AP:64:LYS:HE3	73:Aa:176:ALA:HB3	1.79	0.65
20:BQ:35:PRO:HA	46:Bq:121:LEU:HD11	1.77	0.65
53:B9:69:LEU:H	56:BA:560:A:H62	1.43	0.65
77:Ae:97:MET:HE1	77:Ae:107:VAL:HG21	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BS:68:TRP:CD1	22:BS:68:TRP:H	2.12	0.65
39:Bj:162:ARG:HB3	39:Bj:251:HIS:HB2	1.79	0.65
88:FL:76:LEU:HD12	88:FL:79:ILE:HD11	1.78	0.65
23:BT:61:VAL:HB	77:Ae:90:LEU:HA	1.78	0.65
39:Bj:55:ARG:HG3	39:Bj:238:LEU:HD23	1.78	0.65
82:Aj:132:GLU:HG2	82:Aj:133:GLN:HG3	1.77	0.65
34:Bf:127:GLY:N	56:BA:159:A:OP2	2.30	0.65
56:BA:53:U:O4	56:BA:62:C:N3	2.30	0.65
80:Ah:345:LEU:HD21	81:Ai:26:THR:HG21	1.78	0.65
56:BA:645:U:H2'	56:BA:646:A:H8	1.62	0.65
82:Aj:70:ARG:HH21	82:Aj:141:LEU:HD21	1.61	0.65
6:B5:156:THR:HG22	6:B5:173:ARG:HB3	1.79	0.65
31:Bc:210:ASP:OD2	31:Bc:268:ARG:NH1	2.30	0.65
27:BX:37:GLU:HB3	27:BX:104:THR:HG23	1.79	0.65
11:BE:45:SER:O	31:Bc:303:ARG:NH2	2.30	0.64
79:Ag:241:ILE:HA	79:Ag:244:LYS:HE2	1.78	0.64
84:Am:100:PRO:HD2	84:Am:103:LYS:HD2	1.79	0.64
88:DL:76:LEU:HD12	88:DL:79:ILE:HD11	1.78	0.64
23:BT:96:ARG:NH1	23:BT:285:GLU:OE1	2.31	0.64
41:Bl:138:THR:HG22	41:Bl:149:VAL:HG12	1.78	0.64
56:BA:1066:A:H2'	56:BA:1067:G:H8	1.61	0.64
56:BA:1404:G:N2	56:BA:1404:G:OP2	2.30	0.64
56:BA:1418:G:N2	56:BA:1421:A:OP2	2.26	0.64
11:BE:50:ASP:O	21:BR:139:ARG:NH1	2.30	0.64
86:Ao:586:PHE:HD2	86:Ao:591:ARG:HB3	1.62	0.64
3:B2:228:LEU:HD11	56:BA:11:G:H5'	1.78	0.64
56:BA:877:U:H5''	56:BA:878:G:H5'	1.78	0.64
70:AR:95:ARG:HH12	70:AR:102:GLY:HA2	1.62	0.64
33:Be:44:ARG:HH12	50:Bw:157:ALA:HB3	1.62	0.64
43:Bn:35:ARG:NH1	43:Bn:37:THR:O	2.30	0.64
37:Bh:80:GLN:O	37:Bh:210:ARG:NH2	2.31	0.64
39:Bj:159:LEU:HD11	39:Bj:252:HIS:HB2	1.79	0.64
52:AA:902:C:H5''	85:An:171:ARG:HD2	1.80	0.64
79:Ag:63:GLU:O	79:Ag:350:LYS:NZ	2.31	0.64
12:BF:92:ARG:NH1	56:BA:215:A:OP1	2.30	0.64
32:Bd:76:GLU:OE2	40:Bk:204:LEU:CD1	2.42	0.64
88:EL:76:LEU:HD12	88:EL:79:ILE:HD11	1.78	0.64
19:BP:164:ILE:HG12	19:BP:174:VAL:HG11	1.80	0.64
52:AA:876:A:H5'	52:AA:877:A:H5'	1.80	0.64
58:AC:76:LEU:O	66:AN:103:ARG:NH2	2.29	0.64
79:Ag:240:GLY:HA3	79:Ag:291:ASN:HD22	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:821:A:OP1	61:AG:177:ARG:NH1	2.31	0.64
66:AN:41:ARG:NH1	81:Ai:48:THR:O	2.31	0.64
13:BG:130:LEU:O	13:BG:134:SER:OG	2.14	0.64
50:Bw:344:ASP:OD2	50:Bw:383:ARG:NH2	2.31	0.64
10:BD:76:PRO:HB2	10:BD:103:ARG:HD2	1.79	0.63
88:GL:76:LEU:HD12	88:GL:79:ILE:HD11	1.78	0.63
56:BA:1369:U:H5''	56:BA:1370:U:H5'	1.78	0.63
23:BT:58:PRO:HD2	77:Ae:131:TYR:CA	2.27	0.63
31:Bc:112:MET:HB2	31:Bc:267:PRO:HB3	1.79	0.63
79:Ag:323:LEU:HD13	83:Ak:306:ASP:HB2	1.80	0.63
80:Ah:326:LEU:HB2	80:Ah:347:THR:HG23	1.80	0.63
4:B3:78:ARG:O	4:B3:83:LYS:NZ	2.32	0.63
15:BJ:95:MET:HB2	15:BJ:159:PRO:HB3	1.80	0.63
19:BP:203:ARG:HH21	19:BP:262:PRO:HA	1.62	0.63
29:Ba:367:ASP:O	29:Ba:371:LYS:NZ	2.32	0.63
48:Bu:52:SER:HB3	48:Bu:57:THR:HG21	1.80	0.63
52:AA:283:U:OP1	59:AE:419:ARG:NH1	2.31	0.63
54:AV:54:U:H2'	54:AV:55:U:H5''	1.80	0.63
56:BA:388:A:H2'	56:BA:389:A:H8	1.63	0.63
13:BG:168:ASN:OD1	13:BG:170:ASN:ND2	2.27	0.63
86:Ao:420:GLN:O	86:Ao:463:LYS:NZ	2.31	0.63
17:BN:62:THR:HB	17:BN:129:PRO:HA	1.81	0.63
54:AV:1:U:H2'	54:AV:2:U:C6	2.34	0.63
54:AV:40:U:H2'	54:AV:41:U:C6	2.33	0.63
56:BA:135:G:N1	56:BA:138:A:OP2	2.31	0.63
67:AO:110:MET:SD	67:AO:114:ASN:ND2	2.72	0.63
6:B5:93:ARG:NH2	56:BA:642:G:OP1	2.32	0.63
7:B6:42:THR:HG23	7:B6:57:VAL:HG12	1.81	0.63
63:Aj:179:GLN:HA	83:Ak:149:PHE:HA	1.81	0.63
79:Ag:264:VAL:HG21	79:Ag:307:LEU:HD13	1.79	0.63
3:B2:204:MET:HE3	3:B2:205:PRO:HD2	1.79	0.63
19:BP:72:THR:HB	19:BP:77:ARG:HH21	1.64	0.63
29:Ba:35:VAL:HB	29:Ba:38:THR:HG22	1.80	0.63
77:Ae:162:GLN:OE1	77:Ae:196:ASN:ND2	2.31	0.63
36:B8:123:LEU:HD11	36:B8:147:PHE:HB3	1.81	0.63
56:BA:831:U:OP2	56:BA:836:A:N6	2.23	0.63
56:BA:935:C:H4'	56:BA:1426:G:H1'	1.81	0.63
56:BA:1081:U:O4	56:BA:1135:C:N3	2.31	0.63
13:BG:168:ASN:ND2	65:AL:65:THR:O	2.31	0.62
17:BN:111:MET:HE3	56:BA:571:A:H2	1.64	0.62
46:Bq:68:LEU:HA	46:Bq:73:MET:HE2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B4:51:ARG:HB3	39:Bj:85:SER:HB2	1.81	0.62
19:BP:109:ARG:NH2	41:Bl:91:MET:SD	2.70	0.62
19:BP:208:GLU:HB3	49:Bv:103:LEU:HD21	1.80	0.62
40:Bk:97:ALA:HB3	40:Bk:103:ALA:HB2	1.81	0.62
52:AA:647:A:OP2	62:Al:221:GLN:NE2	2.31	0.62
70:AR:141:TYR:O	71:Au:28:ARG:NH1	2.32	0.62
75:Ac:73:SER:OG	76:Ad:120:ARG:NH2	2.32	0.62
75:Ac:132:ARG:NH1	75:Ac:136:LEU:O	2.33	0.62
22:BS:39:VAL:HB	22:BS:42:GLU:HB2	1.81	0.62
52:AA:587:U:O2	52:AA:707:A:N6	2.32	0.62
57:AB:137:ARG:HD3	74:Ab:34:ILE:HD11	1.82	0.62
58:AC:163:VAL:HG11	58:AC:167:ILE:HB	1.81	0.62
60:AF:27:GLU:HG3	76:Ad:170:ARG:HH12	1.64	0.62
30:Bb:194:THR:OG1	30:Bb:197:GLU:OE1	2.17	0.62
54:AV:27:U:H2'	54:AV:28:U:H6	1.64	0.62
56:BA:869:G:O2'	56:BA:966:U:OP2	2.17	0.62
61:AG:168:TYR:HB3	61:AG:236:LEU:HD13	1.81	0.62
3:B2:172:ARG:NH1	56:BA:22:U:O4	2.32	0.62
73:Aa:205:LYS:NZ	87:Ap:182:GLY:O	2.32	0.62
9:B7:58:PRO:HB2	56:BA:672:G:H4'	1.80	0.62
46:Bq:123:LYS:HG3	56:BA:531:G:H5''	1.81	0.62
47:Bt:23:ARG:NH1	56:BA:464:U:OP1	2.33	0.62
56:BA:843:C:N4	56:BA:871:A:O2'	2.33	0.62
79:Ag:358:TYR:O	79:Ag:362:ASN:ND2	2.32	0.62
5:B4:43:ARG:NH1	5:B4:44:LEU:O	2.32	0.62
15:BJ:237:VAL:HA	88:GL:76:LEU:HD11	1.81	0.62
56:BA:49:A:H2'	56:BA:50:A:C8	2.34	0.62
56:BA:1278:C:H2'	56:BA:1279:G:H8	1.64	0.62
75:Ac:51:ASN:ND2	75:Ac:95:ASN:OD1	2.32	0.62
21:BR:106:ARG:HD3	21:BR:136:LEU:HD11	1.82	0.62
54:AV:36:U:H2'	54:AV:37:U:C6	2.35	0.62
56:BA:776:C:O2'	56:BA:778:A:N7	2.33	0.62
87:Ap:89:ARG:HD3	87:Ap:144:MET:HE3	1.82	0.62
24:BU:85:ALA:O	24:BU:89:ASN:ND2	2.33	0.62
25:BV:198:ARG:NH2	35:Bg:13:SER:OG	2.33	0.62
29:Ba:280:GLN:HG2	50:Bw:152:ARG:HE	1.64	0.61
35:Bg:73:PRO:HB2	35:Bg:89:ILE:HG13	1.81	0.61
51:Bx:164:ASN:O	56:BA:568:C:O2'	2.16	0.61
52:AA:567:C:H2'	52:AA:568:G:H8	1.65	0.61
56:BA:218:A:N6	56:BA:229:A:O4'	2.33	0.61
4:B3:104:PRO:HA	4:B3:107:ASN:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BS:86:THR:O	22:BS:120:ARG:NH1	2.33	0.61
32:Bd:171:PHE:HB3	40:Bk:186:VAL:HB	1.82	0.61
77:Ae:80:TRP:HH2	77:Ae:151:THR:HG23	1.64	0.61
86:Ao:80:ARG:NH1	86:Ao:487:SER:OG	2.32	0.61
1:B0:88:CYS:SG	56:BA:1207:C:O2'	2.58	0.61
10:BD:113:ARG:O	10:BD:148:ARG:NH2	2.33	0.61
13:BG:110:ARG:HG2	13:BG:260:LEU:HD23	1.82	0.61
23:BT:57:PRO:HG3	77:Ae:132:LEU:HD23	1.82	0.61
36:B8:108:LYS:NZ	56:BA:77:U:OP2	2.30	0.61
56:BA:215:A:H61	56:BA:231:C:H42	1.46	0.61
73:Aa:198:GLU:OE2	73:Aa:204:ARG:NH1	2.33	0.61
77:Ae:294:GLY:O	77:Ae:298:ARG:NH1	2.33	0.61
54:AV:38:U:H2'	54:AV:39:U:C6	2.36	0.61
56:BA:376:A:N6	56:BA:1061:U:O2	2.33	0.61
4:B3:134:MET:HE1	44:Bo:78:VAL:HG21	1.82	0.61
52:AA:374:C:OP2	84:Am:9:ARG:NH2	2.31	0.61
83:Ak:216:LEU:O	83:Ak:220:ASN:ND2	2.33	0.61
8:BB:73:A:N3	39:Bj:268:TYR:OH	2.33	0.61
29:Ba:174:GLU:HA	29:Ba:296:SER:HB2	1.82	0.61
31:Bc:183:ASP:HB3	31:Bc:186:LEU:HD13	1.83	0.61
31:Bc:278:SER:O	31:Bc:317:ARG:NH1	2.34	0.61
46:Bq:64:ASP:H	46:Bq:65:PRO:HD2	1.66	0.61
50:Bw:63:VAL:HA	50:Bw:66:TRP:CD1	2.35	0.61
52:AA:57:A:O2'	52:AA:59:C:OP1	2.17	0.61
87:Ap:91:ARG:NH1	87:Ap:101:ALA:O	2.34	0.61
87:Ap:93:MET:HE2	87:Ap:96:ARG:HG2	1.83	0.61
9:B7:85:ARG:HE	9:B7:90:ARG:HG3	1.65	0.61
30:Bb:364:ARG:HD2	56:BA:1194:U:H5''	1.83	0.61
37:Bh:60:ARG:HD2	37:Bh:63:LYS:HD2	1.83	0.61
56:BA:975:G:O2'	56:BA:977:G:OP2	2.19	0.61
57:AB:155:GLU:OE1	62:AI:163:HIS:ND1	2.34	0.61
65:AL:63:LEU:HD11	65:AL:84:ARG:HB2	1.83	0.61
15:BJ:46:LYS:HE3	47:Bt:31:ALA:HB1	1.83	0.61
28:BY:25:ARG:HB3	28:BY:28:SER:HB3	1.83	0.61
62:AI:292:GLY:HA3	62:AI:325:GLY:HA2	1.82	0.61
12:BF:212:TRP:O	12:BF:258:THR:OG1	2.18	0.61
22:BS:104:SER:O	22:BS:135:ARG:NH1	2.32	0.61
40:Bk:94:HIS:ND1	40:Bk:154:GLU:OE2	2.33	0.61
87:Ap:90:THR:H	87:Ap:144:MET:HE2	1.66	0.61
52:AA:542:C:O2	52:AA:824:G:N2	2.34	0.60
68:AP:35:VAL:HG23	68:AP:50:GLN:HA	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Bi:90:PRO:HB2	38:Bi:269:TRP:HH2	1.65	0.60
43:Bn:77:PRO:HG2	43:Bn:80:LEU:HB2	1.83	0.60
68:AP:59:ASN:ND2	68:AP:63:GLU:O	2.34	0.60
80:Ah:284:ARG:HH22	86:Ao:457:ARG:HH11	1.49	0.60
10:BD:207:TYR:OH	10:BD:296:TYR:OH	2.18	0.60
54:AV:9:U:O4	54:AV:20:U:C4	2.47	0.60
54:AV:39:U:H2'	54:AV:40:U:C6	2.36	0.60
61:AG:187:MET:HG2	61:AG:219:VAL:HG21	1.84	0.60
86:Ao:460:TYR:HA	86:Ao:463:LYS:HE2	1.82	0.60
3:B2:119:GLN:NE2	56:BA:702:A:OP1	2.34	0.60
15:BJ:214:LEU:HB2	88:DL:90:LEU:HD11	1.82	0.60
52:AA:438:C:H2'	52:AA:439:A:H8	1.66	0.60
56:BA:1326:A:O2'	56:BA:1328:G:OP2	2.18	0.60
5:B4:43:ARG:NH2	8:BB:32:A:OP1	2.30	0.60
11:BE:236:THR:HG23	11:BE:239:ARG:HD2	1.84	0.60
11:BE:238:ARG:NH2	56:BA:993:U:OP2	2.35	0.60
19:BP:33:SER:O	56:BA:234:G:N2	2.35	0.60
19:BP:44:ARG:HD3	19:BP:45:ARG:HG3	1.83	0.60
52:AA:884:C:OP1	77:Ae:433:ARG:NH1	2.33	0.60
1:B0:59:HIS:NE2	56:BA:412:C:O2'	2.34	0.60
10:BD:262:GLY:HA2	56:BA:311:A:H5'	1.82	0.60
12:BF:221:LEU:HD22	12:BF:264:PRO:HB2	1.83	0.60
23:BT:58:PRO:CD	77:Ae:131:TYR:O	2.50	0.60
50:Bw:49:ALA:O	50:Bw:61:ARG:NH1	2.34	0.60
56:BA:1387:A:O2'	56:BA:1388:A:O5'	2.15	0.60
70:AR:66:CYS:HB3	70:AR:101:CYS:H	1.65	0.60
71:AU:15:GLN:HG2	71:AU:16:GLU:HG2	1.84	0.60
17:BN:68:SER:OG	17:BN:71:LYS:NZ	2.30	0.60
22:BS:154:ALA:HA	22:BS:159:LYS:HE3	1.84	0.60
56:BA:1416:G:H2'	56:BA:1417:A:H8	1.67	0.60
59:AE:150:ARG:HG2	59:AE:155:GLN:HG2	1.83	0.60
62:AI:366:ARG:HB3	62:AI:371:LEU:HD12	1.84	0.60
77:Ae:142:TRP:HZ2	82:Aj:76:LEU:HD11	1.66	0.60
10:BD:110:LEU:HD23	10:BD:113:ARG:HE	1.66	0.60
12:BF:132:GLY:HA3	38:Bi:42:THR:HG21	1.82	0.60
13:BG:111:THR:HG21	13:BG:185:VAL:H	1.66	0.60
27:BX:2:ALA:N	27:BX:7:TYR:HH	1.98	0.60
52:AA:527:G:O2'	52:AA:843:C:OP2	2.18	0.60
64:AK:179:ASP:HB2	71:AU:26:LEU:HD21	1.84	0.60
83:Ak:154:ASP:HB2	83:Ak:174:THR:HB	1.83	0.60
87:Ap:110:ASP:HB3	87:Ap:113:LEU:HD23	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B3:75:THR:HG21	4:B3:86:ILE:HG21	1.83	0.60
22:BS:65:GLU:OE1	22:BS:75:ARG:NH1	2.35	0.60
29:Ba:144:ARG:O	29:Ba:194:LYS:NZ	2.30	0.60
31:Bc:85:PRO:HG2	31:Bc:112:MET:HA	1.84	0.60
40:Bk:48:TYR:N	56:BA:402:A:OP1	2.34	0.60
18:BO:77:ILE:HG22	18:BO:78:ARG:HG3	1.83	0.60
26:BW:131:ASN:O	38:Bi:230:ARG:NH2	2.35	0.60
30:Bb:279:ILE:HD11	30:Bb:310:ALA:HB3	1.84	0.60
51:Bx:70:CYS:SG	51:Bx:108:CYS:N	2.75	0.60
15:BJ:95:MET:HB3	15:BJ:156:SER:HB3	1.82	0.59
27:BX:145:PRO:HG3	38:Bi:176:ILE:HD13	1.84	0.59
30:Bb:240:ILE:HD12	30:Bb:245:VAL:HA	1.83	0.59
54:AV:27:U:H2'	54:AV:28:U:C6	2.37	0.59
56:BA:243:A:N3	56:BA:1266:U:O2'	2.35	0.59
56:BA:993:U:H2'	56:BA:994:A:H8	1.66	0.59
4:B3:72:ILE:HD11	4:B3:118:ARG:HB2	1.82	0.59
4:B3:77:ARG:NH1	56:BA:470:C:OP2	2.34	0.59
9:B7:88:LYS:NZ	56:BA:127:G:OP2	2.30	0.59
22:BS:173:ARG:HE	56:BA:1218:U:H5'	1.67	0.59
35:Bg:48:GLU:OE2	47:Bt:101:TRP:NE1	2.28	0.59
50:Bw:147:GLU:HG3	50:Bw:170:PHE:HA	1.84	0.59
52:AA:847:C:N4	55:AX:6:U:OP1	2.35	0.59
50:Bw:264:LYS:NZ	56:BA:705:U:O4	2.35	0.59
56:BA:148:A:H4'	56:BA:149:A:H5''	1.84	0.59
83:Ak:176:ARG:HG2	83:Ak:208:THR:HG22	1.83	0.59
19:BP:132:SER:OG	56:BA:225:C:OP1	2.17	0.59
23:BT:57:PRO:O	77:Ae:135:PHE:HD2	1.84	0.59
56:BA:611:U:H2'	56:BA:612:A:H8	1.67	0.59
6:B5:95:ARG:NH1	56:BA:157:A:OP2	2.36	0.59
15:BJ:123:MET:HB2	15:BJ:152:LEU:HD11	1.84	0.59
27:BX:71:ARG:NH2	27:BX:73:GLN:OE1	2.36	0.59
46:Bq:71:HIS:HA	46:Bq:86:LEU:HG	1.83	0.59
52:AA:714:U:H2'	52:AA:715:G:H8	1.67	0.59
11:BE:69:ASN:HD21	11:BE:154:HIS:HE1	1.50	0.59
40:Bk:90:VAL:HG12	40:Bk:160:SER:HA	1.84	0.59
52:AA:952:C:OP1	71:AU:52:ARG:NH2	2.36	0.59
56:BA:1281:A:O2'	56:BA:1283:U:O4	2.17	0.59
10:BD:103:ARG:NE	56:BA:735:A:OP1	2.36	0.59
21:BR:141:SER:O	21:BR:147:ASN:ND2	2.34	0.59
32:Bd:76:GLU:HG2	40:Bk:204:LEU:CD2	2.32	0.59
39:Bj:214:LYS:HZ3	39:Bj:230:LYS:HD3	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:AV:19:U:H2'	54:AV:20:U:C6	2.38	0.59
56:BA:220:G:H1'	56:BA:231:C:H1'	1.84	0.59
56:BA:672:G:H21	56:BA:759:C:H5'	1.67	0.59
62:AI:115:GLY:HA3	63:AJ:84:ASP:HB2	1.85	0.59
2:B1:41:VAL:HG21	2:B1:83:GLU:HB3	1.84	0.59
21:BR:13:ARG:NH2	56:BA:995:C:OP1	2.35	0.59
25:BV:88:ASN:ND2	25:BV:206:PRO:O	2.30	0.59
52:AA:579:A:OP2	66:AN:108:ARG:NH1	2.35	0.59
54:AV:18:U:C5	54:AV:44:U:H4'	2.38	0.59
68:AP:102:MET:SD	76:Ad:60:TYR:OH	2.60	0.59
75:Ac:112:THR:HA	75:Ac:115:LYS:HE3	1.85	0.59
2:B1:81:GLY:O	2:B1:130:ARG:NH1	2.35	0.59
13:BG:130:LEU:O	13:BG:134:SER:CB	2.50	0.59
32:Bd:76:GLU:OE1	40:Bk:204:LEU:HD13	1.57	0.59
52:AA:116:G:OP1	67:AO:207:LYS:NZ	2.33	0.59
52:AA:386:U:H4'	60:AF:94:VAL:HG12	1.85	0.59
52:AA:578:G:H5''	52:AA:579:A:H2'	1.84	0.59
53:B9:69:LEU:HD22	53:B9:97:GLN:HB3	1.85	0.59
56:BA:52:A:O2'	56:BA:349:A:N3	2.32	0.59
80:Ah:379:LEU:HD13	80:Ah:386:LEU:HB2	1.84	0.59
5:B4:68:ARG:NH1	40:Bk:99:ASP:OD2	2.36	0.59
12:BF:92:ARG:NH2	41:Bl:144:THR:OG1	2.36	0.59
52:AA:800:G:H2'	52:AA:801:A:C8	2.38	0.59
56:BA:842:U:OP2	56:BA:871:A:N6	2.28	0.59
58:AC:75:ASN:HD21	66:AN:104:TRP:HE1	1.50	0.59
63:AJ:89:ASP:OD1	63:AJ:141:ARG:NH2	2.36	0.59
11:BE:221:ARG:NH1	11:BE:257:MET:O	2.35	0.58
24:BU:146:VAL:HG11	34:Bf:56:ARG:HG2	1.85	0.58
75:Ac:47:PHE:HA	75:Ac:51:ASN:HD22	1.67	0.58
79:Ag:221:LEU:HD21	79:Ag:242:VAL:HG13	1.85	0.58
82:Aj:68:LEU:HD21	82:Aj:100:VAL:HG21	1.84	0.58
11:BE:206:VAL:HG11	11:BE:289:VAL:HG13	1.84	0.58
17:BN:6:LYS:NZ	37:Bh:230:GLU:OE2	2.36	0.58
25:BV:119:LEU:HD11	25:BV:194:GLN:HB3	1.85	0.58
28:BY:65:LEU:HD11	28:BY:121:LYS:HG3	1.84	0.58
38:Bi:192:PRO:HB3	38:Bi:216:MET:HG2	1.84	0.58
76:Ad:112:GLU:OE2	76:Ad:115:ARG:NH2	2.36	0.58
19:BP:16:LEU:HD23	19:BP:19:LEU:HD12	1.84	0.58
52:AA:568:G:H21	63:AJ:126:ILE:HD13	1.68	0.58
10:BD:102:GLN:NE2	56:BA:733:A:OP1	2.37	0.58
10:BD:258:ILE:HG23	10:BD:263:ARG:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BJ:97:ALA:HB3	15:BJ:154:LEU:HB2	1.85	0.58
19:BP:44:ARG:NH2	56:BA:602:G:N7	2.45	0.58
30:Bb:160:ASP:OD2	30:Bb:267:ARG:NH2	2.36	0.58
47:Bt:66:ARG:NH2	56:BA:417:G:OP1	2.34	0.58
52:AA:512:A:H2'	52:AA:513:A:H8	1.67	0.58
26:BW:82:LYS:HD3	26:BW:147:ARG:HB3	1.85	0.58
52:AA:77:G:OP1	82:Aj:3:ARG:NH2	2.35	0.58
56:BA:197:U:H2'	56:BA:198:U:H6	1.68	0.58
56:BA:229:A:H4'	56:BA:230:G:H5'	1.85	0.58
56:BA:266:C:O2'	56:BA:281:A:N6	2.33	0.58
56:BA:1224:C:H2'	56:BA:1225:A:H8	1.67	0.58
75:Ac:29:VAL:HB	75:Ac:79:TYR:HB2	1.84	0.58
87:Ap:105:CYS:HB3	87:Ap:142:VAL:HA	1.85	0.58
19:BP:137:GLY:HA3	19:BP:157:GLN:HG3	1.84	0.58
37:Bh:245:LEU:HB3	37:Bh:250:ILE:HB	1.85	0.58
39:Bj:58:LEU:HD12	39:Bj:153:LEU:HD22	1.85	0.58
42:Bm:76:LYS:HE2	42:Bm:83:VAL:HG21	1.86	0.58
11:BE:104:LEU:HB2	11:BE:121:LEU:HB2	1.85	0.58
32:Bd:76:GLU:HG2	40:Bk:204:LEU:CG	2.34	0.58
56:BA:550:A:N7	56:BA:551:A:N6	2.51	0.58
82:Aj:166:TYR:O	87:Ap:199:TRP:NE1	2.33	0.58
20:BQ:103:GLU:OE2	20:BQ:106:ARG:NH2	2.33	0.58
32:Bd:97:LYS:HB3	39:Bj:84:TYR:HB2	1.86	0.58
33:Be:32:LYS:NZ	56:BA:35:A:OP1	2.31	0.58
52:AA:349:A:OP2	64:AK:121:ASN:ND2	2.37	0.58
56:BA:1338:G:H2'	56:BA:1339:A:H8	1.69	0.58
61:AG:119:LYS:NZ	79:Ag:364:TRP:O	2.30	0.58
79:Ag:174:LYS:HE3	79:Ag:176:ARG:HH12	1.68	0.58
88:EL:89:THR:HG23	88:EL:90:LEU:HG	1.85	0.58
26:BW:105:GLU:OE1	26:BW:116:LYS:NZ	2.37	0.58
31:Bc:204:ARG:NH2	31:Bc:276:GLU:OE2	2.37	0.58
59:AE:191:ARG:NH2	87:Ap:80:ASN:OD1	2.37	0.58
68:AP:111:ARG:NH2	73:Aa:168:LYS:O	2.37	0.58
82:Aj:98:THR:HG22	82:Aj:116:GLY:HA2	1.84	0.58
1:B0:92:LEU:HB3	22:BS:66:ARG:HH21	1.69	0.58
52:AA:950:U:H2'	52:AA:951:G:C8	2.38	0.58
59:AE:289:THR:HG21	59:AE:308:GLN:H	1.68	0.58
26:BW:77:GLN:H	26:BW:171:HIS:CD2	2.22	0.57
50:Bw:240:GLN:OE1	50:Bw:347:ARG:NH1	2.36	0.57
62:AI:120:ARG:NH2	83:Ak:91:TYR:OH	2.37	0.57
23:BT:57:PRO:N	77:Ae:136:ARG:N	2.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Ba:395:LYS:HD3	56:BA:269:U:H5''	1.86	0.57
39:Bj:129:LEU:O	39:Bj:132:LYS:NZ	2.36	0.57
52:AA:217:U:H2'	52:AA:218:A:H8	1.69	0.57
23:BT:183:LEU:HD21	23:BT:219:GLN:HG2	1.85	0.57
25:BV:126:VAL:HG11	25:BV:132:ILE:HD11	1.86	0.57
28:BY:145:ARG:HH22	28:BY:157:PRO:HD3	1.69	0.57
35:Bg:28:ARG:NH1	37:Bh:71:GLU:OE2	2.30	0.57
68:AP:59:ASN:HD21	68:AP:63:GLU:HB2	1.69	0.57
16:BK:17:SER:N	16:BK:72:VAL:O	2.36	0.57
52:AA:210:U:H2'	52:AA:211:A:H8	1.68	0.57
56:BA:198:U:H2'	56:BA:199:A:C8	2.39	0.57
5:B4:62:GLY:HA3	32:Bd:182:ILE:H	1.69	0.57
31:Bc:282:ASN:HD21	31:Bc:289:LEU:HD12	1.69	0.57
52:AA:552:A:H2'	52:AA:553:G:H8	1.69	0.57
52:AA:586:U:OP1	66:AN:36:ARG:NH2	2.37	0.57
56:BA:122:G:N2	56:BA:125:A:OP2	2.36	0.57
64:AK:83:GLU:OE1	64:AK:83:GLU:N	2.37	0.57
79:Ag:160:TRP:O	79:Ag:179:GLN:NE2	2.31	0.57
17:BN:26:GLN:NE2	17:BN:147:GLN:OE1	2.38	0.57
30:Bb:75:ARG:HB3	30:Bb:80:GLU:HB3	1.85	0.57
23:BT:55:GLN:C	77:Ae:132:LEU:O	2.48	0.57
39:Bj:140:ALA:HA	39:Bj:143:LYS:HE2	1.86	0.57
15:BJ:121:ILE:HD13	15:BJ:164:MET:HE3	1.86	0.57
19:BP:261:ASP:HB3	19:BP:264:GLN:HB2	1.86	0.57
52:AA:635:C:H5''	57:AB:213:LYS:HE2	1.87	0.57
59:AE:157:ILE:HD11	86:Ao:116:ALA:HA	1.87	0.57
85:An:177:TRP:HB2	85:An:182:LEU:HB2	1.85	0.57
12:BF:171:VAL:HG13	12:BF:273:LEU:HD22	1.86	0.57
23:BT:79:GLU:OE2	23:BT:103:ARG:NH2	2.38	0.57
36:B8:104:ARG:NH2	36:B8:160:LYS:O	2.38	0.57
52:AA:471:U:OP2	74:Ab:50:ARG:NH2	2.37	0.57
56:BA:1557:C:O2'	56:BA:1558:U:O2	2.21	0.57
83:Ak:213:ARG:NH1	83:Ak:223:TYR:OH	2.38	0.57
13:BG:191:GLU:OE1	13:BG:191:GLU:N	2.36	0.57
20:BQ:63:ARG:NH2	56:BA:1177:U:O2	2.37	0.57
21:BR:38:ARG:NH1	21:BR:82:GLU:OE1	2.38	0.57
22:BS:116:LEU:HD13	30:Bb:130:ILE:HD11	1.86	0.57
23:BT:54:PHE:O	23:BT:56:PRO:HD3	2.05	0.57
23:BT:56:PRO:HB3	77:Ae:135:PHE:C	2.29	0.57
24:BU:16:ASP:OD2	56:BA:607:A:O2'	2.21	0.57
30:Bb:139:TRP:CD1	30:Bb:143:CYS:HG	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Bj:273:ARG:HA	39:Bj:276:LEU:HB3	1.86	0.57
47:Bt:15:ARG:NH1	56:BA:1025:A:OP1	2.37	0.57
50:Bw:82:ILE:O	56:BA:777:A:N6	2.25	0.57
60:AF:119:SER:HB3	60:AF:121:LYS:HE3	1.87	0.57
64:AK:99:ILE:HD11	64:AK:163:ALA:HB1	1.86	0.57
68:AP:63:GLU:HG2	73:Aa:177:LYS:HE3	1.86	0.57
4:B3:99:VAL:HG21	44:Bo:77:VAL:HG22	1.87	0.56
47:Bt:78:GLN:OE1	56:BA:391:A:N6	2.38	0.56
73:Aa:92:PHE:O	73:Aa:98:GLN:NE2	2.37	0.56
86:Ao:533:GLU:HA	86:Ao:536:MET:HE3	1.87	0.56
1:B0:102:GLU:OE2	1:B0:132:HIS:NE2	2.32	0.56
17:BN:114:LYS:NZ	56:BA:1034:G:OP1	2.38	0.56
25:BV:148:LEU:HB2	34:Bf:58:ILE:HB	1.87	0.56
70:AR:125:TYR:HE2	71:Au:4:HIS:HB3	1.69	0.56
5:B4:60:GLN:NE2	5:B4:79:PRO:O	2.31	0.56
12:BF:237:LEU:O	49:Bv:25:TYR:N	2.38	0.56
29:Ba:228:ALA:HB3	29:Ba:292:TYR:HB2	1.88	0.56
29:Ba:361:THR:OG1	29:Ba:363:ASP:OD1	2.24	0.56
36:B8:168:ARG:NH1	36:B8:170:ASN:OD1	2.35	0.56
39:Bj:260:LEU:HD22	39:Bj:273:ARG:HD2	1.86	0.56
43:Bn:57:TYR:OH	49:Bv:28:ARG:O	2.15	0.56
52:AA:29:A:O3'	65:AL:129:LYS:NZ	2.37	0.56
52:AA:468:A:OP2	57:AB:99:ARG:NH2	2.38	0.56
56:BA:29:A:N3	56:BA:35:A:O2'	2.31	0.56
57:AB:192:ILE:HD12	57:AB:211:ALA:HB2	1.86	0.56
59:AE:282:ILE:HG13	59:AE:327:ILE:HD13	1.87	0.56
68:AP:118:VAL:HG21	87:Ap:236:PRO:HB2	1.85	0.56
29:Ba:297:ALA:HB3	29:Ba:303:ARG:HG2	1.87	0.56
32:Bd:73:ARG:HA	32:Bd:77:LYS:NZ	2.20	0.56
57:AB:196:HIS:NE2	57:AB:239:ASP:O	2.38	0.56
63:AJ:123:SER:HB3	63:AJ:127:PHE:HB2	1.87	0.56
28:BY:52:GLU:O	28:BY:143:ARG:NH2	2.38	0.56
41:Bl:96:VAL:HG22	41:Bl:110:ILE:HG12	1.86	0.56
47:Bt:41:THR:O	47:Bt:45:ASN:ND2	2.37	0.56
52:AA:385:C:OP1	70:AR:110:LYS:NZ	2.38	0.56
52:AA:533:C:O2'	84:Am:37:ARG:NH2	2.34	0.56
56:BA:416:U:H2'	56:BA:417:G:C8	2.41	0.56
56:BA:783:A:O2'	56:BA:785:A:OP2	2.22	0.56
56:BA:948:A:O2'	56:BA:1382:C:O2	2.23	0.56
79:Ag:221:LEU:HD11	79:Ag:242:VAL:HG22	1.86	0.56
3:B2:95:LYS:NZ	28:BY:181:ASP:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B3:148:ARG:HB3	4:B3:151:LEU:HD21	1.88	0.56
30:Bb:368:ARG:NH1	56:BA:1196:G:OP2	2.38	0.56
62:AI:381:LYS:HA	62:AI:388:ALA:HB2	1.88	0.56
75:Ac:89:ASP:OD1	76:Ad:120:ARG:NH2	2.38	0.56
80:Ah:366:GLU:O	80:Ah:370:ASN:ND2	2.38	0.56
23:BT:56:PRO:O	77:Ae:131:TYR:O	2.23	0.56
29:Ba:360:ASN:HD22	29:Ba:372:ASN:HA	1.71	0.56
36:B8:110:VAL:O	36:B8:114:PHE:HB2	2.06	0.56
52:AA:158:C:O3'	52:AA:172:A:N6	2.39	0.56
52:AA:285:C:N4	65:AL:43:LYS:O	2.38	0.56
54:AV:39:U:H2'	54:AV:40:U:H6	1.70	0.56
58:AC:112:ARG:HG2	83:Ak:161:ALA:HB1	1.86	0.56
58:AC:157:THR:OG1	86:Ao:92:ASP:OD2	2.22	0.56
76:Ad:166:THR:O	76:Ad:176:ARG:NH2	2.38	0.56
5:B4:47:GLN:NE2	8:BB:33:C:OP1	2.31	0.56
11:BE:76:LYS:HG3	11:BE:170:LEU:HD21	1.88	0.56
44:Bo:23:ALA:N	56:BA:482:G:OP1	2.38	0.56
51:Bx:99:MET:HE3	51:Bx:116:GLU:HG3	1.88	0.56
56:BA:165:A:H2'	56:BA:166:A:C8	2.41	0.56
57:AB:238:ASN:ND2	57:AB:241:SER:OG	2.39	0.56
62:AI:206:LEU:HD12	62:AI:219:TYR:HD1	1.70	0.56
86:Ao:446:ASP:N	86:Ao:446:ASP:OD1	2.37	0.56
20:BQ:66:ARG:HB2	56:BA:441:A:H5''	1.88	0.56
26:BW:67:ARG:NH2	38:Bi:228:PHE:O	2.38	0.56
30:Bb:175:VAL:HG22	30:Bb:204:VAL:HG12	1.88	0.56
38:Bi:142:LYS:HD2	38:Bi:216:MET:HE3	1.86	0.56
52:AA:393:A:H5'	67:AO:133:LEU:HD21	1.87	0.56
52:AA:590:C:H2'	52:AA:591:A:C8	2.40	0.56
56:BA:888:A:O2'	56:BA:891:A:N6	2.38	0.56
4:B3:137:THR:HG21	44:Bo:74:ALA:HB2	1.88	0.56
6:B5:93:ARG:NH1	56:BA:644:G:OP1	2.35	0.56
48:Bu:107:ALA:O	48:Bu:115:ARG:NH2	2.38	0.56
50:Bw:278:ILE:HD11	50:Bw:333:GLN:HG2	1.87	0.56
52:AA:313:A:O2'	52:AA:314:A:O4'	2.23	0.56
52:AA:477:A:H2'	52:AA:478:A:C8	2.41	0.56
58:AC:38:ARG:HG2	58:AC:43:ARG:HH21	1.71	0.56
83:Ak:191:LYS:NZ	83:Ak:237:LYS:O	2.38	0.56
20:BQ:218:ILE:HG23	20:BQ:223:MET:HB2	1.88	0.55
26:BW:55:ILE:O	38:Bi:227:ARG:NH2	2.38	0.55
31:Bc:103:ALA:O	31:Bc:110:TRP:N	2.39	0.55
45:Bp:80:HIS:O	51:Bx:36:ARG:NH1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Bt:100:LYS:NZ	56:BA:614:U:O3'	2.39	0.55
52:AA:3:A:O2'	52:AA:5:A:OP2	2.24	0.55
52:AA:17:G:H2'	52:AA:18:G:C8	2.41	0.55
52:AA:828:U:H2'	52:AA:829:G:H8	1.71	0.55
54:AV:25:U:N3	54:AV:26:U:C4	2.74	0.55
61:AG:71:THR:HG22	62:AI:252:GLN:C	2.31	0.55
75:Ac:78:PHE:HB2	75:Ac:86:VAL:HB	1.88	0.55
10:BD:265:ARG:HE	10:BD:271:PRO:HD3	1.71	0.55
12:BF:66:ILE:HD11	12:BF:80:THR:HB	1.87	0.55
23:BT:86:ARG:HH12	56:BA:1557:C:H4'	1.71	0.55
24:BU:52:LYS:NZ	56:BA:164:A:OP1	2.38	0.55
49:Bv:40:PRO:HG3	49:Bv:51:GLN:HB3	1.87	0.55
52:AA:209:C:H2'	52:AA:210:U:H6	1.70	0.55
52:AA:948:U:H2'	52:AA:949:G:H8	1.72	0.55
56:BA:83:A:OP2	56:BA:1235:C:O2'	2.20	0.55
56:BA:881:C:H4'	56:BA:882:A:H5'	1.88	0.55
58:AC:96:MET:HG3	58:AC:108:LEU:HD21	1.87	0.55
58:AC:136:VAL:HG23	58:AC:153:LEU:HD23	1.88	0.55
67:AO:155:ARG:NE	67:AO:159:MET:SD	2.79	0.55
79:Ag:137:LEU:HD11	79:Ag:260:ALA:HB1	1.88	0.55
86:Ao:137:ILE:HD12	86:Ao:138:PRO:HD2	1.87	0.55
25:BV:133:ARG:NH2	25:BV:155:LYS:O	2.40	0.55
30:Bb:240:ILE:HD13	30:Bb:248:GLY:HA3	1.88	0.55
52:AA:58:U:N3	82:Aj:57:ASP:OD2	2.39	0.55
56:BA:388:A:H2'	56:BA:389:A:C8	2.41	0.55
86:Ao:397:TYR:OH	86:Ao:431:ASP:OD2	2.19	0.55
11:BE:210:THR:OG1	11:BE:262:GLY:O	2.23	0.55
11:BE:239:ARG:NH1	56:BA:1046:A:OP1	2.37	0.55
46:Bq:92:TYR:HB3	46:Bq:96:LEU:HD22	1.89	0.55
56:BA:799:A:H61	56:BA:991:C:N4	2.03	0.55
56:BA:1224:C:H2'	56:BA:1225:A:C8	2.40	0.55
82:Aj:163:SER:HB3	82:Aj:190:MET:HB3	1.89	0.55
43:Bn:32:PHE:HD1	56:BA:199:A:H5''	1.72	0.55
52:AA:194:U:H2'	52:AA:195:G:C8	2.41	0.55
63:AJ:78:VAL:HB	63:AJ:143:LEU:HB2	1.88	0.55
78:Af:141:VAL:HA	78:Af:173:LEU:HA	1.89	0.55
9:B7:85:ARG:NH1	56:BA:125:A:OP1	2.40	0.55
28:BY:112:GLU:OE1	38:Bi:74:ARG:NH1	2.39	0.55
58:AC:133:TYR:HA	58:AC:136:VAL:HG12	1.89	0.55
68:AP:51:LEU:HD13	68:AP:73:ILE:HG12	1.87	0.55
11:BE:152:VAL:O	56:BA:1569:A:N6	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BE:238:ARG:N	56:BA:792:G:OP1	2.40	0.55
16:BK:61:LYS:HD3	46:Bq:79:LYS:HE3	1.89	0.55
23:BT:58:PRO:HD3	77:Ae:135:PHE:N	2.22	0.55
31:Bc:66:HIS:HB2	31:Bc:76:PHE:HE1	1.72	0.55
32:Bd:104:VAL:HG11	39:Bj:80:GLU:HG2	1.89	0.55
52:AA:121:C:H2'	52:AA:122:C:C6	2.42	0.55
52:AA:441:U:H2'	52:AA:442:A:H8	1.71	0.55
52:AA:537:A:C6	52:AA:825:C:N4	2.75	0.55
52:AA:799:A:H2'	52:AA:800:G:H8	1.72	0.55
57:AB:71:PHE:O	57:AB:262:LYS:NZ	2.40	0.55
79:Ag:323:LEU:HB2	79:Ag:326:GLU:HG2	1.88	0.55
6:B5:134:THR:OG1	21:BR:41:ARG:NH2	2.40	0.55
17:BN:104:VAL:HG13	17:BN:127:LEU:HD13	1.89	0.55
56:BA:1450:U:H2'	56:BA:1451:U:C6	2.42	0.55
73:Aa:344:ALA:HB1	73:Aa:348:HIS:HB3	1.89	0.55
12:BF:56:PRO:HG2	12:BF:59:ARG:HB3	1.88	0.55
15:BJ:49:ALA:HB1	47:Bt:32:LYS:HE2	1.89	0.55
50:Bw:242:PRO:HD3	50:Bw:423:PRO:HA	1.89	0.55
52:AA:342:C:OP1	64:AK:96:ASN:ND2	2.40	0.55
58:AC:85:ARG:HH21	83:Ak:162:GLY:HA3	1.71	0.55
77:Ae:131:TYR:O	77:Ae:133:TYR:N	2.40	0.55
50:Bw:63:VAL:HA	50:Bw:66:TRP:HD1	1.71	0.55
54:AV:25:U:O4	54:AV:26:U:O4	2.24	0.55
56:BA:6:A:H2'	56:BA:7:G:C4	2.42	0.55
58:AC:69:LEU:HB3	58:AC:93:ARG:HH22	1.72	0.55
59:AE:392:ARG:HG2	59:AE:394:ASP:H	1.70	0.55
64:AK:160:ARG:NH2	64:AK:179:ASP:OD1	2.39	0.55
82:Aj:88:GLN:O	87:Ap:215:ARG:NH1	2.39	0.55
86:Ao:259:ALA:HA	86:Ao:262:TYR:CZ	2.42	0.55
87:Ap:59:LEU:HD13	87:Ap:121:LYS:HB2	1.89	0.55
1:B0:71:ARG:NH2	56:BA:1163:A:OP1	2.40	0.54
9:B7:91:LYS:N	56:BA:118:U:OP1	2.39	0.54
12:BF:287:ARG:HH21	56:BA:223:A:H62	1.54	0.54
15:BJ:110:LEU:HB3	16:BK:132:LEU:HD23	1.88	0.54
32:Bd:189:GLU:HG2	40:Bk:137:LEU:HD13	1.88	0.54
55:AX:5:U:H2'	55:AX:6:U:C6	2.42	0.54
56:BA:1506:A:H2'	56:BA:1507:G:C8	2.42	0.54
3:B2:200:ARG:N	56:BA:31:A:N1	2.44	0.54
19:BP:14:ASP:OD1	19:BP:17:ARG:NH1	2.39	0.54
52:AA:620:C:H2'	52:AA:621:A:H8	1.71	0.54
56:BA:203:A:O2'	56:BA:239:C:O2	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BA:619:C:H2'	56:BA:620:A:H8	1.72	0.54
6:B5:140:GLN:NE2	6:B5:176:GLU:O	2.21	0.54
8:BB:31:C:H2'	8:BB:32:A:H8	1.72	0.54
17:BN:154:ARG:NH1	17:BN:157:GLU:OE2	2.40	0.54
23:BT:57:PRO:HD3	77:Ae:136:ARG:HB2	1.88	0.54
24:BU:73:THR:HG22	24:BU:83:TYR:HB2	1.88	0.54
25:BV:102:VAL:HB	25:BV:139:LEU:HB3	1.87	0.54
29:Ba:350:ARG:NH1	29:Ba:383:TYR:O	2.40	0.54
30:Bb:138:GLU:HG2	30:Bb:141:ARG:HH12	1.71	0.54
32:Bd:141:GLU:HG3	39:Bj:274:ARG:HH21	1.72	0.54
52:AA:121:C:O2'	69:AQ:23:GLN:O	2.25	0.54
52:AA:782:G:H2'	52:AA:783:A:C8	2.41	0.54
59:AE:243:VAL:HG11	59:AE:268:PHE:HE1	1.73	0.54
63:AJ:55:PRO:HA	86:Ao:443:ASN:HD22	1.71	0.54
77:Ae:213:PHE:HE1	77:Ae:221:LEU:HD12	1.73	0.54
35:Bg:78:GLU:HG2	35:Bg:84:VAL:HG22	1.89	0.54
56:BA:165:A:H2'	56:BA:166:A:H8	1.72	0.54
56:BA:248:A:OP1	56:BA:323:A:N6	2.40	0.54
64:AK:68:ILE:HG12	64:AK:70:GLY:H	1.73	0.54
29:Ba:181:VAL:HG21	29:Ba:294:LEU:HD22	1.88	0.54
43:Bn:113:ARG:NH1	56:BA:348:G:O6	2.39	0.54
48:Bu:101:ARG:HG2	48:Bu:133:ILE:HG12	1.89	0.54
52:AA:11:G:O6	52:AA:524:U:O4	2.26	0.54
52:AA:50:U:H2'	52:AA:51:G:C8	2.39	0.54
56:BA:197:U:H2'	56:BA:198:U:C6	2.42	0.54
56:BA:462:G:HO2'	56:BA:486:A:HO2'	1.52	0.54
56:BA:657:U:H1'	56:BA:658:U:C5	2.43	0.54
49:Bv:33:ARG:NH2	56:BA:96:U:OP1	2.41	0.54
54:AV:13:U:N3	54:AV:14:U:C4	2.76	0.54
56:BA:301:U:H2'	56:BA:302:A:H8	1.72	0.54
56:BA:1230:U:H5'	56:BA:1231:U:H5'	1.89	0.54
57:AB:221:ILE:HA	57:AB:235:VAL:HG23	1.89	0.54
65:AL:96:PRO:O	65:AL:127:ARG:NH1	2.41	0.54
82:Aj:36:LEU:HD11	82:Aj:50:LEU:HD11	1.89	0.54
83:Ak:83:VAL:O	83:Ak:101:LYS:NZ	2.39	0.54
10:BD:258:ILE:O	56:BA:843:C:O2'	2.19	0.54
29:Ba:135:LYS:HD2	29:Ba:239:VAL:HG23	1.90	0.54
52:AA:198:C:N4	52:AA:199:G:O6	2.41	0.54
52:AA:552:A:H2'	52:AA:553:G:C8	2.43	0.54
56:BA:343:C:H2'	56:BA:344:U:C6	2.43	0.54
57:AB:219:VAL:HG22	57:AB:233:TYR:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:AN:54:ILE:HG21	66:AN:75:ILE:HB	1.89	0.54
68:AP:102:MET:O	68:AP:106:ASN:ND2	2.30	0.54
79:Ag:275:ARG:HE	79:Ag:281:ILE:HG22	1.72	0.54
82:Aj:16:ARG:HD3	82:Aj:19:ARG:HH22	1.73	0.54
10:BD:205:ALA:O	10:BD:209:ARG:NH2	2.32	0.54
52:AA:89:U:H3	52:AA:93:A:H61	1.54	0.54
52:AA:542:C:H2'	52:AA:543:A:H8	1.73	0.54
52:AA:882:A:O2'	77:Ae:140:ASN:OD1	2.25	0.54
56:BA:188:C:O2'	56:BA:190:U:OP2	2.22	0.54
60:AF:11:LYS:HB3	60:AF:13:MET:HE3	1.90	0.54
77:Ae:147:TRP:H	77:Ae:147:TRP:CD1	2.24	0.54
83:Ak:55:LEU:HD12	83:Ak:56:PRO:HD2	1.88	0.54
86:Ao:258:ASN:HD22	86:Ao:285:LEU:HA	1.73	0.54
2:B1:167:LEU:HD21	2:B1:202:GLU:HB3	1.89	0.54
12:BF:262:THR:HG22	12:BF:264:PRO:HD2	1.89	0.54
13:BG:84:ASN:HB3	13:BG:87:GLU:HB2	1.89	0.54
31:Bc:76:PHE:HB3	31:Bc:78:MET:HE2	1.89	0.54
31:Bc:230:ASN:HB3	31:Bc:233:LYS:HB2	1.89	0.54
50:Bw:202:PHE:O	50:Bw:226:GLN:NE2	2.41	0.54
52:AA:272:A:H4'	52:AA:274:A:H4'	1.90	0.54
54:AV:1:U:H2'	54:AV:2:U:H6	1.71	0.54
54:AV:50:U:O2	54:AV:54:U:O4	2.25	0.54
56:BA:233:A:H2'	56:BA:234:G:H8	1.73	0.54
82:Aj:68:LEU:HD12	82:Aj:71:LEU:HD12	1.90	0.54
17:BN:3:SER:O	37:Bh:302:ARG:NH2	2.34	0.54
23:BT:59:LYS:HB3	77:Ae:97:MET:HB2	1.88	0.54
26:BW:48:LYS:N	56:BA:2:C:OP1	2.39	0.54
31:Bc:75:VAL:HB	38:Bi:282:ILE:HB	1.90	0.54
39:Bj:245:GLN:HG3	39:Bj:248:LYS:HB3	1.88	0.54
39:Bj:265:LYS:HG3	39:Bj:266:PRO:HD3	1.90	0.54
52:AA:798:A:H2'	52:AA:799:A:H8	1.73	0.54
54:AV:40:U:H2'	54:AV:41:U:H6	1.72	0.54
56:BA:187:G:H1'	56:BA:467:A:N6	2.23	0.54
59:AE:178:GLU:HG2	59:AE:181:ARG:HH21	1.73	0.54
60:AF:3:ARG:NH1	60:AF:70:ALA:O	2.41	0.54
60:AF:49:TYR:OH	60:AF:90:ARG:NH1	2.41	0.54
60:AF:54:HIS:NE2	60:AF:85:ASP:O	2.41	0.54
79:Ag:167:LEU:HD11	79:Ag:177:PHE:HB3	1.90	0.54
12:BF:287:ARG:HD2	49:Bv:33:ARG:HH12	1.73	0.53
52:AA:408:A:H4'	52:AA:949:G:N2	2.23	0.53
59:AE:140:LEU:HD21	59:AE:160:ARG:HE	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BP:104:LEU:HD22	19:BP:109:ARG:HD2	1.90	0.53
23:BT:56:PRO:C	77:Ae:136:ARG:N	2.65	0.53
23:BT:58:PRO:CA	77:Ae:135:PHE:HB3	2.38	0.53
24:BU:34:ARG:NH2	56:BA:1014:A:OP1	2.41	0.53
27:BX:150:LEU:HD13	38:Bi:240:ARG:HG2	1.88	0.53
42:Bm:89:ASP:OD1	42:Bm:125:ARG:NH2	2.41	0.53
52:AA:545:C:OP1	61:AG:185:LYS:NZ	2.41	0.53
56:BA:699:G:H2'	56:BA:700:A:H8	1.73	0.53
79:Ag:74:LEU:HD11	79:Ag:96:ALA:HB2	1.90	0.53
80:Ah:367:TRP:HA	80:Ah:370:ASN:HD21	1.72	0.53
8:BB:63:C:H2'	8:BB:64:A:H8	1.73	0.53
13:BG:120:ALA:HB1	13:BG:127:LYS:HE3	1.90	0.53
14:BI:133:SER:HG	14:BI:136:ASN:HD22	1.56	0.53
15:BJ:219:TYR:CE1	88:EL:86:LEU:HD13	2.42	0.53
23:BT:57:PRO:HG3	77:Ae:132:LEU:HA	1.88	0.53
30:Bb:217:LEU:HD11	30:Bb:233:VAL:HG12	1.91	0.53
31:Bc:61:LYS:HG2	38:Bi:275:PRO:HB3	1.90	0.53
43:Bn:51:ARG:NE	56:BA:612:A:OP1	2.42	0.53
52:AA:601:A:N6	81:Ai:63:GLY:HA3	2.24	0.53
56:BA:73:A:O2'	56:BA:224:A:O2'	2.24	0.53
56:BA:1344:C:O2'	56:BA:1387:A:N3	2.34	0.53
6:B5:156:THR:OG1	21:BR:130:CYS:SG	2.52	0.53
13:BG:163:ARG:HG3	13:BG:170:ASN:HA	1.90	0.53
29:Ba:125:LYS:HZ2	29:Ba:364:LEU:HA	1.74	0.53
30:Bb:124:ARG:HH22	32:Bd:116:LEU:HD23	1.72	0.53
31:Bc:44:LEU:HD21	31:Bc:225:GLU:HG3	1.91	0.53
37:Bh:148:LEU:HD13	37:Bh:149:PRO:HD2	1.90	0.53
56:BA:118:U:O4	56:BA:129:A:N7	2.42	0.53
87:Ap:60:ASP:OD1	87:Ap:121:LYS:NZ	2.36	0.53
10:BD:141:ALA:HB2	10:BD:154:ALA:HB2	1.89	0.53
23:BT:60:PRO:HG2	77:Ae:111:THR:C	2.34	0.53
31:Bc:100:SER:HA	31:Bc:126:THR:HG22	1.90	0.53
31:Bc:187:ASP:HB3	31:Bc:289:LEU:HD11	1.90	0.53
52:AA:279:U:O2'	65:AL:54:GLY:O	2.26	0.53
52:AA:738:U:H3'	61:AG:198:ARG:HH21	1.72	0.53
54:AV:25:U:C4	54:AV:26:U:C4	2.96	0.53
56:BA:414:A:H3'	56:BA:415:A:H8	1.73	0.53
56:BA:790:A:N6	56:BA:1000:A:O2'	2.42	0.53
56:BA:920:C:N4	56:BA:924:G:H22	2.05	0.53
56:BA:1150:G:O2'	56:BA:1319:G:OP1	2.25	0.53
82:Aj:67:LEU:HB2	82:Aj:141:LEU:HD23	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BD:177:ALA:HB1	10:BD:245:VAL:HG11	1.90	0.53
26:BW:90:LYS:HD2	26:BW:93:ARG:HD2	1.91	0.53
29:Ba:207:ASN:HB3	50:Bw:151:LEU:HD11	1.90	0.53
31:Bc:190:MET:HG2	31:Bc:291:ARG:HH12	1.72	0.53
48:Bu:103:HIS:CE1	48:Bu:105:ALA:HB3	2.43	0.53
50:Bw:215:HIS:ND1	56:BA:757:A:OP1	2.36	0.53
50:Bw:233:ASN:HB2	50:Bw:293:PHE:HB2	1.91	0.53
50:Bw:397:GLU:HG2	50:Bw:398:THR:HG22	1.89	0.53
52:AA:430:A:H5'	54:AV:35:U:H5'	1.89	0.53
79:Ag:133:LYS:HG2	79:Ag:344:VAL:HG21	1.91	0.53
11:BE:52:HIS:NE2	31:Bc:301:HIS:O	2.41	0.53
13:BG:228:GLU:OE2	56:BA:1153:G:N2	2.42	0.53
30:Bb:161:LEU:HD13	30:Bb:271:LEU:HD11	1.90	0.53
36:B8:157:LEU:HG	36:B8:161:MET:HE2	1.90	0.53
56:BA:677:C:OP1	56:BA:695:U:O2'	2.19	0.53
61:AG:49:GLU:HG3	61:AG:53:LYS:HE3	1.91	0.53
22:BS:173:ARG:NH1	22:BS:174:GLU:O	2.41	0.53
30:Bb:330:VAL:HG13	30:Bb:334:LEU:HD12	1.90	0.53
37:Bh:52:ARG:NH1	56:BA:148:A:OP1	2.41	0.53
58:AC:108:LEU:HD23	58:AC:110:LEU:HD21	1.91	0.53
77:Ae:392:SER:HB2	77:Ae:395:THR:HG22	1.90	0.53
3:B2:115:LEU:HB3	27:BX:27:GLN:HG2	1.90	0.53
12:BF:69:LEU:HB2	12:BF:190:VAL:HG11	1.91	0.53
38:Bi:124:LYS:HE2	38:Bi:208:ILE:HD13	1.90	0.53
56:BA:1454:C:H2'	56:BA:1455:C:C6	2.44	0.53
79:Ag:180:PRO:HB2	79:Ag:232:VAL:HG12	1.90	0.53
84:Am:88:SER:O	84:Am:92:ASN:ND2	2.42	0.53
12:BF:84:PRO:HA	12:BF:88:SER:HB3	1.91	0.53
13:BG:219:LEU:O	13:BG:223:LYS:HG3	2.09	0.53
29:Ba:300:ARG:NH2	56:BA:727:A:OP2	2.42	0.53
30:Bb:233:VAL:O	30:Bb:296:ARG:NH1	2.41	0.53
50:Bw:87:GLN:HE22	50:Bw:273:GLU:HA	1.74	0.53
50:Bw:195:ASP:HB2	50:Bw:234:GLN:HB2	1.91	0.53
52:AA:168:A:O2'	52:AA:169:A:O4'	2.22	0.53
52:AA:240:C:H2'	52:AA:241:G:H8	1.74	0.53
52:AA:824:G:O2'	52:AA:825:C:OP2	2.22	0.53
56:BA:354:U:O2'	56:BA:1055:A:N1	2.41	0.53
56:BA:1072:A:H2'	56:BA:1073:A:C8	2.43	0.53
58:AC:50:PRO:HB3	58:AC:167:ILE:HG13	1.89	0.53
59:AE:305:MET:HE3	59:AE:332:LEU:HD21	1.90	0.53
86:Ao:338:PHE:HA	86:Ao:341:ILE:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B4:71:GLU:O	5:B4:73:ARG:N	2.40	0.52
11:BE:94:SER:HA	11:BE:182:THR:HG21	1.91	0.52
12:BF:223:HIS:HA	12:BF:226:MET:HE3	1.91	0.52
13:BG:146:VAL:HB	13:BG:178:ILE:HB	1.91	0.52
15:BJ:198:PRO:HB3	15:BJ:202:LEU:HD23	1.91	0.52
17:BN:177:ARG:HB2	51:Bx:36:ARG:HB3	1.90	0.52
22:BS:173:ARG:NE	56:BA:1218:U:H5'	2.24	0.52
26:BW:151:LEU:HB2	26:BW:167:LYS:HB2	1.91	0.52
38:Bi:170:PRO:HA	38:Bi:173:VAL:HG12	1.91	0.52
51:Bx:72:ILE:HG23	51:Bx:77:LEU:HB2	1.91	0.52
60:AF:24:ARG:NH2	60:AF:87:ASP:OD2	2.42	0.52
7:B6:20:MET:HG2	7:B6:58:GLU:HA	1.89	0.52
15:BJ:171:ILE:HD12	15:BJ:172:PRO:HD2	1.91	0.52
19:BP:140:LEU:HD11	19:BP:154:ILE:HG21	1.91	0.52
30:Bb:139:TRP:O	30:Bb:144:GLY:N	2.40	0.52
52:AA:210:U:C2	52:AA:211:A:C8	2.97	0.52
79:Ag:272:THR:HG23	79:Ag:315:LEU:HD13	1.91	0.52
52:AA:162:C:OP2	52:AA:163:A:N6	2.41	0.52
6:B5:126:CYS:HA	6:B5:129:LYS:HE2	1.91	0.52
16:BK:39:LEU:HD12	16:BK:44:VAL:HB	1.92	0.52
16:BK:84:GLN:HG3	16:BK:124:LYS:HA	1.91	0.52
18:BO:131:GLU:O	18:BO:135:SER:OG	2.28	0.52
23:BT:271:ARG:NH1	56:BA:1491:A:O2'	2.42	0.52
32:Bd:110:GLU:HA	32:Bd:113:ARG:HG2	1.92	0.52
32:Bd:133:ARG:HA	32:Bd:136:ILE:HG22	1.90	0.52
52:AA:641:A:H2'	52:AA:642:G:C8	2.45	0.52
57:AB:199:ASN:ND2	57:AB:203:GLU:O	2.43	0.52
58:AC:113:ARG:HB2	63:AJ:166:GLU:HB3	1.92	0.52
18:BO:98:PRO:HA	23:BT:162:ILE:HG12	1.91	0.52
33:Be:21:TRP:O	33:Be:32:LYS:NZ	2.41	0.52
34:Bf:73:LYS:HE3	37:Bh:257:LEU:HD23	1.91	0.52
37:Bh:33:LYS:NZ	56:BA:106:C:OP1	2.42	0.52
52:AA:675:A:OP2	58:AC:37:ASN:ND2	2.41	0.52
52:AA:799:A:H2'	52:AA:800:G:C8	2.45	0.52
59:AE:380:LEU:HD12	59:AE:381:PRO:HD2	1.91	0.52
67:AO:133:LEU:HD12	67:AO:167:MET:HE2	1.90	0.52
69:AQ:72:PRO:HB3	69:AQ:78:LYS:HG2	1.91	0.52
78:Af:151:THR:HG22	78:Af:162:THR:HA	1.92	0.52
88:FL:89:THR:HG23	88:FL:90:LEU:HG	1.91	0.52
15:BJ:85:GLU:OE2	15:BJ:124:LYS:NZ	2.42	0.52
25:BV:138:LEU:HD21	44:Bo:43:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Ba:51:GLU:OE1	29:Ba:51:GLU:N	2.42	0.52
51:Bx:192:LEU:HB3	56:BA:574:A:C8	2.45	0.52
56:BA:343:C:H2'	56:BA:344:U:H6	1.74	0.52
59:AE:95:ALA:HB2	81:Ai:74:GLU:HB3	1.92	0.52
59:AE:312:TYR:HE2	59:AE:333:TYR:HB2	1.75	0.52
79:Ag:122:ARG:HH11	79:Ag:336:LEU:HD13	1.75	0.52
79:Ag:227:GLN:OE1	79:Ag:231:ARG:NH1	2.42	0.52
21:BR:27:HIS:HD1	56:BA:661:U:HO2'	1.45	0.52
21:BR:33:LEU:HD21	21:BR:59:LEU:HD22	1.92	0.52
23:BT:55:GLN:NE2	77:Ae:133:TYR:HB2	2.25	0.52
31:Bc:186:LEU:HG	31:Bc:189:TRP:HE1	1.73	0.52
35:Bg:35:ARG:O	35:Bg:44:ARG:NH1	2.43	0.52
52:AA:57:A:N6	82:Aj:49:ARG:O	2.43	0.52
52:AA:210:U:H2'	52:AA:211:A:C8	2.44	0.52
54:AV:39:U:C2	54:AV:40:U:C5	2.97	0.52
56:BA:53:U:H2'	56:BA:54:A:H8	1.72	0.52
56:BA:476:U:H2'	56:BA:477:A:H8	1.73	0.52
56:BA:1528:A:H2'	56:BA:1529:A:H8	1.74	0.52
57:AB:87:ARG:HB3	57:AB:90:LEU:HD12	1.92	0.52
66:AN:66:ASP:HB3	80:Ah:378:ILE:HD11	1.92	0.52
76:Ad:64:ARG:HA	76:Ad:67:VAL:HG22	1.92	0.52
17:BN:69:GLY:HA2	51:Bx:152:THR:HA	1.92	0.52
28:BY:52:GLU:HB3	28:BY:143:ARG:HH22	1.75	0.52
29:Ba:350:ARG:HH12	29:Ba:381:LEU:HD23	1.75	0.52
52:AA:924:U:OP2	55:AX:4:U:O2'	2.27	0.52
56:BA:868:G:H2'	56:BA:869:G:H8	1.75	0.52
56:BA:983:U:O4	56:BA:984:A:N6	2.43	0.52
56:BA:1072:A:H2'	56:BA:1073:A:H8	1.74	0.52
61:AG:215:ASN:HA	61:AG:220:ILE:HG13	1.91	0.52
2:B1:91:TYR:OH	56:BA:61:U:OP1	2.22	0.52
8:BB:65:U:H2'	8:BB:66:A:C8	2.44	0.52
50:Bw:93:VAL:HB	50:Bw:227:ILE:HG12	1.92	0.52
52:AA:11:G:O4'	52:AA:840:A:O2'	2.26	0.52
61:AG:187:MET:HE1	61:AG:209:LEU:HD23	1.90	0.52
71:AU:72:ILE:HD12	84:Am:104:LEU:HD22	1.92	0.52
79:Ag:120:ALA:HB3	79:Ag:298:ASN:HB2	1.92	0.52
11:BE:231:HIS:NE2	56:BA:805:C:O2	2.38	0.52
15:BJ:127:PRO:HG2	15:BJ:130:VAL:HG12	1.92	0.52
19:BP:57:ARG:HB3	19:BP:62:ARG:HH21	1.75	0.52
26:BW:147:ARG:HH12	56:BA:639:U:H5'	1.73	0.52
41:Bl:96:VAL:O	41:Bl:158:LYS:NZ	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:73:G:H1	52:AA:155:A:H1'	1.74	0.52
52:AA:561:U:H3'	52:AA:562:A:C2	2.44	0.52
56:BA:713:A:H2'	56:BA:714:A:C8	2.45	0.52
15:BJ:143:LEU:HG	15:BJ:146:LEU:HD12	1.91	0.51
26:BW:188:LYS:HD2	26:BW:193:HIS:CE1	2.45	0.51
29:Ba:347:THR:HG22	29:Ba:349:GLY:H	1.75	0.51
40:Bk:94:HIS:HB2	40:Bk:185:SER:HB3	1.92	0.51
47:Bt:9:ARG:NH2	56:BA:564:A:OP1	2.43	0.51
52:AA:437:C:OP1	64:AK:191:ARG:NH2	2.33	0.51
54:AV:18:U:H5	54:AV:44:U:H4'	1.75	0.51
56:BA:301:U:H2'	56:BA:302:A:C8	2.44	0.51
56:BA:1026:A:HO2'	56:BA:1277:G:H21	1.54	0.51
58:AC:76:LEU:HD13	63:AJ:81:LYS:HG3	1.92	0.51
68:AP:42:PRO:HG2	68:AP:45:GLY:HA3	1.92	0.51
79:Ag:106:GLU:OE2	83:Ak:315:LYS:NZ	2.43	0.51
79:Ag:347:TYR:CZ	79:Ag:387:PRO:HB3	2.45	0.51
86:Ao:249:ARG:HA	86:Ao:253:LEU:HD23	1.91	0.51
28:BY:69:ASP:HB3	28:BY:72:LYS:HD2	1.93	0.51
38:Bi:278:LYS:HE3	38:Bi:280:VAL:HG22	1.92	0.51
52:AA:202:A:N1	82:Aj:53:ARG:NH2	2.58	0.51
56:BA:130:A:H2'	56:BA:131:A:O4'	2.10	0.51
56:BA:918:U:H2'	56:BA:919:G:H8	1.75	0.51
56:BA:925:G:N2	56:BA:964:A:OP2	2.35	0.51
66:AN:79:PRO:HG2	66:AN:82:SER:HB3	1.92	0.51
75:Ac:56:GLN:NE2	75:Ac:59:ASN:O	2.43	0.51
79:Ag:267:LEU:O	79:Ag:293:ARG:NH2	2.44	0.51
19:BP:211:VAL:O	19:BP:215:THR:OG1	2.20	0.51
52:AA:15:C:H4'	59:AE:300:ARG:HG3	1.92	0.51
52:AA:209:C:H2'	52:AA:210:U:C6	2.45	0.51
53:B9:87:ILE:HB	53:B9:97:GLN:HB2	1.92	0.51
54:AV:5:U:H2'	54:AV:6:U:H6	1.75	0.51
56:BA:698:U:H2'	56:BA:699:G:H8	1.75	0.51
59:AE:283:GLU:O	59:AE:356:GLN:NE2	2.43	0.51
2:B1:177:HIS:O	2:B1:184:ARG:NH2	2.44	0.51
27:BX:138:ASP:HB3	27:BX:141:ARG:HG2	1.93	0.51
29:Ba:123:LEU:HD22	29:Ba:220:LEU:HD11	1.92	0.51
39:Bj:162:ARG:HH21	39:Bj:164:LYS:HE2	1.76	0.51
52:AA:516:C:H2'	52:AA:517:A:C8	2.46	0.51
56:BA:247:C:H2'	56:BA:248:A:H8	1.75	0.51
56:BA:1131:U:H2'	56:BA:1132:G:H8	1.75	0.51
63:AJ:172:VAL:HB	83:Ak:157:ASP:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Ae:312:ASP:HB2	77:Ae:314:GLN:HG3	1.92	0.51
86:Ao:323:LEU:HD11	86:Ao:341:ILE:HD12	1.92	0.51
87:Ap:213:LEU:HG	87:Ap:217:ARG:HE	1.74	0.51
22:BS:122:VAL:HG22	22:BS:157:SER:HB3	1.93	0.51
35:Bg:27:GLN:HB2	35:Bg:80:LEU:HD12	1.91	0.51
52:AA:122:C:H2'	52:AA:123:U:C6	2.46	0.51
54:AV:62:U:C2	54:AV:63:U:C5	2.98	0.51
56:BA:935:C:H2'	56:BA:936:A:C8	2.45	0.51
65:AL:93:CYS:SG	65:AL:94:PHE:N	2.83	0.51
68:AP:29:ARG:NH1	68:AP:55:ASP:OD1	2.43	0.51
71:AU:67:GLU:HG3	78:Af:155:LEU:HG	1.91	0.51
79:Ag:357:GLN:O	79:Ag:361:GLU:HG2	2.11	0.51
29:Ba:125:LYS:NZ	29:Ba:366:SER:O	2.38	0.51
31:Bc:151:ILE:HA	31:Bc:199:PHE:HE1	1.75	0.51
35:Bg:133:PHE:HB3	37:Bh:259:ARG:HD2	1.93	0.51
37:Bh:72:ILE:HD13	37:Bh:178:LEU:HD23	1.93	0.51
56:BA:144:A:H2'	56:BA:145:A:C8	2.45	0.51
56:BA:176:U:H2'	56:BA:177:U:C6	2.45	0.51
69:AQ:33:LEU:HD21	75:Ac:66:MET:HE1	1.93	0.51
76:Ad:94:LYS:HA	76:Ad:97:GLU:HG2	1.93	0.51
3:B2:100:LEU:HB3	3:B2:144:LEU:HD11	1.92	0.51
7:B6:21:MET:HG2	7:B6:29:SER:HB3	1.91	0.51
12:BF:117:ARG:NH1	56:BA:241:C:OP1	2.42	0.51
14:BI:76:ARG:NH1	56:BA:62:C:OP1	2.44	0.51
23:BT:221:LYS:NZ	23:BT:241:LYS:O	2.36	0.51
25:BV:139:LEU:HD13	25:BV:148:LEU:HD23	1.93	0.51
30:Bb:45:LEU:O	30:Bb:50:LYS:NZ	2.36	0.51
32:Bd:165:ASP:OD2	39:Bj:185:ARG:NH2	2.43	0.51
52:AA:584:C:O2	66:AN:86:ARG:NH1	2.44	0.51
56:BA:1163:A:N6	56:BA:1164:G:O6	2.43	0.51
69:AQ:95:VAL:HG23	69:AQ:96:THR:HG23	1.91	0.51
77:Ae:177:ILE:HG13	77:Ae:179:PRO:HD3	1.92	0.51
2:B1:40:PRO:HG3	2:B1:45:PRO:HG3	1.91	0.51
12:BF:68:SER:O	12:BF:210:ARG:NH2	2.38	0.51
20:BQ:134:LYS:NZ	20:BQ:143:GLY:O	2.44	0.51
23:BT:56:PRO:HD2	77:Ae:133:TYR:O	2.11	0.51
50:Bw:265:LEU:HD23	50:Bw:267:LEU:HG	1.92	0.51
52:AA:708:A:H3'	52:AA:709:A:H8	1.76	0.51
52:AA:717:G:O2'	52:AA:809:G:OP1	2.29	0.51
56:BA:192:A:OP2	56:BA:1322:C:O2'	2.24	0.51
71:AU:30:LEU:HD22	71:AU:35:LEU:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:HL:86:LEU:HA	88:HL:89:THR:HG22	1.93	0.51
12:BF:79:LEU:HD23	42:Bm:95:VAL:HG13	1.93	0.51
12:BF:123:GLY:HA2	12:BF:141:ILE:HG12	1.93	0.51
15:BJ:54:ILE:HD12	20:BQ:211:ASN:HB3	1.93	0.51
23:BT:165:GLU:HB2	23:BT:168:ASN:HB2	1.93	0.51
52:AA:546:U:H2'	52:AA:547:A:C8	2.45	0.51
56:BA:920:C:H42	56:BA:924:G:N2	2.04	0.51
56:BA:1387:A:H2'	56:BA:1388:A:C8	2.46	0.51
70:AR:116:GLN:HB3	70:AR:123:VAL:HG22	1.93	0.51
12:BF:70:ARG:O	12:BF:202:TYR:OH	2.29	0.51
24:BU:114:LYS:HD3	34:Bf:45:CYS:SG	2.51	0.51
29:Ba:334:LYS:H	29:Ba:362:THR:HB	1.76	0.51
52:AA:302:U:OP1	67:AO:163:GLN:NE2	2.43	0.51
52:AA:641:A:H2'	52:AA:642:G:H8	1.76	0.51
52:AA:868:U:H3	52:AA:902:C:H42	1.59	0.51
56:BA:354:U:H2'	56:BA:355:G:H8	1.74	0.51
56:BA:644:G:N2	56:BA:1008:A:OP2	2.44	0.51
56:BA:1292:A:N6	56:BA:1304:G:O2'	2.43	0.51
77:Ae:248:LEU:HD22	77:Ae:263:SER:HB3	1.92	0.51
13:BG:104:ASN:O	13:BG:108:ASN:N	2.44	0.50
23:BT:57:PRO:HD2	77:Ae:136:ARG:CB	2.40	0.50
23:BT:117:LEU:HD22	23:BT:176:VAL:HG22	1.93	0.50
32:Bd:97:LYS:NZ	39:Bj:86:ASP:OD1	2.37	0.50
56:BA:699:G:H2'	56:BA:700:A:C8	2.46	0.50
56:BA:1121:U:H2'	56:BA:1122:A:H8	1.76	0.50
73:Aa:243:GLN:NE2	73:Aa:245:GLN:OE1	2.44	0.50
83:Ak:66:GLN:NE2	86:Ao:81:ASP:OD1	2.44	0.50
83:Ak:268:LEU:HD21	83:Ak:321:LEU:HD11	1.93	0.50
88:DL:86:LEU:HA	88:DL:89:THR:HG22	1.93	0.50
5:B4:46:ARG:NH1	32:Bd:87:ASP:O	2.45	0.50
13:BG:248:GLU:OE2	13:BG:251:ARG:NH2	2.38	0.50
14:BI:102:VAL:HG11	14:BI:105:LEU:HD23	1.94	0.50
15:BJ:64:CYS:HB3	51:Bx:70:CYS:HB2	1.93	0.50
48:Bu:75:ARG:NH1	48:Bu:108:ASP:OD1	2.44	0.50
70:AR:86:SER:OG	70:AR:90:GLY:N	2.43	0.50
73:Aa:224:ARG:NH1	73:Aa:256:GLN:O	2.44	0.50
86:Ao:608:ILE:HG21	86:Ao:642:LEU:HD21	1.93	0.50
6:B5:134:THR:HG23	21:BR:131:LEU:HD22	1.92	0.50
6:B5:181:ARG:NH1	6:B5:187:GLN:OE1	2.44	0.50
12:BF:220:ASP:OD1	12:BF:221:LEU:N	2.45	0.50
19:BP:79:PRO:HB3	56:BA:1234:U:H5'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BW:189:THR:HG23	26:BW:192:ALA:H	1.77	0.50
51:Bx:43:ASP:N	51:Bx:43:ASP:OD1	2.43	0.50
54:AV:31:U:H3'	54:AV:32:U:H6	1.77	0.50
56:BA:1121:U:H2'	56:BA:1122:A:C8	2.47	0.50
62:AI:88:LEU:HD11	62:AI:107:ALA:HB1	1.94	0.50
74:Ab:89:ASN:HB3	74:Ab:92:PHE:HB2	1.93	0.50
75:Ac:90:VAL:HG23	75:Ac:93:LYS:HB2	1.93	0.50
14:BI:95:GLU:OE1	14:BI:95:GLU:N	2.44	0.50
14:BI:102:VAL:HG22	14:BI:128:LEU:HD12	1.92	0.50
19:BP:100:ARG:O	19:BP:104:LEU:HG	2.11	0.50
21:BR:27:HIS:ND1	56:BA:661:U:O2'	2.37	0.50
49:Bv:55:ARG:NH1	56:BA:93:U:OP2	2.44	0.50
52:AA:72:A:H2'	52:AA:73:G:C8	2.47	0.50
52:AA:950:U:H2'	52:AA:951:G:H8	1.76	0.50
56:BA:220:G:N3	56:BA:231:C:O2'	2.41	0.50
56:BA:344:U:H2'	56:BA:345:G:C8	2.47	0.50
56:BA:529:G:O2'	56:BA:548:A:N3	2.42	0.50
56:BA:709:A:H2'	56:BA:710:A:H8	1.76	0.50
57:AB:99:ARG:NH1	74:Ab:50:ARG:O	2.41	0.50
3:B2:71:ASP:OD1	28:BY:175:LYS:NZ	2.36	0.50
11:BE:334:ASP:OD1	11:BE:335:GLU:N	2.44	0.50
29:Ba:201:ARG:HD3	29:Ba:230:LEU:HD21	1.94	0.50
30:Bb:304:TYR:O	30:Bb:308:GLN:HB2	2.11	0.50
52:AA:918:A:H62	65:AL:75:SER:HB2	1.76	0.50
67:AO:71:SER:HA	67:AO:95:SER:HB2	1.93	0.50
67:AO:144:MET:HE1	67:AO:150:ASP:HB3	1.94	0.50
73:Aa:282:ASP:HA	73:Aa:285:ARG:HG2	1.92	0.50
88:EL:86:LEU:HA	88:EL:89:THR:HG22	1.93	0.50
23:BT:122:ALA:O	23:BT:170:ARG:NH2	2.44	0.50
27:BX:46:MET:HG3	33:Be:34:ARG:HB3	1.93	0.50
32:Bd:173:ARG:HB3	40:Bk:184:LEU:HD23	1.94	0.50
52:AA:54:A:OP2	76:Ad:27:ARG:NH1	2.45	0.50
56:BA:108:A:O4'	56:BA:110:A:N6	2.44	0.50
56:BA:193:U:H2'	56:BA:194:G:C8	2.46	0.50
56:BA:1140:A:H2'	56:BA:1141:A:H8	1.76	0.50
56:BA:1399:G:O2'	56:BA:1402:C:OP2	2.23	0.50
56:BA:1458:G:O2'	56:BA:1467:G:O6	2.29	0.50
79:Ag:171:ASN:OD1	79:Ag:175:GLN:NE2	2.45	0.50
86:Ao:541:ASP:OD1	86:Ao:542:GLN:N	2.44	0.50
20:BQ:240:ARG:NH2	20:BQ:246:TYR:OH	2.44	0.50
22:BS:103:VAL:HG13	30:Bb:151:LEU:HD21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BW:75:ARG:HB3	26:BW:78:ILE:HD11	1.94	0.50
52:AA:546:U:H2'	52:AA:547:A:H8	1.77	0.50
56:BA:16:A:H2'	56:BA:17:C:C6	2.47	0.50
56:BA:335:U:OP1	56:BA:338:C:N4	2.34	0.50
6:B5:107:ILE:HG21	26:BW:102:ALA:HB1	1.94	0.50
15:BJ:162:LYS:H	15:BJ:162:LYS:HD2	1.76	0.50
46:Bq:72:ALA:HA	46:Bq:73:MET:HE3	1.93	0.50
52:AA:29:A:H2'	52:AA:30:A:H8	1.76	0.50
52:AA:98:A:H5'	68:AP:11:ALA:HA	1.92	0.50
52:AA:581:A:H61	52:AA:806:A:H3'	1.77	0.50
56:BA:247:C:H2'	56:BA:248:A:C8	2.47	0.50
63:AJ:74:LYS:HB2	63:AJ:177:LEU:HD21	1.92	0.50
79:Ag:312:THR:OG1	93:Ag:500:GTP:O2G	2.28	0.50
10:BD:64:VAL:O	10:BD:80:ARG:NH2	2.45	0.50
10:BD:128:ILE:HD12	10:BD:142:LEU:HG	1.93	0.50
52:AA:535:U:H4'	52:AA:536:C:OP1	2.12	0.50
56:BA:230:G:H2'	56:BA:231:C:C6	2.46	0.50
73:Aa:177:LYS:HB3	73:Aa:199:PRO:HD3	1.94	0.50
79:Ag:162:LYS:HD3	79:Ag:315:LEU:HD21	1.94	0.50
82:Aj:16:ARG:HD3	82:Aj:19:ARG:HH12	1.77	0.50
28:BY:81:ARG:HD3	28:BY:81:ARG:H	1.77	0.49
28:BY:184:GLU:OE1	28:BY:186:THR:OG1	2.29	0.49
38:Bi:197:VAL:HG22	38:Bi:212:VAL:HG13	1.93	0.49
52:AA:306:G:H2'	52:AA:307:A:C8	2.47	0.49
56:BA:740:U:H2'	56:BA:741:A:C8	2.47	0.49
60:AF:42:LEU:HB2	60:AF:63:TYR:HB2	1.93	0.49
63:AJ:121:LEU:HB2	66:AN:108:ARG:HE	1.77	0.49
77:Ae:358:LEU:HB2	77:Ae:361:GLU:HG3	1.94	0.49
78:Af:131:ASP:HB3	78:Af:134:LYS:HD2	1.94	0.49
80:Ah:303:TRP:CZ2	83:Ak:165:ILE:HG12	2.46	0.49
86:Ao:267:ARG:HH22	86:Ao:295:TYR:HB3	1.77	0.49
86:Ao:469:CYS:SG	86:Ao:470:PHE:N	2.85	0.49
3:B2:120:GLU:HG2	27:BX:110:LEU:HD12	1.94	0.49
7:B6:34:ARG:NH1	7:B6:39:GLU:O	2.46	0.49
11:BE:274:TRP:HE1	11:BE:286:ASN:HB2	1.77	0.49
31:Bc:41:GLN:HB3	31:Bc:258:ILE:HD12	1.93	0.49
32:Bd:159:ALA:O	32:Bd:163:LYS:NZ	2.45	0.49
39:Bj:179:GLN:HG2	39:Bj:181:GLY:H	1.77	0.49
50:Bw:85:LYS:HE2	56:BA:777:A:H62	1.76	0.49
50:Bw:241:LEU:HD11	50:Bw:290:HIS:HD1	1.77	0.49
52:AA:590:C:H2'	52:AA:591:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:848:C:H2'	52:AA:849:G:C8	2.47	0.49
56:BA:233:A:H2'	56:BA:234:G:C8	2.47	0.49
79:Ag:271:THR:HG22	79:Ag:273:LEU:H	1.77	0.49
86:Ao:265:MET:HE3	86:Ao:269:MET:HE3	1.93	0.49
86:Ao:342:LEU:HD21	86:Ao:378:VAL:HG23	1.94	0.49
4:B3:114:LYS:NZ	47:Bt:42:GLU:OE2	2.44	0.49
11:BE:127:CYS:HB3	11:BE:193:LEU:HB2	1.94	0.49
23:BT:56:PRO:N	77:Ae:132:LEU:O	2.45	0.49
23:BT:56:PRO:HB2	77:Ae:134:LYS:C	2.37	0.49
39:Bj:235:LYS:HE3	39:Bj:275:PHE:HD1	1.77	0.49
43:Bn:118:TYR:OH	56:BA:87:A:OP1	2.23	0.49
48:Bu:138:CYS:SG	48:Bu:139:SER:N	2.86	0.49
50:Bw:151:LEU:HD23	50:Bw:153:ARG:HH21	1.77	0.49
52:AA:857:C:H2'	52:AA:858:C:H6	1.77	0.49
56:BA:1388:A:H8	56:BA:1388:A:OP2	1.95	0.49
59:AE:374:ARG:HB3	59:AE:377:CYS:HB2	1.94	0.49
62:AI:302:LEU:HD22	79:Ag:384:ASN:HB3	1.94	0.49
21:BR:11:HIS:CG	56:BA:1558:U:H4'	2.47	0.49
52:AA:759:U:H5''	81:Ai:29:LYS:HE3	1.93	0.49
54:AV:30:U:O2	54:AV:34:U:O4	2.30	0.49
56:BA:396:C:O2'	56:BA:415:A:N6	2.45	0.49
56:BA:474:A:O2'	56:BA:596:A:O4'	2.27	0.49
77:Ae:87:ASP:H	77:Ae:118:ASN:HD21	1.58	0.49
83:Ak:78:PHE:HE2	83:Ak:107:LEU:HD13	1.77	0.49
88:GL:86:LEU:HA	88:GL:89:THR:HG22	1.93	0.49
20:BQ:172:VAL:HA	20:BQ:175:PHE:CE2	2.47	0.49
29:Ba:200:ARG:HD2	29:Ba:233:LYS:HD2	1.93	0.49
52:AA:96:U:H2'	52:AA:97:C:C6	2.46	0.49
54:AV:25:U:C2	54:AV:26:U:C5	3.01	0.49
56:BA:164:A:H4'	56:BA:165:A:C8	2.47	0.49
56:BA:187:G:N2	56:BA:1025:A:O4'	2.46	0.49
56:BA:1459:U:O2	56:BA:1468:A:N7	2.45	0.49
73:Aa:100:ILE:HG21	73:Aa:325:LEU:HG	1.95	0.49
77:Ae:74:TYR:OH	77:Ae:409:GLU:O	2.24	0.49
79:Ag:363:ASN:O	79:Ag:366:GLN:NE2	2.45	0.49
88:CL:63:LYS:O	88:CL:66:GLN:HG3	2.13	0.49
12:BF:47:VAL:HG13	12:BF:78:GLY:HA3	1.93	0.49
30:Bb:362:PRO:HB2	30:Bb:364:ARG:HG2	1.93	0.49
31:Bc:313:LEU:O	31:Bc:317:ARG:HG2	2.12	0.49
32:Bd:101:ARG:NH2	39:Bj:79:ILE:O	2.45	0.49
32:Bd:173:ARG:NH2	39:Bj:56:PRO:HB3	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:13:U:H2'	52:AA:14:C:C6	2.47	0.49
56:BA:1092:A:H61	56:BA:1122:A:N6	2.10	0.49
81:Ai:46:LYS:HA	81:Ai:49:TYR:CD1	2.48	0.49
88:FL:86:LEU:HA	88:FL:89:THR:HG22	1.93	0.49
19:BP:189:LYS:HB3	19:BP:192:PRO:HG2	1.95	0.49
40:Bk:90:VAL:HG23	40:Bk:189:HIS:HB3	1.93	0.49
52:AA:185:A:H1'	52:AA:213:G:H22	1.77	0.49
56:BA:645:U:H2'	56:BA:646:A:C8	2.45	0.49
56:BA:1143:U:H2'	56:BA:1144:U:C6	2.47	0.49
56:BA:1450:U:H2'	56:BA:1451:U:H6	1.78	0.49
63:AJ:122:LYS:O	66:AN:112:ARG:NH1	2.43	0.49
64:AK:190:PRO:HG2	71:AU:45:TYR:HB2	1.94	0.49
77:Ae:188:MET:O	77:Ae:192:ILE:HG12	2.13	0.49
77:Ae:222:SER:HA	77:Ae:225:VAL:HG22	1.94	0.49
79:Ag:283:PRO:HB2	79:Ag:293:ARG:HH21	1.78	0.49
86:Ao:603:ARG:HH21	86:Ao:636:LEU:HD12	1.77	0.49
2:B1:96:LYS:O	56:BA:60:U:O2'	2.29	0.49
10:BD:186:GLY:O	10:BD:220:LYS:NZ	2.41	0.49
25:BV:173:LYS:NZ	56:BA:477:A:O3'	2.35	0.49
27:BX:14:ASN:OD1	28:BY:210:HIS:ND1	2.45	0.49
29:Ba:236:LEU:HB3	29:Ba:341:VAL:HG13	1.94	0.49
35:Bg:93:SER:O	35:Bg:97:ILE:HG12	2.13	0.49
52:AA:10:U:N3	52:AA:13:U:OP2	2.27	0.49
52:AA:61:G:N2	52:AA:198:C:O3'	2.46	0.49
56:BA:505:U:C2	56:BA:507:G:H5'	2.48	0.49
56:BA:1570:C:H3'	56:BA:1571:A:H2'	1.95	0.49
77:Ae:164:LYS:O	77:Ae:168:THR:HG23	2.13	0.49
4:B3:75:THR:HB	4:B3:83:LYS:HG2	1.94	0.49
22:BS:43:ALA:HB1	30:Bb:226:LEU:HD21	1.94	0.49
25:BV:71:PRO:HB2	25:BV:76:GLU:HG2	1.95	0.49
42:Bm:117:ARG:O	42:Bm:121:MET:HG2	2.13	0.49
52:AA:524:U:H2'	52:AA:525:U:C6	2.48	0.49
56:BA:1262:A:O2'	56:BA:1423:C:OP1	2.23	0.49
59:AE:296:LEU:HD11	59:AE:303:ILE:HD12	1.93	0.49
61:AG:78:PRO:HG2	61:AG:81:LYS:HB3	1.95	0.49
79:Ag:275:ARG:NH2	79:Ag:285:GLU:OE1	2.45	0.49
86:Ao:67:LYS:HG3	86:Ao:68:VAL:HG13	1.95	0.49
88:EL:82:LEU:HD22	88:FL:67:LEU:HD13	1.95	0.49
1:B0:139:GLU:HG3	30:Bb:344:PHE:HZ	1.76	0.49
3:B2:194:LYS:HG2	56:BA:41:A:H4'	1.95	0.49
6:B5:136:GLU:HB3	6:B5:177:ARG:HH12	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BG:133:ILE:HG22	13:BG:151:PHE:CD1	2.47	0.49
23:BT:58:PRO:HD3	77:Ae:131:TYR:O	2.13	0.49
32:Bd:139:LEU:HD23	40:Bk:169:ILE:HG23	1.95	0.49
52:AA:647:A:N6	71:Au:80:ARG:O	2.39	0.49
57:AB:84:PHE:HZ	78:Af:88:SER:HB2	1.77	0.49
60:AF:3:ARG:NH1	67:AO:98:MET:O	2.46	0.49
70:AR:125:TYR:HB3	71:Au:9:ALA:HB2	1.94	0.49
77:Ae:191:PHE:HA	77:Ae:196:ASN:HD22	1.78	0.49
79:Ag:162:LYS:HB3	79:Ag:315:LEU:HD11	1.95	0.49
88:CL:80:SER:HA	88:CL:83:ASN:ND2	2.28	0.49
41:Bl:111:ARG:NH2	56:BA:216:C:OP2	2.46	0.48
51:Bx:71:PRO:O	51:Bx:74:ARG:HG2	2.13	0.48
52:AA:782:G:N3	54:AV:38:U:O2'	2.44	0.48
73:Aa:99:ASN:OD1	73:Aa:100:ILE:N	2.46	0.48
83:Ak:79:LYS:HD2	86:Ao:91:ASP:HB3	1.95	0.48
83:Ak:292:GLU:OE1	83:Ak:295:ARG:NH2	2.34	0.48
8:BB:42:C:OP2	22:BS:85:ARG:NH2	2.44	0.48
18:BO:81:LYS:NZ	56:BA:1383:G:O3'	2.47	0.48
19:BP:54:LYS:HE3	56:BA:184:U:H5''	1.95	0.48
22:BS:116:LEU:HD21	22:BS:124:ALA:HA	1.95	0.48
26:BW:101:LEU:HD22	26:BW:116:LYS:HG3	1.93	0.48
31:Bc:183:ASP:OD1	31:Bc:184:LYS:N	2.45	0.48
37:Bh:105:ARG:HB2	37:Bh:112:LYS:HD2	1.94	0.48
50:Bw:154:LYS:NZ	56:BA:741:A:OP2	2.46	0.48
52:AA:13:U:H2'	52:AA:14:C:H6	1.77	0.48
56:BA:50:A:H2'	56:BA:51:A:C8	2.48	0.48
79:Ag:154:ILE:HD13	79:Ag:261:VAL:HB	1.95	0.48
86:Ao:461:TYR:CZ	86:Ao:488:VAL:HG11	2.47	0.48
3:B2:231:LYS:NZ	56:BA:11:G:O6	2.41	0.48
12:BF:220:ASP:O	12:BF:245:ALA:N	2.46	0.48
12:BF:230:VAL:HG12	12:BF:242:LEU:HD22	1.94	0.48
29:Ba:233:LYS:HA	29:Ba:286:PRO:HD2	1.95	0.48
29:Ba:392:ILE:HG12	29:Ba:397:VAL:HG22	1.95	0.48
52:AA:525:U:H2'	52:AA:526:G:H8	1.78	0.48
58:AC:72:HIS:NE2	58:AC:75:ASN:OD1	2.44	0.48
58:AC:144:SER:HB3	58:AC:151:VAL:HG22	1.95	0.48
62:AI:318:LEU:HD21	62:AI:329:MET:HE1	1.94	0.48
88:EL:72:ALA:HA	88:HL:76:LEU:CD2	2.43	0.48
3:B2:176:GLY:O	56:BA:22:U:N3	2.35	0.48
58:AC:109:VAL:HB	58:AC:120:CYS:HB2	1.96	0.48
62:AI:158:TYR:CZ	62:AI:218:ASP:HB3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:AP:21:LEU:HD22	68:AP:34:ILE:HG12	1.95	0.48
79:Ag:78:PHE:HZ	79:Ag:142:HIS:HB2	1.78	0.48
11:BE:96:ARG:HH22	11:BE:202:GLN:HE22	1.62	0.48
14:BI:144:LYS:HG2	14:BI:147:ARG:HH12	1.78	0.48
19:BP:177:ALA:HA	19:BP:222:TYR:CD1	2.48	0.48
29:Ba:179:VAL:HG22	50:Bw:198:ARG:HH21	1.78	0.48
29:Ba:301:PRO:HB3	56:BA:721:A:OP1	2.14	0.48
31:Bc:285:THR:OG1	31:Bc:288:SER:O	2.28	0.48
37:Bh:83:PHE:HE2	37:Bh:202:LEU:HB2	1.78	0.48
52:AA:201:A:H2'	52:AA:202:A:C8	2.48	0.48
52:AA:299:U:H2'	52:AA:300:G:C8	2.49	0.48
56:BA:1354:A:H61	56:BA:1465:A:H61	1.61	0.48
62:AI:257:LEU:HD23	62:AI:257:LEU:H	1.76	0.48
86:Ao:89:PHE:HE2	86:Ao:106:PHE:HB2	1.78	0.48
87:Ap:79:ARG:HH12	87:Ap:87:PRO:HD2	1.78	0.48
11:BE:206:VAL:HG13	11:BE:297:VAL:HG13	1.94	0.48
22:BS:180:GLU:HB3	56:BA:1210:A:H5''	1.95	0.48
29:Ba:88:ARG:NH2	56:BA:743:U:O3'	2.46	0.48
29:Ba:249:LYS:HE2	29:Ba:370:VAL:HG22	1.95	0.48
30:Bb:50:LYS:O	30:Bb:52:ARG:NH1	2.46	0.48
31:Bc:289:LEU:HD23	31:Bc:289:LEU:H	1.78	0.48
40:Bk:48:TYR:HE2	56:BA:409:A:H61	1.61	0.48
40:Bk:122:GLU:N	40:Bk:158:GLN:O	2.47	0.48
41:Bl:84:TYR:HA	41:Bl:115:GLY:HA3	1.95	0.48
50:Bw:219:ARG:NH2	56:BA:780:G:OP2	2.40	0.48
56:BA:296:C:OP2	91:BA:1793:SPM:N1	2.46	0.48
56:BA:742:U:H2'	56:BA:743:U:C6	2.49	0.48
59:AE:141:TRP:HH2	86:Ao:120:ILE:HD11	1.79	0.48
73:Aa:254:VAL:HA	73:Aa:264:TYR:HE2	1.78	0.48
73:Aa:338:GLU:HA	73:Aa:341:LYS:HG2	1.95	0.48
76:Ad:168:ILE:HG12	76:Ad:176:ARG:HG3	1.94	0.48
1:B0:71:ARG:NH1	56:BA:1162:G:OP1	2.47	0.48
12:BF:92:ARG:HH12	41:Bl:144:THR:HG23	1.79	0.48
22:BS:104:SER:HG	30:Bb:150:ARG:HH22	1.57	0.48
29:Ba:172:LYS:O	29:Ba:175:THR:OG1	2.26	0.48
31:Bc:223:ALA:HB1	31:Bc:237:ILE:HD13	1.95	0.48
48:Bu:71:ILE:HG21	48:Bu:150:LEU:HD22	1.96	0.48
50:Bw:365:CYS:HB2	50:Bw:388:TRP:HB2	1.94	0.48
56:BA:740:U:H2'	56:BA:741:A:H8	1.78	0.48
56:BA:1066:A:H2'	56:BA:1067:G:C8	2.47	0.48
66:AN:40:ARG:NH1	66:AN:86:ARG:HH21	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Ah:321:HIS:HA	80:Ah:325:PHE:HD2	1.78	0.48
87:Ap:116:ASP:OD1	87:Ap:117:PHE:N	2.47	0.48
88:EL:72:ALA:HA	88:HL:76:LEU:HD22	1.95	0.48
1:B0:78:GLY:HA3	1:B0:132:HIS:CE1	2.48	0.48
52:AA:770:A:H2'	52:AA:771:A:H8	1.78	0.48
52:AA:815:U:H2'	52:AA:816:U:H6	1.79	0.48
56:BA:891:A:H3'	56:BA:892:G:H8	1.77	0.48
56:BA:1160:C:H2'	56:BA:1161:G:H8	1.79	0.48
59:AE:171:ASP:O	59:AE:174:GLN:HG3	2.13	0.48
77:Ae:270:LEU:HD12	77:Ae:273:LYS:HD3	1.94	0.48
86:Ao:353:LYS:HB3	86:Ao:381:LEU:HD22	1.96	0.48
2:B1:6:VAL:HG12	56:BA:21:C:H41	1.79	0.48
4:B3:93:LYS:O	4:B3:96:THR:OG1	2.32	0.48
12:BF:231:VAL:HG13	49:Bv:26:ARG:HD2	1.96	0.48
16:BK:32:GLY:O	16:BK:36:GLY:N	2.46	0.48
19:BP:38:ARG:HD3	19:BP:45:ARG:HH21	1.78	0.48
22:BS:51:ARG:HG3	30:Bb:267:ARG:HH21	1.77	0.48
23:BT:57:PRO:N	77:Ae:132:LEU:O	2.47	0.48
36:B8:172:TYR:HB2	36:B8:175:ASP:HB2	1.96	0.48
37:Bh:184:PHE:O	37:Bh:186:VAL:HG23	2.13	0.48
52:AA:120:A:N6	52:AA:132:A:N1	2.61	0.48
56:BA:368:A:O2'	56:BA:369:G:N7	2.46	0.48
56:BA:1226:C:OP1	56:BA:1227:U:N3	2.47	0.48
56:BA:1357:C:H3'	56:BA:1358:G:H5''	1.96	0.48
62:AI:321:LEU:HD13	62:AI:357:VAL:HG11	1.96	0.48
80:Ah:329:TYR:O	80:Ah:369:ARG:NH2	2.47	0.48
8:BB:4:A:H3'	8:BB:5:A:H5''	1.95	0.48
17:BN:16:ARG:O	37:Bh:261:SER:OG	2.21	0.48
31:Bc:61:LYS:HD2	31:Bc:77:VAL:HG12	1.95	0.48
50:Bw:399:ILE:HG22	50:Bw:404:VAL:HA	1.96	0.48
60:AF:23:LYS:HG3	76:Ad:173:LEU:HD21	1.95	0.48
79:Ag:46:ALA:HB3	79:Ag:357:GLN:HG3	1.95	0.48
25:BV:178:PHE:HD1	25:BV:185:GLN:HG2	1.78	0.47
41:Bl:91:MET:HE3	56:BA:219:A:H5''	1.95	0.47
43:Bn:68:LYS:HG2	43:Bn:72:GLU:HG3	1.95	0.47
52:AA:441:U:H2'	52:AA:442:A:C8	2.48	0.47
56:BA:319:G:H2'	56:BA:320:U:C6	2.48	0.47
56:BA:745:A:H3'	56:BA:746:U:H5''	1.95	0.47
56:BA:1195:A:H3'	56:BA:1196:G:H8	1.79	0.47
56:BA:1236:C:H2'	56:BA:1237:A:H8	1.79	0.47
63:AJ:106:ILE:HD11	63:AJ:143:LEU:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:Ao:423:MET:HB3	86:Ao:463:LYS:HE3	1.95	0.47
3:B2:230:ARG:NH2	56:BA:101:U:O3'	2.47	0.47
7:B6:47:ASP:O	7:B6:51:LYS:N	2.47	0.47
10:BD:216:VAL:HG13	10:BD:228:GLN:HB3	1.95	0.47
18:BO:37:ARG:NH1	56:BA:984:A:OP2	2.47	0.47
20:BQ:49:LYS:HA	20:BQ:113:MET:HE1	1.96	0.47
28:BY:54:TRP:NE1	28:BY:56:LEU:O	2.48	0.47
30:Bb:214:TRP:HB3	30:Bb:272:LEU:HD11	1.96	0.47
49:Bv:28:ARG:NH1	56:BA:100:C:O2'	2.47	0.47
52:AA:293:A:OP1	85:An:129:ASN:ND2	2.47	0.47
54:AV:50:U:N3	54:AV:54:U:C5	2.65	0.47
56:BA:115:U:H2'	56:BA:131:A:H61	1.78	0.47
56:BA:342:C:H2'	56:BA:343:C:H6	1.79	0.47
56:BA:1006:U:H2'	56:BA:1007:G:O4'	2.13	0.47
82:Aj:108:ASN:HB3	82:Aj:110:ASP:OD1	2.14	0.47
83:Ak:153:ILE:HD13	83:Ak:221:TYR:HE1	1.78	0.47
16:BK:35:LEU:HD12	16:BK:38:ILE:HD11	1.94	0.47
22:BS:52:ASN:HD22	30:Bb:267:ARG:HD3	1.79	0.47
31:Bc:278:SER:H	31:Bc:295:GLY:HA2	1.79	0.47
35:Bg:15:LEU:HD11	37:Bh:169:VAL:HG22	1.96	0.47
52:AA:703:U:H2'	52:AA:704:U:C6	2.49	0.47
52:AA:738:U:H2'	61:AG:198:ARG:HE	1.78	0.47
54:AV:47:U:H2'	54:AV:48:U:C6	2.49	0.47
56:BA:648:C:H2'	56:BA:649:A:C8	2.49	0.47
56:BA:744:A:OP1	56:BA:744:A:H4'	2.13	0.47
67:AO:115:LYS:HG3	67:AO:116:VAL:HG23	1.96	0.47
77:Ae:168:THR:O	77:Ae:175:TYR:HB2	2.15	0.47
79:Ag:79:PRO:HG2	79:Ag:193:ALA:HA	1.96	0.47
85:An:173:LEU:HD12	85:An:191:THR:HG23	1.96	0.47
88:EL:77:LEU:HD11	88:HL:72:ALA:HB1	1.96	0.47
2:B1:163:ARG:HD3	2:B1:205:GLY:H	1.78	0.47
13:BG:108:ASN:OD1	13:BG:110:ARG:NH1	2.47	0.47
16:BK:60:ILE:HG22	46:Bq:78:TYR:HA	1.95	0.47
23:BT:53:ALA:HA	82:Aj:108:ASN:HA	1.96	0.47
24:BU:34:ARG:HH21	56:BA:1014:A:H5''	1.78	0.47
27:BX:75:GLY:N	27:BX:91:ASP:OD1	2.39	0.47
29:Ba:112:ARG:HG3	56:BA:719:C:O2'	2.13	0.47
30:Bb:206:TYR:OH	30:Bb:242:GLY:O	2.31	0.47
34:Bf:67:ILE:HG21	37:Bh:258:THR:HG23	1.96	0.47
37:Bh:96:CYS:SG	37:Bh:181:SER:OG	2.67	0.47
56:BA:1336:A:H2'	56:BA:1337:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:Aa:135:GLU:HA	73:Aa:138:LYS:HG2	1.96	0.47
15:BJ:95:MET:HE2	15:BJ:161:VAL:HG22	1.97	0.47
24:BU:137:GLU:HB2	24:BU:138:PRO:HD3	1.97	0.47
30:Bb:138:GLU:O	30:Bb:142:THR:HG22	2.14	0.47
30:Bb:257:PRO:HB3	30:Bb:268:PHE:CZ	2.50	0.47
32:Bd:157:LEU:HD11	39:Bj:178:TRP:HH2	1.78	0.47
50:Bw:132:ASP:OD1	50:Bw:134:THR:OG1	2.22	0.47
52:AA:159:C:P	52:AA:172:A:H61	2.38	0.47
54:AV:5:U:H2'	54:AV:6:U:C6	2.49	0.47
56:BA:339:G:N3	56:BA:1067:G:O2'	2.44	0.47
56:BA:410:U:O2'	56:BA:1169:A:N7	2.44	0.47
56:BA:1023:U:H2'	56:BA:1024:G:C8	2.50	0.47
56:BA:1269:G:N2	56:BA:1272:U:O2	2.43	0.47
66:AN:93:MET:HG3	66:AN:110:VAL:HG11	1.95	0.47
73:Aa:247:VAL:HG22	73:Aa:284:LEU:HD23	1.96	0.47
83:Ak:188:ALA:O	83:Ak:235:SER:OG	2.33	0.47
4:B3:73:LYS:NZ	56:BA:471:U:OP1	2.37	0.47
4:B3:120:LYS:NZ	47:Bt:44:GLU:OE2	2.43	0.47
11:BE:103:LYS:NZ	11:BE:291:GLY:O	2.38	0.47
19:BP:26:ASN:ND2	47:Bt:98:THR:OG1	2.47	0.47
19:BP:99:ASN:HB2	19:BP:144:GLY:HA3	1.96	0.47
22:BS:78:TRP:O	22:BS:96:HIS:ND1	2.48	0.47
31:Bc:127:PHE:HB3	31:Bc:302:LEU:HD11	1.97	0.47
43:Bn:69:HIS:CD2	43:Bn:71:LYS:HG3	2.45	0.47
52:AA:216:A:N7	52:AA:273:A:O2'	2.42	0.47
52:AA:578:G:H3'	52:AA:579:A:H8	1.79	0.47
52:AA:857:C:H2'	52:AA:858:C:C6	2.50	0.47
56:BA:1381:A:H2'	56:BA:1382:C:C6	2.49	0.47
63:AJ:80:VAL:HG21	63:AJ:91:TYR:CE2	2.49	0.47
69:AQ:6:SER:O	69:AQ:11:LYS:NZ	2.48	0.47
73:Aa:104:MET:HG3	73:Aa:318:ASP:HB3	1.95	0.47
77:Ae:188:MET:HE1	77:Ae:200:ALA:HB1	1.97	0.47
1:B0:144:LEU:HD22	22:BS:44:VAL:HG11	1.97	0.47
4:B3:68:ILE:HD11	4:B3:122:LEU:HD13	1.97	0.47
5:B4:59:LYS:HA	5:B4:78:MET:HB2	1.95	0.47
6:B5:155:GLU:HB3	6:B5:172:LYS:HD3	1.97	0.47
12:BF:70:ARG:HA	12:BF:196:PRO:HD3	1.96	0.47
12:BF:279:ARG:H	41:Bl:90:ARG:NH2	2.12	0.47
13:BG:118:LYS:HA	13:BG:129:ALA:HB1	1.97	0.47
17:BN:115:ASN:HB2	56:BA:175:C:H5''	1.97	0.47
25:BV:76:GLU:OE1	25:BV:80:HIS:NE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Bf:49:LEU:HD23	34:Bf:60:CYS:HB3	1.97	0.47
52:AA:62:C:H2'	52:AA:63:G:C8	2.49	0.47
52:AA:65:C:O2'	52:AA:157:A:N6	2.47	0.47
52:AA:240:C:H2'	52:AA:241:G:C8	2.50	0.47
52:AA:248:C:H41	65:AL:78:ARG:HH22	1.61	0.47
52:AA:495:U:H2'	52:AA:496:A:C8	2.49	0.47
52:AA:936:C:H2'	52:AA:937:A:C8	2.50	0.47
52:AA:939:A:H2'	52:AA:940:C:C6	2.49	0.47
54:AV:13:U:C4	54:AV:14:U:C4	3.03	0.47
56:BA:434:U:H2'	56:BA:435:C:C6	2.49	0.47
56:BA:689:A:C5	91:BA:1793:SPM:H82	2.50	0.47
56:BA:1131:U:H2'	56:BA:1132:G:C8	2.49	0.47
57:AB:93:LYS:HE2	78:Af:149:GLU:HB3	1.97	0.47
57:AB:131:THR:HG22	57:AB:256:ILE:HD11	1.97	0.47
58:AC:89:ASP:O	58:AC:93:ARG:HG2	2.14	0.47
59:AE:186:LYS:HD3	59:AE:186:LYS:HA	1.49	0.47
73:Aa:180:PHE:HB2	73:Aa:195:VAL:HG23	1.96	0.47
75:Ac:2:PRO:HB2	75:Ac:11:ARG:HH12	1.79	0.47
77:Ae:131:TYR:O	77:Ae:132:LEU:C	2.57	0.47
77:Ae:370:GLN:O	77:Ae:374:ARG:HG2	2.13	0.47
83:Ak:190:LYS:O	83:Ak:194:LYS:NZ	2.46	0.47
87:Ap:51:TYR:CE2	87:Ap:58:TYR:HB2	2.50	0.47
15:BJ:236:TYR:OH	88:HL:86:LEU:O	2.31	0.47
20:BQ:170:LYS:HB2	46:Bq:132:LEU:HD22	1.95	0.47
23:BT:96:ARG:HA	23:BT:99:MET:SD	2.55	0.47
25:BV:181:ARG:HH21	56:BA:188:C:P	2.38	0.47
36:B8:109:ALA:O	36:B8:113:ARG:HG2	2.15	0.47
52:AA:543:A:H4'	61:AG:159:VAL:HG13	1.97	0.47
52:AA:815:U:H2'	52:AA:816:U:C6	2.49	0.47
55:AX:3:U:O2'	55:AX:4:U:H5	1.95	0.47
56:BA:52:A:H4'	56:BA:245:A:H2	1.80	0.47
56:BA:920:C:O2	56:BA:924:G:O6	2.33	0.47
80:Ah:345:LEU:HB3	81:Ai:34:VAL:HG22	1.97	0.47
86:Ao:472:GLU:HG3	86:Ao:473:GLN:H	1.79	0.47
87:Ap:108:CYS:SG	87:Ap:146:GLN:HG3	2.54	0.47
11:BE:252:TRP:HB3	17:BN:84:PRO:HD3	1.97	0.47
14:BI:139:LEU:O	14:BI:142:GLU:HG3	2.15	0.47
16:BK:139:SER:HB3	56:BA:526:A:H4'	1.96	0.47
23:BT:152:ARG:HD3	23:BT:161:GLU:HG2	1.96	0.47
28:BY:21:TYR:CZ	28:BY:82:GLN:HG2	2.49	0.47
30:Bb:364:ARG:NE	56:BA:1195:A:OP2	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Bm:143:GLU:O	42:Bm:147:SER:OG	2.28	0.47
56:BA:289:U:H2'	56:BA:290:A:H8	1.79	0.47
59:AE:185:MET:HE2	59:AE:185:MET:HB2	1.68	0.47
60:AF:105:CYS:HB2	70:AR:70:GLU:H	1.79	0.47
62:AI:363:GLU:HA	62:AI:366:ARG:HG2	1.96	0.47
67:AO:176:TYR:HB2	69:AQ:89:GLY:HA3	1.97	0.47
82:Aj:135:MET:SD	82:Aj:135:MET:N	2.80	0.47
83:Ak:184:LEU:HD12	83:Ak:188:ALA:HB1	1.97	0.47
13:BG:92:MET:HB3	13:BG:245:THR:HG21	1.97	0.47
22:BS:176:ARG:HH12	56:BA:1211:A:P	2.38	0.47
48:Bu:103:HIS:HE1	48:Bu:105:ALA:HB3	1.77	0.47
52:AA:388:U:H5''	60:AF:72:ALA:HB1	1.96	0.47
56:BA:368:A:H61	56:BA:433:G:H5'	1.80	0.47
59:AE:282:ILE:HD12	59:AE:353:LEU:HB3	1.96	0.47
62:AI:321:LEU:HD12	62:AI:353:LEU:HD13	1.97	0.47
62:AI:323:ARG:HD2	62:AI:327:HIS:HE1	1.79	0.47
77:Ae:97:MET:HE3	77:Ae:97:MET:HB3	1.76	0.47
79:Ag:80:HIS:HB3	79:Ag:155:PRO:HG3	1.96	0.47
88:CL:76:LEU:HB3	88:FL:72:ALA:HA	1.97	0.47
11:BE:215:PHE:O	56:BA:789:A:O2'	2.19	0.46
17:BN:169:VAL:HG13	51:Bx:75:TRP:CD1	2.50	0.46
18:BO:41:VAL:HG12	18:BO:105:VAL:O	2.15	0.46
41:Bl:105:ARG:HD2	56:BA:388:A:H4'	1.97	0.46
44:Bo:23:ALA:O	44:Bo:28:ARG:NH2	2.48	0.46
50:Bw:87:GLN:NE2	50:Bw:274:ASN:OD1	2.47	0.46
52:AA:884:C:N4	77:Ae:144:LEU:O	2.48	0.46
56:BA:199:A:H2'	56:BA:200:A:H8	1.80	0.46
56:BA:548:A:H2'	56:BA:549:C:C6	2.50	0.46
56:BA:723:A:H3'	56:BA:724:A:H5''	1.97	0.46
56:BA:1243:U:H2'	56:BA:1244:U:C6	2.50	0.46
59:AE:305:MET:HE1	59:AE:353:LEU:HD21	1.97	0.46
67:AO:75:LEU:H	67:AO:107:ILE:HD11	1.80	0.46
77:Ae:137:HIS:C	82:Aj:104:TYR:HB2	2.39	0.46
86:Ao:469:CYS:SG	86:Ao:498:ASP:HB3	2.55	0.46
6:B5:90:ASN:O	6:B5:94:ARG:HG2	2.15	0.46
15:BJ:232:LEU:HD21	88:HL:87:LYS:NZ	2.30	0.46
25:BV:162:ALA:HB2	25:BV:199:ILE:HG13	1.98	0.46
29:Ba:363:ASP:OD1	29:Ba:363:ASP:N	2.44	0.46
30:Bb:197:GLU:OE1	30:Bb:197:GLU:N	2.48	0.46
37:Bh:216:ARG:HG3	37:Bh:220:ILE:HD12	1.97	0.46
50:Bw:289:GLY:HA3	50:Bw:329:TRP:CZ2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BA:666:G:O6	56:BA:774:A:N6	2.48	0.46
56:BA:1002:U:C2	56:BA:1003:C:C5	3.03	0.46
56:BA:1060:C:H2'	56:BA:1061:U:H6	1.80	0.46
83:Ak:55:LEU:HB3	86:Ao:93:PRO:HB3	1.96	0.46
10:BD:156:GLU:N	10:BD:247:ARG:O	2.48	0.46
10:BD:207:TYR:O	10:BD:209:ARG:HG3	2.15	0.46
23:BT:60:PRO:HG3	77:Ae:112:ILE:HA	1.97	0.46
28:BY:124:ASP:OD1	28:BY:124:ASP:N	2.49	0.46
32:Bd:193:GLN:HG3	40:Bk:133:GLU:HB3	1.98	0.46
52:AA:787:A:H2'	52:AA:788:G:C8	2.50	0.46
56:BA:289:U:H2'	56:BA:290:A:C8	2.50	0.46
56:BA:877:U:O2'	56:BA:965:A:OP2	2.27	0.46
64:AK:130:ALA:HB1	64:AK:163:ALA:HB2	1.97	0.46
66:AN:34:MET:HE3	81:Ai:52:TYR:CD1	2.51	0.46
74:Ab:19:LEU:HD23	74:Ab:25:LEU:HB2	1.96	0.46
80:Ah:311:ALA:O	83:Ak:166:ARG:NH2	2.47	0.46
84:Am:52:MET:HG3	84:Am:70:ILE:HD13	1.97	0.46
86:Ao:375:TYR:O	86:Ao:379:ILE:HG12	2.15	0.46
88:CL:76:LEU:HD22	88:FL:71:ILE:HG22	1.97	0.46
11:BE:218:VAL:HB	11:BE:258:PRO:HG3	1.97	0.46
14:BI:122:ARG:HE	14:BI:123:LEU:HD12	1.79	0.46
24:BU:71:ARG:NH1	26:BW:208:HIS:O	2.48	0.46
29:Ba:240:ALA:HB2	29:Ba:375:TRP:HH2	1.79	0.46
29:Ba:353:GLN:HE22	29:Ba:379:ASP:H	1.64	0.46
30:Bb:155:CYS:O	30:Bb:267:ARG:NH1	2.49	0.46
39:Bj:152:LYS:HD2	39:Bj:157:LEU:HD21	1.97	0.46
41:Bl:94:ILE:HD11	41:Bl:162:LEU:HG	1.96	0.46
46:Bq:130:ASN:HB3	56:BA:534:A:H5'	1.97	0.46
52:AA:621:A:OP2	58:AC:36:LYS:N	2.48	0.46
56:BA:1329:U:OP2	56:BA:1399:G:N1	2.33	0.46
56:BA:1336:A:H2'	56:BA:1337:G:C8	2.49	0.46
60:AF:105:CYS:CB	70:AR:70:GLU:H	2.29	0.46
64:AK:77:TRP:HB2	64:AK:85:ILE:HD11	1.97	0.46
77:Ae:84:ASP:OD1	77:Ae:84:ASP:N	2.44	0.46
3:B2:185:GLN:OE1	27:BX:9:LEU:N	2.41	0.46
5:B4:53:TYR:CG	5:B4:72:PRO:HB3	2.50	0.46
10:BD:290:LEU:HD12	10:BD:291:PRO:HD2	1.98	0.46
13:BG:79:VAL:HG11	13:BG:82:ILE:HG12	1.98	0.46
13:BG:171:PRO:HB3	13:BG:180:VAL:HG22	1.96	0.46
20:BQ:53:VAL:HG21	20:BQ:102:PHE:HB3	1.98	0.46
30:Bb:35:MET:HB2	30:Bb:38:GLU:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Bd:76:GLU:OE2	40:Bk:204:LEU:HD12	2.11	0.46
51:Bx:79:HIS:HA	51:Bx:184:ASN:HD22	1.79	0.46
52:AA:662:C:H2'	52:AA:663:A:H8	1.81	0.46
54:AV:18:U:H5	54:AV:44:U:H5'	1.81	0.46
54:AV:33:U:H2'	54:AV:34:U:C6	2.51	0.46
56:BA:952:A:H2'	56:BA:953:G:H8	1.81	0.46
56:BA:1021:C:H2'	56:BA:1022:G:C8	2.50	0.46
57:AB:105:LEU:HD21	57:AB:224:THR:HG22	1.97	0.46
70:AR:73:VAL:HG21	70:AR:107:GLU:HB3	1.98	0.46
79:Ag:54:ASP:HB2	79:Ag:57:LYS:HB2	1.96	0.46
86:Ao:551:PHE:CG	86:Ao:585:LEU:HD22	2.50	0.46
2:B1:6:VAL:HG13	2:B1:11:TRP:HE1	1.81	0.46
8:BB:8:U:O2	8:BB:14:A:N6	2.48	0.46
10:BD:231:SER:OG	56:BA:851:G:N7	2.46	0.46
15:BJ:128:ASN:ND2	56:BA:551:A:OP1	2.45	0.46
28:BY:180:GLU:O	28:BY:184:GLU:HB2	2.14	0.46
37:Bh:166:VAL:HG11	37:Bh:192:ARG:HG3	1.98	0.46
52:AA:97:C:H2'	52:AA:98:A:O4'	2.16	0.46
52:AA:242:U:O4	52:AA:259:A:N7	2.48	0.46
52:AA:562:A:H8	52:AA:708:A:H61	1.63	0.46
52:AA:843:C:O2	52:AA:928:A:N6	2.49	0.46
52:AA:939:A:H2'	52:AA:940:C:H6	1.81	0.46
56:BA:199:A:H2'	56:BA:200:A:C8	2.50	0.46
56:BA:731:U:O2'	56:BA:732:A:O5'	2.30	0.46
56:BA:916:C:H2'	56:BA:917:G:C8	2.50	0.46
56:BA:916:C:H2'	56:BA:917:G:H8	1.80	0.46
56:BA:1129:C:H3'	56:BA:1130:A:H8	1.79	0.46
58:AC:101:PRO:HB2	81:Ai:72:ARG:HH21	1.79	0.46
73:Aa:230:VAL:O	73:Aa:236:ASN:ND2	2.42	0.46
76:Ad:55:VAL:O	76:Ad:58:GLU:HG3	2.15	0.46
77:Ae:185:ASN:HD21	77:Ae:217:SER:HB2	1.81	0.46
82:Aj:73:LEU:HD13	82:Aj:76:LEU:HD12	1.97	0.46
82:Aj:102:PRO:HA	82:Aj:112:GLY:HA3	1.97	0.46
12:BF:59:ARG:HH21	19:BP:10:PRO:HG3	1.80	0.46
12:BF:217:LEU:HB2	12:BF:256:HIS:CG	2.51	0.46
17:BN:152:PRO:HB3	51:Bx:84:GLU:HG3	1.97	0.46
22:BS:117:TYR:CD1	30:Bb:114:ARG:HG2	2.51	0.46
24:BU:52:LYS:HG2	24:BU:55:ARG:HH21	1.81	0.46
29:Ba:161:ALA:O	29:Ba:165:HIS:ND1	2.48	0.46
42:Bm:74:HIS:HA	42:Bm:77:GLU:HG2	1.98	0.46
52:AA:729:A:O2'	79:Ag:316:PHE:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BA:344:U:H2'	56:BA:345:G:H8	1.81	0.46
57:AB:161:CYS:SG	57:AB:253:GLN:HA	2.55	0.46
59:AE:93:LEU:H	81:Ai:75:HIS:HD2	1.64	0.46
59:AE:203:LEU:HD21	59:AE:268:PHE:HB3	1.98	0.46
67:AO:140:TYR:HB2	67:AO:157:LEU:HD13	1.96	0.46
68:AP:110:LEU:O	68:AP:114:ARG:HG2	2.16	0.46
69:AQ:69:LEU:HD13	69:AQ:80:GLU:HB2	1.97	0.46
2:B1:133:ASP:OD1	14:BI:120:ARG:NH2	2.49	0.46
31:Bc:206:LEU:HD12	31:Bc:209:LYS:HE3	1.98	0.46
48:Bu:103:HIS:HB3	48:Bu:106:SER:HB2	1.96	0.46
49:Bv:34:SER:O	56:BA:96:U:N3	2.49	0.46
49:Bv:37:PRO:HG3	49:Bv:64:HIS:CG	2.51	0.46
50:Bw:394:PRO:O	50:Bw:408:ASN:ND2	2.37	0.46
56:BA:129:A:H2'	56:BA:130:A:C8	2.51	0.46
56:BA:942:U:H2'	56:BA:943:C:C6	2.51	0.46
58:AC:116:GLN:HB3	58:AC:150:PRO:HG2	1.97	0.46
59:AE:313:GLY:HA2	59:AE:331:ASP:HA	1.98	0.46
61:AG:115:LEU:HD22	61:AG:141:PRO:HB2	1.97	0.46
62:AI:228:ARG:HH11	71:AU:85:GLN:HB3	1.81	0.46
65:AL:70:PRO:HB3	65:AL:117:ASP:HB3	1.97	0.46
68:AP:29:ARG:NH1	68:AP:57:LEU:HB2	2.31	0.46
73:Aa:189:HIS:HB3	73:Aa:215:ILE:HD13	1.96	0.46
3:B2:153:ASP:HA	3:B2:156:ARG:HG2	1.97	0.46
15:BJ:204:GLN:HB3	88:CL:90:LEU:HD21	1.97	0.46
19:BP:73:PRO:HG2	19:BP:76:LEU:HD12	1.97	0.46
29:Ba:409:GLU:HG3	29:Ba:413:LYS:HE3	1.97	0.46
34:Bf:46:LYS:O	34:Bf:63:PRO:HD2	2.15	0.46
52:AA:23:U:H2'	52:AA:24:C:H6	1.80	0.46
52:AA:892:A:C5	82:Aj:21:LEU:HD21	2.50	0.46
66:AN:84:PRO:HG3	81:Ai:43:ALA:HB2	1.98	0.46
73:Aa:324:HIS:CE1	73:Aa:328:ILE:HD11	2.51	0.46
76:Ad:29:THR:N	76:Ad:32:ASP:OD2	2.49	0.46
79:Ag:267:LEU:HD21	79:Ag:292:LEU:HD23	1.98	0.46
79:Ag:389:GLN:HG3	79:Ag:393:LEU:HD13	1.97	0.46
86:Ao:379:ILE:HD12	86:Ao:396:ILE:HG23	1.97	0.46
3:B2:236:LEU:HD13	28:BY:48:PRO:HG3	1.96	0.46
10:BD:198:GLU:HB3	10:BD:241:CYS:HB3	1.97	0.46
11:BE:233:GLN:OE1	56:BA:1402:C:O2'	2.24	0.46
13:BG:167:MET:HE3	13:BG:184:GLN:CD	2.41	0.46
15:BJ:121:ILE:HD12	15:BJ:156:SER:HB2	1.98	0.46
18:BO:33:GLN:H	18:BO:36:THR:HG21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BT:192:ASP:CG	23:BT:230:SER:H	2.24	0.46
27:BX:50:ARG:NH1	27:BX:68:VAL:O	2.49	0.46
29:Ba:140:ALA:HB1	29:Ba:412:ARG:HG2	1.98	0.46
29:Ba:166:SER:HB3	29:Ba:171:PRO:HG3	1.98	0.46
32:Bd:149:GLU:CD	39:Bj:212:HIS:HB3	2.41	0.46
52:AA:93:A:N3	76:Ad:79:ARG:NH2	2.63	0.46
52:AA:823:G:H2'	52:AA:824:G:C8	2.51	0.46
56:BA:1031:C:H2'	56:BA:1032:G:C8	2.51	0.46
56:BA:1344:C:H2'	56:BA:1345:A:C8	2.51	0.46
57:AB:117:LEU:HA	57:AB:120:THR:HB	1.97	0.46
58:AC:154:HIS:CG	83:Ak:77:PRO:HG3	2.51	0.46
60:AF:6:LEU:HB3	60:AF:66:VAL:HB	1.97	0.46
62:AI:323:ARG:HH11	62:AI:327:HIS:CE1	2.34	0.46
67:AO:171:LEU:HG	67:AO:179:PHE:HB2	1.98	0.46
73:Aa:101:LEU:HD22	73:Aa:291:GLY:HA2	1.98	0.46
77:Ae:436:GLU:HA	77:Ae:439:GLU:HG2	1.97	0.46
86:Ao:647:GLY:O	86:Ao:651:ARG:HG2	2.16	0.46
29:Ba:380:GLN:HB3	29:Ba:410:THR:HG22	1.98	0.45
30:Bb:237:VAL:HA	30:Bb:250:GLU:HA	1.97	0.45
33:Be:32:LYS:HG3	56:BA:36:A:C4	2.51	0.45
50:Bw:365:CYS:O	50:Bw:388:TRP:N	2.42	0.45
52:AA:28:U:H2'	52:AA:29:A:H8	1.80	0.45
52:AA:154:C:H2'	52:AA:155:A:H8	1.80	0.45
52:AA:180:U:H2'	52:AA:181:A:C8	2.51	0.45
52:AA:476:A:H8	84:Am:13:LEU:HD22	1.81	0.45
52:AA:533:C:O3'	84:Am:37:ARG:HD3	2.16	0.45
52:AA:542:C:C2	52:AA:824:G:N2	2.84	0.45
52:AA:578:G:H3'	52:AA:579:A:C8	2.51	0.45
52:AA:798:A:H2'	52:AA:799:A:C8	2.51	0.45
52:AA:824:G:HO2'	52:AA:825:C:P	2.36	0.45
54:AV:7:U:H4'	54:AV:8:U:H5''	1.98	0.45
56:BA:570:A:H2'	56:BA:571:A:C8	2.51	0.45
56:BA:1238:A:H3'	56:BA:1239:A:H5''	1.97	0.45
62:AI:157:SER:HB3	62:AI:210:LEU:HD22	1.98	0.45
73:Aa:237:LEU:HG	73:Aa:241:TYR:CZ	2.51	0.45
77:Ae:93:LEU:HD23	77:Ae:96:LEU:HB3	1.99	0.45
78:Af:109:VAL:HG12	78:Af:110:GLU:H	1.81	0.45
79:Ag:246:LEU:O	79:Ag:250:SER:OG	2.26	0.45
86:Ao:427:SER:HA	86:Ao:467:LEU:HD21	1.98	0.45
11:BE:231:HIS:CE1	56:BA:806:U:H1'	2.51	0.45
15:BJ:181:ILE:O	15:BJ:184:THR:OG1	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BP:51:ARG:HD3	43:Bn:126:LYS:HD2	1.98	0.45
24:BU:54:THR:HG21	25:BV:176:MET:H	1.81	0.45
32:Bd:143:GLN:HG3	40:Bk:169:ILE:HD11	1.99	0.45
37:Bh:96:CYS:HG	37:Bh:181:SER:HG	1.60	0.45
39:Bj:235:LYS:NZ	39:Bj:275:PHE:O	2.32	0.45
52:AA:893:A:H2'	52:AA:894:U:O4'	2.15	0.45
56:BA:364:A:O2'	56:BA:385:U:OP1	2.34	0.45
56:BA:860:G:H2'	56:BA:860:G:N3	2.30	0.45
56:BA:1021:C:H2'	56:BA:1022:G:H8	1.81	0.45
56:BA:1459:U:H2'	56:BA:1460:A:H8	1.81	0.45
57:AB:101:MET:HE2	57:AB:228:PRO:HD3	1.98	0.45
57:AB:116:ASP:OD1	57:AB:116:ASP:N	2.43	0.45
61:AG:153:GLU:HA	61:AG:183:ALA:HB2	1.97	0.45
64:AK:102:VAL:HG12	64:AK:108:PRO:HA	1.97	0.45
79:Ag:47:ILE:HG23	79:Ag:65:GLN:HE22	1.81	0.45
80:Ah:307:ILE:HB	83:Ak:159:VAL:HG12	1.97	0.45
88:CL:80:SER:HA	88:CL:83:ASN:HD21	1.80	0.45
5:B4:41:LEU:HD11	39:Bj:67:GLN:HB3	1.98	0.45
19:BP:76:LEU:O	56:BA:1234:U:O2'	2.28	0.45
26:BW:48:LYS:NZ	56:BA:148:A:O2'	2.50	0.45
34:Bf:71:HIS:HA	35:Bg:141:GLY:H	1.82	0.45
50:Bw:251:ILE:HG22	50:Bw:253:ILE:H	1.81	0.45
52:AA:154:C:H2'	52:AA:155:A:C8	2.52	0.45
52:AA:515:U:H2'	52:AA:516:C:C6	2.51	0.45
52:AA:942:G:H2'	52:AA:944:A:OP2	2.15	0.45
56:BA:476:U:H2'	56:BA:477:A:C8	2.51	0.45
56:BA:607:A:N1	56:BA:627:C:O2'	2.48	0.45
56:BA:1060:C:H2'	56:BA:1061:U:C6	2.52	0.45
59:AE:289:THR:HG22	59:AE:290:ILE:H	1.81	0.45
64:AK:68:ILE:HG23	64:AK:71:GLN:HG2	1.97	0.45
79:Ag:191:LYS:HD3	79:Ag:229:ILE:HD12	1.97	0.45
83:Ak:286:LEU:HA	83:Ak:291:VAL:HG21	1.99	0.45
2:B1:202:GLU:HG3	2:B1:203:TRP:CD1	2.51	0.45
8:BB:9:A:H8	8:BB:11:C:H41	1.64	0.45
9:B7:81:VAL:HG22	9:B7:84:ARG:HH22	1.82	0.45
11:BE:67:ASP:OD1	11:BE:68:GLU:N	2.50	0.45
21:BR:32:LEU:HB3	21:BR:52:LEU:HD22	1.97	0.45
23:BT:188:LEU:HD22	23:BT:191:ARG:HH12	1.82	0.45
30:Bb:239:ASN:HD22	30:Bb:278:ARG:HH11	1.64	0.45
35:Bg:4:ARG:NH2	56:BA:167:G:O6	2.50	0.45
37:Bh:215:ILE:HG23	37:Bh:219:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:129:G:H2'	52:AA:130:G:C8	2.52	0.45
52:AA:800:G:H2'	52:AA:801:A:H8	1.80	0.45
53:B9:78:LEU:HD11	53:B9:85:TRP:HB3	1.99	0.45
56:BA:353:C:O2	56:BA:1267:A:O2'	2.35	0.45
56:BA:1405:A:H2'	56:BA:1406:G:C8	2.50	0.45
77:Ae:243:ASN:OD1	77:Ae:244:PHE:N	2.48	0.45
86:Ao:427:SER:HA	86:Ao:467:LEU:HD11	1.98	0.45
3:B2:175:PHE:HA	9:B7:83:LEU:HD21	1.99	0.45
4:B3:109:LYS:O	4:B3:113:VAL:HG22	2.15	0.45
15:BJ:44:ARG:NH1	20:BQ:234:ASP:OD2	2.50	0.45
52:AA:689:G:O2'	81:Ai:75:HIS:NE2	2.39	0.45
52:AA:928:A:O2'	52:AA:929:A:H5'	2.16	0.45
54:AV:4:U:H2'	54:AV:5:U:C6	2.51	0.45
56:BA:342:C:H2'	56:BA:343:C:C6	2.52	0.45
61:AG:196:HIS:HB3	61:AG:199:VAL:HG23	1.99	0.45
80:Ah:354:PRO:HA	83:Ak:215:PRO:HG3	1.97	0.45
81:Ai:27:ASP:OD1	81:Ai:27:ASP:N	2.44	0.45
83:Ak:89:MET:HE2	83:Ak:106:GLU:HB3	1.99	0.45
87:Ap:215:ARG:HG3	87:Ap:218:ARG:NH2	2.32	0.45
3:B2:221:ILE:HG12	3:B2:224:ARG:NH2	2.31	0.45
11:BE:106:MET:H	23:BT:91:LYS:HZ1	1.65	0.45
15:BJ:65:LEU:HD12	15:BJ:66:PRO:HD2	1.97	0.45
19:BP:193:PHE:HE2	19:BP:200:ILE:HG12	1.81	0.45
23:BT:56:PRO:CA	77:Ae:132:LEU:O	2.65	0.45
31:Bc:101:ILE:HD12	31:Bc:126:THR:HA	1.98	0.45
40:Bk:92:ASN:OD1	40:Bk:158:GLN:NE2	2.49	0.45
50:Bw:145:LEU:HD22	50:Bw:402:ASN:HA	1.97	0.45
52:AA:602:A:H2'	52:AA:603:U:C6	2.51	0.45
52:AA:888:A:H2'	52:AA:889:U:C6	2.52	0.45
56:BA:695:U:H3	56:BA:696:A:N6	2.14	0.45
56:BA:1157:C:H2'	56:BA:1158:C:C6	2.51	0.45
56:BA:1315:U:H2'	56:BA:1316:U:C6	2.50	0.45
56:BA:1502:U:H2'	56:BA:1503:C:C6	2.52	0.45
67:AO:112:LEU:HD23	67:AO:131:VAL:HG13	1.99	0.45
87:Ap:215:ARG:HG3	87:Ap:218:ARG:HH21	1.82	0.45
10:BD:275:LEU:HB2	56:BA:329:A:C5	2.52	0.45
12:BF:123:GLY:HA3	12:BF:142:ARG:HG2	1.99	0.45
18:BO:55:PRO:HB3	18:BO:77:ILE:HG12	1.98	0.45
18:BO:78:ARG:NH1	52:AA:866:U:OP1	2.50	0.45
26:BW:95:MET:HG2	26:BW:184:ARG:HH22	1.82	0.45
52:AA:620:C:H4'	63:AJ:122:LYS:HG2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:AV:33:U:C5	54:AV:34:U:C4	3.05	0.45
56:BA:183:U:H2'	56:BA:184:U:C6	2.51	0.45
56:BA:636:U:O4	56:BA:637:A:N6	2.50	0.45
56:BA:1020:C:H2'	56:BA:1021:C:C6	2.52	0.45
56:BA:1031:C:H2'	56:BA:1032:G:H8	1.81	0.45
56:BA:1323:U:H5'	56:BA:1324:C:OP2	2.16	0.45
59:AE:162:LYS:O	59:AE:166:GLU:HG2	2.16	0.45
77:Ae:96:LEU:O	77:Ae:100:THR:HG23	2.16	0.45
3:B2:156:ARG:HA	33:Be:128:LEU:HD13	1.97	0.45
7:B6:50:VAL:HG23	7:B6:52:LYS:HB2	1.99	0.45
9:B7:85:ARG:HH12	33:Be:17:ARG:HH12	1.65	0.45
11:BE:329:PRO:HD2	11:BE:332:LEU:HD21	1.99	0.45
17:BN:78:SER:HB2	56:BA:568:C:N3	2.31	0.45
19:BP:180:ASP:OD1	19:BP:180:ASP:N	2.50	0.45
19:BP:216:ASP:OD1	19:BP:217:ALA:N	2.50	0.45
23:BT:148:THR:HG22	23:BT:165:GLU:HG2	1.97	0.45
52:AA:117:C:H42	67:AO:208:LYS:HE2	1.82	0.45
52:AA:461:A:H2'	52:AA:462:A:H8	1.82	0.45
54:AV:3:U:H2'	54:AV:4:U:C6	2.52	0.45
54:AV:17:U:H2'	54:AV:19:U:H5'	1.99	0.45
56:BA:306:A:H2'	56:BA:307:G:C8	2.51	0.45
56:BA:1251:C:H5'	56:BA:1253:G:H5'	1.99	0.45
56:BA:1343:C:H2'	56:BA:1344:C:C6	2.52	0.45
62:AI:273:GLY:HA3	62:AI:352:ALA:HB2	1.98	0.45
65:AL:129:LYS:HD3	65:AL:129:LYS:HA	1.77	0.45
66:AN:63:LEU:HB3	66:AN:67:LEU:HD11	1.98	0.45
68:AP:101:PRO:HB3	76:Ad:59:ARG:HB3	1.99	0.45
83:Ak:76:ALA:O	83:Ak:112:ASN:ND2	2.37	0.45
5:B4:56:LEU:HD22	5:B4:75:MET:HE2	1.99	0.45
15:BJ:40:MET:HE2	20:BQ:242:TRP:CG	2.52	0.45
26:BW:162:PHE:HB3	56:BA:762:A:N1	2.31	0.45
27:BX:68:VAL:HG22	27:BX:97:VAL:HG12	1.98	0.45
31:Bc:156:LYS:HD2	31:Bc:158:GLU:HG2	1.99	0.45
39:Bj:243:PHE:HZ	39:Bj:248:LYS:HE2	1.82	0.45
52:AA:418:C:O2'	64:AK:189:ARG:O	2.35	0.45
56:BA:175:C:H2'	56:BA:176:U:C6	2.52	0.45
56:BA:411:U:H2'	56:BA:412:C:C6	2.51	0.45
56:BA:1146:G:H2'	56:BA:1147:G:C8	2.52	0.45
71:AU:83:PRO:HG2	71:AU:84:TRP:CD1	2.52	0.45
80:Ah:301:LYS:HE2	86:Ao:140:LEU:HD21	1.99	0.45
83:Ak:67:ASP:N	83:Ak:67:ASP:OD1	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Ak:68:TRP:N	83:Ak:69:PRO:HD2	2.32	0.45
83:Ak:70:SER:HA	86:Ao:78:VAL:HG23	1.99	0.45
13:BG:167:MET:HG3	13:BG:169:LEU:HG	1.98	0.45
18:BO:119:ILE:HG21	18:BO:123:ILE:HD11	1.98	0.45
19:BP:260:LYS:HE3	19:BP:267:PHE:CZ	2.51	0.45
29:Ba:139:LEU:HD22	29:Ba:416:ALA:HA	1.99	0.45
52:AA:164:C:H3'	52:AA:165:G:H8	1.82	0.45
52:AA:953:U:H2'	52:AA:954:U:C6	2.52	0.45
54:AV:38:U:H2'	54:AV:39:U:C5	2.52	0.45
56:BA:232:U:H2'	56:BA:233:A:C8	2.51	0.45
56:BA:477:A:N6	56:BA:478:G:O6	2.50	0.45
56:BA:515:A:N1	56:BA:540:A:O2'	2.49	0.45
56:BA:838:A:H1'	56:BA:933:A:N6	2.33	0.45
59:AE:369:HIS:HA	59:AE:387:PRO:HD3	1.98	0.45
61:AG:172:VAL:HG22	61:AG:240:ARG:HD3	1.99	0.45
82:Aj:90:ASP:OD2	87:Ap:215:ARG:NH2	2.50	0.45
87:Ap:62:GLU:OE1	87:Ap:66:ASN:ND2	2.50	0.45
1:B0:85:LYS:NZ	56:BA:1207:C:OP1	2.47	0.44
4:B3:130:THR:HG23	4:B3:132:GLU:H	1.82	0.44
12:BF:62:VAL:HG13	12:BF:82:LEU:HB2	1.98	0.44
17:BN:21:LEU:HB3	17:BN:59:ILE:HG12	1.99	0.44
17:BN:80:HIS:CD2	17:BN:82:GLY:H	2.35	0.44
19:BP:127:VAL:HG21	19:BP:138:VAL:HG21	1.98	0.44
30:Bb:224:HIS:HA	30:Bb:232:TYR:CZ	2.53	0.44
45:Bp:10:LEU:HD23	45:Bp:42:VAL:HG13	1.99	0.44
46:Bq:88:PRO:HG2	46:Bq:91:GLU:HG2	1.98	0.44
52:AA:285:C:H41	65:AL:43:LYS:C	2.25	0.44
52:AA:364:U:H2'	52:AA:365:A:H8	1.82	0.44
52:AA:638:A:H1'	52:AA:639:A:H2'	1.99	0.44
56:BA:713:A:H2'	56:BA:714:A:H8	1.82	0.44
59:AE:136:ARG:N	81:Ai:67:PHE:O	2.49	0.44
70:AR:87:PRO:HA	70:AR:126:LYS:HB3	1.98	0.44
83:Ak:68:TRP:HZ2	83:Ak:114:LEU:HD13	1.82	0.44
83:Ak:123:ARG:HG2	86:Ao:77:THR:HB	1.98	0.44
29:Ba:122:TRP:HE3	29:Ba:123:LEU:HD23	1.82	0.44
29:Ba:209:LEU:O	29:Ba:223:HIS:HA	2.17	0.44
51:Bx:60:SER:HB2	51:Bx:75:TRP:CH2	2.52	0.44
52:AA:122:C:H4'	69:AQ:24:LYS:HD2	1.99	0.44
52:AA:182:A:C6	65:AL:56:PRO:HD2	2.52	0.44
52:AA:394:U:H2'	67:AO:129:ARG:HD3	1.99	0.44
52:AA:489:G:H2'	52:AA:490:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:662:C:O2'	58:AC:64:HIS:ND1	2.35	0.44
52:AA:807:G:H2'	52:AA:809:G:C8	2.52	0.44
56:BA:619:C:H2'	56:BA:620:A:C8	2.52	0.44
61:AG:112:THR:HG23	79:Ag:396:TYR:HB3	1.98	0.44
62:AI:263:TYR:HD1	62:AI:268:MET:HA	1.82	0.44
79:Ag:103:PRO:HG3	79:Ag:344:VAL:HG12	1.99	0.44
79:Ag:125:LEU:HD23	79:Ag:342:ILE:HB	2.00	0.44
12:BF:59:ARG:NH2	12:BF:88:SER:O	2.50	0.44
56:BA:276:G:C2	56:BA:827:U:H1'	2.52	0.44
56:BA:1003:C:C2	56:BA:1004:A:C8	3.06	0.44
62:AI:202:ILE:HG13	62:AI:205:GLU:H	1.81	0.44
73:Aa:189:HIS:O	73:Aa:211:ARG:NH2	2.50	0.44
77:Ae:93:LEU:HD23	77:Ae:96:LEU:HD23	1.99	0.44
84:Am:56:TRP:HB3	84:Am:61:PHE:CD2	2.53	0.44
84:Am:66:CYS:SG	84:Am:69:GLU:HB2	2.58	0.44
4:B3:73:LYS:HA	56:BA:472:U:OP1	2.17	0.44
10:BD:203:ARG:HH21	10:BD:206:GLN:HE22	1.66	0.44
15:BJ:63:ARG:NH2	51:Bx:102:ARG:HH21	2.16	0.44
15:BJ:89:VAL:O	15:BJ:93:ASN:ND2	2.50	0.44
16:BK:140:VAL:O	16:BK:144:ILE:HG12	2.17	0.44
23:BT:55:GLN:O	23:BT:57:PRO:HD3	2.16	0.44
23:BT:60:PRO:HD2	77:Ae:97:MET:HE2	1.99	0.44
23:BT:96:ARG:O	23:BT:99:MET:HG2	2.18	0.44
44:Bo:34:ALA:HB2	44:Bo:40:TYR:CE2	2.53	0.44
49:Bv:109:ALA:O	49:Bv:113:LYS:HG2	2.18	0.44
52:AA:56:U:H1'	52:AA:198:C:H1'	2.00	0.44
52:AA:269:C:H2'	52:AA:270:C:C6	2.52	0.44
52:AA:644:A:H5''	52:AA:651:G:OP2	2.18	0.44
52:AA:836:G:H2'	52:AA:837:C:C6	2.52	0.44
52:AA:956:G:H2'	52:AA:957:A:H8	1.82	0.44
56:BA:102:G:H2'	56:BA:103:A:C8	2.52	0.44
56:BA:392:U:H2'	56:BA:393:A:C8	2.44	0.44
56:BA:635:U:H2'	56:BA:636:U:C6	2.52	0.44
91:BA:1794:SPM:H122	91:BA:1794:SPM:H91	1.84	0.44
58:AC:62:ILE:HG12	58:AC:66:LYS:HE3	2.00	0.44
60:AF:40:GLU:OE1	76:Ad:187:TYR:OH	2.29	0.44
77:Ae:131:TYR:C	77:Ae:133:TYR:N	2.75	0.44
79:Ag:54:ASP:N	79:Ag:54:ASP:OD1	2.49	0.44
12:BF:287:ARG:HD2	49:Bv:33:ARG:NH1	2.32	0.44
13:BG:107:LEU:HD12	13:BG:193:LEU:HD22	1.99	0.44
13:BG:201:THR:HG22	13:BG:205:LYS:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BP:47:ARG:NE	56:BA:183:U:OP1	2.46	0.44
45:Bp:72:HIS:CD2	45:Bp:97:ARG:HD3	2.53	0.44
51:Bx:94:ARG:NE	56:BA:1518:A:H4'	2.32	0.44
52:AA:29:A:H2'	52:AA:30:A:C8	2.52	0.44
52:AA:824:G:O2'	61:AG:241:TRP:NE1	2.44	0.44
52:AA:825:C:P	52:AA:825:C:O4'	2.76	0.44
56:BA:322:G:C6	56:BA:341:G:C8	3.06	0.44
56:BA:688:A:H3'	56:BA:689:A:H4'	1.99	0.44
60:AF:2:PRO:N	60:AF:69:TYR:HH	2.16	0.44
77:Ae:135:PHE:C	77:Ae:135:PHE:CD1	2.94	0.44
86:Ao:397:TYR:CE1	86:Ao:434:LEU:HD13	2.53	0.44
10:BD:198:GLU:OE2	10:BD:204:GLY:N	2.42	0.44
12:BF:190:VAL:O	12:BF:262:THR:HA	2.17	0.44
13:BG:100:LYS:HG2	13:BG:104:ASN:ND2	2.32	0.44
18:BO:114:PRO:HG3	18:BO:137:VAL:HA	2.00	0.44
22:BS:113:LYS:HE2	30:Bb:110:LEU:HD11	1.99	0.44
23:BT:61:VAL:HG23	77:Ae:89:HIS:O	2.18	0.44
23:BT:246:ASP:OD1	23:BT:246:ASP:N	2.50	0.44
28:BY:178:SER:OG	28:BY:180:GLU:OE1	2.32	0.44
30:Bb:175:VAL:HB	30:Bb:187:VAL:HB	1.99	0.44
31:Bc:169:VAL:HG12	31:Bc:322:GLU:HB3	1.98	0.44
37:Bh:271:PHE:CZ	37:Bh:285:PRO:HB3	2.52	0.44
41:Bl:128:LEU:HB2	41:Bl:136:PRO:HG3	1.98	0.44
52:AA:15:C:OP1	59:AE:339:SER:OG	2.18	0.44
52:AA:277:A:H2'	52:AA:278:A:H8	1.83	0.44
52:AA:368:A:H2'	52:AA:368:A:N3	2.32	0.44
52:AA:603:U:H2'	52:AA:605:C:H4'	1.99	0.44
56:BA:657:U:H1'	56:BA:658:U:H5	1.83	0.44
56:BA:1079:U:H2'	56:BA:1080:A:H8	1.83	0.44
59:AE:286:GLU:HB2	59:AE:288:HIS:CE1	2.53	0.44
62:AI:323:ARG:HH11	62:AI:327:HIS:HE1	1.64	0.44
66:AN:62:ILE:HG21	80:Ah:341:HIS:HB3	1.98	0.44
84:Am:17:ARG:HH21	84:Am:20:ILE:HD11	1.82	0.44
4:B3:105:SER:HB3	56:BA:416:U:H1'	2.00	0.44
12:BF:65:TRP:CD1	42:Bm:118:LEU:HD11	2.53	0.44
14:BI:105:LEU:HD12	14:BI:112:VAL:HG21	2.00	0.44
17:BN:111:MET:HG2	56:BA:571:A:N3	2.33	0.44
21:BR:79:TRP:NE1	23:BT:269:MET:SD	2.91	0.44
21:BR:86:ILE:HB	21:BR:87:PRO:HD3	1.99	0.44
23:BT:57:PRO:CD	77:Ae:136:ARG:N	2.77	0.44
24:BU:69:ILE:O	24:BU:73:THR:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BW:204:ARG:HA	56:BA:170:U:N3	2.33	0.44
43:Bn:48:ASN:ND2	43:Bn:51:ARG:H	2.16	0.44
52:AA:56:U:O2	52:AA:198:C:O2'	2.32	0.44
52:AA:924:U:H2'	55:AX:4:U:H4'	1.98	0.44
56:BA:671:C:H2'	56:BA:672:G:H8	1.83	0.44
56:BA:838:A:H1'	56:BA:933:A:H61	1.82	0.44
56:BA:1287:G:H1	56:BA:1309:U:H3	1.64	0.44
56:BA:1459:U:H2'	56:BA:1460:A:C8	2.53	0.44
91:BA:1793:SPM:H62	91:BA:1793:SPM:H91	1.76	0.44
62:AI:139:GLN:HB2	62:AI:140:TRP:CE3	2.53	0.44
63:AJ:145:LEU:HB3	63:AJ:148:LEU:HD11	1.98	0.44
73:Aa:307:LEU:HD23	73:Aa:364:ILE:HD13	2.00	0.44
77:Ae:235:ASP:OD1	77:Ae:235:ASP:N	2.44	0.44
79:Ag:72:GLN:HA	79:Ag:75:LYS:HE3	1.99	0.44
86:Ao:419:PHE:HE2	86:Ao:450:LEU:HD13	1.83	0.44
87:Ap:72:PRO:HD2	87:Ap:75:ALA:HB2	1.98	0.44
3:B2:128:MET:HE3	3:B2:131:PRO:HA	2.00	0.44
3:B2:212:ARG:HD3	43:Bn:104:ILE:HD11	2.00	0.44
6:B5:125:TYR:O	6:B5:129:LYS:HG3	2.18	0.44
15:BJ:225:GLN:HB3	15:BJ:226:PRO:HD3	1.99	0.44
28:BY:96:ARG:HB3	56:BA:140:A:H4'	2.00	0.44
30:Bb:44:ASP:HB3	30:Bb:47:ARG:HG2	2.00	0.44
30:Bb:360:ARG:NH1	56:BA:1204:A:N7	2.63	0.44
31:Bc:212:PRO:HG3	31:Bc:268:ARG:NH1	2.33	0.44
50:Bw:242:PRO:HB3	50:Bw:424:LYS:HG2	2.00	0.44
52:AA:123:U:H2'	52:AA:124:A:C4	2.53	0.44
56:BA:902:C:O5'	56:BA:924:G:O2'	2.34	0.44
56:BA:1065:G:H2'	56:BA:1066:A:C8	2.53	0.44
66:AN:36:ARG:O	66:AN:40:ARG:HG3	2.18	0.44
73:Aa:210:GLU:O	73:Aa:214:MET:HE2	2.18	0.44
11:BE:211:ILE:HG12	11:BE:292:HIS:HB3	2.00	0.44
12:BF:279:ARG:H	41:Bl:90:ARG:HH21	1.64	0.44
13:BG:130:LEU:O	13:BG:134:SER:HB3	2.18	0.44
38:Bi:197:VAL:HG13	38:Bi:212:VAL:HG22	2.00	0.44
50:Bw:55:SER:HB2	56:BA:659:U:H5''	2.00	0.44
52:AA:438:C:H2'	52:AA:439:A:C8	2.50	0.44
56:BA:440:A:H2'	56:BA:441:A:H8	1.83	0.44
56:BA:1000:A:H2'	56:BA:1001:A:C8	2.53	0.44
16:BK:85:PRO:HG2	46:Bq:77:ILE:HD11	1.99	0.43
19:BP:111:ASP:OD1	19:BP:111:ASP:N	2.51	0.43
26:BW:157:HIS:O	91:BA:1793:SPM:N1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Bj:162:ARG:HD3	39:Bj:171:TRP:HE3	1.83	0.43
50:Bw:87:GLN:HG3	56:BA:773:C:O2'	2.18	0.43
50:Bw:205:LEU:HG	50:Bw:224:ARG:HG2	2.00	0.43
52:AA:789:C:H4'	52:AA:790:A:H5'	2.00	0.43
61:AG:176:ASP:HA	61:AG:179:ARG:HE	1.81	0.43
8:BB:1:G:O6	8:BB:70:A:N6	2.51	0.43
13:BG:107:LEU:O	13:BG:256:LYS:NZ	2.44	0.43
23:BT:57:PRO:O	77:Ae:135:PHE:HB3	2.17	0.43
29:Ba:105:TYR:HB2	29:Ba:220:LEU:HD23	2.00	0.43
41:Bl:139:GLN:HA	47:Bt:85:HIS:CD2	2.53	0.43
52:AA:81:U:O4	52:AA:102:G:N1	2.50	0.43
52:AA:95:A:H2'	52:AA:96:U:C6	2.54	0.43
52:AA:816:U:H2'	52:AA:817:G:O4'	2.18	0.43
54:AV:33:U:H2'	54:AV:34:U:O4'	2.18	0.43
56:BA:1239:A:H5'	56:BA:1240:A:H2	1.83	0.43
58:AC:99:THR:O	58:AC:101:PRO:HD3	2.18	0.43
64:AK:65:TYR:CG	70:AR:131:LEU:HD21	2.53	0.43
65:AL:82:ARG:HE	65:AL:90:GLU:HG2	1.83	0.43
67:AO:144:MET:HE2	67:AO:144:MET:HA	2.01	0.43
77:Ae:135:PHE:C	77:Ae:137:HIS:H	2.25	0.43
79:Ag:135:LEU:HG	93:Ag:500:GTP:C4	2.53	0.43
82:Aj:41:MET:HE3	82:Aj:50:LEU:HD12	1.99	0.43
12:BF:291:CYS:HB3	41:Bl:54:PRO:HA	2.00	0.43
20:BQ:105:MET:HG2	20:BQ:179:VAL:HG13	2.00	0.43
27:BX:5:VAL:HG21	33:Be:135:ARG:HD2	1.99	0.43
29:Ba:337:GLU:HG2	29:Ba:338:GLN:HG2	2.00	0.43
38:Bi:124:LYS:O	38:Bi:127:GLU:HG3	2.18	0.43
39:Bj:191:THR:HG23	39:Bj:195:LEU:HD13	1.99	0.43
47:Bt:82:PHE:CG	47:Bt:83:PRO:HD2	2.54	0.43
50:Bw:185:HIS:O	50:Bw:422:ARG:NH2	2.45	0.43
52:AA:155:A:H2'	52:AA:156:C:C6	2.54	0.43
52:AA:265:U:H2'	52:AA:266:U:H6	1.83	0.43
52:AA:277:A:H2'	52:AA:278:A:C8	2.54	0.43
52:AA:408:A:H4'	52:AA:949:G:H22	1.83	0.43
52:AA:892:A:C6	82:Aj:21:LEU:HD11	2.53	0.43
56:BA:53:U:H2'	56:BA:54:A:C8	2.52	0.43
56:BA:1061:U:O4	56:BA:1062:A:N6	2.51	0.43
56:BA:1236:C:H2'	56:BA:1237:A:C8	2.53	0.43
56:BA:1448:A:H2'	56:BA:1449:U:C6	2.53	0.43
57:AB:242:PRO:HA	57:AB:245:VAL:HG22	2.00	0.43
58:AC:72:HIS:HB3	58:AC:112:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Ag:178:ASP:HB2	79:Ag:236:THR:HG21	2.00	0.43
84:Am:11:ALA:O	84:Am:12:ARG:NH1	2.41	0.43
1:B0:76:HIS:O	1:B0:130:PHE:HA	2.18	0.43
15:BJ:46:LYS:HE2	47:Bt:35:MET:HE3	1.99	0.43
29:Ba:85:PRO:HB3	56:BA:744:A:OP2	2.17	0.43
36:B8:133:LEU:N	56:BA:1244:U:OP1	2.50	0.43
56:BA:230:G:H2'	56:BA:231:C:H6	1.83	0.43
56:BA:306:A:H2'	56:BA:307:G:H8	1.83	0.43
56:BA:424:U:H2'	56:BA:425:A:C8	2.54	0.43
56:BA:792:G:H2'	56:BA:793:A:H8	1.83	0.43
56:BA:993:U:H2'	56:BA:994:A:C8	2.50	0.43
56:BA:1501:C:H2'	56:BA:1502:U:C6	2.53	0.43
70:AR:67:ILE:H	70:AR:67:ILE:HD12	1.84	0.43
79:Ag:273:LEU:HB2	79:Ag:281:ILE:HD11	2.00	0.43
82:Aj:78:ARG:HH11	82:Aj:144:LYS:HE2	1.84	0.43
10:BD:168:ASP:HA	10:BD:184:PRO:HD3	2.00	0.43
12:BF:250:VAL:HA	12:BF:253:MET:HE3	2.00	0.43
13:BG:111:THR:HG21	13:BG:185:VAL:N	2.32	0.43
20:BQ:105:MET:SD	20:BQ:183:LEU:HD21	2.58	0.43
21:BR:153:LEU:HG	31:Bc:315:ARG:HD2	1.99	0.43
28:BY:189:PRO:O	33:Be:93:THR:OG1	2.23	0.43
31:Bc:197:HIS:NE2	31:Bc:201:LYS:HE3	2.33	0.43
34:Bf:75:ILE:HG23	37:Bh:289:VAL:HG11	2.01	0.43
50:Bw:188:VAL:HG21	50:Bw:423:PRO:HD2	1.99	0.43
52:AA:458:C:O2'	52:AA:460:A:OP2	2.37	0.43
52:AA:534:U:H5'	84:Am:38:ARG:HB2	2.01	0.43
52:AA:749:C:H2'	52:AA:750:G:O4'	2.19	0.43
56:BA:1001:A:H2'	56:BA:1002:U:H6	1.83	0.43
56:BA:1414:C:N4	56:BA:1415:G:O6	2.51	0.43
63:AJ:71:THR:O	63:AJ:150:GLY:N	2.51	0.43
80:Ah:344:GLU:HG3	80:Ah:345:LEU:N	2.32	0.43
6:B5:130:VAL:HG11	21:BR:134:LEU:HD23	2.01	0.43
11:BE:126:ASP:HB2	11:BE:150:LYS:HA	2.00	0.43
27:BX:66:ALA:HB2	27:BX:100:ALA:HA	2.01	0.43
27:BX:131:GLN:HA	27:BX:134:LYS:HG2	2.00	0.43
30:Bb:35:MET:HE3	30:Bb:36:PRO:HD2	2.01	0.43
32:Bd:73:ARG:HA	32:Bd:77:LYS:CE	2.49	0.43
32:Bd:128:GLU:HA	32:Bd:131:MET:HG2	2.00	0.43
38:Bi:137:PHE:N	38:Bi:138:PRO:HD2	2.34	0.43
39:Bj:74:LEU:HD23	39:Bj:77:ILE:HD11	1.99	0.43
39:Bj:203:LYS:HB2	39:Bj:239:LEU:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Bn:36:VAL:HG23	43:Bn:37:THR:HG23	2.00	0.43
47:Bt:17:TRP:CH2	47:Bt:23:ARG:HD3	2.54	0.43
52:AA:356:A:H2'	52:AA:357:G:H8	1.84	0.43
52:AA:491:G:H5''	85:An:135:ARG:NH1	2.33	0.43
52:AA:616:C:OP1	59:AE:108:ALA:N	2.52	0.43
52:AA:681:A:H5''	59:AE:114:ARG:HH22	1.84	0.43
52:AA:740:U:OP1	61:AG:197:ARG:NH2	2.49	0.43
52:AA:941:U:H2'	52:AA:942:G:C8	2.54	0.43
56:BA:562:A:H2'	56:BA:563:U:O4'	2.19	0.43
57:AB:171:LYS:HE3	57:AB:171:LYS:HB2	1.89	0.43
61:AG:71:THR:HB	62:AI:254:LYS:HE3	2.00	0.43
70:AR:66:CYS:HB2	70:AR:100:LEU:HA	2.00	0.43
79:Ag:300:TRP:HH2	79:Ag:305:ILE:HD11	1.83	0.43
83:Ak:66:GLN:HE22	86:Ao:83:THR:HG22	1.83	0.43
8:BB:65:U:H2'	8:BB:66:A:H8	1.83	0.43
15:BJ:96:ILE:HB	15:BJ:180:CYS:SG	2.59	0.43
17:BN:75:LYS:HB2	51:Bx:174:MET:HE1	2.00	0.43
25:BV:133:ARG:N	44:Bo:50:SER:O	2.42	0.43
32:Bd:138:SER:O	32:Bd:141:GLU:HG2	2.19	0.43
32:Bd:180:PRO:HG3	39:Bj:136:ARG:HA	2.01	0.43
33:Be:22:THR:HA	33:Be:32:LYS:HZ3	1.84	0.43
36:B8:126:LYS:HG2	36:B8:144:LEU:HA	1.99	0.43
38:Bi:160:LEU:O	38:Bi:164:VAL:HG22	2.19	0.43
49:Bv:129:PRO:HA	49:Bv:132:ILE:HG12	2.01	0.43
54:AV:33:U:H2'	54:AV:34:U:H6	1.83	0.43
56:BA:124:A:N3	56:BA:251:C:O2'	2.42	0.43
56:BA:347:U:O4'	56:BA:349:A:H5'	2.19	0.43
56:BA:1009:A:H2'	56:BA:1010:A:C8	2.53	0.43
56:BA:1479:G:H2'	56:BA:1480:G:H8	1.84	0.43
71:AU:80:ARG:NH1	78:Af:112:ASP:OD2	2.41	0.43
79:Ag:182:GLU:HA	79:Ag:185:THR:HG22	2.00	0.43
87:Ap:73:VAL:O	87:Ap:109:ARG:NH2	2.52	0.43
10:BD:199:SER:HB2	10:BD:203:ARG:HD3	2.01	0.43
12:BF:92:ARG:HD2	12:BF:92:ARG:HA	1.86	0.43
17:BN:67:PHE:HB2	17:BN:72:TRP:CD1	2.54	0.43
25:BV:115:GLU:HG2	35:Bg:19:LEU:HD11	2.01	0.43
37:Bh:148:LEU:HD22	37:Bh:305:PHE:HB3	2.00	0.43
51:Bx:121:MET:HE3	51:Bx:151:LEU:HA	2.00	0.43
52:AA:168:A:O2'	52:AA:170:A:N1	2.51	0.43
56:BA:527:U:H2'	56:BA:529:G:N7	2.33	0.43
62:AI:247:ARG:HD3	62:AI:247:ARG:HA	1.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AK:161:LEU:HD13	71:AU:23:TYR:CG	2.54	0.43
86:Ao:81:ASP:HB3	86:Ao:84:ALA:HB3	2.00	0.43
86:Ao:398:ASP:OD1	86:Ao:399:ILE:N	2.51	0.43
86:Ao:520:LYS:O	86:Ao:527:ARG:NH2	2.52	0.43
88:GL:75:THR:HG22	88:GL:78:GLU:HG2	2.01	0.43
4:B3:129:PRO:HG3	4:B3:147:VAL:HG22	2.01	0.43
16:BK:66:LEU:HD13	16:BK:82:ILE:HG23	2.00	0.43
18:BO:77:ILE:HD12	18:BO:107:LEU:HD21	2.00	0.43
40:Bk:125:TYR:CE2	40:Bk:197:ARG:HD3	2.53	0.43
52:AA:16:U:HO2'	52:AA:294:A:N6	2.17	0.43
52:AA:265:U:H2'	52:AA:266:U:C6	2.54	0.43
52:AA:567:C:H2'	52:AA:568:G:C8	2.49	0.43
52:AA:792:U:H2'	52:AA:793:A:H8	1.84	0.43
52:AA:848:C:H2'	52:AA:849:G:H8	1.83	0.43
56:BA:738:U:H2'	56:BA:739:U:C6	2.53	0.43
73:Aa:307:LEU:HD21	73:Aa:350:ILE:HG23	2.00	0.43
79:Ag:298:ASN:O	79:Ag:298:ASN:ND2	2.52	0.43
11:BE:334:ASP:HB3	11:BE:337:VAL:HG23	2.01	0.43
12:BF:103:GLN:HE22	12:BF:250:VAL:H	1.65	0.43
23:BT:58:PRO:HD2	77:Ae:131:TYR:O	2.19	0.43
28:BY:108:MET:HE1	38:Bi:169:PHE:HB3	2.01	0.43
37:Bh:170:ALA:HB1	37:Bh:175:VAL:HB	2.01	0.43
40:Bk:49:ARG:HA	40:Bk:54:HIS:CD2	2.54	0.43
47:Bt:71:PHE:CE2	47:Bt:75:LYS:HD2	2.53	0.43
51:Bx:146:ARG:HH21	56:BA:1531:C:P	2.42	0.43
52:AA:542:C:C2	52:AA:543:A:C8	3.07	0.43
56:BA:913:G:H21	56:BA:914:A:N6	2.17	0.43
56:BA:937:C:H3'	56:BA:938:U:H5''	2.00	0.43
56:BA:952:A:H2'	56:BA:953:G:C8	2.53	0.43
56:BA:1154:U:C2	56:BA:1155:G:C8	3.07	0.43
56:BA:1239:A:H5'	56:BA:1240:A:C2	2.54	0.43
59:AE:191:ARG:O	87:Ap:78:ARG:NH1	2.49	0.43
77:Ae:408:CYS:O	77:Ae:411:GLU:HG2	2.19	0.43
79:Ag:66:HIS:HB3	79:Ag:97:CYS:HB3	2.00	0.43
88:DL:75:THR:HG22	88:DL:78:GLU:HG2	2.01	0.43
88:EL:75:THR:HG22	88:EL:78:GLU:HG2	2.01	0.43
4:B3:77:ARG:NH1	56:BA:469:C:OP2	2.52	0.42
11:BE:292:HIS:CG	56:BA:1558:U:H2'	2.54	0.42
20:BQ:98:HIS:HB3	20:BQ:151:VAL:HG12	2.00	0.42
23:BT:114:GLY:HA3	23:BT:182:ARG:HG3	2.01	0.42
35:Bg:35:ARG:HA	35:Bg:44:ARG:HD3	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Bh:188:PRO:N	37:Bh:189:PRO:HD2	2.34	0.42
40:Bk:117:LEU:HB3	40:Bk:166:PHE:HZ	1.84	0.42
46:Bq:122:ARG:O	46:Bq:126:ILE:HG12	2.19	0.42
52:AA:534:U:O5'	84:Am:37:ARG:NH1	2.51	0.42
52:AA:704:U:H2'	52:AA:705:G:C8	2.54	0.42
52:AA:936:C:H2'	52:AA:937:A:H8	1.84	0.42
56:BA:385:U:H2'	56:BA:386:U:H6	1.83	0.42
56:BA:516:G:N3	56:BA:533:A:O2'	2.43	0.42
56:BA:1000:A:H2'	56:BA:1001:A:H8	1.84	0.42
56:BA:1183:U:C6	56:BA:1230:U:H2'	2.54	0.42
58:AC:110:LEU:HD22	58:AC:119:ILE:HG12	2.00	0.42
62:AI:137:ALA:O	62:AI:139:GLN:NE2	2.51	0.42
68:AP:29:ARG:NH2	68:AP:55:ASP:OD2	2.49	0.42
77:Ae:171:ASN:CG	77:Ae:174:GLN:HB3	2.44	0.42
79:Ag:259:VAL:HB	79:Ag:305:ILE:HD13	2.02	0.42
9:B7:69:TRP:CE2	56:BA:34:A:C2	3.07	0.42
10:BD:202:GLY:O	29:Ba:30:ALA:N	2.52	0.42
15:BJ:219:TYR:OH	88:EL:90:LEU:HB2	2.19	0.42
19:BP:191:VAL:HB	19:BP:192:PRO:HD3	2.01	0.42
21:BR:113:ARG:HB2	21:BR:121:MET:SD	2.59	0.42
23:BT:182:ARG:HD3	23:BT:187:LEU:HD22	2.01	0.42
24:BU:52:LYS:HD3	56:BA:165:A:N3	2.33	0.42
29:Ba:351:LEU:HD11	29:Ba:379:ASP:HA	2.01	0.42
30:Bb:217:LEU:HD13	30:Bb:236:LEU:HD13	2.00	0.42
38:Bi:72:LEU:HD22	56:BA:139:G:C6	2.54	0.42
50:Bw:87:GLN:HE22	50:Bw:274:ASN:H	1.68	0.42
51:Bx:146:ARG:HD3	51:Bx:146:ARG:HA	1.93	0.42
52:AA:15:C:H2'	52:AA:16:U:C6	2.53	0.42
52:AA:25:U:H2'	52:AA:26:A:H8	1.84	0.42
52:AA:294:A:H3'	52:AA:294:A:OP2	2.19	0.42
52:AA:297:A:H5'	52:AA:298:G:H5''	2.01	0.42
52:AA:534:U:C5'	84:Am:38:ARG:HB2	2.50	0.42
52:AA:589:C:H2'	52:AA:590:C:C6	2.54	0.42
52:AA:858:C:H2'	52:AA:859:U:H6	1.84	0.42
56:BA:622:A:N6	56:BA:623:G:O6	2.52	0.42
56:BA:1135:C:H2'	56:BA:1136:U:C6	2.54	0.42
59:AE:137:HIS:ND1	81:Ai:67:PHE:HB3	2.33	0.42
59:AE:296:LEU:HG	59:AE:303:ILE:HB	2.01	0.42
62:AI:294:ILE:HG12	62:AI:329:MET:HG3	2.01	0.42
73:Aa:104:MET:HG2	73:Aa:290:PHE:HE2	1.84	0.42
86:Ao:305:ALA:HB2	86:Ao:319:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B0:78:GLY:HA3	1:B0:132:HIS:ND1	2.34	0.42
17:BN:15:ALA:HB1	37:Bh:269:VAL:HG21	2.01	0.42
23:BT:56:PRO:O	77:Ae:133:TYR:C	2.59	0.42
31:Bc:52:GLN:HG3	31:Bc:216:LEU:HD11	2.01	0.42
31:Bc:190:MET:HG2	31:Bc:291:ARG:NH1	2.34	0.42
37:Bh:98:ILE:HG12	37:Bh:119:LEU:HD12	2.00	0.42
50:Bw:271:GLN:NE2	56:BA:667:C:O2	2.49	0.42
51:Bx:77:LEU:HD13	51:Bx:88:LEU:HD22	2.02	0.42
52:AA:226:G:H2'	52:AA:227:A:H8	1.84	0.42
52:AA:601:A:H2'	52:AA:602:A:C8	2.54	0.42
52:AA:728:U:H2'	52:AA:729:A:C8	2.55	0.42
52:AA:883:C:H1'	52:AA:886:A:N6	2.34	0.42
54:AV:31:U:H3'	54:AV:32:U:C6	2.53	0.42
54:AV:47:U:C4	54:AV:48:U:C4	3.07	0.42
56:BA:10:A:N6	56:BA:11:G:N3	2.67	0.42
56:BA:269:U:H2'	56:BA:270:U:C6	2.55	0.42
56:BA:568:C:H2'	56:BA:569:C:O4'	2.19	0.42
56:BA:987:G:N2	56:BA:991:C:O2'	2.51	0.42
56:BA:1415:G:H2'	56:BA:1416:G:H8	1.85	0.42
56:BA:1415:G:H2'	56:BA:1416:G:C8	2.54	0.42
56:BA:1416:G:H2'	56:BA:1417:A:C8	2.50	0.42
56:BA:1420:A:H8	56:BA:1420:A:OP2	2.02	0.42
77:Ae:261:LEU:HD11	77:Ae:302:VAL:HB	2.00	0.42
12:BF:120:VAL:HG21	12:BF:142:ARG:HB3	2.01	0.42
20:BQ:103:GLU:CD	20:BQ:106:ARG:HH21	2.25	0.42
21:BR:149:LEU:HD23	31:Bc:312:LEU:HD13	2.00	0.42
32:Bd:164:ARG:HH12	40:Bk:91:LEU:HD21	1.84	0.42
50:Bw:99:ALA:HB3	50:Bw:102:ALA:HB2	2.01	0.42
52:AA:389:A:H5''	67:AO:101:GLN:HB2	2.02	0.42
52:AA:634:C:H2'	52:AA:635:C:C6	2.54	0.42
52:AA:734:A:H2'	52:AA:735:G:C8	2.54	0.42
56:BA:246:C:H2'	56:BA:247:C:C6	2.54	0.42
56:BA:421:U:H2'	56:BA:422:U:C6	2.54	0.42
56:BA:869:G:H2'	56:BA:870:C:C6	2.54	0.42
56:BA:1338:G:H2'	56:BA:1339:A:C8	2.50	0.42
58:AC:69:LEU:HD13	83:Ak:109:LYS:HE2	2.02	0.42
59:AE:119:LYS:H	59:AE:119:LYS:HG2	1.65	0.42
59:AE:243:VAL:HG11	59:AE:268:PHE:CE1	2.54	0.42
60:AF:96:HIS:O	60:AF:99:THR:HG22	2.19	0.42
64:AK:120:ARG:HD3	64:AK:120:ARG:HA	1.85	0.42
74:Ab:18:ASP:OD1	74:Ab:19:LEU:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:Ad:51:THR:HG21	87:Ap:228:SER:H	1.84	0.42
84:Am:72:ASP:OD1	84:Am:73:PHE:N	2.52	0.42
12:BF:184:GLN:HE22	19:BP:22:VAL:HG23	1.84	0.42
12:BF:249:ASN:OD1	12:BF:249:ASN:N	2.51	0.42
22:BS:68:TRP:C	22:BS:70:THR:H	2.28	0.42
23:BT:58:PRO:HD3	77:Ae:134:LYS:C	2.45	0.42
24:BU:34:ARG:NH2	56:BA:1014:A:H5''	2.34	0.42
27:BX:56:TYR:HE1	27:BX:61:TYR:HE1	1.68	0.42
29:Ba:115:GLU:HB2	29:Ba:119:GLN:HG3	2.01	0.42
29:Ba:299:LEU:O	29:Ba:303:ARG:HG3	2.19	0.42
30:Bb:258:PHE:HA	30:Bb:327:VAL:HG13	2.02	0.42
33:Be:28:ARG:N	56:BA:671:C:OP1	2.48	0.42
35:Bg:15:LEU:HD11	37:Bh:169:VAL:HA	2.00	0.42
50:Bw:267:LEU:HD23	50:Bw:267:LEU:HA	1.91	0.42
52:AA:499:C:H2'	52:AA:500:G:C8	2.54	0.42
52:AA:883:C:H3'	77:Ae:433:ARG:HH12	1.84	0.42
56:BA:562:A:H3'	56:BA:562:A:N3	2.34	0.42
56:BA:1165:U:OP2	56:BA:1166:A:O2'	2.28	0.42
56:BA:1462:G:N2	56:BA:1464:A:H3'	2.35	0.42
61:AG:240:ARG:HG2	61:AG:242:TRP:H	1.84	0.42
77:Ae:93:LEU:HD23	77:Ae:93:LEU:HA	1.92	0.42
83:Ak:93:VAL:HB	83:Ak:96:GLY:H	1.84	0.42
84:Am:40:LYS:HD3	84:Am:40:LYS:HA	1.41	0.42
86:Ao:543:HIS:H	86:Ao:588:ARG:NH1	2.17	0.42
88:HL:75:THR:HG22	88:HL:78:GLU:HG2	2.01	0.42
13:BG:223:LYS:HG2	13:BG:231:ILE:HG13	2.00	0.42
19:BP:78:ILE:O	36:B8:113:ARG:HD3	2.19	0.42
23:BT:60:PRO:HG2	77:Ae:111:THR:CB	2.50	0.42
25:BV:165:ILE:HD11	25:BV:198:ARG:HB2	2.01	0.42
27:BX:86:ARG:HH12	33:Be:18:MET:HB2	1.84	0.42
29:Ba:50:TYR:OH	29:Ba:72:ARG:O	2.30	0.42
44:Bo:91:TRP:CD2	47:Bt:58:GLN:HG2	2.55	0.42
45:Bp:17:ARG:HE	45:Bp:65:ASP:HB2	1.84	0.42
47:Bt:14:GLY:H	56:BA:1279:G:H5''	1.84	0.42
48:Bu:118:LEU:HD11	48:Bu:157:ILE:HD13	2.02	0.42
52:AA:938:U:H2'	52:AA:939:A:C8	2.55	0.42
57:AB:242:PRO:N	57:AB:243:PRO:HD2	2.35	0.42
59:AE:296:LEU:HD22	59:AE:352:GLY:HA3	2.02	0.42
68:AP:95:GLY:O	82:Aj:167:PRO:HB2	2.20	0.42
69:AQ:13:VAL:HG23	69:AQ:66:LEU:HB2	2.02	0.42
77:Ae:433:ARG:O	77:Ae:436:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Ai:66:ARG:HA	81:Ai:71:TYR:O	2.19	0.42
85:An:174:LYS:HE2	85:An:178:GLN:OE1	2.20	0.42
86:Ao:430:ARG:HD2	86:Ao:470:PHE:HZ	1.84	0.42
11:BE:221:ARG:HA	11:BE:261:LEU:HD22	2.02	0.42
17:BN:67:PHE:HB2	17:BN:72:TRP:NE1	2.35	0.42
30:Bb:183:ASP:OD2	48:Bu:188:ARG:NE	2.31	0.42
30:Bb:237:VAL:HG22	30:Bb:240:ILE:HD11	2.02	0.42
30:Bb:307:HIS:HB2	30:Bb:311:MET:HE2	2.00	0.42
32:Bd:173:ARG:HH21	40:Bk:175:HIS:HD2	1.67	0.42
33:Be:51:ILE:HG22	33:Be:53:GLU:H	1.85	0.42
51:Bx:65:ASN:O	51:Bx:74:ARG:HB2	2.20	0.42
52:AA:568:G:N2	63:AJ:126:ILE:HG21	2.35	0.42
56:BA:302:A:H2'	56:BA:303:G:C8	2.55	0.42
56:BA:668:A:H2'	56:BA:669:C:C6	2.55	0.42
59:AE:324:CYS:HB3	59:AE:329:ILE:HB	2.01	0.42
62:AI:281:LYS:HE3	62:AI:281:LYS:HB2	1.91	0.42
74:Ab:67:GLU:OE1	74:Ab:71:ARG:NH2	2.53	0.42
75:Ac:120:LYS:HA	75:Ac:123:LEU:HD23	2.01	0.42
77:Ae:208:MET:HA	77:Ae:213:PHE:CE2	2.54	0.42
79:Ag:66:HIS:CD2	79:Ag:99:MET:HB2	2.55	0.42
86:Ao:611:ALA:HA	86:Ao:614:LEU:HD23	2.00	0.42
2:B1:222:ASP:N	2:B1:222:ASP:OD1	2.50	0.42
10:BD:296:TYR:OH	56:BA:852:C:OP2	2.37	0.42
13:BG:109:ILE:HG12	13:BG:166:GLY:HA3	2.02	0.42
25:BV:168:THR:OG1	25:BV:169:GLU:N	2.51	0.42
40:Bk:85:ASP:OD1	40:Bk:85:ASP:N	2.43	0.42
41:Bl:141:ASN:ND2	56:BA:214:A:OP1	2.47	0.42
50:Bw:89:MET:HG3	50:Bw:269:LYS:HB3	2.01	0.42
52:AA:133:G:H2'	52:AA:133:G:N3	2.34	0.42
52:AA:729:A:H2'	52:AA:730:C:O4'	2.19	0.42
52:AA:792:U:H4'	62:AI:389:ARG:HG3	2.02	0.42
52:AA:920:G:H1'	56:BA:908:A:O2'	2.20	0.42
56:BA:207:A:H61	56:BA:236:U:H3'	1.83	0.42
56:BA:266:C:HO2'	56:BA:281:A:N6	2.18	0.42
56:BA:1001:A:C4	56:BA:1002:U:C5	3.08	0.42
57:AB:269:LEU:O	57:AB:273:GLN:HG3	2.20	0.42
63:AJ:128:LYS:HG2	63:AJ:131:ARG:HH21	1.84	0.42
66:AN:56:SER:O	66:AN:60:ASN:ND2	2.53	0.42
68:AP:102:MET:HA	68:AP:105:THR:HG22	2.01	0.42
68:AP:108:GLU:HG2	87:Ap:231:PRO:HG3	2.02	0.42
77:Ae:160:GLY:C	77:Ae:162:GLN:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BE:104:LEU:HD11	11:BE:123:GLN:HB2	2.02	0.42
13:BG:74:ILE:HD11	13:BG:85:LEU:HD11	2.01	0.42
15:BJ:104:LEU:HB2	45:Bp:43:ARG:HH12	1.85	0.42
20:BQ:124:VAL:HG12	20:BQ:158:ARG:NE	2.35	0.42
23:BT:56:PRO:HD2	77:Ae:133:TYR:C	2.45	0.42
28:BY:133:VAL:HG11	28:BY:145:ARG:HD2	2.01	0.42
29:Ba:203:CYS:H	50:Bw:173:GLN:NE2	2.17	0.42
31:Bc:63:GLU:O	31:Bc:119:SER:OG	2.36	0.42
42:Bm:91:SER:HB2	42:Bm:123:ARG:HH11	1.84	0.42
44:Bo:48:ASP:OD1	44:Bo:48:ASP:N	2.52	0.42
46:Bq:119:ARG:NE	56:BA:529:G:OP1	2.52	0.42
52:AA:762:G:N1	52:AA:765:A:OP2	2.53	0.42
56:BA:77:U:H2'	56:BA:78:A:C8	2.55	0.42
56:BA:415:A:H2'	56:BA:416:U:O4'	2.19	0.42
56:BA:454:U:C2	56:BA:455:A:C8	3.07	0.42
56:BA:743:U:H3'	56:BA:744:A:C5'	2.49	0.42
61:AG:116:GLU:OE2	79:Ag:85:ARG:NH2	2.51	0.42
76:Ad:56:LEU:HG	76:Ad:60:TYR:CE2	2.55	0.42
77:Ae:404:GLN:O	77:Ae:407:THR:OG1	2.30	0.42
80:Ah:367:TRP:HA	80:Ah:370:ASN:ND2	2.35	0.42
83:Ak:58:ARG:O	83:Ak:62:MET:HG2	2.20	0.42
5:B4:41:LEU:HD22	39:Bj:71:ALA:HB2	2.02	0.42
6:B5:93:ARG:HH12	56:BA:644:G:P	2.42	0.42
16:BK:35:LEU:HA	16:BK:38:ILE:HD11	2.01	0.42
20:BQ:75:PRO:HB3	20:BQ:241:TYR:CZ	2.54	0.42
25:BV:167:LYS:HB2	35:Bg:106:ASP:HB3	2.02	0.42
28:BY:15:LEU:HD11	28:BY:26:PRO:HB3	2.02	0.42
31:Bc:163:LEU:O	31:Bc:230:ASN:ND2	2.53	0.42
36:B8:98:SER:OG	56:BA:76:G:O6	2.31	0.42
37:Bh:60:ARG:NH1	37:Bh:63:LYS:HB2	2.35	0.42
49:Bv:29:PRO:HA	49:Bv:30:PRO:HD3	1.94	0.42
52:AA:584:C:O2	66:AN:86:ARG:HG2	2.20	0.42
52:AA:856:U:H2'	52:AA:857:C:C6	2.55	0.42
54:AV:38:U:H2'	54:AV:39:U:H6	1.84	0.42
56:BA:1387:A:N6	56:BA:1450:U:O2'	2.53	0.42
56:BA:1448:A:C8	56:BA:1503:C:H2'	2.54	0.42
56:BA:1518:A:H2'	56:BA:1519:U:C6	2.55	0.42
62:AI:198:SER:HB3	62:AI:246:ARG:HD2	2.01	0.42
77:Ae:172:LYS:HE2	77:Ae:209:MET:CB	2.46	0.42
81:Ai:68:LEU:HD13	86:Ao:120:ILE:HD12	2.01	0.42
11:BE:215:PHE:CE1	11:BE:259:GLY:HA2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BG:184:GLN:HB3	13:BG:187:ARG:HD2	2.02	0.41
17:BN:171:SER:OG	51:Bx:58:GLN:OE1	2.25	0.41
33:Be:67:LYS:HE3	33:Be:67:LYS:HB2	1.89	0.41
41:Bl:154:ASP:OD1	41:Bl:154:ASP:N	2.53	0.41
50:Bw:90:LYS:HD2	50:Bw:226:GLN:HB2	2.02	0.41
52:AA:153:C:C2	52:AA:154:C:C5	3.08	0.41
52:AA:212:A:C2	52:AA:213:G:C8	3.08	0.41
52:AA:419:A:H2'	52:AA:420:A:O4'	2.20	0.41
56:BA:1183:U:H2'	56:BA:1184:G:H8	1.84	0.41
56:BA:1373:U:H2'	56:BA:1374:U:C6	2.55	0.41
56:BA:1451:U:H2'	56:BA:1452:C:C6	2.55	0.41
71:Au:82:ASP:OD1	71:Au:82:ASP:N	2.49	0.41
76:Ad:199:ARG:HA	76:Ad:200:PRO:HD3	1.91	0.41
77:Ae:415:VAL:HA	77:Ae:418:GLN:HG2	2.01	0.41
79:Ag:73:GLU:OE2	79:Ag:142:HIS:NE2	2.50	0.41
86:Ao:289:ARG:NH1	86:Ao:289:ARG:HA	2.35	0.41
2:B1:215:GLN:NE2	2:B1:219:GLU:OE2	2.39	0.41
7:B6:17:LEU:HD11	7:B6:31:ASN:HB3	2.02	0.41
9:B7:60:ASN:ND2	33:Be:25:ARG:O	2.53	0.41
11:BE:183:GLU:CD	11:BE:183:GLU:H	2.28	0.41
16:BK:156:VAL:HG11	16:BK:159:LEU:HB2	2.02	0.41
17:BN:136:ASP:OD1	17:BN:137:ILE:HG13	2.20	0.41
22:BS:52:ASN:OD1	22:BS:55:ASN:N	2.53	0.41
22:BS:54:ARG:HG3	22:BS:58:LEU:HG	2.01	0.41
24:BU:11:ARG:NH1	24:BU:13:ARG:HD2	2.35	0.41
31:Bc:66:HIS:HB3	31:Bc:74:THR:HB	2.01	0.41
38:Bi:288:LYS:HE2	38:Bi:291:GLU:HG3	2.02	0.41
52:AA:199:G:N2	52:AA:201:A:H3'	2.35	0.41
52:AA:287:C:C2	75:Ac:2:PRO:HB3	2.55	0.41
52:AA:303:U:H1'	67:AO:197:HIS:CE1	2.55	0.41
52:AA:562:A:H1'	52:AA:708:A:H61	1.85	0.41
52:AA:922:C:C2	52:AA:923:G:C8	3.08	0.41
56:BA:211:U:H2'	56:BA:212:C:C6	2.55	0.41
61:AG:71:THR:CG2	62:AI:252:GLN:C	2.92	0.41
62:AI:251:ILE:H	62:AI:251:ILE:HG12	1.44	0.41
65:AL:129:LYS:HG3	65:AL:130:TYR:H	1.84	0.41
67:AO:201:HIS:HE1	67:AO:203:ARG:HE	1.68	0.41
76:Ad:68:ARG:HH12	82:Aj:198:ILE:HD13	1.85	0.41
77:Ae:218:THR:HG21	77:Ae:254:LYS:HG2	2.01	0.41
79:Ag:99:MET:H	93:Ag:500:GTP:HN1	1.68	0.41
80:Ah:287:GLN:NE2	80:Ah:291:GLU:HG3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:BK:113:THR:OG1	16:BK:114:LEU:N	2.54	0.41
21:BR:62:TYR:HE2	23:BT:269:MET:HG2	1.85	0.41
29:Ba:60:TYR:HB3	29:Ba:70:LEU:HD12	2.02	0.41
31:Bc:230:ASN:O	31:Bc:234:LEU:HG	2.20	0.41
45:Bp:10:LEU:HD12	45:Bp:10:LEU:HA	1.84	0.41
52:AA:220:U:H2'	52:AA:221:A:C8	2.55	0.41
52:AA:472:A:H4'	59:AE:299:LYS:HB3	2.02	0.41
52:AA:499:C:H2'	52:AA:500:G:H8	1.85	0.41
52:AA:641:A:N7	59:AE:260:LYS:NZ	2.69	0.41
52:AA:884:C:H5	77:Ae:143:TYR:HA	1.86	0.41
56:BA:119:A:C4	56:BA:129:A:N6	2.88	0.41
56:BA:232:U:H2'	56:BA:233:A:H8	1.85	0.41
56:BA:316:U:H2'	56:BA:317:A:C8	2.55	0.41
56:BA:363:G:H2'	56:BA:364:A:C8	2.55	0.41
56:BA:1156:A:H2'	56:BA:1157:C:H6	1.85	0.41
56:BA:1531:C:H3'	56:BA:1532:U:H5''	2.03	0.41
59:AE:93:LEU:H	81:Ai:75:HIS:CD2	2.39	0.41
63:AJ:73:TYR:HE2	63:AJ:150:GLY:HA2	1.85	0.41
65:AL:55:ARG:HD2	65:AL:58:LEU:HD21	2.02	0.41
73:Aa:197:ARG:CZ	73:Aa:203:LEU:HB2	2.50	0.41
79:Ag:334:ASP:OD1	83:Ak:302:LYS:NZ	2.51	0.41
10:BD:281:GLY:O	56:BA:885:G:N2	2.41	0.41
11:BE:48:TRP:CE2	11:BE:51:GLU:HB2	2.55	0.41
17:BN:67:PHE:HD1	17:BN:71:LYS:HE2	1.86	0.41
31:Bc:145:MET:HE3	31:Bc:259:ASP:HB3	2.02	0.41
33:Be:28:ARG:HD2	56:BA:670:A:H5''	2.01	0.41
37:Bh:61:SER:HA	37:Bh:66:TRP:CG	2.54	0.41
37:Bh:164:GLU:H	37:Bh:164:GLU:CD	2.27	0.41
38:Bi:226:ASP:OD1	38:Bi:227:ARG:N	2.52	0.41
39:Bj:187:THR:HG23	39:Bj:190:ARG:HH21	1.85	0.41
52:AA:15:C:H2'	52:AA:16:U:H6	1.85	0.41
52:AA:397:U:H2'	52:AA:398:G:O4'	2.20	0.41
52:AA:769:A:H2'	52:AA:770:A:H8	1.86	0.41
52:AA:881:A:H61	52:AA:888:A:N6	2.18	0.41
56:BA:365:G:N1	56:BA:598:U:OP2	2.42	0.41
56:BA:420:U:H2'	56:BA:421:U:C6	2.55	0.41
56:BA:447:A:N6	56:BA:449:C:O2	2.54	0.41
56:BA:1477:A:H2'	56:BA:1478:U:C6	2.55	0.41
56:BA:1527:U:O2	56:BA:1527:U:H2'	2.20	0.41
57:AB:56:ASP:OD1	57:AB:56:ASP:N	2.52	0.41
59:AE:224:GLU:OE2	59:AE:226:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AI:241:PHE:O	62:AI:244:ARG:HG2	2.20	0.41
62:AI:318:LEU:HD23	62:AI:353:LEU:HD11	2.02	0.41
62:AI:350:ALA:HB1	62:AI:370:LEU:HB3	2.01	0.41
64:AK:177:ILE:HD11	71:AU:19:VAL:HG13	2.03	0.41
66:AN:91:CYS:HB3	66:AN:96:ARG:H	1.86	0.41
73:Aa:325:LEU:HD23	73:Aa:325:LEU:HA	1.95	0.41
82:Aj:120:PHE:CD2	82:Aj:121:LYS:HG2	2.56	0.41
85:An:179:LYS:HE3	85:An:179:LYS:HB3	1.90	0.41
86:Ao:436:TYR:HD1	86:Ao:436:TYR:HA	1.76	0.41
1:B0:144:LEU:HB3	22:BS:46:PRO:HB3	2.03	0.41
2:B1:163:ARG:NH1	29:Ba:55:LEU:HD11	2.35	0.41
3:B2:201:PHE:HB2	29:Ba:65:HIS:CD2	2.56	0.41
9:B7:85:ARG:HH12	33:Be:17:ARG:NH1	2.18	0.41
13:BG:230:THR:HG23	20:BQ:136:MET:HE1	2.03	0.41
19:BP:231:GLU:O	19:BP:235:GLU:HG2	2.20	0.41
20:BQ:76:SER:HB2	20:BQ:155:LYS:HB2	2.02	0.41
32:Bd:164:ARG:HE	32:Bd:168:LEU:HD23	1.84	0.41
36:B8:124:ARG:NH2	56:BA:1203:C:H5''	2.36	0.41
37:Bh:258:THR:HG22	37:Bh:259:ARG:HG3	2.01	0.41
41:Bl:150:LYS:NZ	47:Bt:79:ALA:O	2.52	0.41
46:Bq:95:TRP:HA	46:Bq:98:GLU:HG3	2.03	0.41
52:AA:554:C:H2'	52:AA:555:C:C6	2.56	0.41
52:AA:638:A:H4'	52:AA:639:A:H5'	2.02	0.41
52:AA:712:A:H2'	52:AA:713:A:H8	1.84	0.41
53:B9:74:ARG:NH1	56:BA:545:U:O2'	2.54	0.41
54:AV:56:U:H2'	54:AV:57:U:H6	1.85	0.41
56:BA:417:G:H2'	56:BA:418:U:C6	2.56	0.41
56:BA:1155:G:C6	56:BA:1156:A:C5	3.08	0.41
56:BA:1513:U:H5''	56:BA:1525:C:H42	1.86	0.41
57:AB:119:GLN:O	57:AB:123:HIS:ND1	2.29	0.41
61:AG:203:GLU:OE2	61:AG:207:GLN:NE2	2.53	0.41
68:AP:59:ASN:HB2	75:Ac:145:GLY:O	2.21	0.41
81:Ai:86:LYS:HG3	81:Ai:89:ARG:NH2	2.35	0.41
83:Ak:92:PRO:HB3	83:Ak:98:PRO:HD3	2.02	0.41
86:Ao:579:LEU:HD11	86:Ao:599:LEU:HD12	2.02	0.41
88:FL:75:THR:HG22	88:FL:78:GLU:HG2	2.01	0.41
2:B1:69:VAL:HG12	2:B1:86:VAL:HG22	2.03	0.41
8:BB:30:G:H2'	8:BB:31:C:C6	2.56	0.41
15:BJ:150:HIS:ND1	56:BA:551:A:H5'	2.35	0.41
26:BW:132:VAL:HG11	26:BW:138:LEU:HD21	2.02	0.41
27:BX:50:ARG:NH1	27:BX:69:ARG:HA	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Bd:150:LEU:HD13	32:Bd:158:HIS:HA	2.02	0.41
35:Bg:44:ARG:NH1	47:Bt:100:LYS:HA	2.35	0.41
38:Bi:251:HIS:HD2	38:Bi:254:ASP:HB2	1.86	0.41
40:Bk:86:TYR:HD1	40:Bk:88:TYR:HD2	1.68	0.41
43:Bn:32:PHE:CD1	56:BA:199:A:H5''	2.54	0.41
47:Bt:57:GLU:CD	47:Bt:57:GLU:H	2.28	0.41
52:AA:62:C:H2'	52:AA:63:G:H8	1.86	0.41
52:AA:66:C:H5'	68:AP:13:ARG:HH12	1.86	0.41
56:BA:191:A:N6	56:BA:1029:G:OP1	2.53	0.41
56:BA:341:G:H2'	56:BA:342:C:C6	2.55	0.41
56:BA:507:G:H2'	56:BA:508:G:H8	1.86	0.41
56:BA:1019:C:H2'	56:BA:1020:C:H6	1.85	0.41
56:BA:1407:U:H2'	56:BA:1408:U:C6	2.56	0.41
73:Aa:193:PHE:CE2	82:Aj:173:MET:HG2	2.56	0.41
77:Ae:80:TRP:HA	77:Ae:83:ARG:HD2	2.02	0.41
77:Ae:86:GLU:HB2	77:Ae:118:ASN:OD1	2.20	0.41
86:Ao:617:PHE:HD2	86:Ao:633:LEU:HD11	1.85	0.41
4:B3:73:LYS:HE2	4:B3:73:LYS:HB3	1.90	0.41
13:BG:129:ALA:HB3	13:BG:132:GLN:HG3	2.02	0.41
17:BN:68:SER:O	17:BN:71:LYS:NZ	2.37	0.41
21:BR:49:VAL:HG13	21:BR:124:ILE:HB	2.01	0.41
21:BR:94:ALA:HB3	21:BR:95:PRO:HD3	2.02	0.41
26:BW:167:LYS:HA	56:BA:1007:G:OP1	2.20	0.41
31:Bc:61:LYS:HD3	31:Bc:61:LYS:HA	1.92	0.41
40:Bk:172:GLU:HA	40:Bk:175:HIS:ND1	2.35	0.41
47:Bt:18:ILE:HD11	56:BA:468:A:C2	2.55	0.41
52:AA:204:U:H2'	52:AA:205:U:C6	2.55	0.41
52:AA:447:U:H2'	52:AA:448:A:C8	2.56	0.41
52:AA:526:G:H1'	59:AE:231:MET:HG3	2.02	0.41
54:AV:18:U:C4	54:AV:45:U:OP2	2.74	0.41
54:AV:33:U:C6	54:AV:34:U:C5	3.09	0.41
56:BA:322:G:C5	56:BA:341:G:C8	3.09	0.41
61:AG:161:ILE:HD12	61:AG:170:VAL:HG21	2.02	0.41
63:AJ:75:ARG:H	63:AJ:175:THR:HB	1.85	0.41
73:Aa:150:MET:HE2	73:Aa:150:MET:HB3	1.92	0.41
73:Aa:190:ARG:HH21	87:Ap:177:PHE:HD1	1.68	0.41
1:B0:116:LEU:O	1:B0:120:LEU:HG	2.21	0.41
1:B0:122:GLN:HA	30:Bb:51:TYR:CD2	2.56	0.41
11:BE:69:ASN:HD21	11:BE:154:HIS:CE1	2.35	0.41
13:BG:117:ASP:HA	13:BG:136:ILE:HD12	2.02	0.41
19:BP:62:ARG:HG3	43:Bn:128:ARG:HE	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Bb:303:PHE:CE2	30:Bb:311:MET:HE1	2.56	0.41
33:Be:87:LYS:HE3	33:Be:87:LYS:HB2	1.89	0.41
43:Bn:92:ILE:HD13	43:Bn:114:ILE:HD13	2.03	0.41
52:AA:869:A:N1	52:AA:899:C:O2'	2.54	0.41
56:BA:48:U:O2'	56:BA:49:A:H4'	2.21	0.41
56:BA:150:A:N3	56:BA:198:U:O2'	2.46	0.41
56:BA:157:A:H2'	56:BA:158:A:H8	1.85	0.41
56:BA:978:G:H4'	56:BA:1429:C:H4'	2.02	0.41
56:BA:1390:G:H2'	56:BA:1391:U:C6	2.56	0.41
56:BA:1448:A:H2'	56:BA:1449:U:H6	1.84	0.41
73:Aa:217:VAL:HG22	73:Aa:226:ILE:HD13	2.02	0.41
77:Ae:80:TRP:HB2	77:Ae:154:ARG:NH1	2.36	0.41
77:Ae:86:GLU:CD	77:Ae:114:ARG:HG2	2.45	0.41
77:Ae:164:LYS:HE2	77:Ae:164:LYS:HB3	1.96	0.41
78:Af:144:ARG:NH1	78:Af:171:LEU:HD21	2.36	0.41
86:Ao:432:LEU:HD13	86:Ao:471:MET:HB3	2.01	0.41
86:Ao:491:PRO:HB3	86:Ao:495:THR:HB	2.02	0.41
87:Ap:188:PRO:HA	87:Ap:189:PRO:HD3	1.97	0.41
8:BB:37:A:H4'	40:Bk:111:HIS:CD2	2.55	0.41
10:BD:162:ASP:OD1	10:BD:163:THR:N	2.43	0.41
12:BF:83:HIS:HD2	12:BF:85:ASP:H	1.68	0.41
12:BF:249:ASN:ND2	43:Bn:55:GLY:O	2.54	0.41
16:BK:115:LYS:HD2	46:Bq:92:TYR:CE2	2.56	0.41
16:BK:124:LYS:HE3	16:BK:124:LYS:HB3	1.85	0.41
17:BN:78:SER:HB2	56:BA:568:C:C2	2.56	0.41
18:BO:42:ASP:HB3	18:BO:106:VAL:HG23	2.02	0.41
18:BO:85:LEU:HD23	18:BO:137:VAL:HG11	2.03	0.41
23:BT:102:ARG:NH2	23:BT:169:PRO:HA	2.35	0.41
27:BX:145:PRO:HB3	38:Bi:175:ASP:HB2	2.03	0.41
28:BY:36:PRO:O	28:BY:39:THR:HG22	2.20	0.41
28:BY:133:VAL:HG13	28:BY:145:ARG:HB3	2.02	0.41
29:Ba:233:LYS:HG2	29:Ba:284:PRO:O	2.21	0.41
31:Bc:99:LYS:HE2	31:Bc:99:LYS:HB3	1.85	0.41
31:Bc:181:VAL:HG22	31:Bc:290:VAL:HG22	2.02	0.41
33:Be:45:ASP:OD1	33:Be:45:ASP:N	2.52	0.41
41:Bl:111:ARG:HD2	56:BA:217:A:H62	1.86	0.41
52:AA:66:C:H5'	68:AP:13:ARG:HH22	1.85	0.41
52:AA:182:A:H62	65:AL:55:ARG:HG2	1.86	0.41
52:AA:405:G:N1	52:AA:452:C:O2'	2.27	0.41
52:AA:489:G:H2'	52:AA:490:A:C8	2.55	0.41
52:AA:514:C:C2	52:AA:515:U:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:669:C:O2'	61:AG:35:SER:O	2.36	0.41
56:BA:157:A:H2'	56:BA:158:A:C8	2.55	0.41
56:BA:211:U:H2'	56:BA:212:C:H6	1.86	0.41
56:BA:331:A:N6	56:BA:1068:C:H4'	2.36	0.41
56:BA:644:G:O2'	56:BA:1007:G:O6	2.30	0.41
56:BA:653:A:H2'	56:BA:654:G:O4'	2.20	0.41
56:BA:919:G:H2'	56:BA:920:C:C6	2.56	0.41
56:BA:1029:G:H2'	56:BA:1030:G:C8	2.55	0.41
56:BA:1127:A:H2'	56:BA:1128:A:C8	2.56	0.41
56:BA:1191:A:H2'	56:BA:1192:U:H6	1.86	0.41
56:BA:1349:G:H1	56:BA:1360:U:H3	1.69	0.41
56:BA:1366:A:N7	56:BA:1537:A:O2'	2.54	0.41
58:AC:163:VAL:HG21	58:AC:167:ILE:HD12	2.02	0.41
59:AE:163:GLU:O	59:AE:167:LYS:HG2	2.20	0.41
59:AE:278:TYR:HB3	74:Ab:6:LEU:HD21	2.03	0.41
61:AG:90:VAL:HG12	61:AG:145:PHE:HE2	1.85	0.41
65:AL:72:LYS:N	65:AL:73:PRO:HD2	2.36	0.41
68:AP:29:ARG:HH11	68:AP:57:LEU:HB2	1.86	0.41
69:AQ:13:VAL:O	69:AQ:65:LEU:HD12	2.21	0.41
73:Aa:295:TRP:HA	73:Aa:298:VAL:HG22	2.03	0.41
77:Ae:109:SER:HA	77:Ae:112:ILE:HG22	2.03	0.41
77:Ae:298:ARG:O	77:Ae:301:GLN:HG2	2.21	0.41
77:Ae:406:PRO:HA	77:Ae:409:GLU:HG2	2.02	0.41
78:Af:115:ILE:HD13	78:Af:141:VAL:HG21	2.03	0.41
79:Ag:364:TRP:HZ2	79:Ag:395:ALA:HA	1.85	0.41
80:Ah:379:LEU:HB2	80:Ah:386:LEU:HD12	2.03	0.41
86:Ao:431:ASP:HB3	86:Ao:434:LEU:HD12	2.03	0.41
86:Ao:434:LEU:O	86:Ao:438:VAL:HG23	2.21	0.41
87:Ap:63:GLU:OE1	87:Ap:112:LYS:NZ	2.51	0.41
11:BE:60:PHE:HB2	21:BR:154:ARG:NH1	2.36	0.41
12:BF:50:LYS:HE2	12:BF:50:LYS:HB2	1.96	0.41
14:BI:99:THR:OG1	14:BI:127:GLY:O	2.39	0.41
23:BT:87:THR:HG21	23:BT:91:LYS:HD3	2.03	0.41
37:Bh:97:TYR:O	37:Bh:101:GLU:HG2	2.20	0.41
44:Bo:45:GLU:OE2	44:Bo:70:ARG:NH2	2.54	0.41
50:Bw:240:GLN:NE2	50:Bw:349:PHE:HA	2.36	0.41
52:AA:397:U:H5''	52:AA:462:A:O2'	2.20	0.41
52:AA:925:A:O2'	52:AA:946:A:H5'	2.21	0.41
56:BA:1070:U:H1'	56:BA:1420:A:H2	1.86	0.41
60:AF:28:ALA:O	60:AF:32:ARG:HG2	2.21	0.41
62:AI:88:LEU:HA	62:AI:91:MET:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AI:259:GLU:O	62:AI:355:SER:OG	2.34	0.41
63:AJ:163:ASN:HB3	83:Ak:116:LEU:HD11	2.03	0.41
65:AL:69:LYS:HA	65:AL:70:PRO:HD3	1.96	0.41
88:EL:76:LEU:HD21	88:GL:90:LEU:HD21	2.02	0.41
10:BD:128:ILE:HD11	10:BD:144:ALA:HB2	2.02	0.40
12:BF:195:LEU:HD23	12:BF:195:LEU:HA	1.91	0.40
16:BK:127:ASP:O	16:BK:131:ALA:HB2	2.21	0.40
23:BT:58:PRO:CD	77:Ae:135:PHE:N	2.84	0.40
31:Bc:298:LEU:HG	31:Bc:309:TRP:HZ3	1.86	0.40
34:Bf:126:ARG:HD3	34:Bf:126:ARG:HA	1.98	0.40
35:Bg:146:ARG:HD3	35:Bg:146:ARG:HA	1.90	0.40
37:Bh:90:THR:HG23	37:Bh:120:LYS:O	2.22	0.40
39:Bj:199:ASN:OD1	39:Bj:199:ASN:N	2.48	0.40
50:Bw:420:LEU:O	50:Bw:422:ARG:HG3	2.20	0.40
52:AA:295:A:N3	52:AA:487:C:H1'	2.36	0.40
52:AA:534:U:H2'	52:AA:535:U:C6	2.57	0.40
52:AA:914:A:H2'	52:AA:915:G:C8	2.56	0.40
56:BA:51:A:H2'	56:BA:52:A:N3	2.36	0.40
56:BA:300:A:H2'	56:BA:301:U:H6	1.85	0.40
56:BA:443:G:O2'	56:BA:446:C:N4	2.36	0.40
56:BA:1362:U:H2'	56:BA:1363:U:C6	2.56	0.40
57:AB:145:SER:O	57:AB:167:THR:HA	2.20	0.40
58:AC:72:HIS:HD2	58:AC:74:GLY:H	1.69	0.40
61:AG:82:THR:OG1	61:AG:87:GLU:OE2	2.34	0.40
61:AG:170:VAL:HG13	61:AG:237:ALA:HA	2.02	0.40
75:Ac:7:PHE:O	75:Ac:10:ARG:HG2	2.20	0.40
79:Ag:144:CYS:SG	79:Ag:258:LEU:HD22	2.60	0.40
86:Ao:581:TYR:O	86:Ao:585:LEU:HG	2.21	0.40
1:B0:71:ARG:NH1	56:BA:1162:G:H5''	2.36	0.40
4:B3:101:LYS:HB3	44:Bo:84:MET:HE1	2.03	0.40
30:Bb:136:ARG:NE	30:Bb:140:GLU:OE2	2.54	0.40
51:Bx:60:SER:HB2	51:Bx:75:TRP:HH2	1.86	0.40
52:AA:421:A:H3'	52:AA:422:C:H6	1.86	0.40
52:AA:554:C:H2'	52:AA:555:C:H6	1.86	0.40
52:AA:945:A:H5''	85:An:138:MET:HE1	2.04	0.40
56:BA:342:C:C2	56:BA:343:C:C5	3.09	0.40
56:BA:1543:U:H2'	56:BA:1544:A:H8	1.86	0.40
63:AJ:53:ASP:OD1	63:AJ:53:ASP:N	2.48	0.40
69:AQ:35:LEU:HB2	69:AQ:42:TYR:CE1	2.56	0.40
69:AQ:69:LEU:HD12	69:AQ:70:PRO:HD2	2.02	0.40
73:Aa:194:ILE:HG13	73:Aa:211:ARG:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:Ab:119:VAL:O	74:Ab:123:LYS:HG2	2.20	0.40
75:Ac:105:ILE:HG13	75:Ac:106:LEU:HG	2.02	0.40
77:Ac:359:ASP:OD1	77:Ac:359:ASP:N	2.54	0.40
86:Ao:343:LYS:O	86:Ao:346:ARG:HG2	2.22	0.40
3:B2:119:GLN:HG2	27:BX:29:VAL:HG12	2.03	0.40
10:BD:258:ILE:HG22	56:BA:843:C:H4'	2.02	0.40
10:BD:285:ARG:NH1	10:BD:287:ILE:HD11	2.37	0.40
11:BE:105:GLY:HA3	23:BT:91:LYS:HD2	2.03	0.40
11:BE:179:PHE:CZ	11:BE:298:LYS:HG3	2.57	0.40
19:BP:72:THR:HA	19:BP:73:PRO:HD3	1.97	0.40
29:Ba:313:MET:HE1	29:Ba:353:GLN:HB2	2.03	0.40
35:Bg:144:ARG:HB2	35:Bg:147:GLU:HB2	2.04	0.40
39:Bj:189:GLU:O	39:Bj:192:LEU:HG	2.21	0.40
40:Bk:96:ILE:HB	40:Bk:183:LYS:HB2	2.02	0.40
50:Bw:131:LEU:H	50:Bw:131:LEU:HG	1.67	0.40
52:AA:88:C:H2'	52:AA:89:U:C6	2.57	0.40
52:AA:251:C:P	65:AL:116:GLN:HE21	2.45	0.40
54:AV:18:U:H5	54:AV:44:U:C5'	2.34	0.40
56:BA:320:U:H2'	56:BA:325:G:O2'	2.22	0.40
56:BA:516:G:H1'	56:BA:533:A:H2'	2.02	0.40
56:BA:1002:U:N3	56:BA:1003:C:C5	2.89	0.40
56:BA:1122:A:H2'	56:BA:1123:A:H8	1.86	0.40
56:BA:1156:A:H2'	56:BA:1157:C:C6	2.56	0.40
62:AI:224:ARG:O	62:AI:227:GLU:HG3	2.21	0.40
75:Ac:90:VAL:HG21	75:Ac:98:ILE:HD11	2.03	0.40
79:Ag:207:TYR:HE1	79:Ag:244:LYS:HE3	1.86	0.40
82:Aj:88:GLN:HA	87:Ap:215:ARG:HD3	2.04	0.40
87:Ap:100:VAL:HG11	87:Ap:104:PRO:HG3	2.03	0.40
13:BG:75:ASN:OD1	13:BG:77:ALA:HB3	2.22	0.40
15:BJ:99:CYS:SG	15:BJ:100:GLN:N	2.94	0.40
19:BP:40:PRO:HG3	56:BA:204:G:H2'	2.03	0.40
22:BS:51:ARG:NH2	30:Bb:229:ASP:HA	2.36	0.40
29:Ba:43:PRO:HA	29:Ba:44:PRO:HD3	1.94	0.40
29:Ba:277:THR:OG1	29:Ba:278:GLY:N	2.54	0.40
31:Bc:240:LYS:HD3	31:Bc:240:LYS:HA	1.92	0.40
32:Bd:117:LEU:HD23	39:Bj:73:LEU:HD22	2.04	0.40
51:Bx:71:PRO:HD2	51:Bx:107:LEU:HD23	2.02	0.40
52:AA:209:C:C2	52:AA:210:U:C5	3.10	0.40
52:AA:220:U:H2'	52:AA:221:A:H8	1.86	0.40
52:AA:308:A:C2	75:Ac:36:THR:HG21	2.56	0.40
52:AA:328:A:H2	64:AK:185:HIS:HB2	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AA:432:A:H4'	52:AA:433:U:H5''	2.04	0.40
52:AA:541:C:H2'	52:AA:542:C:O4'	2.22	0.40
52:AA:855:C:H2'	52:AA:856:U:C6	2.56	0.40
54:AV:56:U:H2'	54:AV:57:U:C6	2.56	0.40
56:BA:1487:C:H2'	56:BA:1488:C:C6	2.56	0.40
60:AF:90:ARG:NH1	70:AR:117:ILE:O	2.54	0.40
61:AG:234:ARG:HG3	64:AK:128:ILE:HD12	2.04	0.40
63:AJ:72:LEU:HB3	63:AJ:177:LEU:HD12	2.01	0.40
67:AO:110:MET:HE3	67:AO:110:MET:HB3	2.00	0.40
80:Ah:287:GLN:OE1	80:Ah:287:GLN:N	2.54	0.40
86:Ao:86:PRO:HG2	86:Ao:89:PHE:CD1	2.57	0.40
4:B3:35:LYS:HE2	56:BA:453:U:H1'	2.04	0.40
5:B4:64:THR:HG21	39:Bj:133:LEU:HD22	2.02	0.40
12:BF:114:THR:O	12:BF:156:ARG:NH1	2.55	0.40
13:BG:229:ASP:CG	56:BA:1153:G:H22	2.30	0.40
14:BI:59:TRP:CD1	14:BI:79:VAL:HG12	2.57	0.40
23:BT:63:VAL:O	77:Ae:89:HIS:HB3	2.22	0.40
25:BV:120:ILE:HG22	25:BV:122:ASN:H	1.85	0.40
29:Ba:302:ARG:HA	29:Ba:302:ARG:HD3	1.89	0.40
52:AA:224:U:H3	52:AA:225:A:N6	2.20	0.40
52:AA:278:A:H2'	52:AA:279:U:C6	2.57	0.40
52:AA:278:A:H2'	52:AA:279:U:H6	1.87	0.40
52:AA:525:U:H2'	52:AA:526:G:C8	2.55	0.40
52:AA:541:C:H2'	52:AA:542:C:C6	2.57	0.40
52:AA:882:A:H5'	77:Ae:108:SER:HB2	2.02	0.40
56:BA:189:A:N1	56:BA:1028:A:C2	2.89	0.40
56:BA:303:G:H2'	56:BA:304:U:O4'	2.22	0.40
56:BA:1387:A:N6	56:BA:1450:U:HO2'	2.19	0.40
59:AE:425:LEU:HD13	87:Ap:85:ILE:HG21	2.03	0.40
63:AJ:92:GLU:HG3	63:AJ:108:VAL:HG11	2.04	0.40
79:Ag:205:GLU:HB3	79:Ag:207:TYR:CE2	2.56	0.40
79:Ag:364:TRP:CZ2	79:Ag:395:ALA:HA	2.55	0.40
82:Aj:31:SER:HG	82:Aj:32:GLN:H	1.69	0.40
83:Ak:266:GLU:O	83:Ak:270:GLN:HG2	2.22	0.40
86:Ao:559:LYS:HE3	86:Ao:574:TRP:HZ2	1.87	0.40
88:DL:64:ILE:O	88:DL:68:VAL:HG23	2.22	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%)	107 (99%)	1 (1%)	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%)	55 (92%)	5 (8%)	0	100	100
6	B5	108/188 (57%)	107 (99%)	1 (1%)	0	100	100
7	B6	50/65 (77%)	50 (100%)	0	0	100	100
9	B7	44/95 (46%)	44 (100%)	0	0	100	100
10	BD	238/306 (78%)	230 (97%)	8 (3%)	0	100	100
11	BE	305/399 (76%)	292 (96%)	13 (4%)	0	100	100
12	BF	248/294 (84%)	244 (98%)	4 (2%)	0	100	100
13	BG	191/257 (74%)	172 (90%)	19 (10%)	0	100	100
14	BI	96/268 (36%)	96 (100%)	0	0	100	100
15	BJ	210/262 (80%)	200 (95%)	10 (5%)	0	100	100
16	BK	174/192 (91%)	172 (99%)	2 (1%)	0	100	100
17	BN	175/178 (98%)	171 (98%)	4 (2%)	0	100	100
18	BO	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
19	BP	286/296 (97%)	276 (96%)	10 (4%)	0	100	100
20	BQ	220/251 (88%)	217 (99%)	3 (1%)	0	100	100
21	BR	151/169 (89%)	143 (95%)	8 (5%)	0	100	100
22	BS	141/180 (78%)	132 (94%)	9 (6%)	0	100	100
23	BT	226/292 (77%)	217 (96%)	8 (4%)	1 (0%)	30	67
24	BU	138/149 (93%)	138 (100%)	0	0	100	100
25	BV	153/209 (73%)	150 (98%)	3 (2%)	0	100	100
26	BW	164/210 (78%)	161 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	BX	147/150 (98%)	143 (97%)	4 (3%)	0	100	100
28	BY	204/216 (94%)	201 (98%)	3 (2%)	0	100	100
29	Ba	391/423 (92%)	380 (97%)	11 (3%)	0	100	100
30	Bb	352/380 (93%)	338 (96%)	14 (4%)	0	100	100
31	Bc	293/334 (88%)	282 (96%)	11 (4%)	0	100	100
32	Bd	136/206 (66%)	130 (96%)	6 (4%)	0	100	100
33	Be	120/135 (89%)	115 (96%)	5 (4%)	0	100	100
34	Bf	106/142 (75%)	102 (96%)	2 (2%)	2 (2%)	6	32
35	Bg	146/159 (92%)	137 (94%)	9 (6%)	0	100	100
36	B8	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
37	Bh	287/332 (86%)	275 (96%)	12 (4%)	0	100	100
38	Bi	258/306 (84%)	253 (98%)	5 (2%)	0	100	100
39	Bj	211/279 (76%)	205 (97%)	6 (3%)	0	100	100
40	Bk	151/269 (56%)	149 (99%)	2 (1%)	0	100	100
41	Bl	131/166 (79%)	129 (98%)	2 (2%)	0	100	100
42	Bm	107/198 (54%)	105 (98%)	2 (2%)	0	100	100
43	Bn	95/128 (74%)	90 (95%)	5 (5%)	0	100	100
44	Bo	95/124 (77%)	94 (99%)	1 (1%)	0	100	100
45	Bp	95/112 (85%)	92 (97%)	3 (3%)	0	100	100
46	Bq	78/138 (56%)	73 (94%)	4 (5%)	1 (1%)	9	41
47	Bt	92/102 (90%)	89 (97%)	3 (3%)	0	100	100
48	Bu	147/205 (72%)	140 (95%)	5 (3%)	2 (1%)	9	39
49	Bv	133/222 (60%)	132 (99%)	1 (1%)	0	100	100
50	Bw	385/433 (89%)	365 (95%)	20 (5%)	0	100	100
51	Bx	160/196 (82%)	155 (97%)	5 (3%)	0	100	100
53	B9	36/100 (36%)	36 (100%)	0	0	100	100
57	AB	218/289 (75%)	214 (98%)	4 (2%)	0	100	100
58	AC	130/167 (78%)	123 (95%)	7 (5%)	0	100	100
59	AE	341/430 (79%)	332 (97%)	9 (3%)	0	100	100
60	AF	120/276 (44%)	119 (99%)	1 (1%)	0	100	100
61	AG	206/242 (85%)	206 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AI	326/397 (82%)	315 (97%)	11 (3%)	0	100	100
63	AJ	138/200 (69%)	127 (92%)	11 (8%)	0	100	100
64	AK	135/196 (69%)	129 (96%)	6 (4%)	0	100	100
65	AL	107/139 (77%)	103 (96%)	4 (4%)	0	100	100
66	AN	99/128 (77%)	99 (100%)	0	0	100	100
67	AO	173/239 (72%)	166 (96%)	7 (4%)	0	100	100
68	AP	115/135 (85%)	112 (97%)	3 (3%)	0	100	100
69	AQ	110/130 (85%)	108 (98%)	2 (2%)	0	100	100
70	AR	95/143 (66%)	94 (99%)	1 (1%)	0	100	100
71	AU	84/87 (97%)	84 (100%)	0	0	100	100
73	Aa	290/382 (76%)	285 (98%)	5 (2%)	0	100	100
74	Ab	133/190 (70%)	132 (99%)	1 (1%)	0	100	100
75	Ac	167/173 (96%)	165 (99%)	2 (1%)	0	100	100
76	Ad	175/205 (85%)	175 (100%)	0	0	100	100
77	Ae	386/455 (85%)	356 (92%)	27 (7%)	3 (1%)	16	53
78	Af	97/188 (52%)	93 (96%)	4 (4%)	0	100	100
79	Ag	351/410 (86%)	339 (97%)	12 (3%)	0	100	100
80	Ah	118/387 (30%)	118 (100%)	0	0	100	100
81	Ai	97/106 (92%)	97 (100%)	0	0	100	100
82	Aj	211/218 (97%)	206 (98%)	5 (2%)	0	100	100
83	Ak	273/325 (84%)	264 (97%)	9 (3%)	0	100	100
84	Am	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
85	An	70/199 (35%)	69 (99%)	1 (1%)	0	100	100
86	Ao	532/690 (77%)	518 (97%)	14 (3%)	0	100	100
87	Ap	188/258 (73%)	183 (97%)	5 (3%)	0	100	100
88	CL	43/198 (22%)	41 (95%)	2 (5%)	0	100	100
88	DL	25/198 (13%)	25 (100%)	0	0	100	100
88	EL	26/198 (13%)	26 (100%)	0	0	100	100
88	FL	25/198 (13%)	25 (100%)	0	0	100	100
88	GL	25/198 (13%)	25 (100%)	0	0	100	100
88	HL	24/198 (12%)	24 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	14350/19681 (73%)	13925 (97%)	416 (3%)	9 (0%)	49	83

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	Bf	78	PRO
34	Bf	80	PRO
48	Bu	167	PRO
46	Bq	64	ASP
77	Ae	136	ARG
23	BT	58	PRO
77	Ae	342	PRO
77	Ae	341	GLN
48	Bu	166	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B0	90/115 (78%)	88 (98%)	2 (2%)	45	64
2	B1	219/229 (96%)	218 (100%)	1 (0%)	81	81
3	B2	164/228 (72%)	162 (99%)	2 (1%)	63	73
4	B3	110/150 (73%)	109 (99%)	1 (1%)	70	76
5	B4	45/114 (40%)	42 (93%)	3 (7%)	15	36
6	B5	99/163 (61%)	98 (99%)	1 (1%)	68	76
7	B6	49/60 (82%)	48 (98%)	1 (2%)	48	65
9	B7	41/78 (53%)	40 (98%)	1 (2%)	43	63
10	BD	193/248 (78%)	188 (97%)	5 (3%)	40	60
11	BE	263/320 (82%)	260 (99%)	3 (1%)	65	74
12	BF	217/251 (86%)	213 (98%)	4 (2%)	51	67
13	BG	173/224 (77%)	164 (95%)	9 (5%)	21	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	BI	88/228 (39%)	87 (99%)	1 (1%)	65	74
15	BJ	192/230 (84%)	190 (99%)	2 (1%)	68	76
16	BK	129/151 (85%)	129 (100%)	0	100	100
17	BN	156/157 (99%)	156 (100%)	0	100	100
18	BO	99/123 (80%)	98 (99%)	1 (1%)	68	76
19	BP	245/249 (98%)	243 (99%)	2 (1%)	73	77
20	BQ	190/210 (90%)	188 (99%)	2 (1%)	65	74
21	BR	132/143 (92%)	131 (99%)	1 (1%)	73	77
22	BS	123/153 (80%)	122 (99%)	1 (1%)	73	77
23	BT	208/258 (81%)	204 (98%)	4 (2%)	50	66
24	BU	118/127 (93%)	118 (100%)	0	100	100
25	BV	136/178 (76%)	133 (98%)	3 (2%)	45	64
26	BW	144/180 (80%)	144 (100%)	0	100	100
27	BX	116/134 (87%)	116 (100%)	0	100	100
28	BY	185/192 (96%)	182 (98%)	3 (2%)	55	69
29	Ba	348/365 (95%)	343 (99%)	5 (1%)	59	71
30	Bb	310/328 (94%)	307 (99%)	3 (1%)	68	76
31	Bc	271/299 (91%)	269 (99%)	2 (1%)	76	79
32	Bd	127/181 (70%)	122 (96%)	5 (4%)	28	49
33	Be	100/108 (93%)	100 (100%)	0	100	100
34	Bf	80/133 (60%)	80 (100%)	0	100	100
35	Bg	128/136 (94%)	123 (96%)	5 (4%)	28	49
36	B8	87/162 (54%)	85 (98%)	2 (2%)	44	63
37	Bh	251/284 (88%)	250 (100%)	1 (0%)	84	82
38	Bi	236/275 (86%)	232 (98%)	4 (2%)	53	67
39	Bj	190/242 (78%)	188 (99%)	2 (1%)	65	74
40	Bk	135/226 (60%)	134 (99%)	1 (1%)	76	79
41	Bl	122/147 (83%)	120 (98%)	2 (2%)	55	69
42	Bm	103/178 (58%)	103 (100%)	0	100	100
43	Bn	88/113 (78%)	86 (98%)	2 (2%)	44	63
44	Bo	77/97 (79%)	77 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	Bp	79/88 (90%)	77 (98%)	2 (2%)	42	62
46	Bq	70/114 (61%)	66 (94%)	4 (6%)	18	40
47	Bt	75/82 (92%)	75 (100%)	0	100	100
48	Bu	126/177 (71%)	126 (100%)	0	100	100
49	Bv	115/183 (63%)	115 (100%)	0	100	100
50	Bw	340/373 (91%)	336 (99%)	4 (1%)	63	73
51	Bx	149/173 (86%)	146 (98%)	3 (2%)	48	65
53	B9	36/77 (47%)	35 (97%)	1 (3%)	38	59
57	AB	187/233 (80%)	186 (100%)	1 (0%)	81	81
58	AC	115/142 (81%)	114 (99%)	1 (1%)	70	76
59	AE	282/351 (80%)	273 (97%)	9 (3%)	34	55
60	AF	107/210 (51%)	105 (98%)	2 (2%)	50	66
61	AG	181/205 (88%)	180 (99%)	1 (1%)	78	80
62	AI	273/333 (82%)	267 (98%)	6 (2%)	45	64
63	AJ	130/180 (72%)	128 (98%)	2 (2%)	57	70
64	AK	103/151 (68%)	102 (99%)	1 (1%)	68	76
65	AL	92/116 (79%)	92 (100%)	0	100	100
66	AN	92/114 (81%)	91 (99%)	1 (1%)	65	74
67	AO	159/205 (78%)	158 (99%)	1 (1%)	78	80
68	AP	97/113 (86%)	97 (100%)	0	100	100
69	AQ	97/114 (85%)	95 (98%)	2 (2%)	47	65
70	AR	89/127 (70%)	87 (98%)	2 (2%)	45	64
71	AU	77/78 (99%)	76 (99%)	1 (1%)	61	72
73	Aa	258/330 (78%)	251 (97%)	7 (3%)	39	59
74	Ab	113/162 (70%)	112 (99%)	1 (1%)	70	76
75	Ac	152/155 (98%)	150 (99%)	2 (1%)	61	72
76	Ad	149/168 (89%)	144 (97%)	5 (3%)	32	54
77	Ae	325/393 (83%)	316 (97%)	9 (3%)	38	59
78	Af	86/160 (54%)	84 (98%)	2 (2%)	44	63
79	Ag	312/361 (86%)	305 (98%)	7 (2%)	45	64
80	Ah	109/346 (32%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	Ai	86/93 (92%)	85 (99%)	1 (1%)	63	73
82	Aj	188/190 (99%)	185 (98%)	3 (2%)	55	69
83	Ak	249/289 (86%)	244 (98%)	5 (2%)	48	65
84	Am	100/102 (98%)	92 (92%)	8 (8%)	11	31
85	An	66/174 (38%)	66 (100%)	0	100	100
86	Ao	478/541 (88%)	468 (98%)	10 (2%)	47	65
87	Ap	170/225 (76%)	168 (99%)	2 (1%)	63	73
88	CL	30/157 (19%)	30 (100%)	0	100	100
88	DL	26/157 (17%)	26 (100%)	0	100	100
88	EL	27/157 (17%)	27 (100%)	0	100	100
88	FL	26/157 (17%)	26 (100%)	0	100	100
88	GL	26/157 (17%)	26 (100%)	0	100	100
88	HL	25/157 (16%)	25 (100%)	0	100	100
All	All	12649/16737 (76%)	12456 (98%)	193 (2%)	55	70

All (193) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B0	53	ILE
1	B0	117	VAL
2	B1	126	THR
3	B2	92	LEU
3	B2	197	ASN
4	B3	86	ILE
5	B4	48	THR
5	B4	58	VAL
5	B4	80	VAL
6	B5	153	THR
7	B6	16	ILE
9	B7	73	LEU
10	BD	125	GLU
10	BD	190	VAL
10	BD	208	ILE
10	BD	216	VAL
10	BD	240	THR
11	BE	127	CYS
11	BE	236	THR

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Mol	Chain	Res	Type
11	BE	245	THR
12	BF	47	VAL
12	BF	62	VAL
12	BF	120	VAL
12	BF	262	THR
13	BG	82	ILE
13	BG	103	PHE
13	BG	105	LYS
13	BG	143	LEU
13	BG	163	ARG
13	BG	164	GLU
13	BG	187	ARG
13	BG	224	ASP
13	BG	228	GLU
14	BI	107	VAL
15	BJ	39	VAL
15	BJ	161	VAL
18	BO	58	ILE
19	BP	61	THR
19	BP	286	THR
20	BQ	59	VAL
20	BQ	136	MET
21	BR	144	THR
22	BS	141	ILE
23	BT	55	GLN
23	BT	58	PRO
23	BT	59	LYS
23	BT	187	LEU
25	BV	55	VAL
25	BV	103	VAL
25	BV	113	THR
28	BY	86	VAL
28	BY	98	VAL
28	BY	186	THR
29	Ba	74	VAL
29	Ba	273	VAL
29	Ba	341	VAL
29	Ba	342	VAL
29	Ba	391	VAL
30	Bb	179	VAL
30	Bb	189	HIS
30	Bb	233	VAL

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Mol	Chain	Res	Type
31	Bc	56	THR
31	Bc	283	LEU
32	Bd	74	ARG
32	Bd	76	GLU
32	Bd	79	SER
32	Bd	136	ILE
32	Bd	150	LEU
35	Bg	14	VAL
35	Bg	61	VAL
35	Bg	75	VAL
35	Bg	112	VAL
35	Bg	127	GLN
36	B8	137	THR
36	B8	163	THR
37	Bh	267	LEU
38	Bi	153	ASN
38	Bi	186	VAL
38	Bi	221	THR
38	Bi	238	VAL
39	Bj	47	LEU
39	Bj	84	TYR
40	Bk	84	THR
41	Bl	42	VAL
41	Bl	109	VAL
43	Bn	43	VAL
43	Bn	44	VAL
45	Bp	27	VAL
45	Bp	75	ILE
46	Bq	66	PHE
46	Bq	73	MET
46	Bq	77	ILE
46	Bq	101	VAL
50	Bw	47	ILE
50	Bw	131	LEU
50	Bw	255	VAL
50	Bw	370	THR
51	Bx	70	CYS
51	Bx	152	THR
51	Bx	159	VAL
53	B9	65	THR
57	AB	201	VAL
58	AC	52	THR

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Mol	Chain	Res	Type
59	AE	184	LYS
59	AE	185	MET
59	AE	186	LYS
59	AE	187	VAL
59	AE	188	LYS
59	AE	189	ARG
59	AE	289	THR
59	AE	336	VAL
59	AE	401	VAL
60	AF	105	CYS
60	AF	111	VAL
61	AG	208	GLU
62	AI	71	VAL
62	AI	247	ARG
62	AI	249	ILE
62	AI	251	ILE
62	AI	253	SER
62	AI	286	VAL
63	AJ	54	VAL
63	AJ	97	LEU
64	AK	68	ILE
66	AN	35	LEU
67	AO	72	MET
69	AQ	71	VAL
69	AQ	84	ILE
70	AR	69	CYS
70	AR	133	ASP
71	AU	14	VAL
73	Aa	129	THR
73	Aa	150	MET
73	Aa	153	VAL
73	Aa	196	VAL
73	Aa	276	ASP
73	Aa	329	LEU
73	Aa	352	VAL
74	Ab	132	LEU
75	Ac	90	VAL
75	Ac	106	LEU
76	Ad	29	THR
76	Ad	44	THR
76	Ad	109	ASN
76	Ad	145	GLU

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Mol	Chain	Res	Type
76	Ad	169	THR
77	Ae	93	LEU
77	Ae	135	PHE
77	Ae	137	HIS
77	Ae	138	SER
77	Ae	172	LYS
77	Ae	234	THR
77	Ae	280	LEU
77	Ae	360	VAL
77	Ae	388	VAL
78	Af	109	VAL
78	Af	173	LEU
79	Ag	47	ILE
79	Ag	208	VAL
79	Ag	212	ARG
79	Ag	236	THR
79	Ag	261	VAL
79	Ag	306	VAL
79	Ag	336	LEU
81	Ai	27	ASP
82	Aj	40	THR
82	Aj	86	LEU
82	Aj	151	THR
83	Ak	93	VAL
83	Ak	165	ILE
83	Ak	204	THR
83	Ak	227	LEU
83	Ak	246	THR
84	Am	37	ARG
84	Am	38	ARG
84	Am	39	GLU
84	Am	40	LYS
84	Am	64	GLU
84	Am	66	CYS
84	Am	96	LEU
84	Am	98	SER
86	Ao	78	VAL
86	Ao	115	ASN
86	Ao	137	ILE
86	Ao	294	VAL
86	Ao	341	ILE
86	Ao	349	TYR

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Mol	Chain	Res	Type
86	Ao	387	SER
86	Ao	436	TYR
86	Ao	489	PHE
86	Ao	644	VAL
87	Ap	115	VAL
87	Ap	179	THR

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

Mol	Chain	Res	Type
2	B1	13	GLN
3	B2	91	GLN
4	B3	136	ASN
5	B4	37	ASN
6	B5	115	HIS
6	B5	188	ASN
7	B6	31	ASN
9	B7	87	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
12	BF	251	HIS
15	BJ	93	ASN
15	BJ	101	HIS
17	BN	40	GLN
17	BN	89	GLN
17	BN	94	GLN
19	BP	84	ASN
19	BP	87	HIS
21	BR	100	GLN
23	BT	55	GLN
24	BU	89	ASN
28	BY	119	GLN
29	Ba	149	ASN
29	Ba	231	ASN
29	Ba	360	ASN

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Mol	Chain	Res	Type
30	Bb	220	ASN
30	Bb	308	GLN
30	Bb	354	GLN
31	Bc	282	ASN
35	Bg	107	GLN
35	Bg	120	HIS
36	B8	154	GLN
37	Bh	69	HIS
38	Bi	167	ASN
38	Bi	196	GLN
39	Bj	212	HIS
40	Bk	81	ASN
40	Bk	136	GLN
40	Bk	158	GLN
41	Bl	93	ASN
42	Bm	107	ASN
42	Bm	151	HIS
43	Bn	120	HIS
45	Bp	80	HIS
46	Bq	135	ASN
47	Bt	10	ASN
47	Bt	21	HIS
49	Bv	81	GLN
50	Bw	60	GLN
50	Bw	67	GLN
50	Bw	87	GLN
50	Bw	228	ASN
50	Bw	234	GLN
50	Bw	352	GLN
50	Bw	376	GLN
51	Bx	69	GLN
51	Bx	76	ASN
51	Bx	109	GLN
51	Bx	184	ASN
57	AB	119	GLN
57	AB	238	ASN
59	AE	151	ASN
59	AE	155	GLN
59	AE	356	GLN
59	AE	361	GLN
59	AE	369	HIS
60	AF	81	HIS

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Mol	Chain	Res	Type
61	AG	233	ASN
62	AI	90	ASN
62	AI	175	HIS
62	AI	327	HIS
62	AI	385	GLN
65	AL	74	ASN
66	AN	60	ASN
67	AO	201	HIS
67	AO	213	GLN
69	AQ	79	HIS
71	AU	3	ASN
73	Aa	270	HIS
73	Aa	334	GLN
75	Ac	51	ASN
75	Ac	95	ASN
75	Ac	118	GLN
75	Ac	128	HIS
76	Ad	65	GLN
76	Ad	109	ASN
76	Ad	188	ASN
77	Ae	127	HIS
79	Ag	68	ASN
79	Ag	301	GLN
79	Ag	363	ASN
80	Ah	370	ASN
80	Ah	387	ASN
83	Ak	66	GLN
83	Ak	104	ASN
83	Ak	183	ASN
83	Ak	307	ASN
84	Am	15	ASN
84	Am	92	ASN
85	An	166	GLN
86	Ao	543	HIS
87	Ap	147	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	AA	959/962 (99%)	176 (18%)	3 (0%)
54	AV	70/71 (98%)	28 (40%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
55	AX	4/5 (80%)	1 (25%)	0
56	BA	1542/1571 (98%)	412 (26%)	2 (0%)
8	BB	64/73 (87%)	17 (26%)	0
All	All	2639/2682 (98%)	634 (24%)	5 (0%)

All (634) 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
52	AA	5	A
52	AA	10	U
52	AA	27	U
52	AA	34	U
52	AA	42	A
52	AA	43	U
52	AA	54	A
52	AA	58	U
52	AA	63	G
52	AA	65	C
52	AA	75	A
52	AA	81	U
52	AA	83	C
52	AA	102	G
52	AA	115	A
52	AA	120	A
52	AA	127	A

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Mol	Chain	Res	Type
52	AA	147	G
52	AA	152	A
52	AA	161	C
52	AA	164	C
52	AA	165	G
52	AA	170	A
52	AA	171	C
52	AA	173	G
52	AA	175	A
52	AA	186	U
52	AA	191	C
52	AA	194	U
52	AA	212	A
52	AA	216	A
52	AA	217	U
52	AA	219	U
52	AA	222	A
52	AA	223	U
52	AA	224	U
52	AA	231	G
52	AA	235	A
52	AA	238	C
52	AA	244	C
52	AA	247	G
52	AA	253	G
52	AA	256	G
52	AA	257	U
52	AA	258	C
52	AA	273	A
52	AA	281	G
52	AA	287	C
52	AA	288	G
52	AA	294	A
52	AA	296	G
52	AA	297	A
52	AA	308	A
52	AA	309	A
52	AA	310	A
52	AA	314	A
52	AA	315	U
52	AA	316	C
52	AA	317	A

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Mol	Chain	Res	Type
52	AA	320	A
52	AA	328	A
52	AA	337	C
52	AA	345	U
52	AA	354	C
52	AA	355	U
52	AA	361	A
52	AA	362	A
52	AA	368	A
52	AA	372	C
52	AA	395	C
52	AA	399	A
52	AA	407	U
52	AA	417	C
52	AA	421	A
52	AA	433	U
52	AA	455	A
52	AA	457	C
52	AA	458	C
52	AA	461	A
52	AA	464	A
52	AA	471	U
52	AA	472	A
52	AA	477	A
52	AA	479	C
52	AA	498	U
52	AA	502	A
52	AA	503	A
52	AA	518	A
52	AA	531	U
52	AA	532	G
52	AA	534	U
52	AA	536	C
52	AA	538	C
52	AA	540	U
52	AA	561	U
52	AA	566	U
52	AA	571	A
52	AA	574	C
52	AA	576	C
52	AA	589	C
52	AA	592	A

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Mol	Chain	Res	Type
52	AA	593	C
52	AA	596	U
52	AA	597	U
52	AA	604	U
52	AA	616	C
52	AA	618	G
52	AA	619	C
52	AA	625	U
52	AA	633	C
52	AA	639	A
52	AA	644	A
52	AA	645	A
52	AA	646	C
52	AA	647	A
52	AA	649	U
52	AA	665	A
52	AA	681	A
52	AA	682	G
52	AA	696	U
52	AA	698	A
52	AA	699	U
52	AA	707	A
52	AA	708	A
52	AA	709	A
52	AA	711	A
52	AA	720	A
52	AA	722	A
52	AA	731	A
52	AA	732	U
52	AA	739	A
52	AA	743	A
52	AA	746	A
52	AA	771	A
52	AA	775	A
52	AA	780	A
52	AA	781	G
52	AA	790	A
52	AA	791	G
52	AA	802	A
52	AA	803	U
52	AA	807	G
52	AA	808	U

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Mol	Chain	Res	Type
52	AA	823	G
52	AA	825	C
52	AA	838	A
52	AA	841	C
52	AA	842	A
52	AA	854	C
52	AA	863	G
52	AA	869	A
52	AA	870	G
52	AA	876	A
52	AA	877	A
52	AA	883	C
52	AA	885	U
52	AA	886	A
52	AA	893	A
52	AA	894	U
52	AA	897	C
52	AA	899	C
52	AA	902	C
52	AA	910	G
52	AA	918	A
52	AA	919	A
52	AA	923	G
52	AA	925	A
52	AA	928	A
52	AA	930	G
52	AA	932	U
52	AA	943	G
52	AA	946	A
52	AA	955	G
52	AA	956	G
52	AA	959	U
52	AA	960	A
54	AV	6	U
54	AV	8	U
54	AV	9	U
54	AV	10	U
54	AV	11	U
54	AV	12	U
54	AV	13	U
54	AV	14	U
54	AV	16	U

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Mol	Chain	Res	Type
54	AV	17	U
54	AV	18	U
54	AV	24	U
54	AV	30	U
54	AV	38	U
54	AV	43	U
54	AV	44	U
54	AV	45	U
54	AV	46	U
54	AV	49	U
54	AV	55	U
54	AV	56	U
54	AV	60	U
54	AV	62	U
54	AV	64	U
54	AV	65	U
54	AV	68	U
54	AV	69	C
54	AV	71	A
55	AX	3	U
56	BA	4	A
56	BA	7	G
56	BA	11	G
56	BA	15	A
56	BA	19	U
56	BA	20	A
56	BA	21	C
56	BA	22	U
56	BA	26	C
56	BA	27	A
56	BA	31	A
56	BA	32	C
56	BA	36	A
56	BA	37	A
56	BA	40	C
56	BA	41	A
56	BA	45	A
56	BA	46	A
56	BA	49	A
56	BA	56	A
56	BA	57	A
56	BA	59	A

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Mol	Chain	Res	Type
56	BA	60	U
56	BA	63	A
56	BA	66	U
56	BA	67	A
56	BA	68	A
56	BA	82	G
56	BA	83	A
56	BA	96	U
56	BA	97	A
56	BA	105	G
56	BA	109	U
56	BA	118	U
56	BA	119	A
56	BA	122	G
56	BA	129	A
56	BA	130	A
56	BA	132	G
56	BA	135	G
56	BA	139	G
56	BA	140	A
56	BA	141	A
56	BA	142	U
56	BA	143	A
56	BA	146	A
56	BA	147	U
56	BA	163	C
56	BA	164	A
56	BA	168	A
56	BA	172	C
56	BA	178	C
56	BA	180	A
56	BA	182	C
56	BA	190	U
56	BA	192	A
56	BA	205	A
56	BA	218	A
56	BA	219	A
56	BA	223	A
56	BA	225	C
56	BA	229	A
56	BA	231	C
56	BA	237	A

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Mol	Chain	Res	Type
56	BA	238	C
56	BA	239	C
56	BA	243	A
56	BA	245	A
56	BA	254	G
56	BA	263	G
56	BA	265	G
56	BA	271	U
56	BA	272	A
56	BA	273	A
56	BA	275	A
56	BA	277	A
56	BA	295	G
56	BA	309	A
56	BA	311	A
56	BA	313	U
56	BA	322	G
56	BA	323	A
56	BA	324	G
56	BA	329	A
56	BA	330	A
56	BA	331	A
56	BA	336	A
56	BA	337	A
56	BA	338	C
56	BA	340	A
56	BA	351	A
56	BA	352	G
56	BA	359	G
56	BA	366	A
56	BA	368	A
56	BA	369	G
56	BA	373	U
56	BA	374	U
56	BA	376	A
56	BA	389	A
56	BA	390	A
56	BA	393	A
56	BA	394	C
56	BA	398	A
56	BA	404	C
56	BA	409	A

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Mol	Chain	Res	Type
56	BA	413	C
56	BA	414	A
56	BA	417	G
56	BA	427	G
56	BA	428	A
56	BA	432	A
56	BA	433	G
56	BA	446	C
56	BA	447	A
56	BA	448	G
56	BA	459	A
56	BA	460	C
56	BA	467	A
56	BA	468	A
56	BA	472	U
56	BA	473	G
56	BA	474	A
56	BA	479	A
56	BA	480	G
56	BA	488	U
56	BA	490	U
56	BA	491	U
56	BA	492	A
56	BA	493	A
56	BA	494	U
56	BA	497	U
56	BA	498	A
56	BA	499	C
56	BA	500	C
56	BA	501	A
56	BA	503	A
56	BA	505	U
56	BA	509	C
56	BA	514	A
56	BA	515	A
56	BA	516	G
56	BA	517	C
56	BA	518	A
56	BA	526	A
56	BA	527	U
56	BA	530	A
56	BA	532	A

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Mol	Chain	Res	Type
56	BA	533	A
56	BA	541	A
56	BA	547	A
56	BA	548	A
56	BA	549	C
56	BA	550	A
56	BA	551	A
56	BA	553	U
56	BA	554	U
56	BA	557	C
56	BA	560	A
56	BA	561	C
56	BA	562	A
56	BA	563	U
56	BA	570	A
56	BA	574	A
56	BA	576	U
56	BA	578	A
56	BA	579	U
56	BA	584	A
56	BA	586	C
56	BA	592	G
56	BA	595	C
56	BA	596	A
56	BA	618	A
56	BA	625	A
56	BA	626	G
56	BA	631	A
56	BA	633	U
56	BA	634	G
56	BA	640	A
56	BA	648	C
56	BA	649	A
56	BA	654	G
56	BA	660	C
56	BA	665	C
56	BA	673	C
56	BA	674	U
56	BA	675	U
56	BA	683	U
56	BA	684	A
56	BA	689	A

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Mol	Chain	Res	Type
56	BA	694	A
56	BA	695	U
56	BA	697	C
56	BA	704	U
56	BA	707	A
56	BA	713	A
56	BA	719	C
56	BA	720	C
56	BA	722	A
56	BA	723	A
56	BA	724	A
56	BA	725	C
56	BA	727	A
56	BA	728	C
56	BA	737	G
56	BA	744	A
56	BA	745	A
56	BA	746	U
56	BA	747	U
56	BA	748	A
56	BA	763	C
56	BA	764	A
56	BA	774	A
56	BA	777	A
56	BA	778	A
56	BA	780	G
56	BA	782	A
56	BA	783	A
56	BA	784	G
56	BA	814	C
56	BA	819	A
56	BA	825	C
56	BA	835	A
56	BA	847	U
56	BA	848	C
56	BA	852	C
56	BA	854	U
56	BA	855	U
56	BA	856	A
56	BA	859	A
56	BA	864	U
56	BA	872	A

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Mol	Chain	Res	Type
56	BA	878	G
56	BA	883	G
56	BA	889	C
56	BA	892	G
56	BA	894	U
56	BA	895	U
56	BA	896	A
56	BA	897	A
56	BA	899	G
56	BA	900	G
56	BA	902	C
56	BA	909	U
56	BA	910	U
56	BA	922	A
56	BA	923	A
56	BA	924	G
56	BA	925	G
56	BA	926	U
56	BA	931	U
56	BA	933	A
56	BA	935	C
56	BA	938	U
56	BA	939	U
56	BA	947	A
56	BA	948	A
56	BA	950	U
56	BA	958	U
56	BA	959	G
56	BA	960	U
56	BA	962	U
56	BA	964	A
56	BA	965	A
56	BA	967	G
56	BA	970	C
56	BA	977	G
56	BA	983	U
56	BA	986	U
56	BA	987	G
56	BA	992	U
56	BA	1015	C
56	BA	1016	C
56	BA	1018	U

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Mol	Chain	Res	Type
56	BA	1025	A
56	BA	1026	A
56	BA	1027	G
56	BA	1028	A
56	BA	1038	A
56	BA	1041	A
56	BA	1045	U
56	BA	1050	C
56	BA	1055	A
56	BA	1056	G
56	BA	1057	A
56	BA	1063	U
56	BA	1064	G
56	BA	1071	U
56	BA	1072	A
56	BA	1074	U
56	BA	1075	U
56	BA	1081	U
56	BA	1089	G
56	BA	1091	U
56	BA	1092	A
56	BA	1093	A
56	BA	1127	A
56	BA	1129	C
56	BA	1138	G
56	BA	1140	A
56	BA	1146	G
56	BA	1167	C
56	BA	1168	A
56	BA	1169	A
56	BA	1180	G
56	BA	1183	U
56	BA	1194	U
56	BA	1195	A
56	BA	1204	A
56	BA	1206	U
56	BA	1207	C
56	BA	1217	A
56	BA	1218	U
56	BA	1219	A
56	BA	1220	A
56	BA	1221	C

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Mol	Chain	Res	Type
56	BA	1222	A
56	BA	1226	C
56	BA	1231	U
56	BA	1233	A
56	BA	1237	A
56	BA	1238	A
56	BA	1239	A
56	BA	1240	A
56	BA	1241	U
56	BA	1242	U
56	BA	1246	A
56	BA	1247	U
56	BA	1249	A
56	BA	1252	G
56	BA	1253	G
56	BA	1254	A
56	BA	1258	A
56	BA	1264	C
56	BA	1270	G
56	BA	1271	A
56	BA	1287	G
56	BA	1288	U
56	BA	1291	U
56	BA	1294	A
56	BA	1298	C
56	BA	1299	C
56	BA	1314	U
56	BA	1321	C
56	BA	1323	U
56	BA	1325	G
56	BA	1326	A
56	BA	1328	G
56	BA	1332	G
56	BA	1336	A
56	BA	1341	A
56	BA	1342	C
56	BA	1352	G
56	BA	1357	C
56	BA	1358	G
56	BA	1385	U
56	BA	1386	U
56	BA	1387	A

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Mol	Chain	Res	Type
56	BA	1388	A
56	BA	1389	A
56	BA	1390	G
56	BA	1395	A
56	BA	1396	C
56	BA	1405	A
56	BA	1407	U
56	BA	1409	C
56	BA	1420	A
56	BA	1425	A
56	BA	1426	G
56	BA	1429	C
56	BA	1432	U
56	BA	1433	U
56	BA	1436	U
56	BA	1438	U
56	BA	1445	U
56	BA	1448	A
56	BA	1451	U
56	BA	1455	C
56	BA	1457	A
56	BA	1464	A
56	BA	1468	A
56	BA	1473	A
56	BA	1474	G
56	BA	1475	A
56	BA	1476	A
56	BA	1493	A
56	BA	1494	A
56	BA	1498	C
56	BA	1504	A
56	BA	1505	G
56	BA	1509	U
56	BA	1514	A
56	BA	1518	A
56	BA	1521	U
56	BA	1522	A
56	BA	1526	U
56	BA	1527	U
56	BA	1528	A
56	BA	1529	A
56	BA	1531	C

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Mol	Chain	Res	Type
56	BA	1532	U
56	BA	1533	A
56	BA	1536	U
56	BA	1548	A
56	BA	1549	A
56	BA	1551	C
56	BA	1552	C
56	BA	1553	A
56	BA	1558	U
56	BA	1559	A
56	BA	1569	A
56	BA	1571	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	AA	535	U
52	AA	824	G
52	AA	918	A
56	BA	48	U
56	BA	1241	U

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 338 ligands modelled in this entry, 333 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
91	SPM	BA	1793	-	13,13,13	0.35	0	12,12,12	0.77	0
91	SPM	BA	1794	-	13,13,13	0.34	0	12,12,12	0.79	0
91	SPM	AA	3001	-	13,13,13	0.34	0	12,12,12	0.79	0
92	5GP	BA	1792	89	26,26,26	0.99	2 (7%)	40,40,40	1.67	8 (20%)
93	GTP	Ag	500	89	30,34,34	0.82	1 (3%)	46,54,54	1.79	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
91	SPM	BA	1793	-	-	2/11/11/11	-
91	SPM	BA	1794	-	-	3/11/11/11	-
91	SPM	AA	3001	-	-	2/11/11/11	-
92	5GP	BA	1792	89	-	0/10/26/26	0/3/3/3
93	GTP	Ag	500	89	-	3/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	BA	1792	5GP	C6-N1	-2.53	1.34	1.38
93	Ag	500	GTP	C2-N3	2.20	1.38	1.33
92	BA	1792	5GP	C5-N7	-2.04	1.35	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	BA	1792	5GP	C5-C4-N3	-5.59	119.40	128.46
93	Ag	500	GTP	C5-C4-N3	-5.33	119.82	128.46
93	Ag	500	GTP	C2-N3-C4	4.70	120.68	112.30
92	BA	1792	5GP	C2-N3-C4	4.26	119.88	112.30
93	Ag	500	GTP	PA-O3A-PB	-3.92	119.36	132.83
93	Ag	500	GTP	N9-C4-N3	3.48	132.93	125.94
92	BA	1792	5GP	N9-C4-N3	3.45	132.88	125.94
93	Ag	500	GTP	PB-O3B-PG	-3.36	121.31	132.83
93	Ag	500	GTP	C2-N1-C6	-2.95	119.72	125.10
93	Ag	500	GTP	C5-C6-N1	2.57	119.72	113.19
92	BA	1792	5GP	C5-C6-N1	2.44	119.38	113.19
93	Ag	500	GTP	C8-N7-C5	2.42	108.63	104.24
93	Ag	500	GTP	O6-C6-C5	-2.41	120.20	126.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
93	Ag	500	GTP	N9-C8-N7	-2.39	108.89	113.39
92	BA	1792	5GP	O6-C6-C5	-2.37	120.32	126.60
93	Ag	500	GTP	C3'-C2'-C1'	2.34	105.86	101.43
92	BA	1792	5GP	C2-N1-C6	-2.32	120.86	125.10
92	BA	1792	5GP	N9-C8-N7	-2.26	109.14	113.39
92	BA	1792	5GP	C4-C5-N7	-2.06	107.46	110.72

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
91	BA	1794	SPM	N5-C6-C7-C8
91	AA	3001	SPM	C8-C9-N10-C11
91	BA	1794	SPM	C8-C9-N10-C11
91	BA	1793	SPM	C6-C7-C8-C9
91	BA	1794	SPM	C6-C7-C8-C9
91	BA	1793	SPM	C7-C8-C9-N10
91	AA	3001	SPM	C6-C7-C8-C9
93	Ag	500	GTP	C4'-C5'-O5'-PA
93	Ag	500	GTP	O4'-C4'-C5'-O5'
93	Ag	500	GTP	C3'-C4'-C5'-O5'

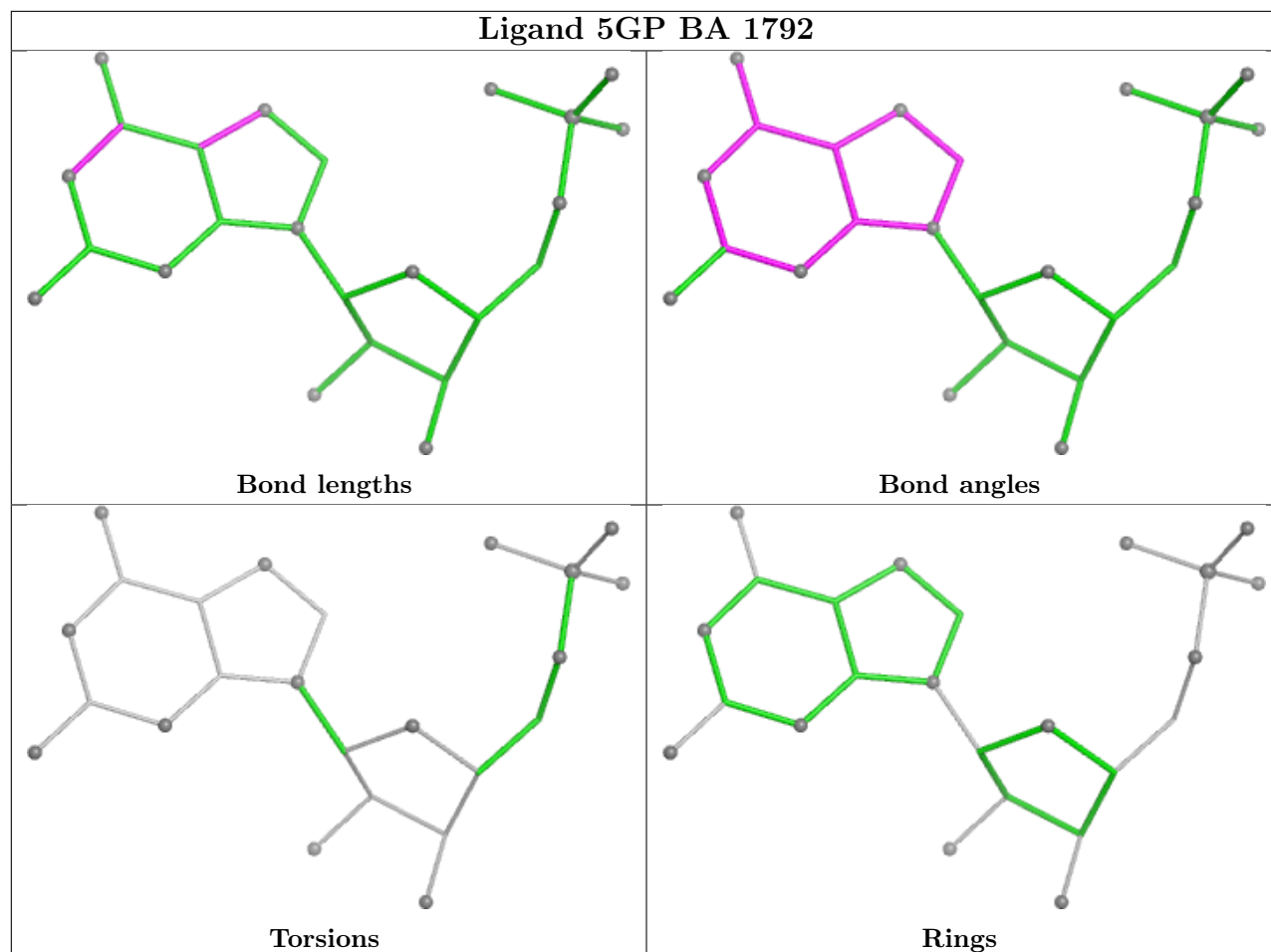
There are no ring outliers.

3 monomers are involved in 8 short contacts:

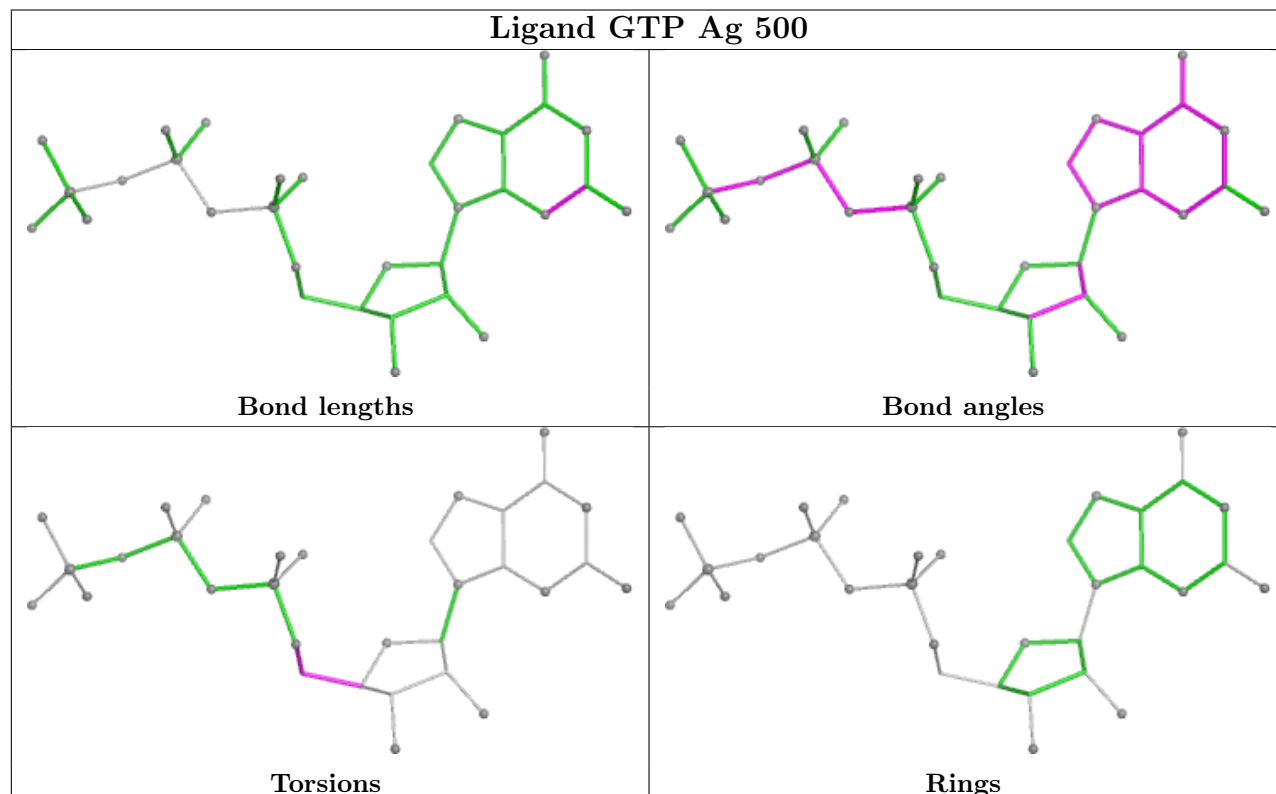
Mol	Chain	Res	Type	Clashes	Symm-Clashes
91	BA	1793	SPM	4	0
91	BA	1794	SPM	1	0
93	Ag	500	GTP	3	0

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

Ligand 5GP BA 1792



Ligand GTP Ag 500



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
86	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	7.63

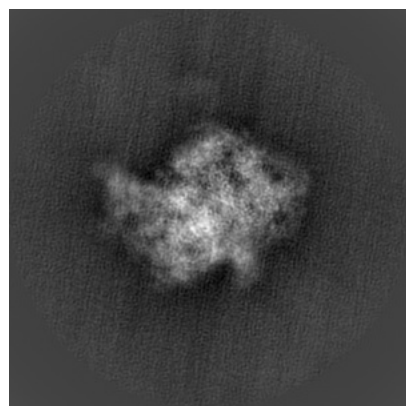
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12568. These allow visual inspection of the internal detail of the map and identification of artifacts.

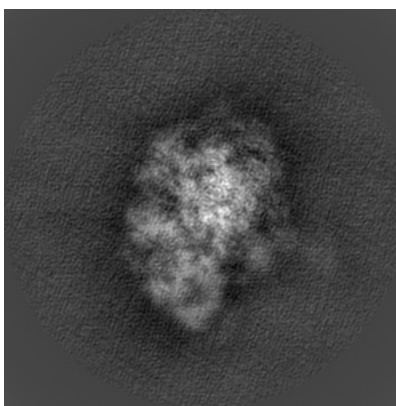
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

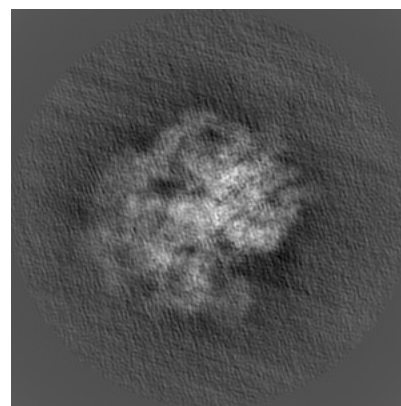
6.1.1 Primary map



X

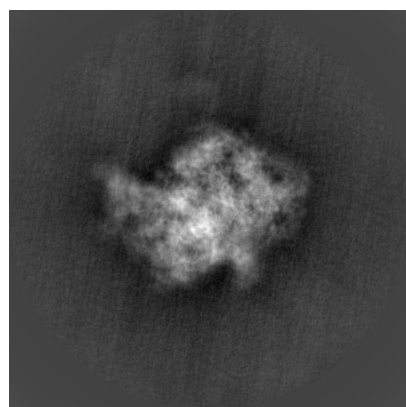


Y

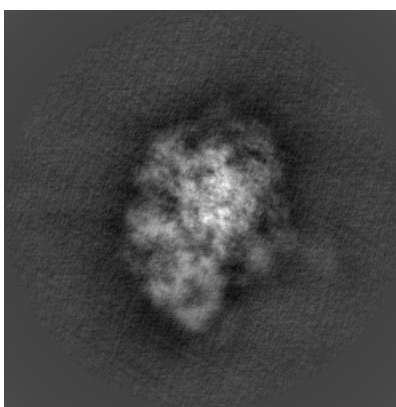


Z

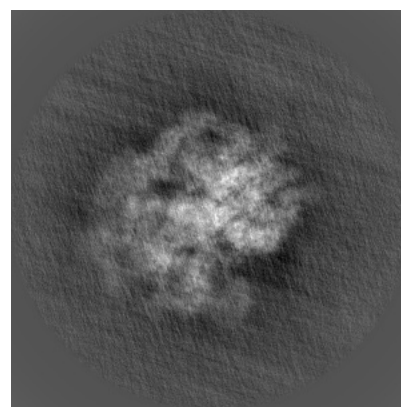
6.1.2 Raw map



X



Y

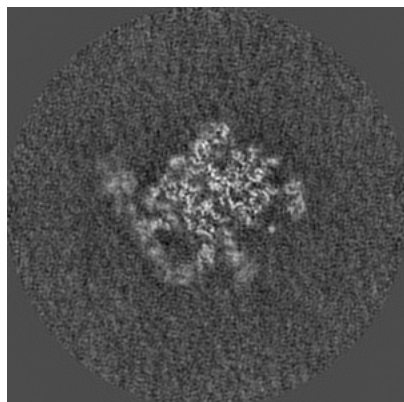


Z

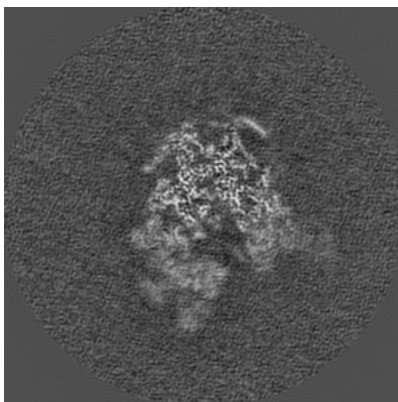
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

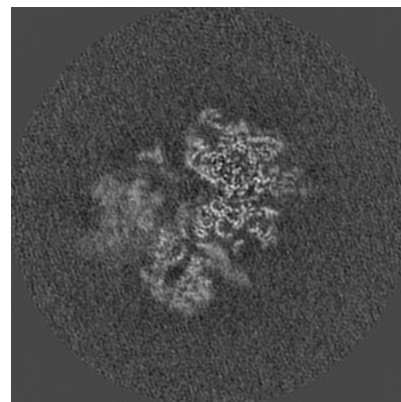
6.2.1 Primary map



X Index: 240

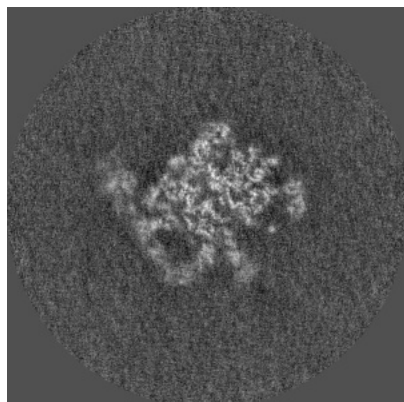


Y Index: 240

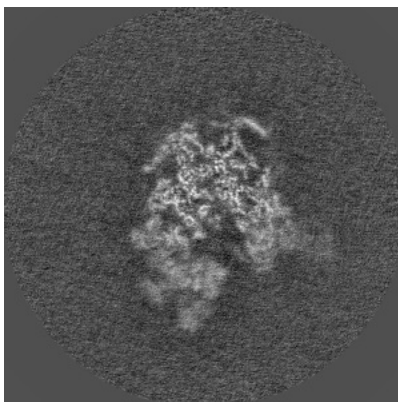


Z Index: 240

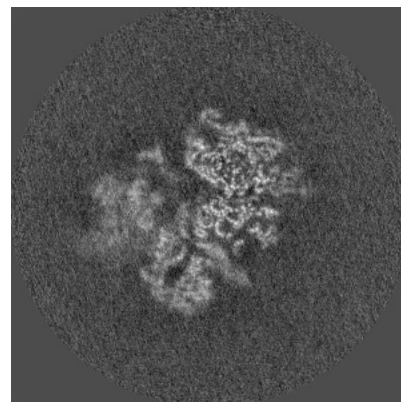
6.2.2 Raw map



X Index: 240



Y Index: 240

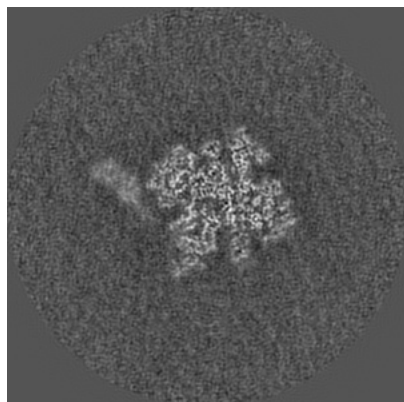


Z Index: 240

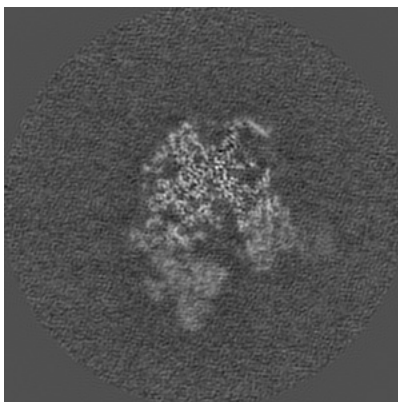
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

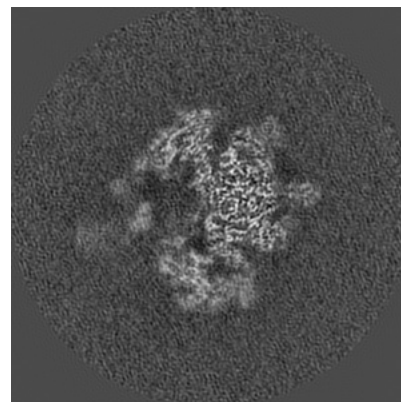
6.3.1 Primary map



X Index: 268

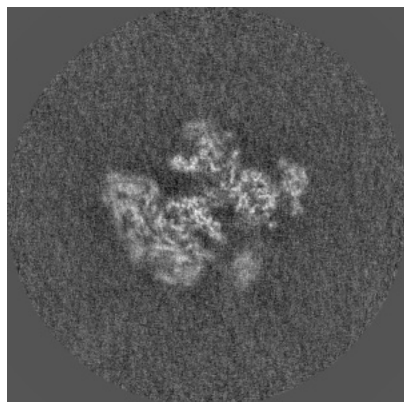


Y Index: 238

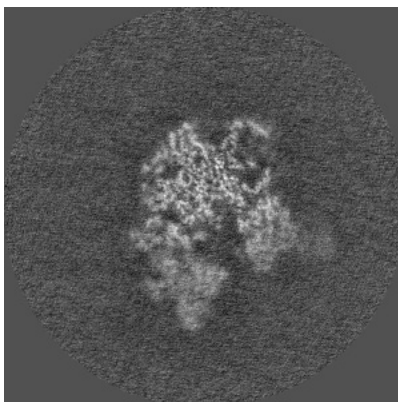


Z Index: 262

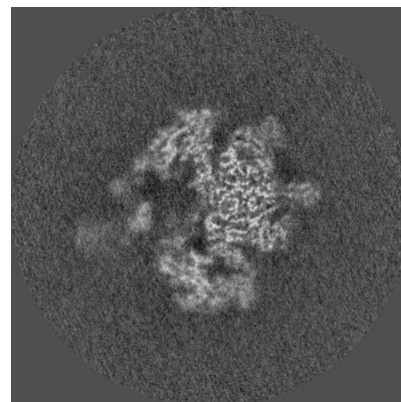
6.3.2 Raw map



X Index: 228



Y Index: 237

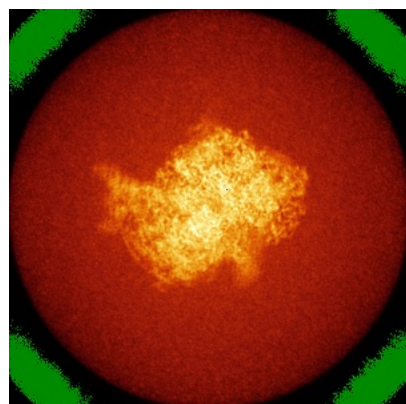


Z Index: 262

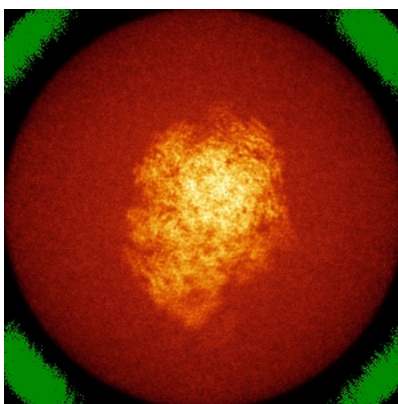
The images above show the largest variance slices of the map in three orthogonal directions.

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

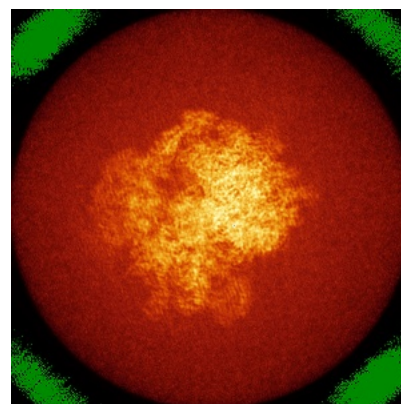
6.4.1 Primary map



X

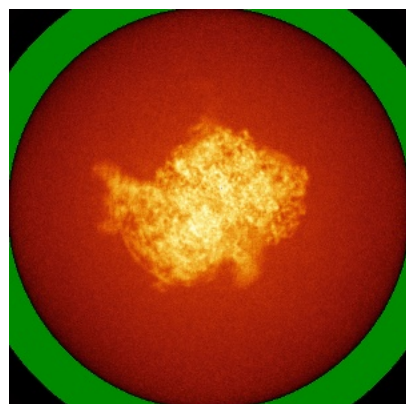


Y

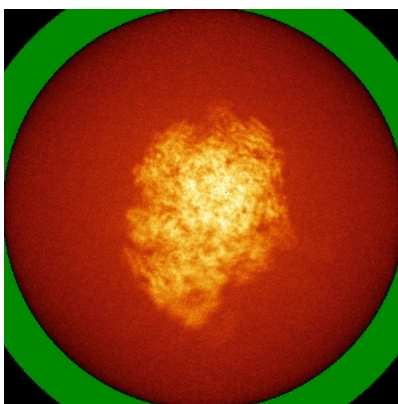


Z

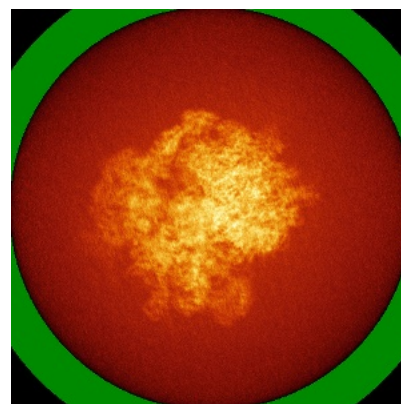
6.4.2 Raw map



X



Y

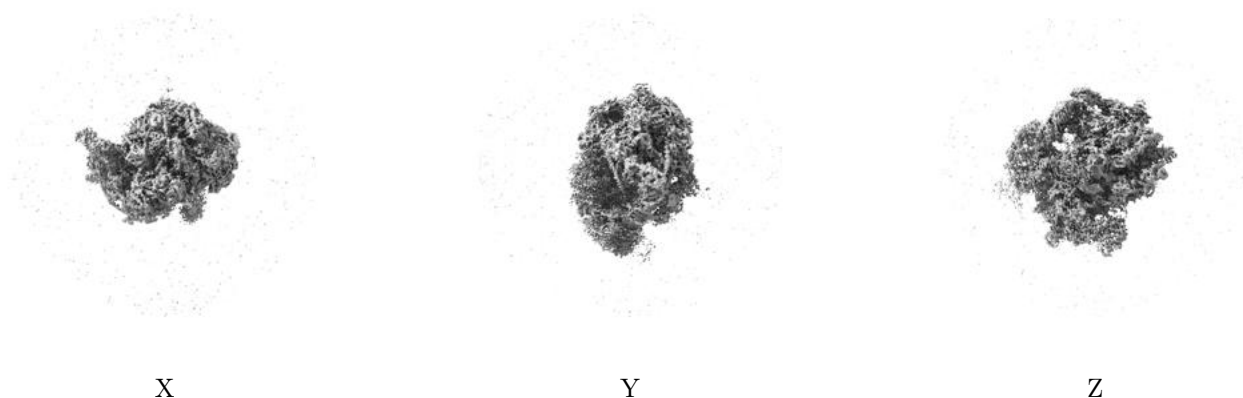


Z

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.

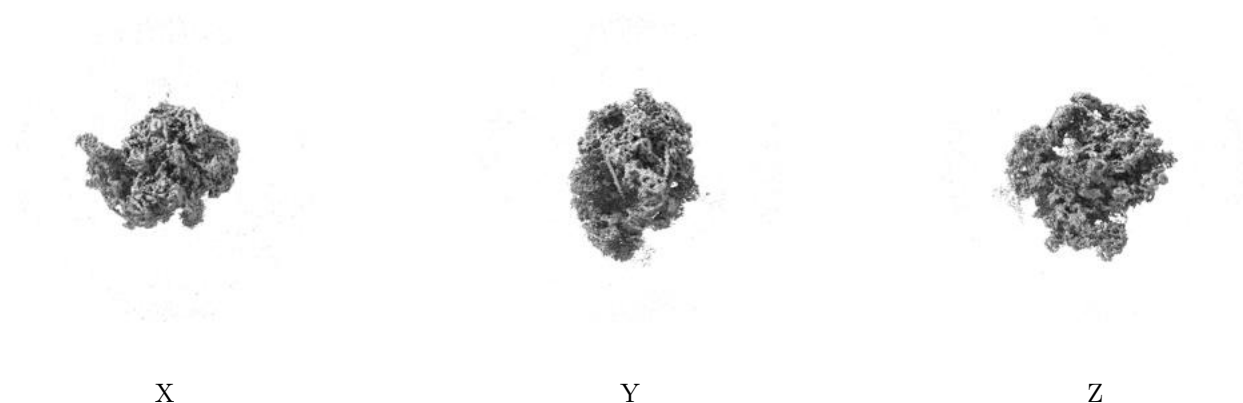
6.5 Orthogonal surface views [i](#)

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.

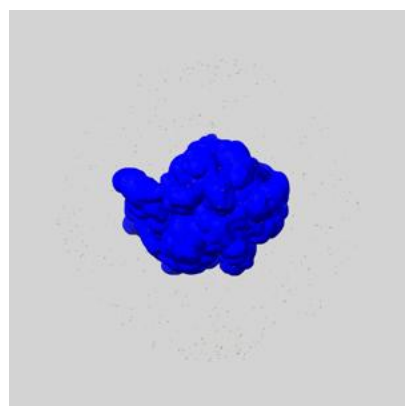
6.6 Mask visualisation [i](#)

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

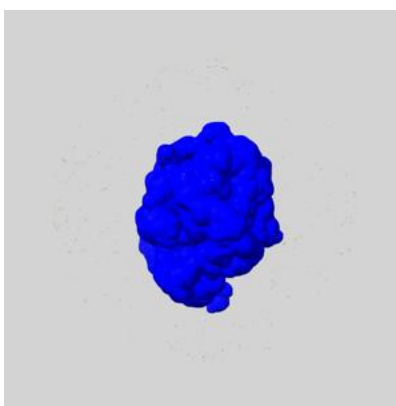
A mask typically either:

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

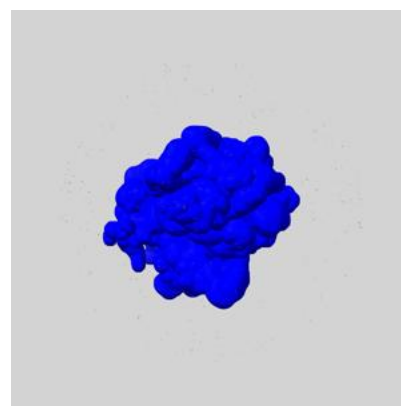
6.6.1 emd_12568_msk_1.map [i](#)



X



Y

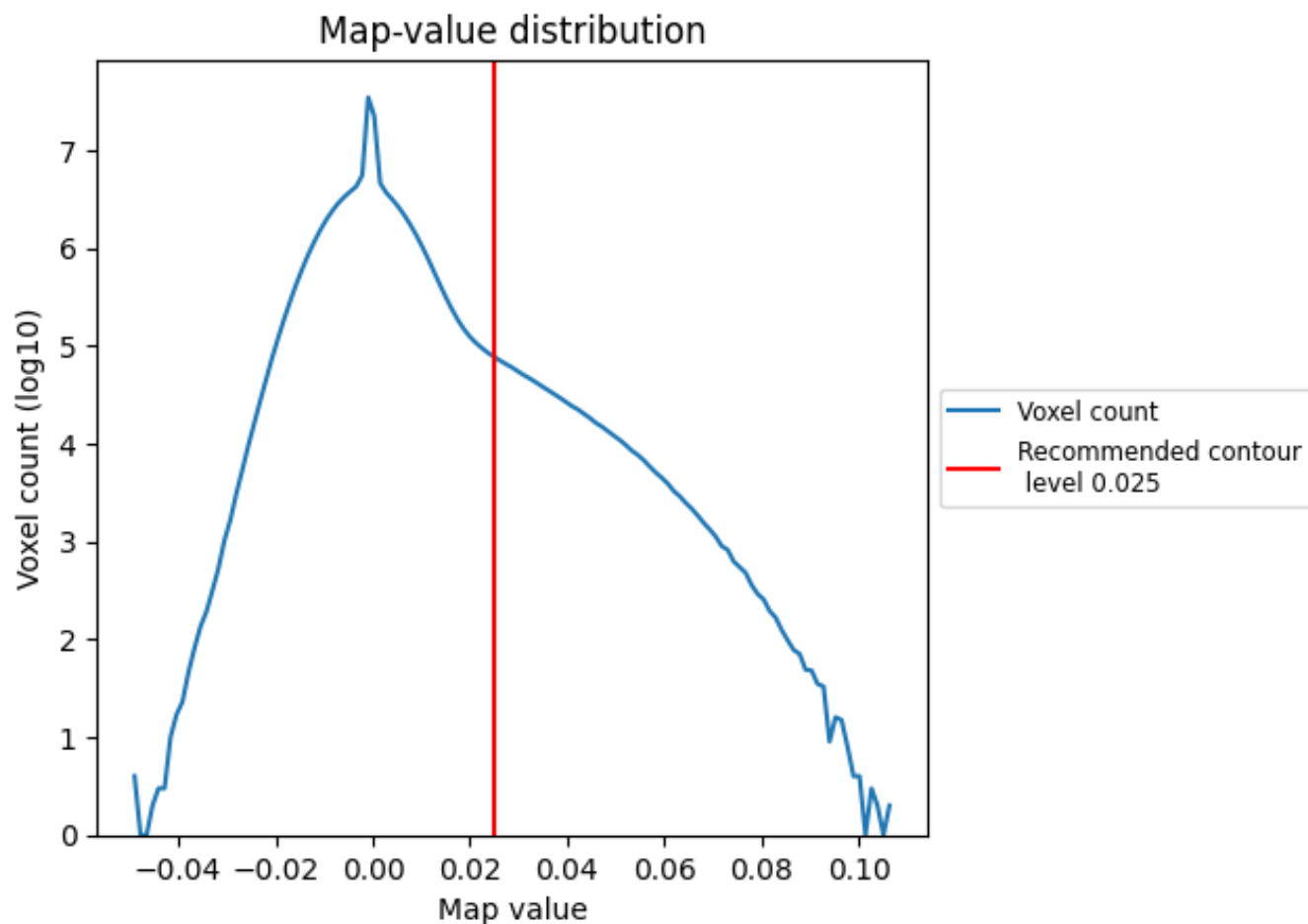


Z

7 Map analysis [i](#)

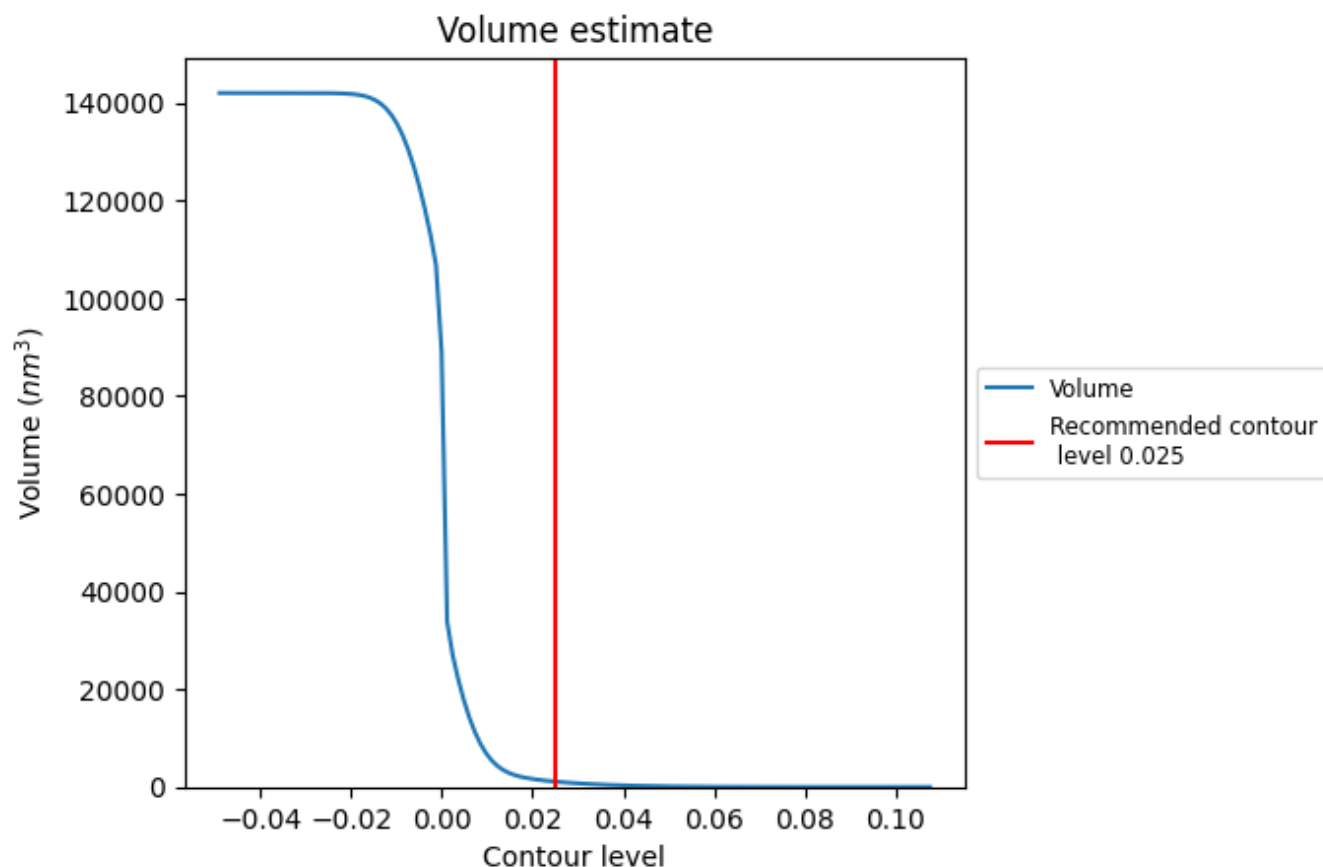
This section contains the results of statistical analysis of the map.

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.

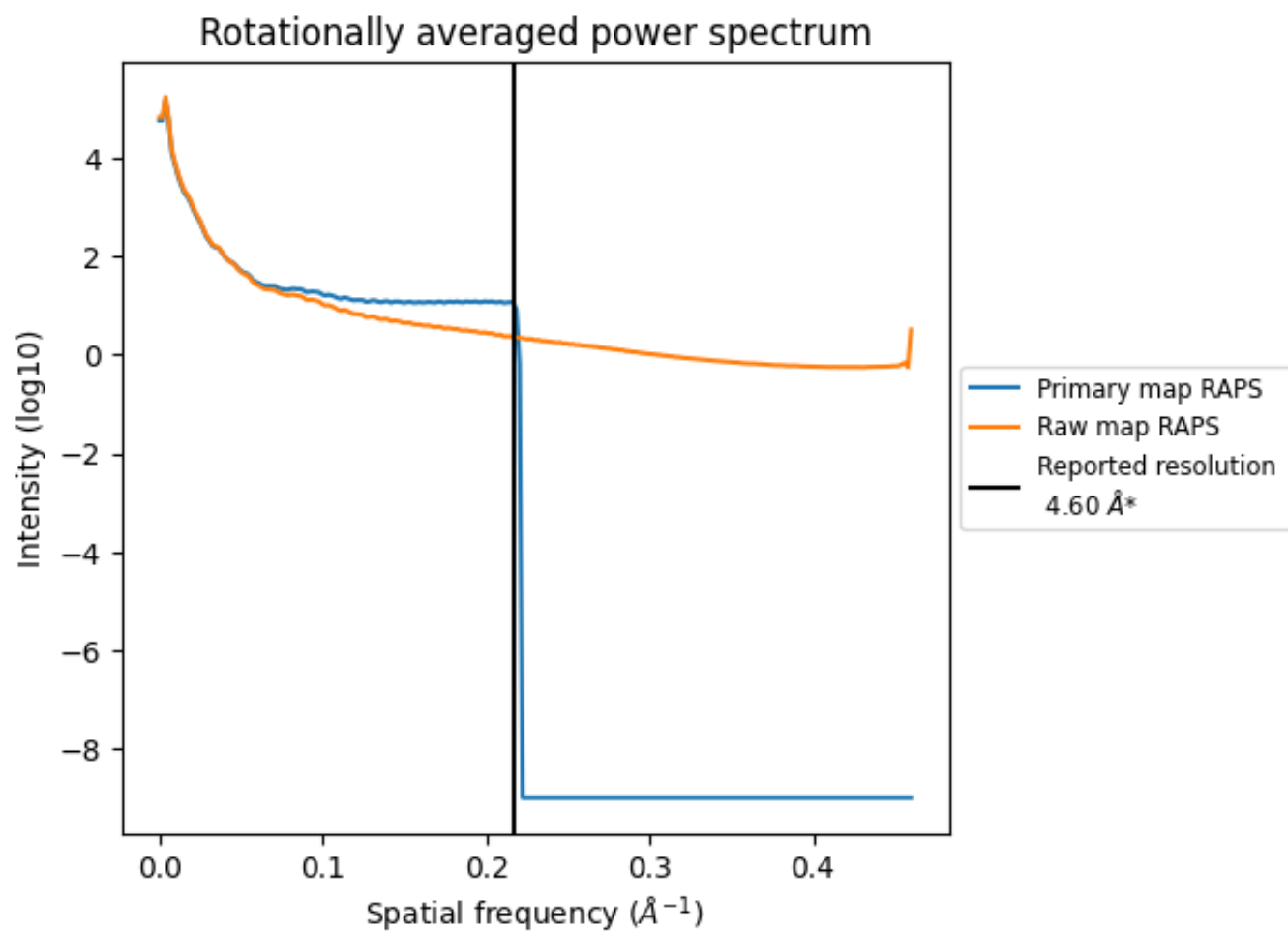
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1096 nm³; this corresponds to an approximate mass of 990 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 ⓘ

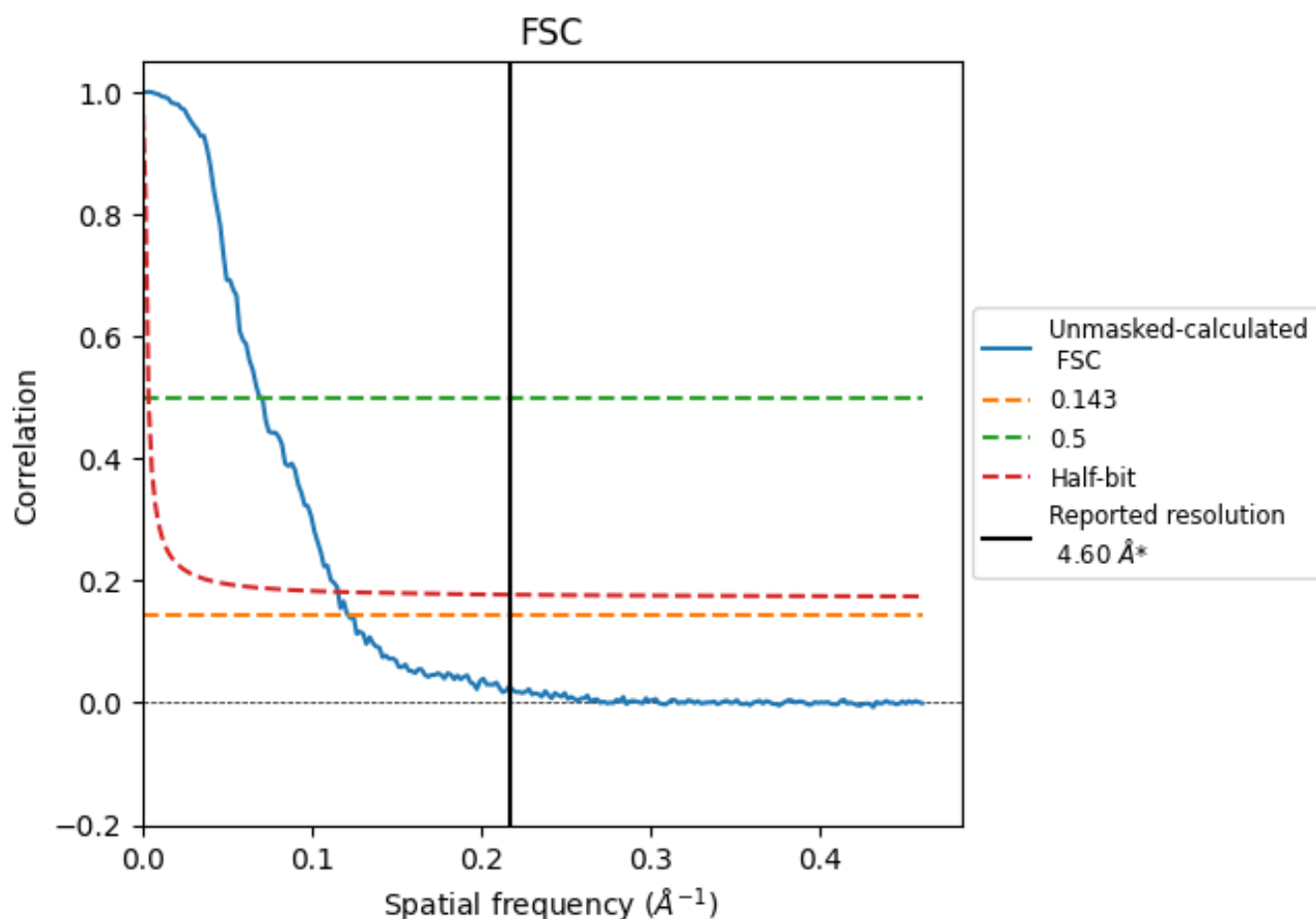


*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

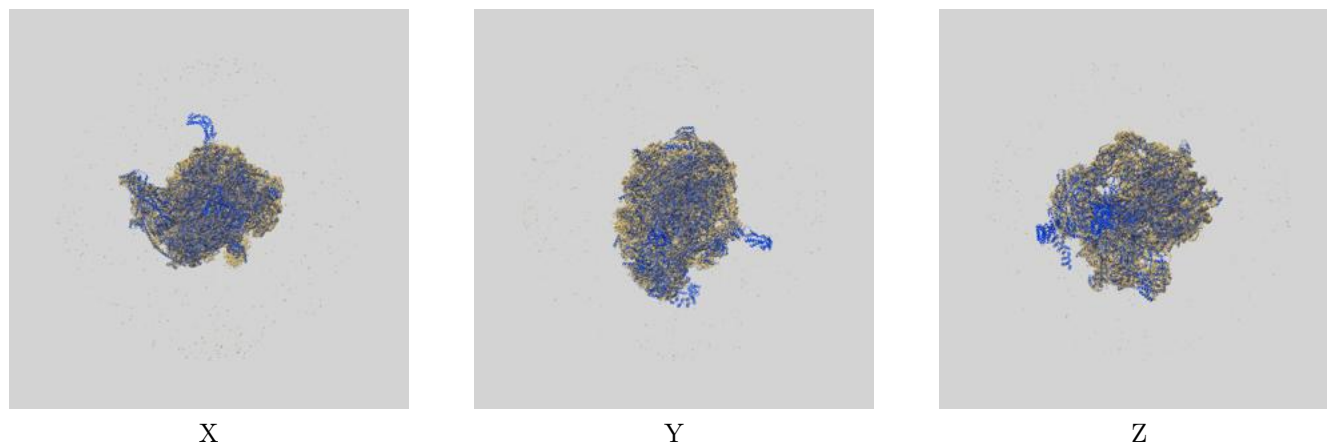
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.23	14.27	8.67

*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 8.23 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

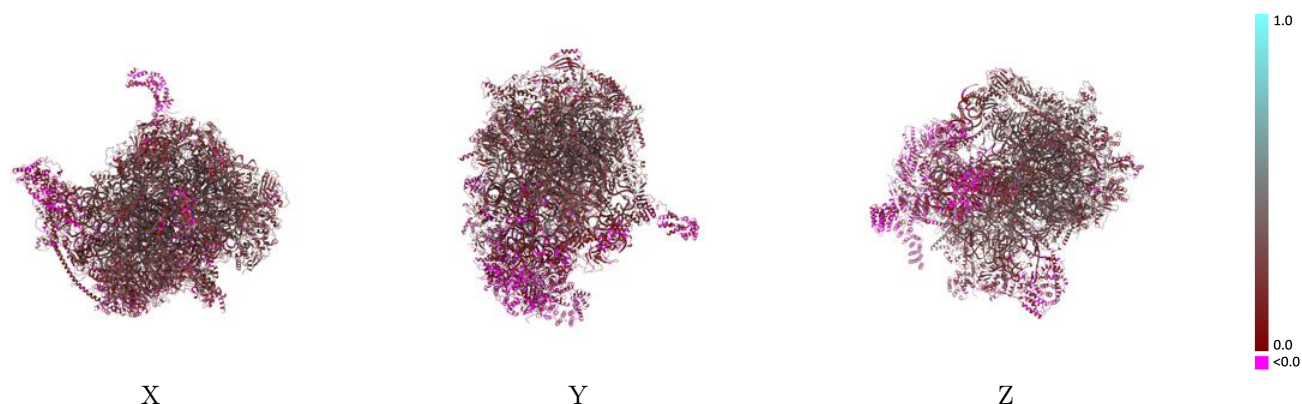
This section contains information regarding the fit between EMDB map EMD-12568 and PDB model 7NSI. Per-residue inclusion information can be found in section 3 on page 25.

9.1 Map-model overlay [i](#)



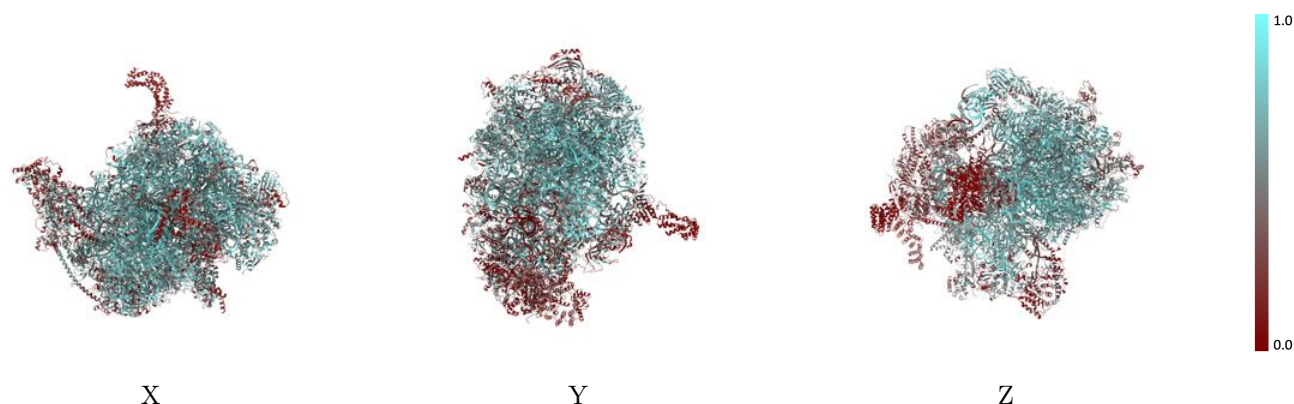
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



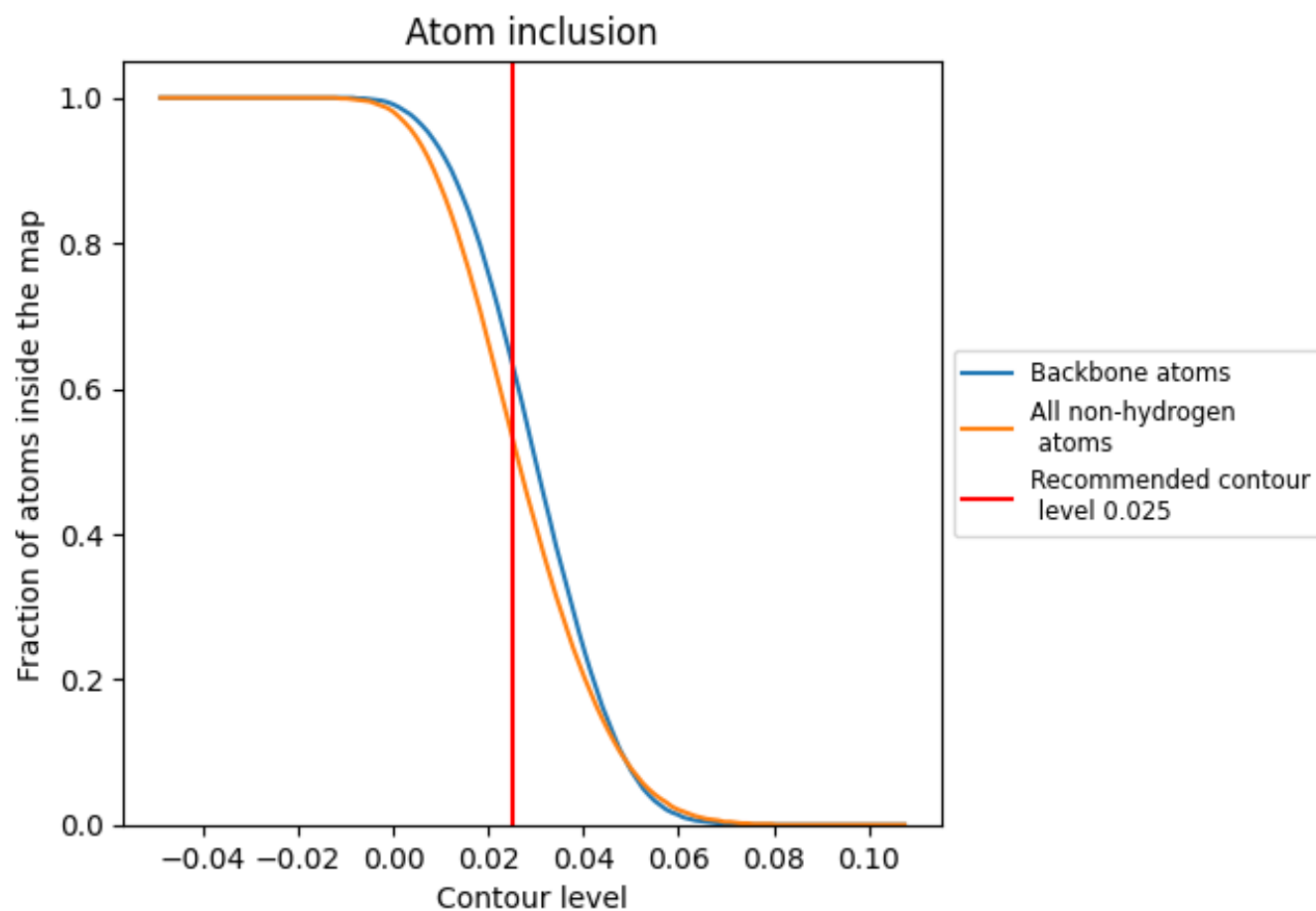
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 64% of all backbone atoms, 53% 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	 0.5340	 0.2280
AA	 0.6890	 0.2170
AB	 0.5250	 0.2150
AC	 0.1830	 0.0880
AE	 0.3340	 0.1870
AF	 0.3370	 0.1520
AG	 0.1940	 0.0770
AI	 0.3060	 0.1310
AJ	 0.1530	 0.0960
AK	 0.3260	 0.1580
AL	 0.5040	 0.2670
AN	 0.2900	 0.0890
AO	 0.3610	 0.1490
AP	 0.3990	 0.1650
AQ	 0.5060	 0.2070
AR	 0.4070	 0.1650
AU	 0.4600	 0.2290
AV	 0.0510	 0.0580
AX	 0.2570	 0.1710
AZ	 0.2000	 0.0460
Aa	 0.3470	 0.1680
Ab	 0.4290	 0.1700
Ac	 0.4960	 0.2360
Ad	 0.4520	 0.1500
Ae	 0.2290	 0.0670
Af	 0.3910	 0.1710
Ag	 0.2110	 0.0390
Ah	 0.1470	 0.0680
Ai	 0.1950	 0.0780
Aj	 0.2810	 0.1280
Ak	 0.1720	 0.0830
Am	 0.2310	 0.1380
An	 0.4160	 0.2230
Ao	 0.0280	 0.0320
Ap	 0.4140	 0.1650



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Chain	Atom inclusion	Q-score
B0	 0.6790	 0.3260
B1	 0.5260	 0.2690
B2	 0.6330	 0.2840
B3	 0.6340	 0.3080
B4	 0.3490	 0.1400
B5	 0.6050	 0.3010
B6	 0.4420	 0.2420
B7	 0.6400	 0.3080
B8	 0.6200	 0.3330
B9	 0.6600	 0.2820
BA	 0.8150	 0.3280
BB	 0.6640	 0.1730
BD	 0.6250	 0.2940
BE	 0.6580	 0.3080
BF	 0.6030	 0.3000
BG	 0.1480	 0.2050
BI	 0.4650	 0.2480
BJ	 0.2340	 0.1720
BK	 0.1280	 0.1290
BN	 0.6510	 0.3100
BO	 0.6160	 0.3250
BP	 0.6080	 0.3050
BQ	 0.6150	 0.3010
BR	 0.6370	 0.3100
BS	 0.6540	 0.2770
BT	 0.5810	 0.2740
BU	 0.6340	 0.2990
BV	 0.6290	 0.3150
BW	 0.5910	 0.3220
BX	 0.5570	 0.2900
BY	 0.3040	 0.2500
Ba	 0.6320	 0.2600
Bb	 0.6530	 0.2620
Bc	 0.5880	 0.2640
Bd	 0.3450	 0.1410
Be	 0.4980	 0.2550
Bf	 0.5560	 0.2740
Bg	 0.6360	 0.3140
Bh	 0.6060	 0.2640
Bi	 0.2920	 0.1930
Bj	 0.3550	 0.1100
Bk	 0.3360	 0.1580

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Chain	Atom inclusion	Q-score
Bl	 0.6260	 0.2970
Bm	 0.2140	 0.2230
Bn	 0.6030	 0.3070
Bo	 0.6470	 0.2850
Bp	 0.2740	 0.1740
Bq	 0.2070	 0.1870
Bt	 0.6710	 0.3010
Bu	 0.4750	 0.2240
Bv	 0.5020	 0.2260
Bw	 0.6090	 0.2730
Bx	 0.6020	 0.2640
CL	 0.0220	 0.1070
DL	 0.0050	 0.0340
EL	 0.0000	 -0.0180
FL	 0.0000	 -0.0030
GL	 0.0000	 0.0180
HL	 0.0000	 -0.0550