



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 06:09 PM UTC

PDB ID : 7L08 / pdb_00007l08
EMDB ID : EMD-23096
Title : Cryo-EM structure of the human 55S mitoribosome-RRFmt complex.
Authors : Koripella, R.; Agrawal, E.K.; Deep, A.; Agrawal, R.K.
Deposited on : 2020-12-11
Resolution : 3.49 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

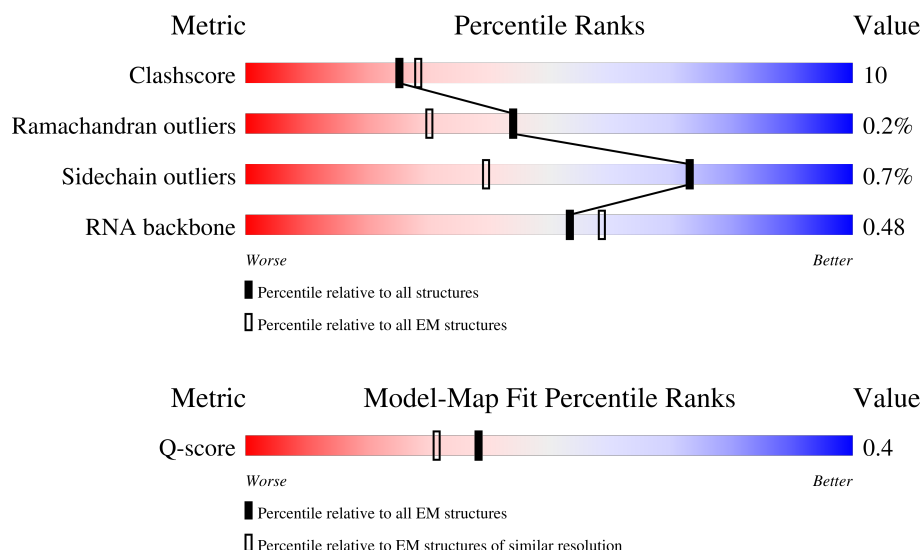
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.49 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.



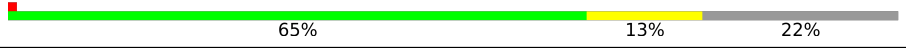
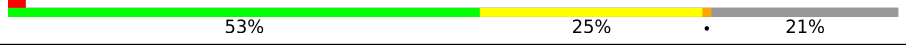
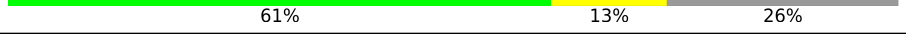
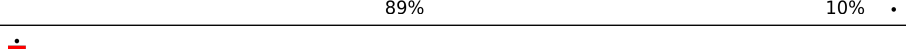
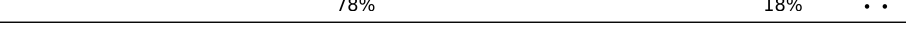
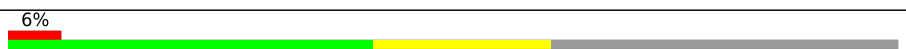
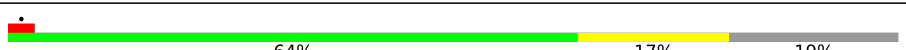
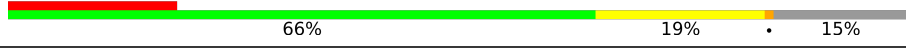
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13600 (2.99 - 3.99)

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

Mol	Chain	Length	Quality of chain
1	AA	954	
2	AB	296	
3	AC	167	

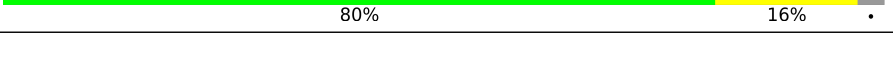
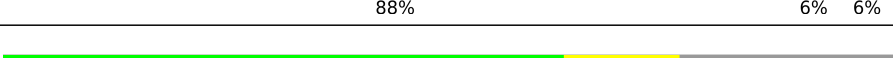
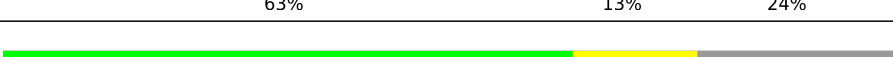
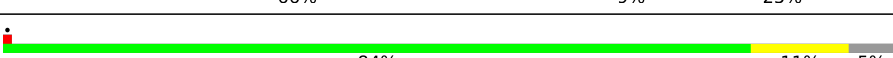
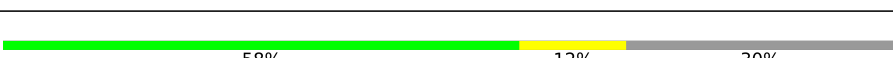
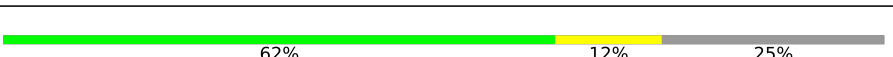
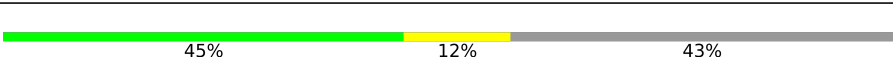
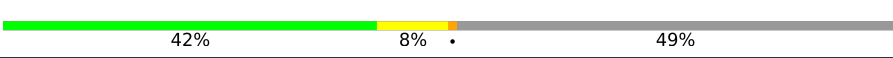
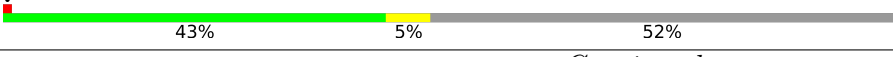
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Mol	Chain	Length	Quality of chain
4	AE	125	
5	AI	194	
6	AJ	138	
7	AK	128	
8	AM	137	
9	AN	130	
10	AO	258	
11	AP	142	
12	AQ	87	
13	AT	173	
14	AW	187	
15	AX	398	
16	A2	118	
17	AH	201	
18	AL	257	
19	AR	360	
20	AS	190	
21	AU	205	
22	AV	414	
23	AY	395	
24	AZ	106	
25	A1	323	
26	A0	218	
27	A3	199	
28	A4	689	

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Mol	Chain	Length	Quality of chain
29	AD	430	
30	AF	242	
31	AG	396	
32	A	1559	
33	B	73	
34	D	305	
35	F	311	
36	H	267	
37	K	178	
38	L	145	
39	M	296	
40	O	175	
41	R	149	
42	S	205	
43	T	212	
44	W	148	
45	X	256	
46	Y	250	
47	Z	161	
48	0	188	
49	1	65	
50	2	92	
51	3	188	
52	4	103	
53	8	206	

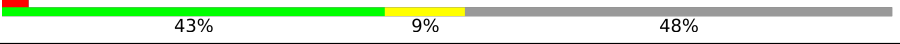
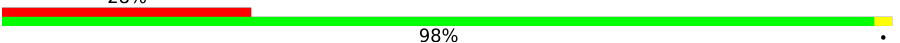
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Mol	Chain	Length	Quality of chain
54	b	155	
55	e	279	
56	g	166	
57	i	128	
58	j	123	
59	m	128	
60	o	102	
61	q	222	
62	r	196	
63	J	192	
64	I	261	
65	N	251	
66	P	179	
67	U	153	
68	V	216	
69	E	348	
70	5	423	
71	6	380	
72	7	338	
73	9	137	
74	a	142	
75	c	332	
76	d	306	
77	f	194	
78	h	158	

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Mol	Chain	Length	Quality of chain
79	k	112	
80	l	138	
81	p	206	
82	s	439	
83	Q	292	
84	u	65	
85	TA	198	
85	TB	198	
86	z	204	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 168922 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 RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	944	Total	C	N	O	P	0	0
			20030	8980	3612	6494	944		

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	220	Total	C	N	O	S	0	0
			1787	1141	324	312	10		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	132	Total	C	N	O	S	0	0
			1082	699	195	184	4		

- Molecule 4 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AE	122	Total	C	N	O	S	0	0
			972	614	177	177	4		

- Molecule 5 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AI	136	Total	C	N	O	S	0	0
			1011	637	192	178	4		

- Molecule 6 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AJ	108	Total	C	N	O	S	0	0
			838	521	169	142	6		

- Molecule 7 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AK	101	Total	C	N	O	S	0	0
			861	537	179	140	5		

- Molecule 8 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AM	116	Total	C	N	O	S	0	0
			920	582	182	150	6		

- Molecule 9 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AN	107	Total	C	N	O	S	0	0
			846	549	153	141	3		

- Molecule 10 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AO	190	Total	C	N	O	S	0	0
			1570	998	291	274	7		

- Molecule 11 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AP	96	Total	C	N	O	S	0	0
			774	498	133	135	8		

- Molecule 12 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AQ	86	Total	C	N	O	S	0	0
			740	458	150	124	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	50	ARG	CYS	variant	UNP P82921

- Molecule 13 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AT	168	Total	C	N	O	S	0	0
			1371	877	239	244	11		

- Molecule 14 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AW	97	Total	C	N	O	S	0	0
			766	486	137	139	4		

- Molecule 15 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AX	353	Total	C	N	O	S	0	0
			2860	1828	503	518	11		

- Molecule 16 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A2	116	Total	C	N	O	S	0	0
			925	574	181	162	8		

- Molecule 17 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AH	122	Total	C	N	O	S	0	0
			1014	656	172	183	3		

- Molecule 18 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AL	174	Total	C	N	O	S	0	0
			1451	924	271	249	7		

- Molecule 19 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AR	292	Total	C	N	O	S	0	0
			2388	1521	410	449	8		

- Molecule 20 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AS	135	Total	C	N	O	S	0	0
			1111	716	198	196	1		

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	177	Total	C	N	O	S	0	0
			1499	922	305	268	4		

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	367	Total	C	N	O	S	0	0
			3009	1931	502	564	12		

- Molecule 23 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AY	120	Total	C	N	O	S	0	0
			1016	657	167	190	2		

- Molecule 24 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AZ	99	Total	C	N	O	S	0	0
			833	531	152	146	4		

- Molecule 25 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A1	275	Total	C	N	O	S	0	0
			2231	1414	380	426	11		

- Molecule 26 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A0	214	Total	C	N	O	S	0	0
			1781	1125	341	310	5		

- Molecule 27 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A3	72	Total	C	N	O	S	0	0
			639	409	137	92	1		

- Molecule 28 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A4	549	Total	C	N	O	S	0	0
			3010	1841	573	593	3		

- Molecule 29 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AD	343	Total	C	N	O	S	0	0
			2731	1713	518	487	13		

- Molecule 30 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	208	Total	C	N	O	S	0	0
			1724	1103	312	298	11		

- Molecule 31 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AG	315	Total	C	N	O	S	0	0
			2587	1640	462	471	14		

- Molecule 32 is a RNA chain called 16S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A	1527	Total	C	N	O	P	0	0
			32395	14536	5844	10488	1527		

- Molecule 33 is a RNA chain called tRNAVAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1601	C	-	insertion	GB 1896813692

- Molecule 34 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	D	239	Total	C	N	O	S	0	0
			1866	1162	377	318	9		

- Molecule 35 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 36 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	H	98	Total	C	N	O	S	0	0
			806	510	156	140			

- Molecule 37 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 38 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 40 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 41 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 42 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 43 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 44 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	W	111	Total	C	N	O	S	0	0
			871	558	164	146	3		

- Molecule 45 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	X	243	Total	C	N	O	S	0	0
			2027	1310	350	362	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	148	ALA	THR	variant	UNP Q13084
X	149	SER	PRO	variant	UNP Q13084
X	150	GLY	LYS	variant	UNP Q13084

- Molecule 46 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 47 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 48 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 49 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 50 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 51 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 52 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 53 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 54 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 55 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 56 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	g	132	Total	C	N	O	S	0	0
			1096	709	191	194	2		

- Molecule 57 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 58 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	j	93	Total	C	N	O	S	0	0
			740	460	143	135	2		

- Molecule 59 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	m	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 60 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	o	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 61 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	q	168	Total	C	N	O	S	0	0
			1293	801	254	233	5		

- Molecule 62 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	r	162	Total	C	N	O	S	0	0
			1322	839	252	223	8		

- Molecule 63 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	J	175	Total	C	N	O	S	0	0
			1330	847	237	244	2		

- Molecule 64 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	I	179	Total	C	N	O	S	0	0
			1435	925	258	242	10		

- Molecule 65 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	N	222	Total	C	N	O	S	0	0
			1786	1143	326	307	10		

- Molecule 66 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	P	143	Total	C	N	O	S	0	0
			1165	729	223	208	5		

- Molecule 67 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	U	152	Total	C	N	O	S	0	0
			1222	773	233	213	3		

- Molecule 68 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	V	206	Total	C	N	O	S	0	0
			1682	1071	299	304	8		

- Molecule 69 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	E	306	Total	C	N	O	S	0	0
			2410	1547	419	433	11		

- Molecule 70 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	5	393	Total	C	N	O	S	0	0
			3205	2070	559	565	11		

- Molecule 71 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 72 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	7	297	Total	C	N	O	S	0	0
			2410	1540	409	443	18		

- Molecule 73 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 74 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	a	108	Total	C	N	O	S	0	0
			896	560	162	169	5		

- Molecule 75 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	c	289	Total	C	N	O	S	0	0
			2322	1483	400	430	9		

- Molecule 76 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	d	257	Total	C	N	O	S	0	0
			2075	1326	363	372	14		

- Molecule 77 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	f	146	Total	C	N	O	S	0	0
			1126	714	186	222	4		

- Molecule 78 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	h	110	Total	C	N	O	S	0	0
			894	568	156	167	3		

- Molecule 79 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	k	96	Total	C	N	O	S	0	0
			743	462	143	133	5		

- Molecule 80 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	l	72	Total	C	N	O	S	0	0
			619	394	112	111	2		

- Molecule 81 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	p	152	Total	C	N	O	S	0	0
			1227	762	232	229	4		

- Molecule 82 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	s	393	Total	C	N	O	S	0	0
			3178	2036	565	563	14		

- Molecule 83 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Q	227	Total	C	N	O	S	0	0
			1894	1211	338	336	9		

- Molecule 84 is a protein called P-site finger.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	u	65	Total	C	N	O	0	0
			325	195	65	65		

- Molecule 85 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	TA	45	Total	C	N	O	0	0
			345	222	54	69		
85	TB	27	Total	C	N	O	0	0
			213	137	33	43		

- Molecule 86 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	z	197	Total	C	N	O	S	0	0
			1525	942	274	301	8		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	AA	27	Total	Mg	0
			27	27	
87	AG	1	Total	Mg	0
			1	1	

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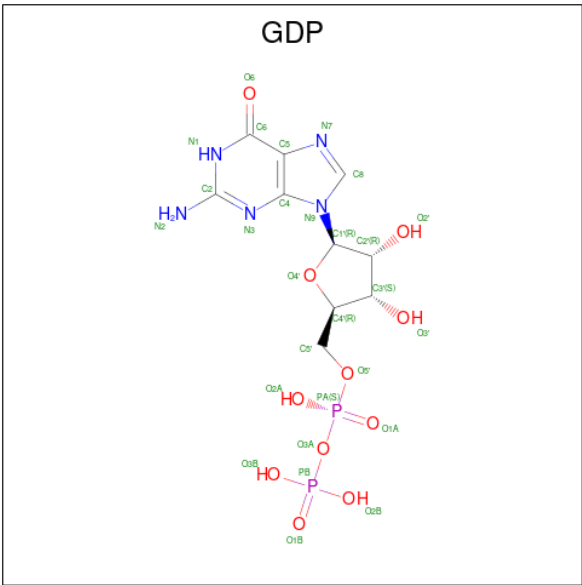
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Mol	Chain	Residues	Atoms		AltConf
87	A	94	Total 94	Mg 94	0
87	D	1	Total 1	Mg 1	0
87	M	1	Total 1	Mg 1	0
87	W	1	Total 1	Mg 1	0
87	g	1	Total 1	Mg 1	0
87	E	1	Total 1	Mg 1	0

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	AB	1	Total 1	Zn 1	0
88	AO	1	Total 1	Zn 1	0
88	AP	1	Total 1	Zn 1	0
88	AT	1	Total 1	Zn 1	0
88	0	1	Total 1	Zn 1	0
88	4	1	Total 1	Zn 1	0
88	r	1	Total 1	Zn 1	0

- Molecule 89 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

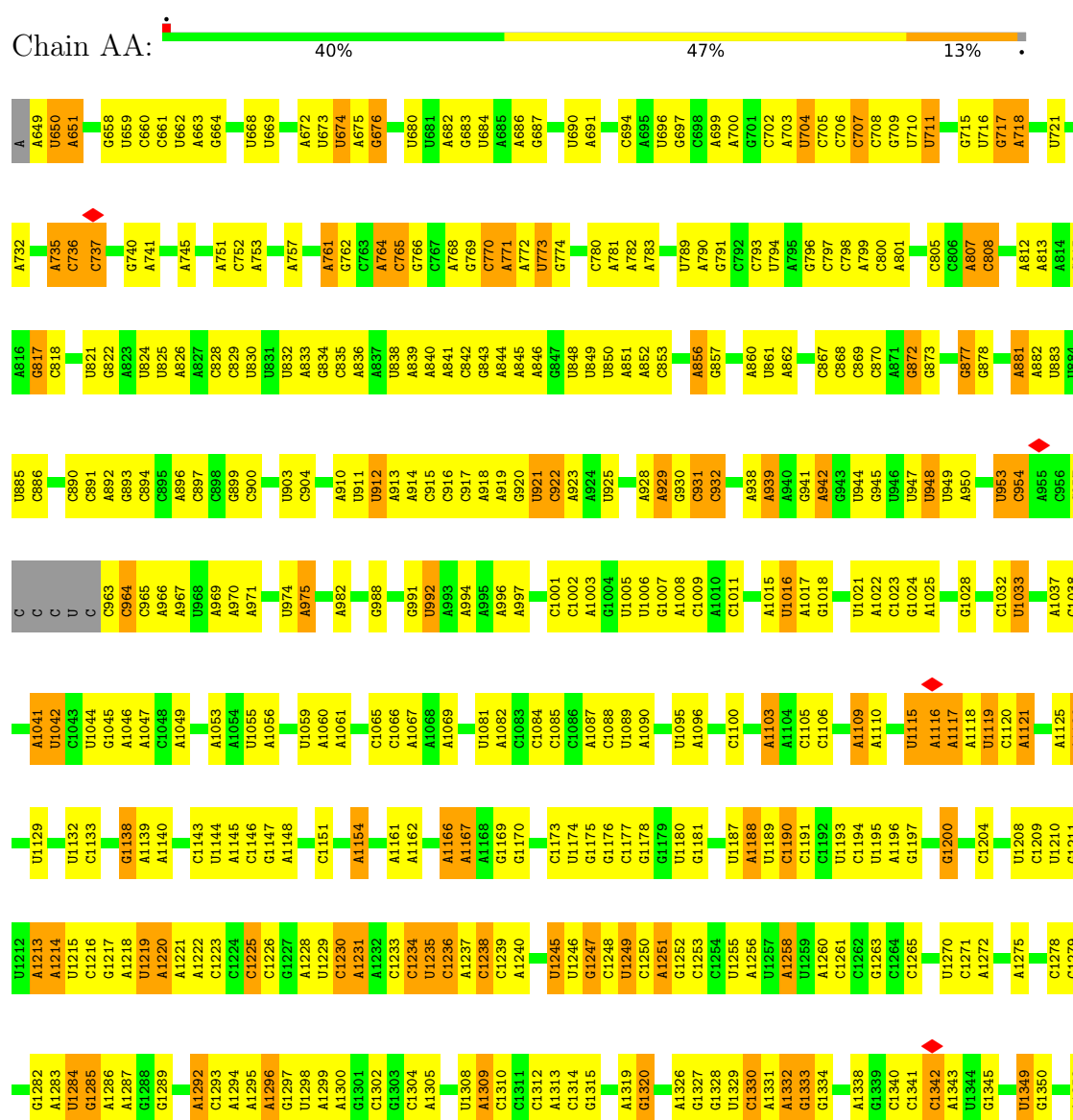


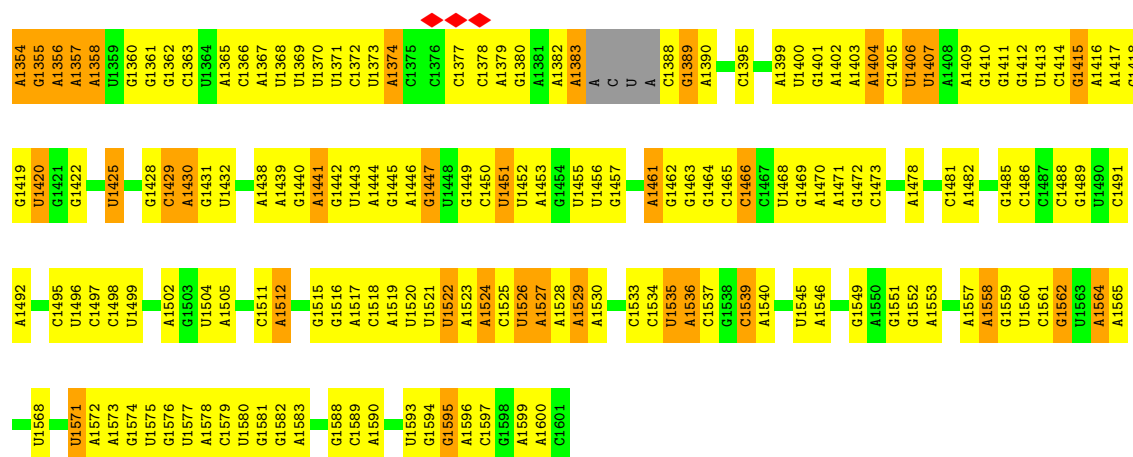
Mol	Chain	Residues	Atoms					AltConf
89	AX	1	Total	C	N	O	P	0
			28	10	5	11	2	

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.

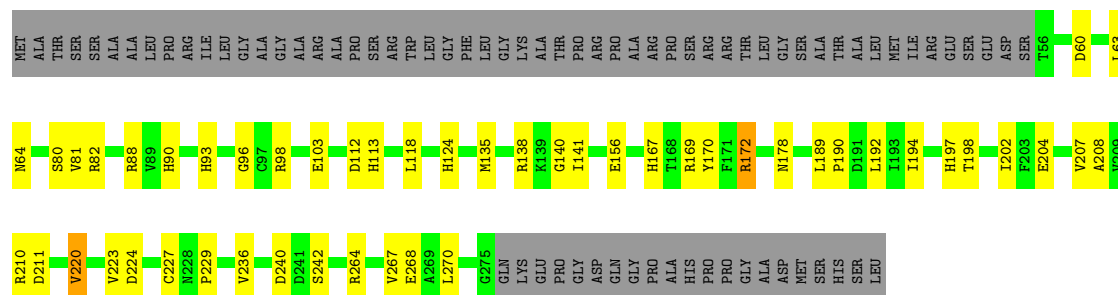
• Molecule 1: 12S rRNA





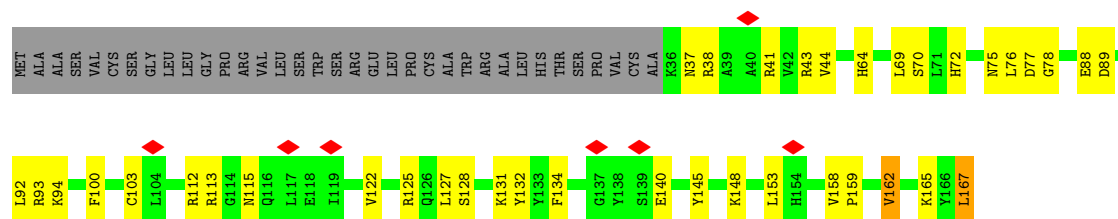
- Molecule 2: 28S ribosomal protein S2, mitochondrial

Chain AB: 57% 16% 26%



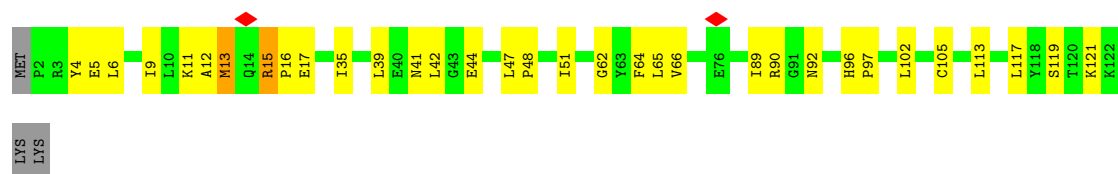
- Molecule 3: 28S ribosomal protein S24, mitochondrial

Chain AC: 56% 22% 21%



- Molecule 4: 28S ribosomal protein S6, mitochondrial

Chain AE: 70% 26%



- Molecule 5: 28S ribosomal protein S11, mitochondrial

Chain AI:  55% 13% 30%

MET GLN ALA VAL ARG ASN ARG ALA GLY SER ARG ARG PHE LEU LEU ARG SER TRP THR TRP PRO PRO GLN THR ALA ALA GLY VAL VAL VAL ALA ARG THR PRO ALA GLY THR ILE CYS THR GLY ALA ARG GLN LEU LEU GLN ASP ALA ALA LYS GLN LYS VAL GLU GLN ASN ALA ALA PRO SER HIS THR K59

E69 E81 P84 T85 A86 H87 S91 H92 N93 H94 T95 V99 V100 S101 E105 A108 R118 R119 A120 K121 K122 A139 K140 V144 I145 K152 G153 L154 R158 M162 D177 P182 H183 F184 G185 R192 K193 L194

- Molecule 6: 28S ribosomal protein S12, mitochondrial

Chain AJ:  65% 13% 22%

MET SER TRP LEU LEU GLY HIS LEU ASN THR SER LEU THR CYS GLY PRO ALA LEU VAL PRO ARG TRP LEU ALA THR CYS MET A31 P42 E53 G54 R55 P56 Q57 F66 T67 K72 P73 N74 S75 A76 R77 R79 R82 E98 Q103 L109

D117 K129 K138

- Molecule 7: 28S ribosomal protein S14, mitochondrial

Chain AK:  53% 25% 21%

MET ALA ALA PHE MET LEU GLY SER LEU LEU ARG ARG THR PHE LYS GLN MET VAL PRO SER ALA ALA GLY GLN TRP ARG SER H28 Y29 V30 R36 K39 R40 R41 Y45 A48 R53 I54 N55 S56 L57 R58 K59 N60 T61 I62 L63 P64 K65 I66 E74 I75 A76

V85 R86 R90 R96 P97 R98 R102 R108 I109 R112 Q119 L120 S121 W128

- Molecule 8: 28S ribosomal protein S16, mitochondrial

Chain AM:  69% 15% 15%

MET VAL HIS LEU THR THR LEU LEU CYS K10 R13 H16 R20 L21 A22 L23 R29 Y32 H38 N39 P42 R43 R46 Y64 V66 A67 L68 H100 P101 M102 M103 I104 A121 S122 Q123 K124 T125 ASP ALA GLU ALA THR ASP THR THR ALA LEU THR GLU ASN

THR

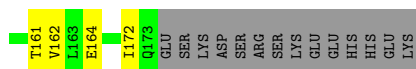
- Molecule 9: 28S ribosomal protein S17, mitochondrial

Chain AN:  62% 21% 18%

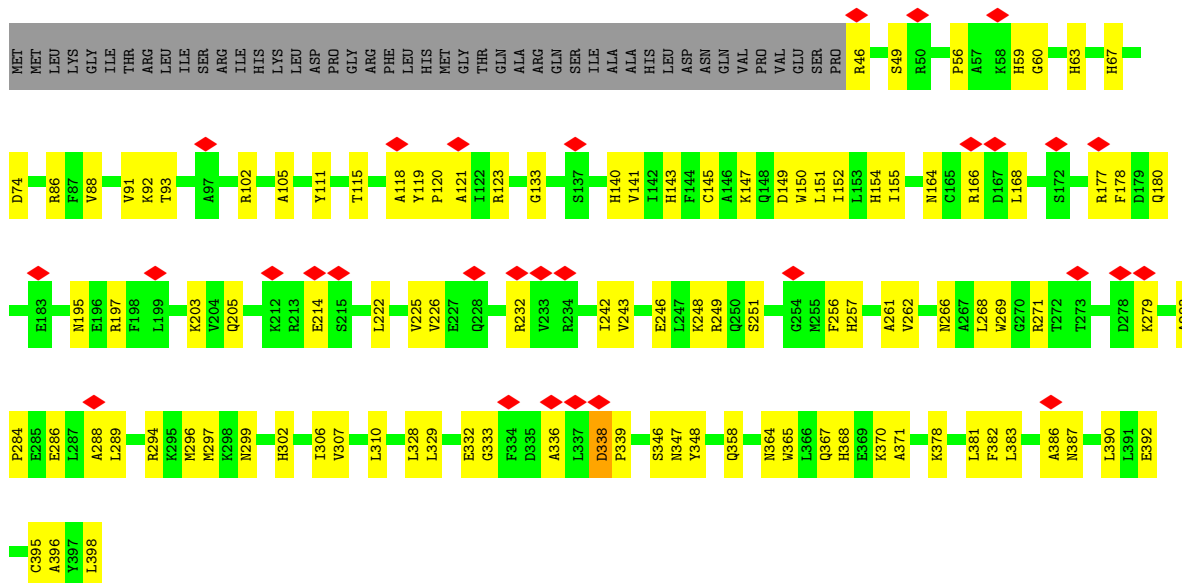
MET SER VAL VAL S6 S7 R11 W12 I13 V14 V17 I18 K24 V28 R29 V30 T31 R46 K47 V64 L65 L66 R67 A68 L69 R73 V91 K98 P99 C100 L106 P109 L110 S111 SER GLU THR THR THR GLN LEU SER LYS ASN LEU GLU ASN

ILE SER SER ALA GLN

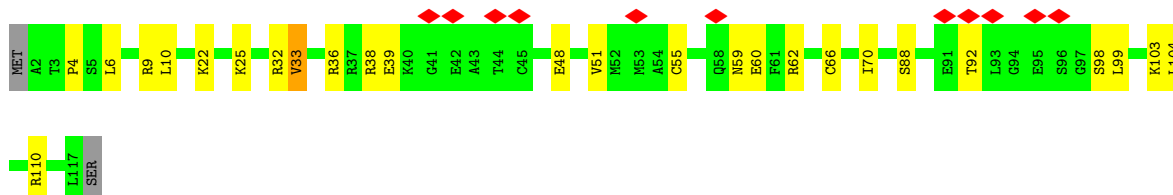
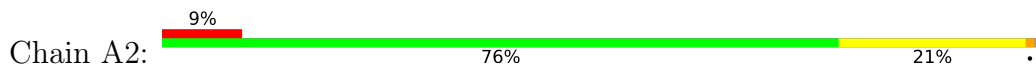
- | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|
| GLU | LEU | LEU | LEU | GLN | LYS | VAL | GLU | THR | ARG | CYS | LEU | ALA | ALA | MET | | | | | | | | | | | | | | | | |
| V77 | M63 | L84 | S87 | P88 | Q91 | A95 | V100 | I104 | I107 | V108 | F109 | D110 | I112 | Y113 | I114 | G117 | K118 | G119 | R125 | D130 | K133 | Y134 | L142 | R143 | L144 | L149 | T150 | S151 | A152 | |
| LEU | LEU | LEU | LEU | GLN | LYS | VAL | GLU | THR | ARG | CYS | LEU | ALA | ALA | MET | LEU | LEU | GLU | LYS | PRO | LYS | THR | ARG | ALA | GLY | GLY | GLY | GLY | ARG | HIS | SER |



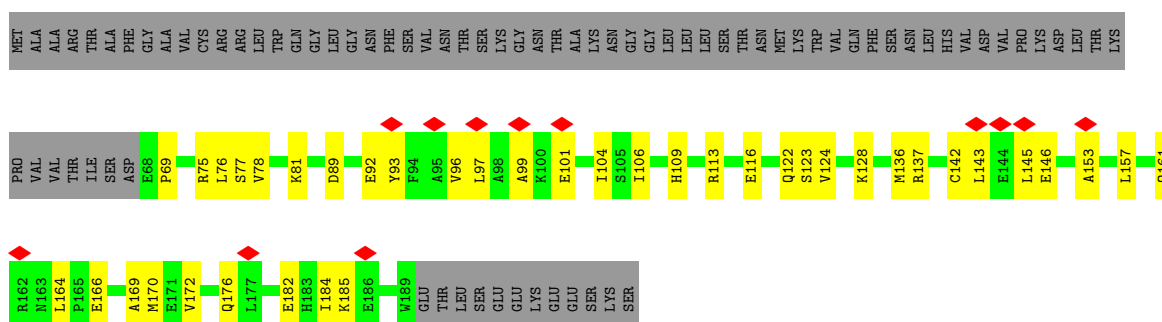
- Molecule 15: 28S ribosomal protein S29, mitochondrial



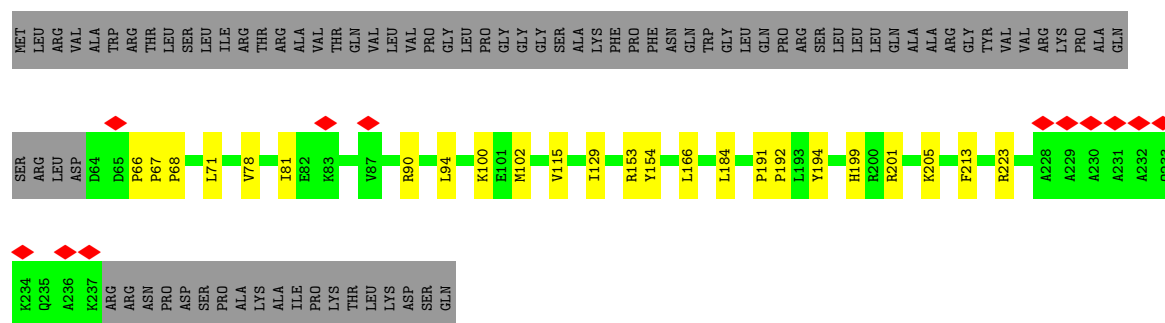
- Molecule 16: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1



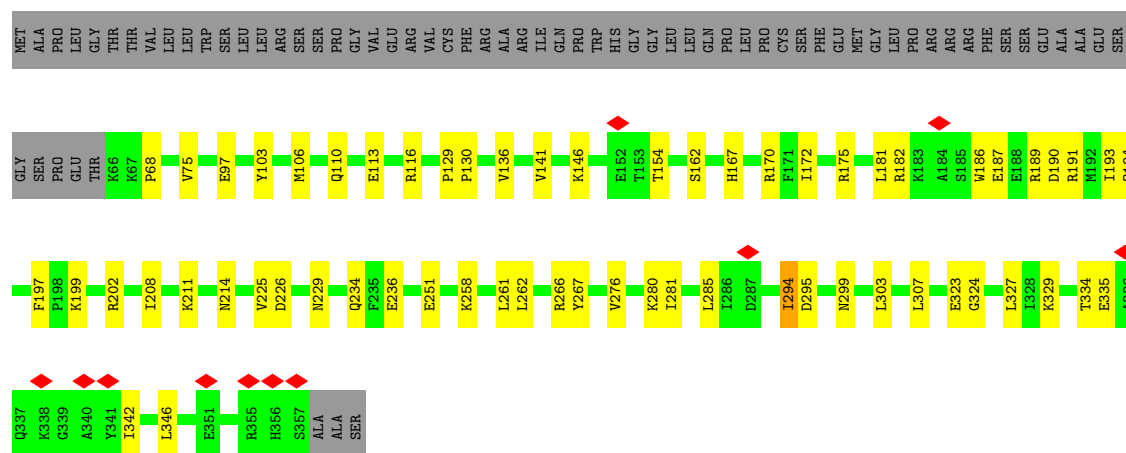
- Molecule 17: 28S ribosomal protein S10, mitochondrial



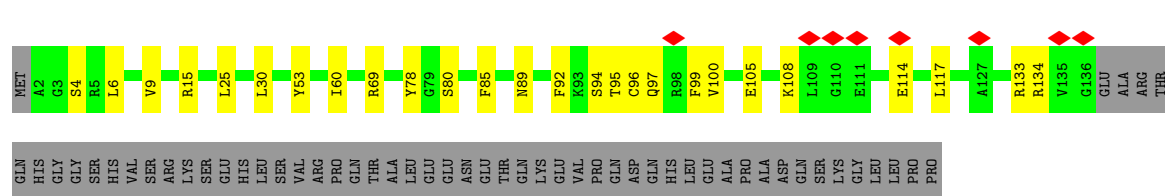
- Molecule 18: 28S ribosomal protein S15, mitochondrial



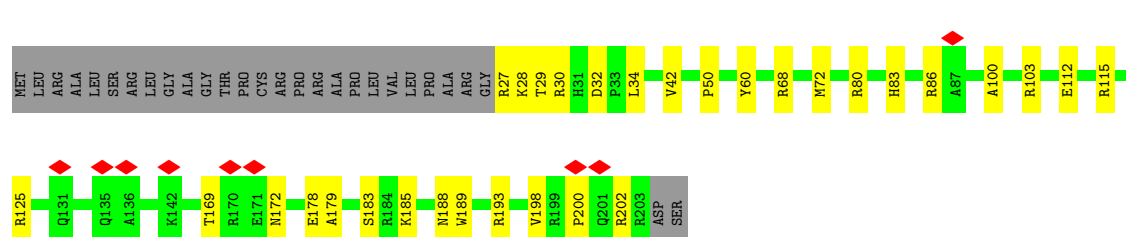
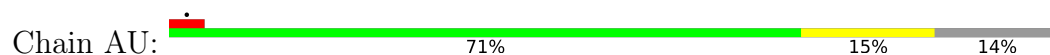
- Molecule 19: 28S ribosomal protein S22, mitochondrial

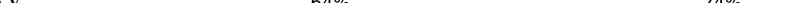


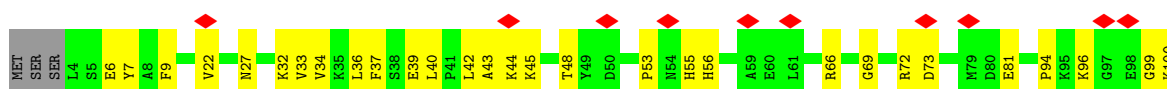
- Molecule 20: 28S ribosomal protein S23, mitochondrial

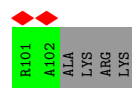


- Molecule 21: 28S ribosomal protein S26, mitochondrial

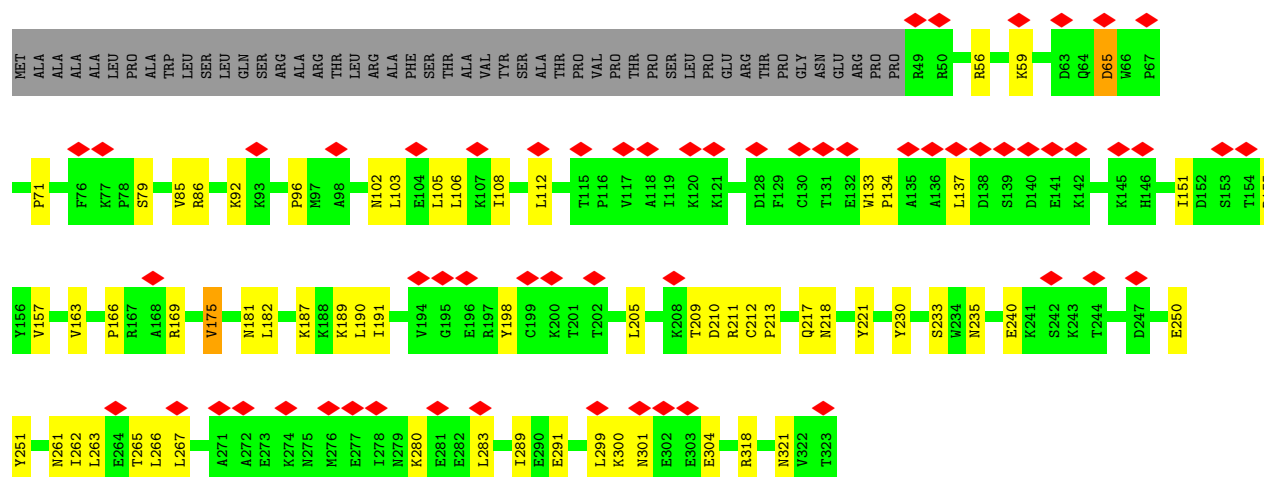


- Chain AV: 

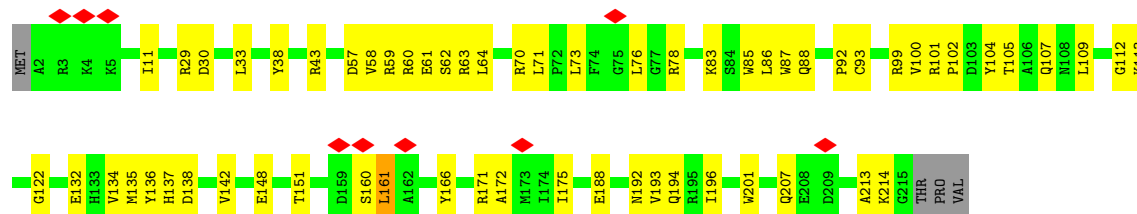




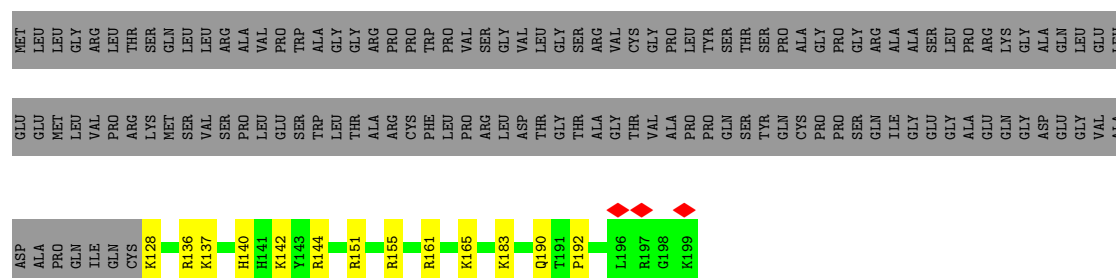
- Molecule 25: 28S ribosomal protein S35, mitochondrial



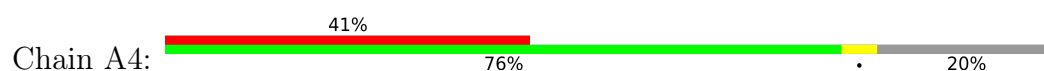
- Molecule 26: 28S ribosomal protein S34, mitochondrial

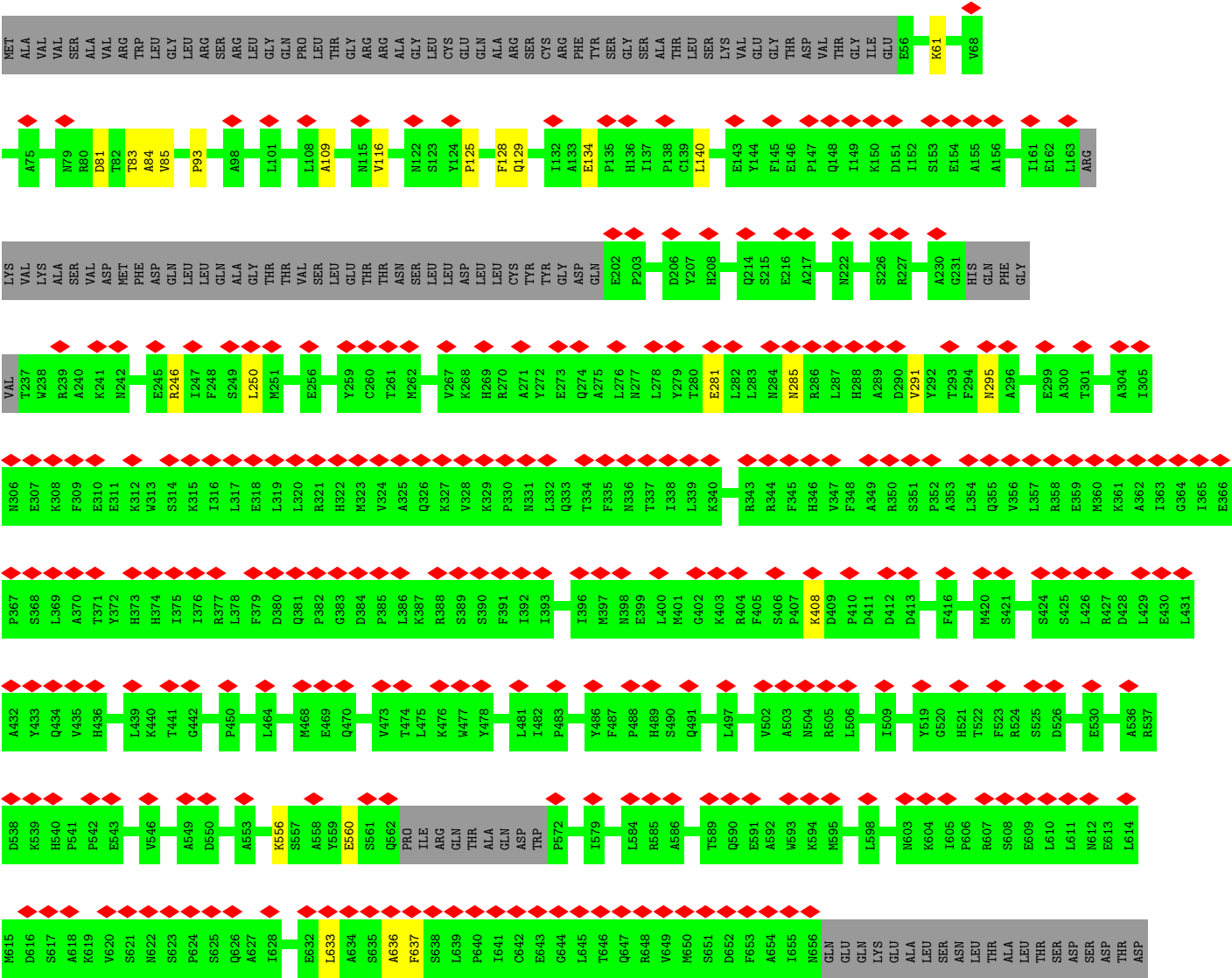


- Molecule 27: Aurora kinase A-interacting protein

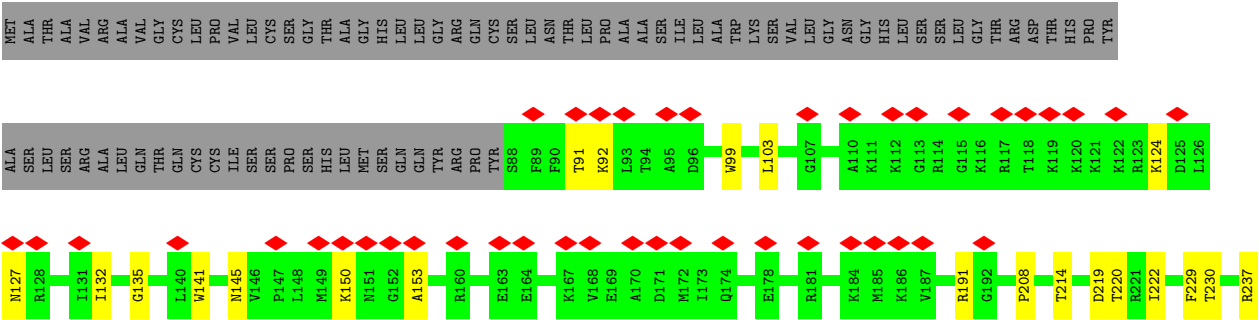


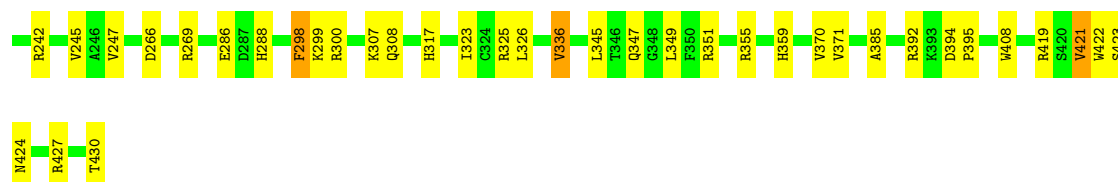
- Molecule 28: Pentatricopeptide repeat domain-containing protein 3, mitochondrial



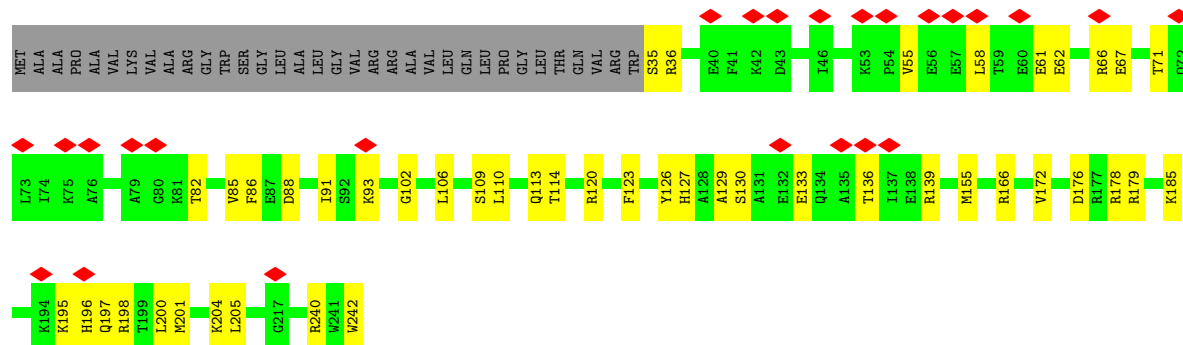


• Molecule 29: 28S ribosomal protein S5, mitochondrial

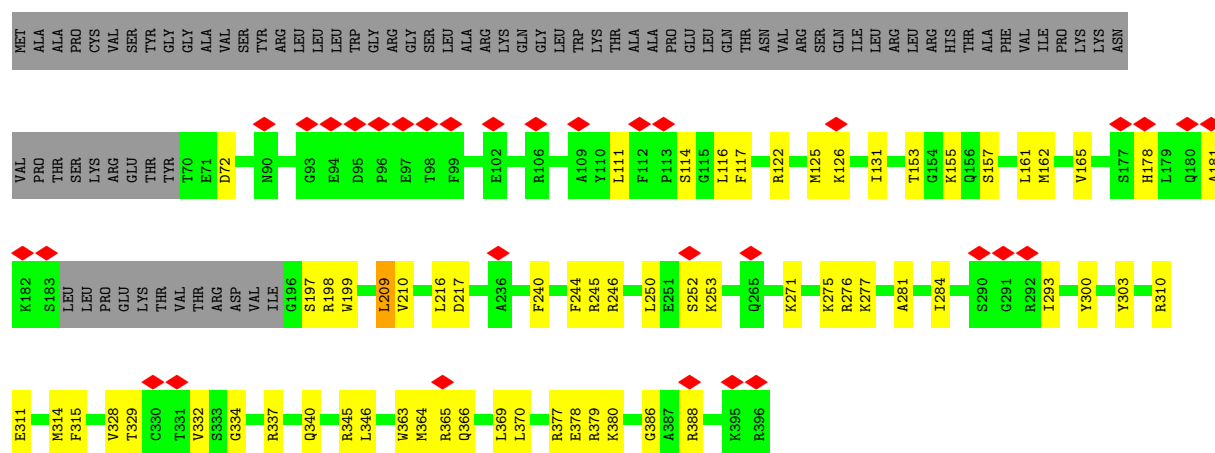




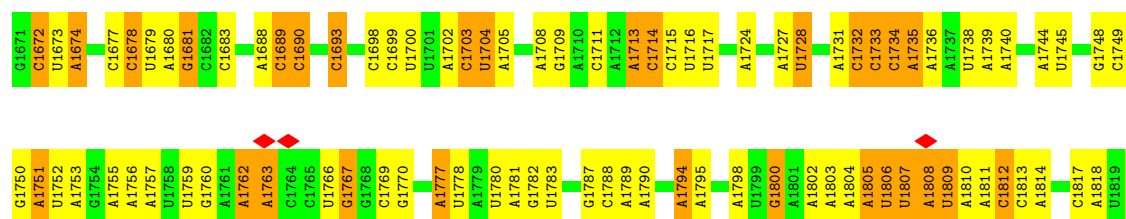
- Molecule 30: 28S ribosomal protein S7, mitochondrial



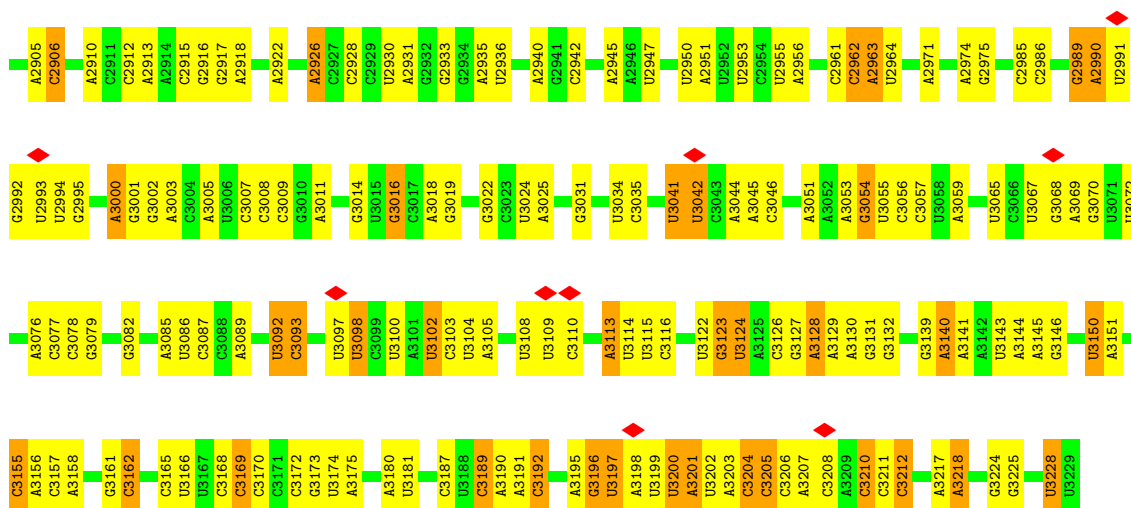
- Molecule 31: 28S ribosomal protein S9, mitochondrial



- Molecule 32: 16S rRNA



G2810	U2744	U2599	U2515	C2415	G2345	C2261	A2192	A2124	U2048	G1889	A1821
G2811	A2745	A2600	C2516	C2415	U2346	C2262	U2193	C2125	U2049	C1890	U1822
G2814	U2746	U2601	U2517	U2420	C2347	C2263	U2194	U2126	A2050	A1891	A1823
	U2747	U2602	U2518	G2421	A2348	A2264	A2195		A2051	A1892	U1824
C2818	U2750	C2603	G2519	C2427	G2349	U2265	A2196	A2131	G2052	A1893	A1825
C2819	G2751	A2604	C2520		A2350	U2266	G2197	A2132	U2055	G1894	G1826
C2820	G2752	C2605	A2521	C2431	U2352	U2274	A2198	A2133	C2056	C1895	C1827
A2821	C2753	U2606	U2522	A2432	U2353	U2275	A2199	A2134	G2057	A1896	A1828
C2822	A2754	G2607	C2523	C2433	A2354	U2276	U2204	C2136	C2058	G1897	A1829
	C2822	G2608	A2524	A2434	U2355	U2277	U2205	C2137	C2059	G1901	G1830
C2829	A2755	A2615	A2527	U2439	A2356	U2278	U2206	U2138	A2060	C1902	A1832
C2830	G2756	G2616	G2528	U2440	C2357	U2279	A2207	G2140	C2061	C1903	C1833
C2831	A2757	A2617	U2529	G2441	U2360	C2284	A2208	U2141	A2065	G1906	U1834
A2832	G2758	U2618	U2530	U2442	G2361	U2285	G2209	A2142	C2066	A1907	A1835
A2833	U2759	A2619	U2531	A2443	A2362	U2286	C2210	G2143	C2067	A1907	A1836
	A2760	G2620	U2532	A2444	U2363	U2287	U2211	A2144	G2002	G1911	C1838
C	C	G2621	A2533	U2445	A2364		C2212	G2145	C2068	A1912	C1839
U	A	G2622	U2536	A2446	U2365	A2283	A2213	A2146	U2069	G1913	C1840
A	A	A2623	G2537	A2447	U2366	A2294	A2214	G2147	C2070	A1914	U1841
C	C	C2624			A2367	U2295		A2148		G1915	A1842
C	A	G2625	C2540	U2456	A2368	U2296	C2217		A2074	G1916	U1843
A	A	U2626	U2545	A2457	A2370	A2297	C2218	A2152	U2075	A1917	U1844
A	A	G2627	U2546	A2458	U2371	U2298	C2219	A2153	C2079	G1918	C1845
A	C	U2628			U2372	U2299	A2220	A2154	U2080		C1846
C	C	A2629		A2461	A2373	G2300	C2221	A2155	U2081	U1924	U1847
C	C	U2630	C2549	A2462	A2374	U2301	U2222	A2156	G2082	A1925	U1848
A	A	G2631	U2550	A2463	U2375	U2302	A2223	A2157	U2083	A1926	C1849
A	A	A2632	A2551		G2377	A2303	C2224	U2158	U2084	A1935	U1850
C	C	A2633	G2552	A2469	C2378	A2306	C2225	U2159	A2085	A1936	G1851
A	A	G2634	U2553	G2470	C2379	U2307	U2226	A2160	A2086	A1937	C1852
A	G	G2635	G2554	G2471	C2380	A2308	A2227	C2163	U2087	A1938	U1853
C	U	U2636	C2557	A2472	A2381	A2309	A2228	A2164	U2088	A1939	U1854
C	C	G2637	U2558	A2473	U2382	G2310	A2229	C2165	U2089	A1940	A1855
C	C	U2638	U2559	C2474	U2383	G2311	A2230	A2167	A2091	G1941	A1856
C	U	G2639	G2560		U2384			A2168	C2092	C1942	U1857
A	A	A2640	U2561	G2478	U2385	A2315	U2233	U2169	A2093	A1943	U1861
A	A	G2641	U2562	C2479	U2386	A2316	C2234	A2170	U2094	A1944	U1862
A	A	U2642	C2570	C2484	U2387	A2317	C2235	U2171	G2094	A1945	A1863
C	C	G2643	U2571	A2493	C2388	A2318	C2236	A2172	A2097	U1952	A1864
	U2766	A2644	U2572	C2494	A2389	A2319	C2237	A2173	G2098	U1953	A1867
A	A2787	G2645	A2573	U2495	A2390	A2320	A2238	G2174	U2099	A1953	G1868
C	C2788	U2652	A2574	U2498	C2393	C2322	A2239	C2175	C2100	G1958	A1869
C	A	G2653	C2577	U2499	A2394	A2323	C2240	C2176			A1870
U	U2791	U2654	C2578	U2500	U2395	U2324	A2241		A2103	U1871	U1872
A	A	U2655	U2582	A2501	C2396	C2326		A2160	A2104	U1877	U1878
A	G2796	U2656	C2584	C2501	A2402	C2326	A2245	A2161	G2105	U1964	A1881
A	U2800	G2659	U2585	A2504	G2403	C2332	A2246	G2162		A1965	A1882
A	A2801	U2660	G2587		U2404	C2333		A2184	U2037	G1966	G1883
A2802	A2802	U2661	U2587	A2507	U2407	U2336	U2253	G2185	A2038	G1968	A1884
A2803	A2803	A2662	A2589	C2508	U2408	A2337	C2254	C2186	G2040	G1973	A1885
A2804	A2804	G2663	A2590	A2509	U2409	A2338	C2255	C2187	U2042	A1974	A1886
A2805	A2805	C2664	U2510	U2510	U2410	A2339	U2256	A2188	C2043	U1975	
A2806	U2806	U2665	C2511	C2511	U2411	G2340	C2257	C2189	A2044	U1976	
A2807	U2807	U2666	U2593	U2593	U2412	U2341	A2258	G2121	C2045	U1977	
U2808	U2808	A2668	U2594	C2514	A2412	U2342	C2259	A2122	A1887	A1887	
C2809	C2809	A2669			C2413		A2260	C2123			

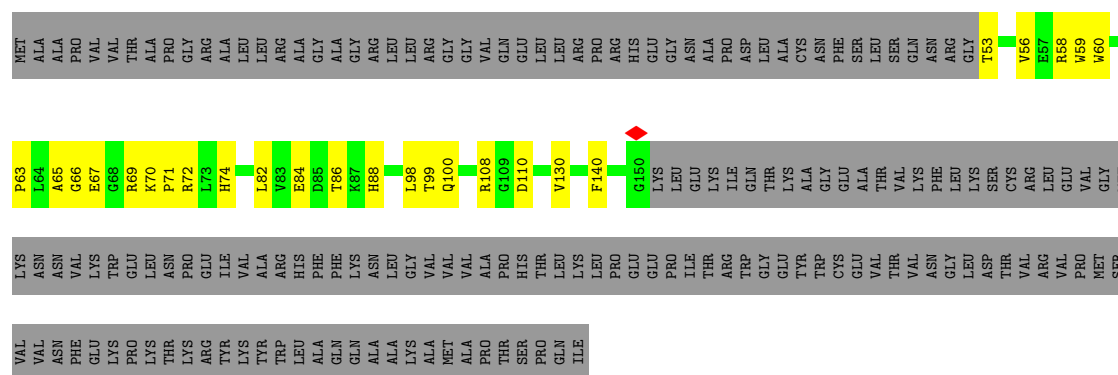


• Molecule 33: tRNAVAL

Chain B: 47% 29% 23%

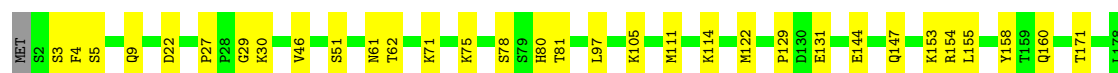


Chain H:  27% 9% 63%



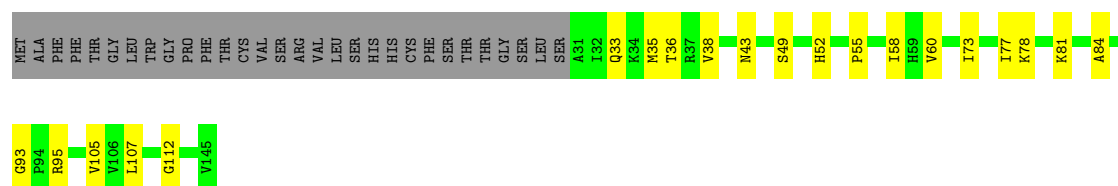
- Molecule 37: 39S ribosomal protein L13, mitochondrial

Chain K:  81% 18% .



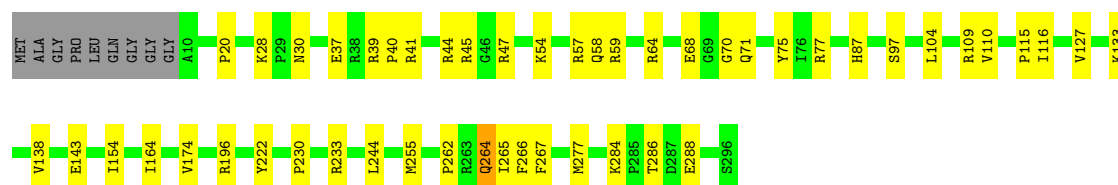
- Molecule 38: 39S ribosomal protein L14, mitochondrial

Chain L:  66% 14% 21%



- Molecule 39: 39S ribosomal protein L15, mitochondrial

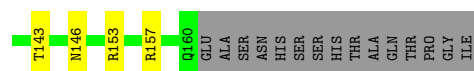
Chain M:  80% 16% .



- Molecule 40: 39S ribosomal protein L17, mitochondrial

Chain O:  69% 18% 13%





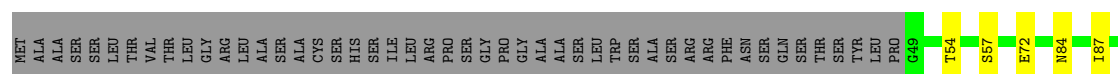
- Molecule 41: 39S ribosomal protein L20, mitochondrial

Chain R: 88% 6% 6%



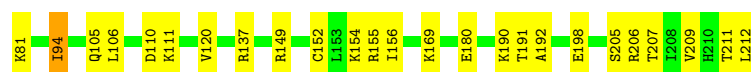
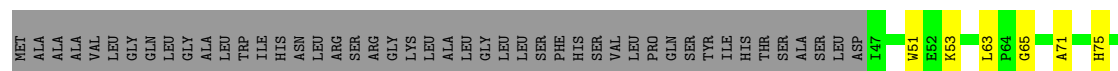
- Molecule 42: 39S ribosomal protein L21, mitochondrial

Chain S: 63% 13% 24%



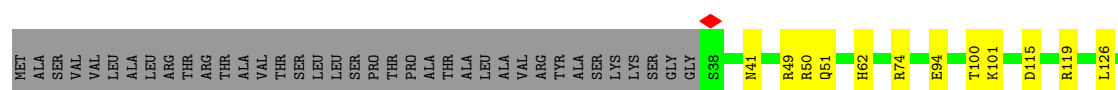
- Molecule 43: 39S ribosomal protein L22, mitochondrial

Chain T: 64% 14% 22%



- Molecule 44: 39S ribosomal protein L27, mitochondrial

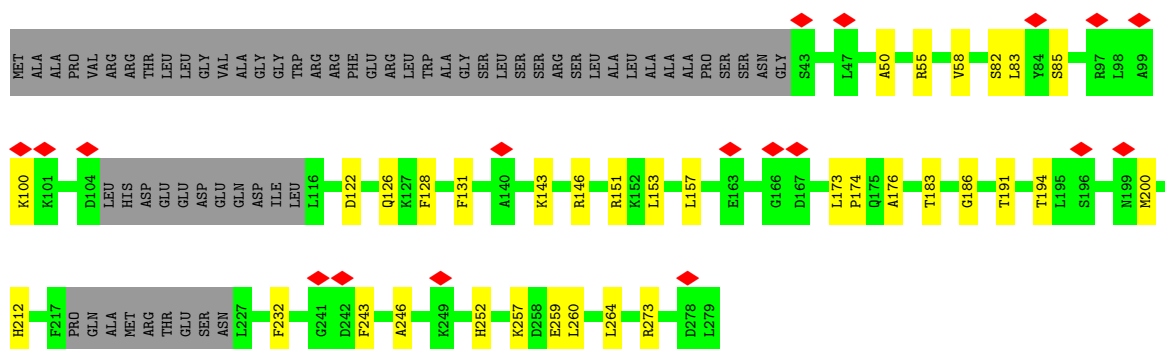
Chain W: 66% 9% 25%



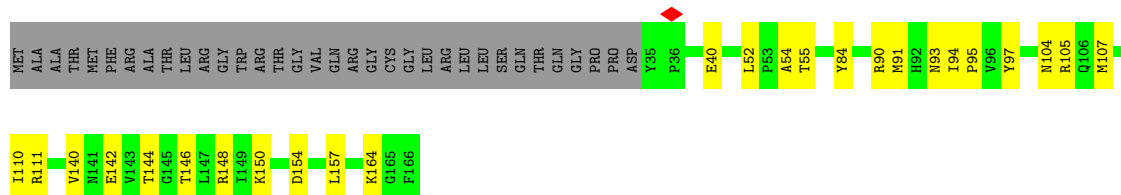
- Molecule 45: 39S ribosomal protein L28, mitochondrial

Chain X: 84% 11% 5%

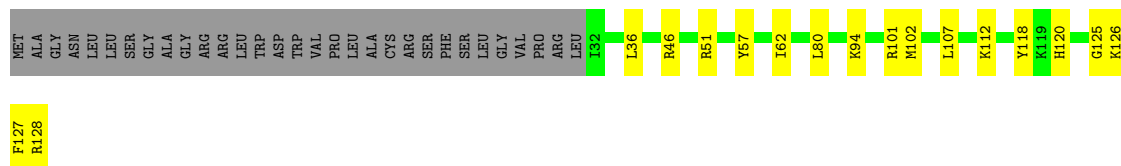




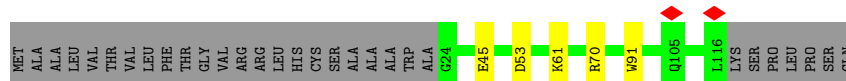
- Molecule 56: 39S ribosomal protein L49, mitochondrial



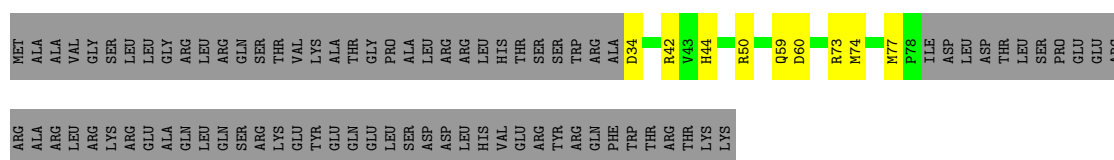
- Molecule 57: 39S ribosomal protein L51, mitochondrial



- Molecule 58: cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA



- Molecule 59: 39S ribosomal protein L55, mitochondrial



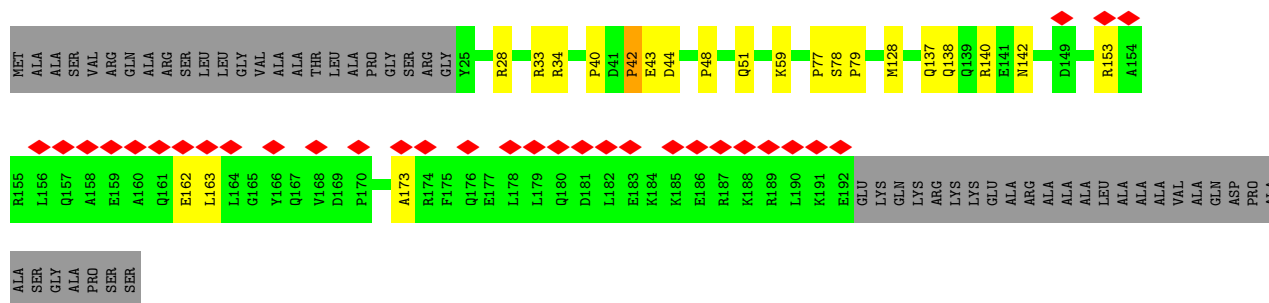
- Molecule 60: Ribosomal protein 63, mitochondrial

Chain o: 



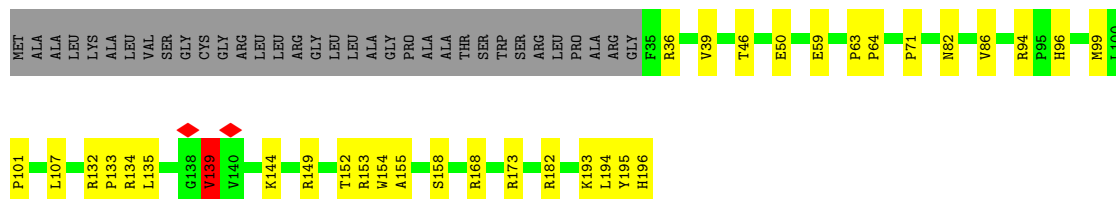
- Molecule 61: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q: 



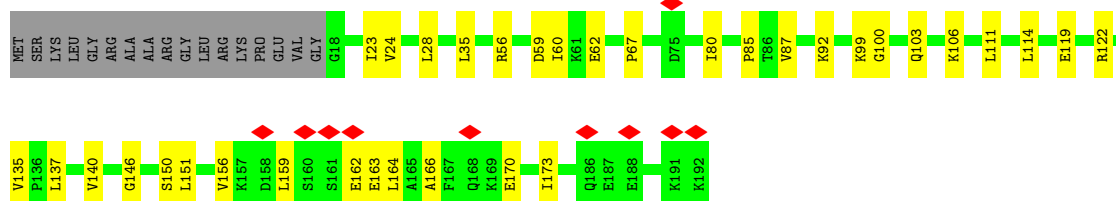
- Molecule 62: 39S ribosomal protein S18a, mitochondrial

Chain r: 



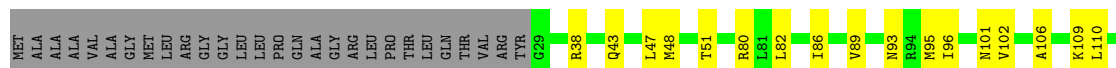
- Molecule 63: 39S ribosomal protein L11, mitochondrial

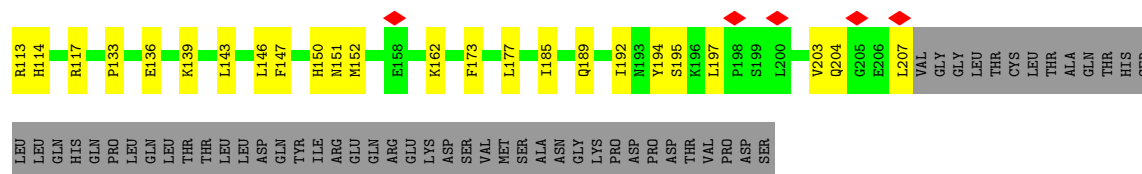
Chain J: 



- Molecule 64: 39S ribosomal protein L10, mitochondrial

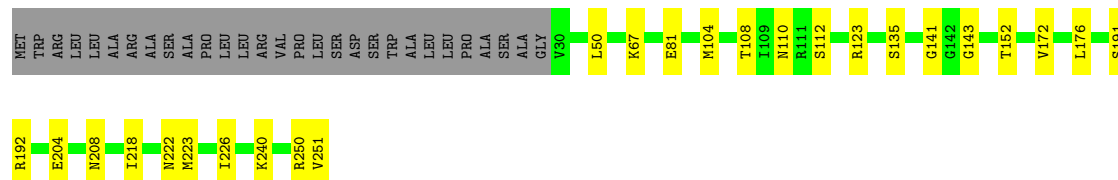
Chain I: 





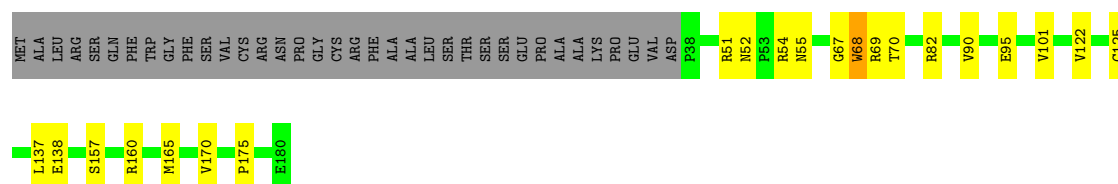
- Molecule 65: 39S ribosomal protein L16, mitochondrial

Chain N: 78% 10% 12%



- Molecule 66: Mitochondrial ribosomal protein L18, isoform CRA_b

Chain P: 68% 11% 20%



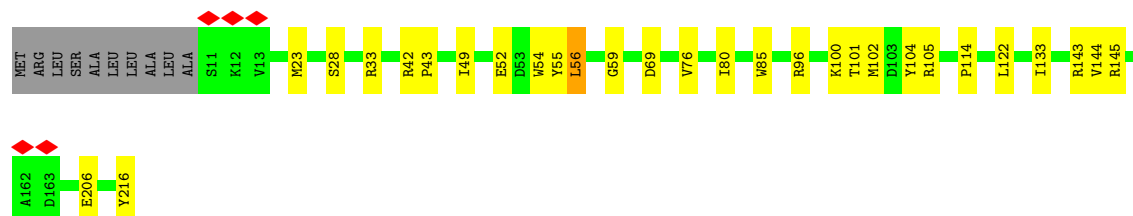
- Molecule 67: 39S ribosomal protein L23, mitochondrial

Chain U: 88% 12% 0%



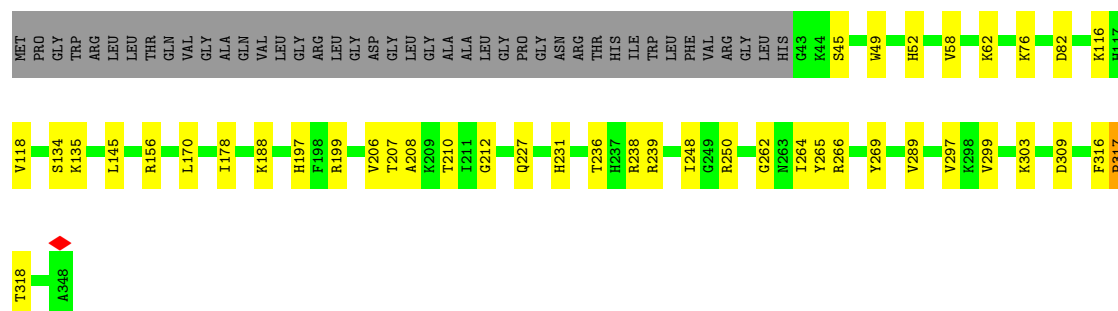
- Molecule 68: 39S ribosomal protein L24, mitochondrial

Chain V: 82% 13% 5%



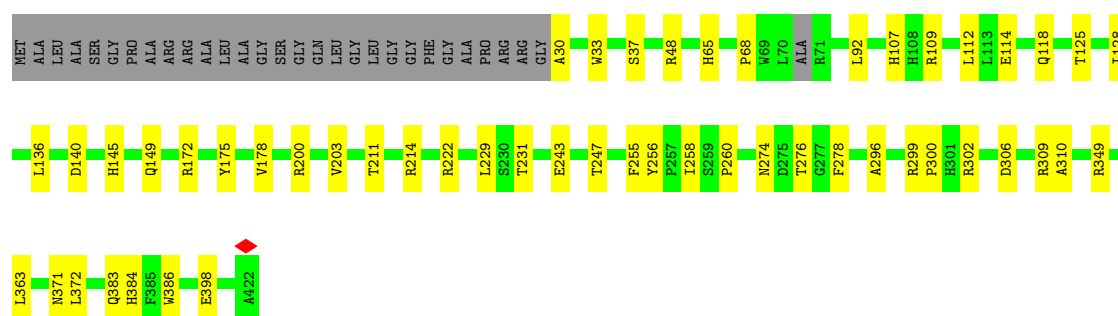
- Molecule 69: 39S ribosomal protein L3, mitochondrial

Chain E: 76% 12% 12%



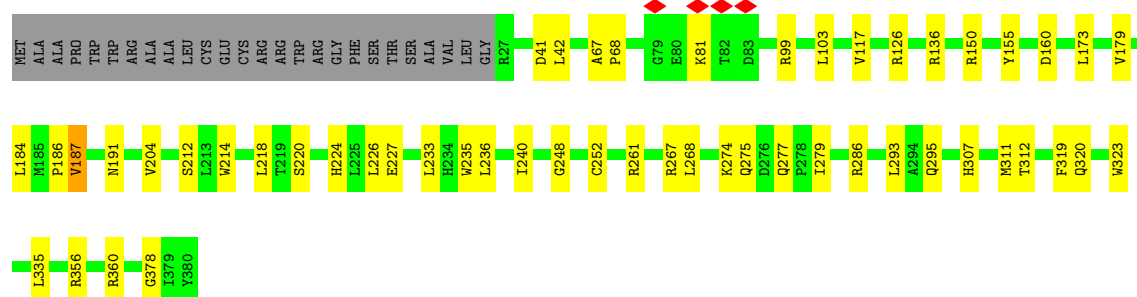
- Molecule 70: 39S ribosomal protein L37, mitochondrial

Chain 5: 81% 12% 7%



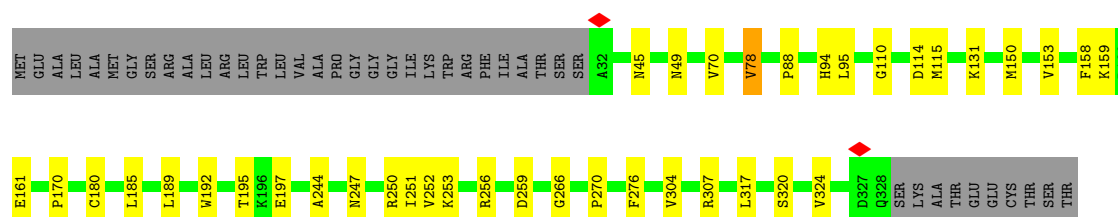
- Molecule 71: 39S ribosomal protein L38, mitochondrial

Chain 6: 79% 14% 7%



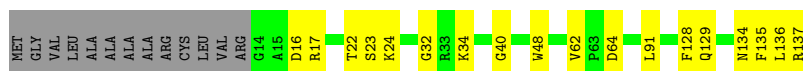
- Molecule 72: 39S ribosomal protein L39, mitochondrial

Chain 7: 76% 11% 12%



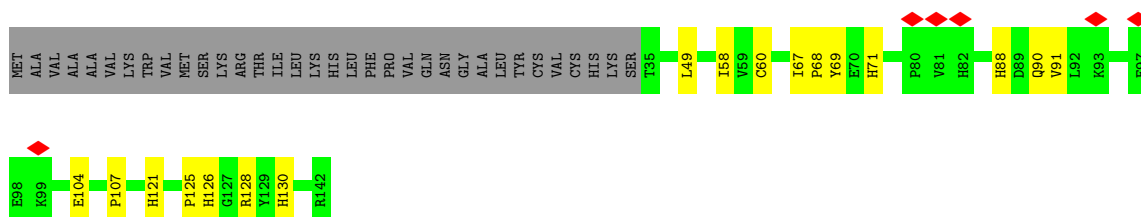
- Molecule 73: 39S ribosomal protein L41, mitochondrial

Chain 9:  77% 13% 9%



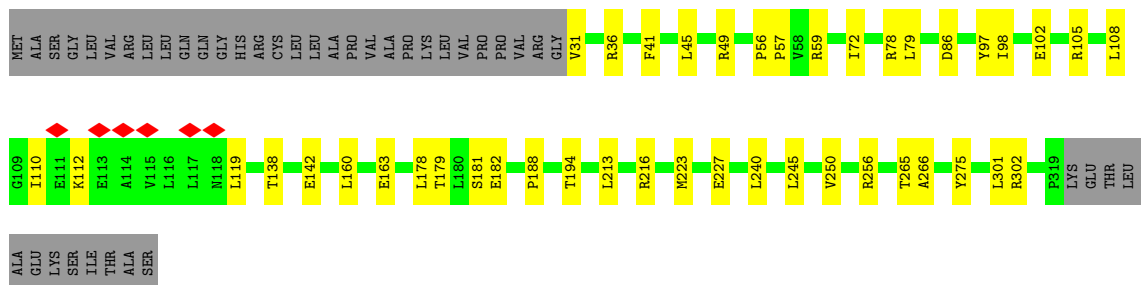
- Molecule 74: 39S ribosomal protein L42, mitochondrial

Chain a:  64% 12% 24%



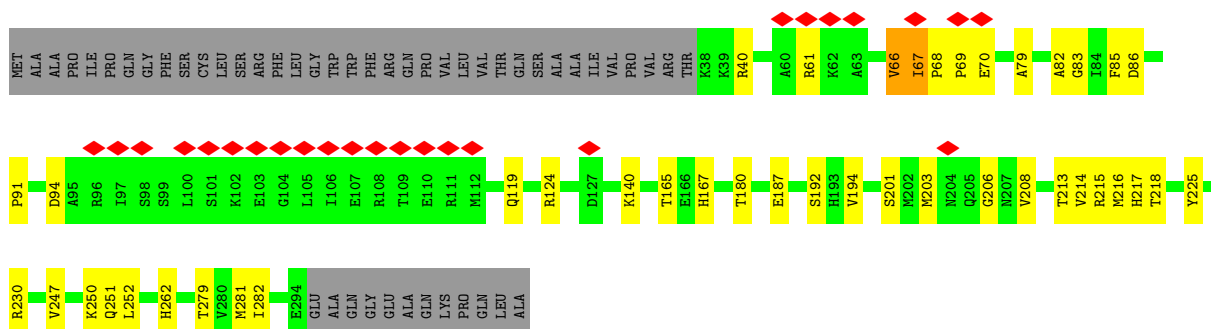
- Molecule 75: 39S ribosomal protein L44, mitochondrial

Chain c:  74% 13% 13%



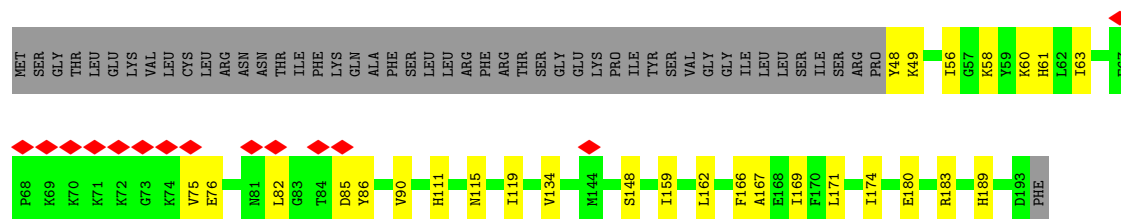
- Molecule 76: 39S ribosomal protein L45, mitochondrial

Chain d:  8% 70% 13% 16%

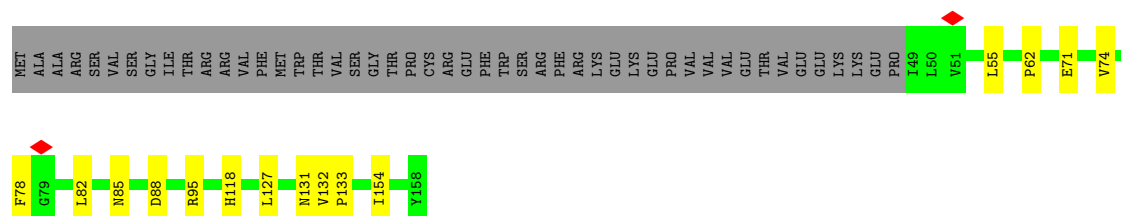


- Molecule 77: 39S ribosomal protein L48, mitochondrial

Chain f:  7% 61% 14% 25%



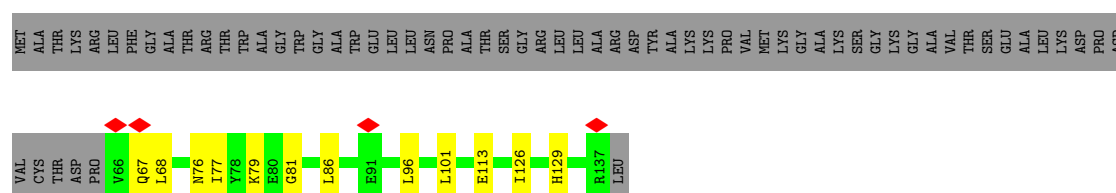
- Molecule 78: 39S ribosomal protein L50, mitochondrial



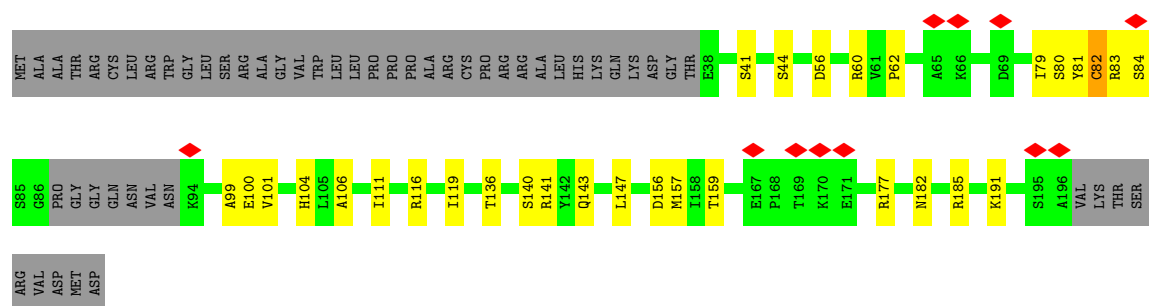
- Molecule 79: 39S ribosomal protein L53, mitochondrial



- Molecule 80: 39S ribosomal protein L54, mitochondrial



- Molecule 81: Peptidyl-tRNA hydrolase ICT1, mitochondrial

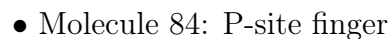


- Molecule 82: 39S ribosomal protein S30, mitochondrial

Frequency	Percentage
Daily	76%
Weekly	14%
Monthly	10%

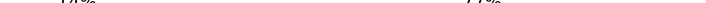


Frequency	Percentage
Daily	66%
Weekly	10%
Monthly	22%

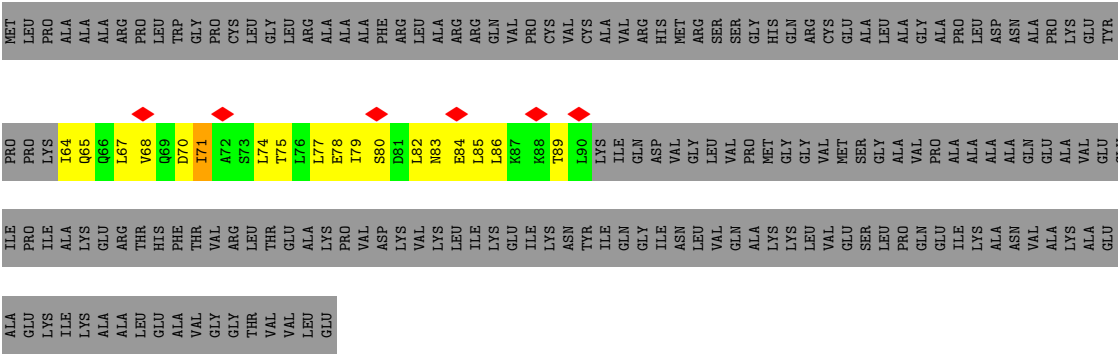


Category	Percentage
Red Bar	28%
Green Bar	98%

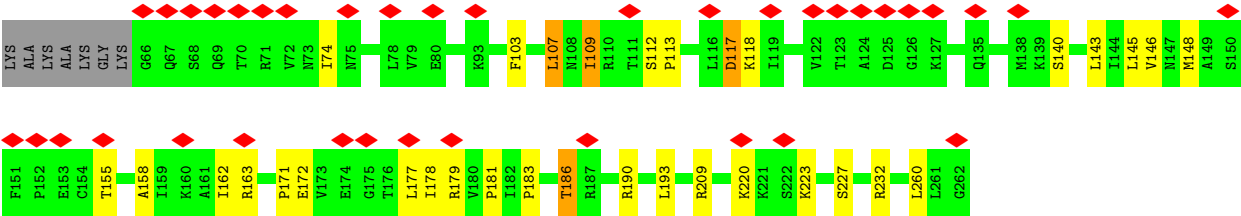
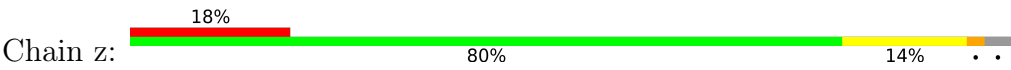


A: 





● Molecule 86: Ribosome-recycling factor, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	93212	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 ($e^-/\text{\AA}^2$)	69.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.359	Depositor
Minimum map value	-1.343	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.110	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	429.30002, 429.30002, 429.30002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07325, 1.07325, 1.07325	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	AA	0.09	0/22406	0.23	0/34881
2	AB	0.40	0/1830	0.63	0/2477
3	AC	0.32	0/1112	0.60	0/1505
4	AE	0.37	0/989	0.78	1/1335 (0.1%)
5	AI	0.35	0/1031	0.69	0/1390
6	AJ	0.52	0/854	0.76	0/1148
7	AK	0.33	0/879	0.69	0/1182
8	AM	0.42	0/941	0.63	0/1265
9	AN	0.42	0/864	0.65	0/1169
10	AO	0.36	0/1624	0.63	0/2209
11	AP	0.38	0/791	0.64	0/1062
12	AQ	0.38	0/752	0.63	0/1001
13	AT	0.45	0/1402	0.60	0/1883
14	AW	0.38	0/778	0.72	1/1048 (0.1%)
15	AX	0.33	0/2932	0.66	0/3968
16	A2	0.38	0/939	0.69	0/1256
17	AH	0.35	0/1037	0.65	0/1403
18	AL	0.36	0/1475	0.64	1/1970 (0.1%)
19	AR	0.33	0/2435	0.61	1/3288 (0.0%)
20	AS	0.37	0/1138	0.58	0/1533
21	AU	0.33	0/1521	0.58	0/2039
22	AV	0.33	0/3071	0.70	2/4147 (0.0%)
23	AY	0.30	0/1046	0.59	0/1410
24	AZ	0.30	0/851	0.62	0/1133
25	A1	0.30	0/2277	0.64	0/3079
26	A0	0.35	0/1827	0.62	0/2473
27	A3	0.45	0/650	0.65	0/855
28	A4	0.23	0/3028	0.53	0/4197
29	AD	0.41	0/2783	0.63	2/3724 (0.1%)
30	AF	0.33	0/1765	0.63	0/2369
31	AG	0.33	0/2642	0.63	0/3538
32	A	0.10	0/36245	0.25	0/56418

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B	0.19	0/1328	0.36	0/2056
34	D	0.23	0/1904	0.52	0/2561
35	F	0.28	0/2071	0.61	1/2817 (0.0%)
36	H	0.23	0/820	0.61	0/1102
37	K	0.26	0/1495	0.58	2/2029 (0.1%)
38	L	0.25	0/904	0.55	2/1218 (0.2%)
39	M	0.27	0/2359	0.65	0/3185
40	O	0.27	0/1269	0.58	0/1708
41	R	0.27	0/1174	0.60	0/1572
42	S	0.26	0/1276	0.57	0/1729
43	T	0.25	0/1402	0.55	0/1886
44	W	0.26	0/893	0.56	0/1204
45	X	0.23	0/2081	0.58	0/2812
46	Y	0.24	0/1552	0.52	0/2079
47	Z	0.25	0/1003	0.56	0/1354
48	0	0.25	0/895	0.63	0/1201
49	1	0.21	0/438	0.49	0/583
50	2	0.26	0/382	0.51	0/507
51	3	0.25	0/852	0.50	0/1136
52	4	0.25	0/350	0.52	0/461
53	8	0.24	0/855	0.59	0/1152
54	b	0.25	0/1202	0.53	0/1626
55	e	0.24	0/1797	0.60	0/2422
56	g	0.26	0/1132	0.55	2/1543 (0.1%)
57	i	0.27	0/849	0.61	0/1135
58	j	0.26	0/755	0.50	0/1016
59	m	0.23	0/379	0.56	0/510
60	o	0.26	0/818	0.60	0/1097
61	q	0.23	0/1323	0.60	0/1794
62	r	0.27	0/1362	0.59	2/1846 (0.1%)
63	J	0.25	0/1348	0.59	0/1813
64	I	0.26	0/1467	0.65	0/1984
65	N	0.23	0/1833	0.49	0/2468
66	P	0.24	0/1191	0.64	2/1611 (0.1%)
67	U	0.26	0/1252	0.49	0/1697
68	V	0.22	0/1727	0.49	0/2341
69	E	0.23	0/2479	0.53	2/3360 (0.1%)
70	5	0.24	0/3300	0.53	0/4495
71	6	0.23	0/3043	0.53	1/4140 (0.0%)
72	7	0.23	0/2467	0.53	0/3337
73	9	0.23	0/1025	0.52	0/1379
74	a	0.25	0/923	0.53	0/1254
75	c	0.22	0/2371	0.52	0/3205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	d	0.23	0/2132	0.58	0/2887
77	f	0.26	0/1144	0.57	0/1551
78	h	0.23	0/917	0.60	0/1249
79	k	0.23	0/754	0.59	0/1017
80	l	0.23	0/636	0.46	0/860
81	p	0.24	0/1246	0.58	0/1675
82	s	0.31	2/3262 (0.1%)	0.58	2/4435 (0.0%)
83	Q	0.24	0/1938	0.53	0/2610
85	TA	0.22	0/349	0.63	0/475
85	TB	0.26	0/212	0.57	0/286
86	z	0.13	0/1534	0.29	0/2063
All	All	0.24	2/177385 (0.0%)	0.49	24/251888 (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
2	AB	0	1
4	AE	0	2
5	AI	0	2
7	AK	0	1
10	AO	0	1
11	AP	0	1
14	AW	0	1
15	AX	0	1
31	AG	0	1
34	D	0	1
37	K	0	2
39	M	0	4
40	O	0	1
41	R	0	1
43	T	0	1
46	Y	0	1
47	Z	0	1
61	q	0	2
66	P	0	1
69	E	0	1
76	d	0	1
78	h	0	2
81	p	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
83	Q	0	1
All	All	0	33

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	s	164	HIS	CE1-NE2	7.70	1.40	1.32
82	s	164	HIS	CG-CD2	5.09	1.41	1.35

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AW	110	ASN	N-CA-C	-6.03	107.75	114.62
66	P	67	GLY	CA-C-N	5.91	132.84	121.54
66	P	67	GLY	C-N-CA	5.91	132.84	121.54
38	L	112	GLY	CA-C-N	5.88	132.29	121.70
38	L	112	GLY	C-N-CA	5.88	132.29	121.70
82	s	285	GLY	N-CA-C	-5.55	107.35	114.85
29	AD	298	PHE	CA-C-N	5.34	131.75	121.54
29	AD	298	PHE	C-N-CA	5.34	131.75	121.54
82	s	164	HIS	CB-CG-CD2	-5.34	124.26	131.20
71	6	117	VAL	N-CA-C	-5.28	107.68	112.96
35	F	128	TRP	CA-CB-CG	5.25	123.58	113.60
69	E	317	PRO	CA-C-N	5.25	131.57	121.54
69	E	317	PRO	C-N-CA	5.25	131.57	121.54
62	r	139	VAL	CA-C-N	5.24	123.54	120.24
62	r	139	VAL	C-N-CA	5.24	123.54	120.24
22	AV	154	LYS	CA-C-N	5.20	131.47	121.54
22	AV	154	LYS	C-N-CA	5.20	131.47	121.54
37	K	144	GLU	CA-C-N	5.15	128.50	120.68
37	K	144	GLU	C-N-CA	5.15	128.50	120.68
19	AR	324	GLY	N-CA-C	5.11	118.42	112.50
4	AE	12	ALA	N-CA-C	5.08	121.62	110.80
56	g	54	ALA	CA-C-N	5.05	131.19	121.54
56	g	54	ALA	C-N-CA	5.05	131.19	121.54
18	AL	71	LEU	CA-CB-CG	5.04	133.95	116.30

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	172	ARG	Peptide
4	AE	11	LYS	Peptide
4	AE	13	MET	Peptide
31	AG	209	LEU	Peptide
5	AI	119	ASN	Peptide
5	AI	144	VAL	Peptide
7	AK	64	PRO	Peptide
10	AO	98	ASN	Peptide
11	AP	140	TYR	Peptide
14	AW	108	VAL	Peptide
15	AX	338	ASP	Peptide
34	D	206	TYR	Peptide
69	E	316	PHE	Peptide
37	K	3	SER	Peptide
37	K	5	SER	Peptide
39	M	110	VAL	Peptide
39	M	20	PRO	Peptide
39	M	264	GLN	Peptide
39	M	286	THR	Peptide
40	O	110	ILE	Peptide
66	P	68	TRP	Peptide
83	Q	67	ARG	Peptide
41	R	137	GLU	Peptide
43	T	94	ILE	Peptide
46	Y	202	LEU	Peptide
47	Z	141	SER	Peptide
76	d	70	GLU	Peptide
78	h	132	VAL	Peptide
78	h	82	LEU	Peptide
81	p	82	CYS	Peptide
81	p	83	ARG	Peptide
61	q	77	PRO	Peptide
61	q	78	SER	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	20030	0	10172	588	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AB	1787	0	1779	35	0
3	AC	1082	0	1088	33	0
4	AE	972	0	1000	22	0
5	AI	1011	0	1052	24	0
6	AJ	838	0	887	51	0
7	AK	861	0	885	43	0
8	AM	920	0	951	17	0
9	AN	846	0	908	18	0
10	AO	1570	0	1533	34	0
11	AP	774	0	803	20	0
12	AQ	740	0	754	24	0
13	AT	1371	0	1394	25	0
14	AW	766	0	785	32	0
15	AX	2860	0	2857	84	0
16	A2	925	0	961	27	0
17	AH	1014	0	1036	31	0
18	AL	1451	0	1543	29	0
19	AR	2388	0	2410	41	0
20	AS	1111	0	1115	31	0
21	AU	1499	0	1512	29	0
22	AV	3009	0	3005	75	0
23	AY	1016	0	962	27	0
24	AZ	833	0	853	27	0
25	A1	2231	0	2261	55	0
26	A0	1781	0	1791	61	0
27	A3	639	0	715	13	0
28	A4	3010	0	1760	21	0
29	AD	2731	0	2804	62	0
30	AF	1724	0	1763	45	0
31	AG	2587	0	2572	51	0
32	A	32395	0	16446	1087	0
33	B	1191	0	607	6	0
34	D	1866	0	1927	59	0
35	F	2013	0	2044	41	0
36	H	806	0	849	37	0
37	K	1451	0	1448	45	0
38	L	889	0	941	34	0
39	M	2305	0	2378	51	0
40	O	1245	0	1283	24	0
41	R	1153	0	1214	9	0
42	S	1251	0	1322	23	0
43	T	1368	0	1410	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	W	871	0	898	21	0
45	X	2027	0	2040	23	0
46	Y	1517	0	1561	25	0
47	Z	978	0	1030	19	0
48	0	880	0	903	33	0
49	1	433	0	475	8	0
50	2	376	0	406	16	0
51	3	831	0	883	17	0
52	4	342	0	361	10	0
53	8	836	0	844	9	0
54	b	1178	0	1180	30	0
55	e	1762	0	1767	28	0
56	g	1096	0	1081	25	0
57	i	827	0	857	32	0
58	j	740	0	741	8	0
59	m	372	0	387	7	0
60	o	797	0	804	34	0
61	q	1293	0	1176	16	0
62	r	1322	0	1347	44	0
63	J	1330	0	1407	56	0
64	I	1435	0	1519	53	0
65	N	1786	0	1817	20	0
66	P	1165	0	1162	14	0
67	U	1222	0	1187	20	0
68	V	1682	0	1692	21	0
69	E	2410	0	2418	50	0
70	5	3205	0	3201	59	0
71	6	2948	0	2841	35	0
72	7	2410	0	2415	24	0
73	9	997	0	987	29	0
74	a	896	0	847	20	0
75	c	2322	0	2338	40	0
76	d	2075	0	2037	28	0
77	f	1126	0	1106	17	0
78	h	894	0	881	9	0
79	k	743	0	758	22	0
80	l	619	0	611	15	0
81	p	1227	0	1239	32	0
82	s	3178	0	3124	55	0
83	Q	1894	0	1927	46	0
84	u	325	0	76	2	0
85	TA	345	0	364	138	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	TB	213	0	234	87	0
86	z	1525	0	1602	43	0
87	A	94	0	0	0	0
87	AA	27	0	0	0	0
87	AG	1	0	0	0	0
87	D	1	0	0	0	0
87	E	1	0	0	0	0
87	M	1	0	0	0	0
87	W	1	0	0	0	0
87	g	1	0	0	0	0
88	0	1	0	0	0	0
88	4	1	0	0	0	0
88	AB	1	0	0	0	0
88	AO	1	0	0	0	0
88	AP	1	0	0	0	0
88	AT	1	0	0	0	0
88	r	1	0	0	0	0
89	AX	28	0	11	1	0
All	All	168922	0	142322	3207	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 10.

All (3207) 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)
85:TA:85:LEU:CD2	85:TB:64:ILE:HG13	1.25	1.67
55:e:243:PHE:CE2	55:e:246:ALA:HA	1.16	1.61
37:K:155:LEU:HA	37:K:158:TYR:CE2	1.09	1.55
55:e:243:PHE:HE2	55:e:246:ALA:CA	1.17	1.54
32:A:1834:U:C4	43:T:206:ARG:HA	1.43	1.50
1:AA:826:A:N6	6:AJ:56:PRO:HD2	1.19	1.48
32:A:2198:A:N6	63:J:150:SER:HB2	1.18	1.47
1:AA:826:A:C6	6:AJ:56:PRO:HD2	1.49	1.46
32:A:3199:U:C5'	32:A:3201:A:N7	1.78	1.45
32:A:3199:U:H5''	32:A:3201:A:N7	1.30	1.44
32:A:2198:A:N6	63:J:150:SER:CB	1.78	1.44
32:A:3199:U:H5''	32:A:3201:A:C8	1.53	1.43
37:K:155:LEU:CA	37:K:158:TYR:CE2	1.99	1.42
32:A:2198:A:H61	63:J:150:SER:CB	1.32	1.42
32:A:1939:G:N2	32:A:2495:U:H1'	1.30	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1939:G:N2	32:A:2495:U:C1'	1.82	1.40
32:A:2060:A:C5	32:A:2079:C:N3	1.90	1.38
32:A:3203:A:H1'	69:E:303:LYS:NZ	1.06	1.36
85:TA:85:LEU:CD2	85:TB:64:ILE:CG1	2.05	1.34
32:A:2493:C:C5	32:A:2540:C:C4	2.17	1.33
32:A:2155:A:C2	60:o:26:PHE:CE1	2.17	1.32
32:A:2155:A:N1	60:o:26:PHE:CZ	1.98	1.32
85:TA:85:LEU:HD23	85:TB:64:ILE:CG1	1.57	1.31
26:A0:171:ARG:HH12	26:A0:188:GLU:CD	1.39	1.29
32:A:3203:A:C1'	69:E:303:LYS:NZ	1.98	1.25
85:TA:85:LEU:O	85:TB:68:VAL:HG22	1.30	1.25
85:TA:81:ASP:HB3	85:TB:64:ILE:CD1	1.66	1.24
37:K:155:LEU:HA	37:K:158:TYR:CZ	1.73	1.24
32:A:1731:A:N6	57:i:118:TYR:CD1	2.04	1.24
32:A:1939:G:C2	32:A:2495:U:H1'	1.72	1.24
1:AA:826:A:N1	6:AJ:56:PRO:CG	2.00	1.23
32:A:2176:C:OP2	63:J:99:LYS:NZ	1.69	1.22
81:p:81:TYR:OH	81:p:147:LEU:HB2	1.40	1.21
32:A:2065:A:C8	44:W:74:ARG:HA	1.74	1.20
32:A:3110:C:H42	32:A:3203:A:N6	1.38	1.20
32:A:2155:A:C2	60:o:26:PHE:CZ	2.28	1.18
32:A:3110:C:N4	32:A:3203:A:H61	1.38	1.18
32:A:3189:C:O2	62:r:154:TRP:CD2	1.97	1.18
69:E:269:TYR:CE1	69:E:303:LYS:HE2	1.79	1.18
32:A:2257:C:OP1	58:j:61:LYS:HB2	1.40	1.17
32:A:2606:U:H5	86:z:209:ARG:CZ	1.56	1.16
32:A:1834:U:O4	43:T:206:ARG:CA	1.92	1.16
32:A:1834:U:O4	43:T:206:ARG:HA	1.43	1.16
32:A:1834:U:N3	43:T:206:ARG:HA	1.61	1.15
32:A:2379:C:C5	73:9:48:TRP:CE2	2.35	1.15
32:A:2615:A:C6	38:L:58:ILE:HB	1.81	1.15
85:TA:85:LEU:HD22	85:TB:64:ILE:C	1.70	1.15
6:AJ:103:GLN:OE1	86:z:181:PRO:CB	1.95	1.14
85:TA:85:LEU:HD22	85:TB:64:ILE:HG13	1.18	1.14
1:AA:826:A:C6	6:AJ:56:PRO:CD	2.30	1.14
32:A:2606:U:C5	86:z:209:ARG:CZ	2.30	1.14
32:A:2961:C:C4	32:A:2962:C:C4	2.35	1.14
32:A:3157:C:O2'	83:Q:84:ARG:O	1.63	1.14
30:AF:123:PHE:CZ	30:AF:139:ARG:HD3	1.83	1.13
70:5:255:PHE:CE1	70:5:258:ILE:O	2.01	1.13
6:AJ:103:GLN:OE1	86:z:181:PRO:HB2	1.46	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:TA:85:LEU:O	85:TB:68:VAL:CG2	1.97	1.12
85:TA:85:LEU:HA	85:TA:88:LYS:HE3	1.28	1.12
32:A:1834:U:O4	43:T:206:ARG:CB	1.98	1.12
32:A:3199:U:H5'	32:A:3201:A:N7	1.64	1.11
32:A:1834:U:C4	43:T:206:ARG:CA	2.33	1.11
83:Q:73:ARG:NH1	83:Q:215:VAL:CG1	2.14	1.10
1:AA:826:A:N6	6:AJ:56:PRO:CD	2.13	1.10
32:A:3203:A:C1'	69:E:303:LYS:HZ3	1.63	1.09
1:AA:826:A:C2	6:AJ:56:PRO:HG2	1.87	1.09
36:H:99:THR:C	36:H:108:ARG:HD3	1.79	1.08
85:TA:81:ASP:CB	85:TB:64:ILE:CD1	2.30	1.08
32:A:2131:A:C4	62:r:168:ARG:NH1	2.21	1.08
32:A:2155:A:C2	60:o:26:PHE:CD1	2.42	1.08
12:AQ:77:ARG:CZ	14:AW:149:LEU:HD13	1.83	1.07
85:TA:85:LEU:HD11	85:TB:67:LEU:HB2	1.15	1.07
32:A:2818:C:O2	86:z:227:SER:OG	1.71	1.07
69:E:269:TYR:HE1	69:E:303:LYS:HE2	0.99	1.07
32:A:2065:A:H8	44:W:74:ARG:HA	0.92	1.07
32:A:3203:A:C2	32:A:3204:C:O2	2.08	1.07
1:AA:892:A:OP2	6:AJ:76:ALA:HB1	1.55	1.06
85:TA:85:LEU:CD1	85:TB:67:LEU:HB2	1.83	1.06
32:A:2060:A:N7	32:A:2079:C:N3	2.03	1.06
85:TB:75:THR:HG22	85:TB:78:GLU:HB2	1.37	1.06
32:A:1853:A:OP2	42:S:177:ARG:NH2	1.89	1.06
85:TA:64:ILE:HG22	85:TB:85:LEU:CD2	1.86	1.06
85:TA:85:LEU:CA	85:TA:88:LYS:HE3	1.85	1.06
32:A:2172:A:H2'	63:J:23:ILE:CG1	1.86	1.05
79:k:57:HIS:CG	85:TA:53:LEU:HB3	1.90	1.05
32:A:2615:A:N6	38:L:58:ILE:HB	1.71	1.05
85:TA:85:LEU:HA	85:TA:88:LYS:CE	1.85	1.05
12:AQ:77:ARG:NH2	14:AW:149:LEU:HD13	1.71	1.05
22:AV:52:ASP:HB2	83:Q:67:ARG:HH12	1.22	1.04
32:A:2189:C:O2'	32:A:2198:A:N3	1.91	1.04
1:AA:1115:U:N3	20:AS:53:TYR:HB2	1.72	1.03
85:TA:85:LEU:HD23	85:TB:64:ILE:CD1	1.88	1.03
32:A:2060:A:C6	32:A:2079:C:N3	2.21	1.03
81:p:81:TYR:CE1	81:p:99:ALA:HB2	1.92	1.03
32:A:3210:C:N4	69:E:156:ARG:O	1.90	1.02
85:TA:81:ASP:HB3	85:TB:64:ILE:HD12	1.06	1.02
1:AA:699:A:N7	21:AU:28:LYS:HE2	1.74	1.01
1:AA:826:A:N1	6:AJ:56:PRO:CD	2.24	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AO:199:TRP:HZ2	26:A0:171:ARG:HE	1.07	1.00
37:K:155:LEU:HA	37:K:158:TYR:CD2	1.96	1.00
1:AA:826:A:N1	6:AJ:56:PRO:HG2	1.70	1.00
26:A0:171:ARG:NH1	26:A0:188:GLU:CD	2.19	1.00
32:A:2065:A:H8	44:W:74:ARG:CA	1.74	1.00
32:A:2131:A:C5	62:r:168:ARG:NH1	2.30	1.00
32:A:2615:A:C2	38:L:58:ILE:HD12	1.96	1.00
32:A:2606:U:C4	86:z:209:ARG:NH1	2.29	1.00
6:AJ:103:GLN:OE1	86:z:181:PRO:CG	2.09	1.00
1:AA:1126:A:C2	20:AS:53:TYR:CD2	2.50	0.99
32:A:2240:C:N4	62:r:196:HIS:HB2	1.76	0.99
37:K:155:LEU:HA	37:K:158:TYR:HE2	1.26	0.99
79:k:58:ASP:CG	85:TA:53:LEU:HD21	1.86	0.99
32:A:1939:G:N2	32:A:2495:U:O4'	1.95	0.99
32:A:2493:C:N4	32:A:2540:C:C2	2.30	0.99
1:AA:1154:A:OP2	27:A3:155:ARG:NH1	1.96	0.98
32:A:3203:A:C1'	69:E:303:LYS:HZ2	1.65	0.98
64:I:189:GLN:HG2	85:TA:55:ASN:ND2	1.72	0.98
1:AA:1526:U:C5	22:AV:102:TRP:CD2	2.51	0.98
26:A0:171:ARG:NH1	26:A0:188:GLU:OE2	1.97	0.98
12:AQ:77:ARG:HH12	14:AW:149:LEU:CB	1.76	0.98
85:TA:81:ASP:CB	85:TB:64:ILE:HD12	1.94	0.97
32:A:1751:A:H4'	39:M:64:ARG:CZ	1.94	0.97
32:A:1902:C:O2	57:i:127:PHE:CD2	2.17	0.97
12:AQ:77:ARG:NH1	14:AW:149:LEU:HD13	1.79	0.97
32:A:1832:A:N6	54:b:4:ARG:NH1	2.12	0.97
32:A:2379:C:N4	73:9:48:TRP:CZ2	2.33	0.97
32:A:2172:A:O2'	63:J:23:ILE:HG13	1.65	0.97
32:A:2606:U:C5	86:z:209:ARG:NH1	2.32	0.96
33:B:1607:U:H3	33:B:1664:G:H1	0.97	0.96
32:A:2172:A:H2'	63:J:23:ILE:HG13	1.46	0.96
32:A:2753:A:H1'	36:H:88:HIS:CE1	1.99	0.96
32:A:2176:C:P	63:J:99:LYS:HZ1	1.87	0.96
32:A:2388:A:H61	34:D:127:ILE:HG21	1.26	0.96
32:A:2172:A:C2'	63:J:23:ILE:HG13	1.96	0.96
32:A:2155:A:C6	60:o:26:PHE:CE2	2.53	0.96
32:A:2155:A:H2	60:o:26:PHE:CE1	1.75	0.96
85:TA:82:LEU:HD23	85:TB:67:LEU:HD13	1.48	0.95
85:TA:85:LEU:HA	85:TA:88:LYS:CD	1.95	0.95
1:AA:1265:C:OP1	7:AK:112:ARG:NH1	1.99	0.95
1:AA:1515:G:O3'	18:AL:223:ARG:NH1	1.99	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2058:C:O2	47:Z:109:LYS:NZ	1.97	0.95
32:A:2155:A:N1	60:o:26:PHE:CE2	2.34	0.95
32:A:2235:C:C5	37:K:78:SER:HB2	2.01	0.95
55:e:243:PHE:CE2	55:e:246:ALA:CA	2.07	0.95
81:p:81:TYR:CE1	81:p:99:ALA:CB	2.49	0.95
1:AA:1526:U:C5	22:AV:102:TRP:CE3	2.55	0.95
15:AX:364:ASN:OD1	30:AF:139:ARG:NH1	2.00	0.95
36:H:99:THR:C	36:H:108:ARG:CD	2.40	0.95
32:A:2094:G:OP2	39:M:57:ARG:NH2	1.98	0.95
32:A:2442:U:H4'	82:s:85:LYS:HD2	1.49	0.94
32:A:3199:U:C5'	32:A:3201:A:C8	2.37	0.94
32:A:2442:U:H5''	82:s:81:ARG:HH22	1.31	0.94
32:A:2198:A:C6	63:J:150:SER:HB2	2.03	0.94
85:TA:74:LEU:HD13	85:TA:78:GLU:HB3	1.49	0.94
32:A:2065:A:C8	44:W:74:ARG:CA	2.48	0.94
85:TA:81:ASP:CG	85:TB:64:ILE:HD13	1.93	0.94
1:AA:826:A:N1	6:AJ:56:PRO:HD2	1.83	0.94
1:AA:826:A:H62	6:AJ:55:ARG:HG3	1.33	0.94
85:TA:85:LEU:HD23	85:TB:64:ILE:HG13	0.96	0.94
32:A:2189:C:O2'	32:A:2198:A:C2	2.21	0.94
32:A:1812:C:O2	75:c:45:LEU:HD22	1.66	0.93
32:A:3203:A:C4	32:A:3204:C:O2	2.22	0.92
85:TA:64:ILE:HG22	85:TB:85:LEU:HD22	1.50	0.92
32:A:2131:A:C5	62:r:168:ARG:CZ	2.45	0.92
32:A:2370:A:OP1	67:U:41:GLN:NE2	2.01	0.92
32:A:2493:C:C6	32:A:2540:C:N4	2.38	0.92
1:AA:1589:C:OP2	12:AQ:47:LYS:NZ	2.02	0.92
32:A:2606:U:O4	86:z:209:ARG:NH1	2.03	0.92
1:AA:826:A:H62	6:AJ:55:ARG:CG	1.83	0.92
32:A:2198:A:N6	63:J:150:SER:HB3	1.82	0.92
32:A:1811:A:N6	75:c:49:ARG:NE	2.18	0.91
22:AV:52:ASP:CB	83:Q:67:ARG:HH12	1.84	0.91
1:AA:699:A:N6	21:AU:32:ASP:OD2	2.04	0.91
32:A:2274:A:OP1	75:c:36:ARG:HD2	1.70	0.91
83:Q:71:PRO:O	83:Q:212:ASN:ND2	2.02	0.91
32:A:2493:C:C6	32:A:2540:C:C4	2.59	0.91
32:A:1811:A:H61	75:c:49:ARG:NE	1.69	0.91
32:A:2372:U:C6	67:U:96:TYR:CD1	2.59	0.90
32:A:1939:G:H21	32:A:2495:U:H1'	1.36	0.90
37:K:155:LEU:CB	37:K:158:TYR:HE2	1.83	0.90
32:A:2065:A:C8	44:W:74:ARG:CB	2.55	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1832:A:N6	54:b:4:ARG:HH12	1.70	0.90
1:AA:1560:U:HO2'	32:A:2582:A:H2	0.94	0.90
32:A:2379:C:C5	73:9:48:TRP:NE1	2.39	0.89
32:A:2388:A:N6	34:D:127:ILE:HG21	1.86	0.89
64:I:189:GLN:CG	85:TA:55:ASN:HD21	1.85	0.89
83:Q:73:ARG:NH1	83:Q:215:VAL:HG13	1.84	0.89
83:Q:73:ARG:HH12	83:Q:215:VAL:CG1	1.81	0.89
32:A:1731:A:C6	57:i:118:TYR:CD1	2.60	0.89
32:A:2155:A:C2	60:o:26:PHE:CE2	2.60	0.89
32:A:3127:G:H2'	32:A:3128:A:H2'	1.52	0.89
83:Q:73:ARG:HH11	83:Q:215:VAL:HG13	1.36	0.89
12:AQ:77:ARG:HH12	14:AW:149:LEU:HB3	1.36	0.88
32:A:2501:C:H41	50:2:49:ARG:HB3	1.36	0.88
64:I:189:GLN:CG	85:TA:55:ASN:ND2	2.29	0.88
1:AA:826:A:C2	6:AJ:56:PRO:CG	2.52	0.88
1:AA:826:A:H61	6:AJ:56:PRO:HD2	1.12	0.88
1:AA:812:A:P	38:L:43:ASN:HD21	1.96	0.88
32:A:3203:A:N3	32:A:3204:C:O2	2.07	0.88
1:AA:925:U:O2'	6:AJ:54:GLY:O	1.91	0.88
32:A:3110:C:N3	32:A:3203:A:N1	2.21	0.88
1:AA:649:A:C6	29:AD:422:TRP:CE2	2.61	0.88
1:AA:1380:G:H1'	15:AX:164:ASN:ND2	1.89	0.88
32:A:2239:A:OP2	37:K:75:LYS:NZ	2.06	0.88
69:E:269:TYR:HE1	69:E:303:LYS:CE	1.86	0.88
32:A:2240:C:OP2	37:K:71:LYS:NZ	2.08	0.87
32:A:2395:A:C8	70:5:384:HIS:CE1	2.63	0.87
32:A:2176:C:P	63:J:99:LYS:NZ	2.45	0.87
32:A:2493:C:C5	32:A:2540:C:N3	2.43	0.87
85:TA:85:LEU:HD22	85:TB:64:ILE:O	1.74	0.87
1:AA:928:A:C2	29:AD:421:VAL:HG11	2.09	0.87
32:A:2379:C:C6	73:9:48:TRP:CD1	2.63	0.87
1:AA:1287:A:OP1	29:AD:230:THR:OG1	1.92	0.87
32:A:3189:C:O2	62:r:154:TRP:CE3	2.28	0.87
85:TA:85:LEU:HD11	85:TB:67:LEU:CB	2.04	0.87
32:A:2373:A:C2	82:s:274:PHE:CG	2.63	0.87
32:A:2499:U:OP2	32:A:2504:A:N6	2.07	0.87
32:A:1883:G:H5'	56:g:91:MET:HE3	1.56	0.86
32:A:2615:A:C6	38:L:58:ILE:CB	2.57	0.86
32:A:2961:C:C5	32:A:2962:C:N4	2.44	0.86
32:A:3189:C:O2	62:r:154:TRP:CG	2.27	0.86
32:A:2442:U:H5''	82:s:81:ARG:NH2	1.89	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1811:A:N6	75:c:49:ARG:CZ	2.38	0.86
32:A:2214:A:H5'	80:l:126:ILE:HD11	1.57	0.85
85:TA:68:VAL:HG21	85:TB:85:LEU:CG	2.06	0.85
85:TA:85:LEU:CD2	85:TB:64:ILE:O	2.24	0.85
1:AA:1341:C:OP1	24:AZ:99:GLY:HA3	1.75	0.85
32:A:2615:A:N6	38:L:58:ILE:CB	2.40	0.85
32:A:3203:A:C2	32:A:3204:C:C2	2.63	0.85
32:A:2257:C:OP1	58:j:61:LYS:CB	2.24	0.85
1:AA:1115:U:C5	20:AS:53:TYR:O	2.30	0.84
81:p:81:TYR:CD1	81:p:99:ALA:HB2	2.12	0.84
32:A:1834:U:C2	43:T:205:SER:O	2.30	0.84
32:A:2017:U:OP1	39:M:54:LYS:NZ	2.09	0.84
36:H:100:GLN:N	36:H:108:ARG:HD3	1.91	0.84
32:A:2529:U:OP2	34:D:208:ARG:NE	2.10	0.84
1:AA:1038:C:O2'	18:AL:154:TYR:OH	1.94	0.84
32:A:2060:A:C5	32:A:2079:C:C4	2.66	0.84
1:AA:764:A:O4'	1:AA:765:C:N3	2.11	0.83
32:A:2175:C:OP1	63:J:99:LYS:HE2	1.79	0.83
32:A:1902:C:C2	57:i:127:PHE:CD2	2.66	0.83
81:p:81:TYR:OH	81:p:147:LEU:CB	2.25	0.83
85:TA:85:LEU:CB	85:TA:88:LYS:HE3	2.09	0.83
1:AA:881:A:N6	10:AO:82:LYS:HG3	1.93	0.83
32:A:2493:C:C5	32:A:2540:C:N4	2.45	0.83
1:AA:1382:A:C5'	15:AX:166:ARG:NH1	2.42	0.83
85:TA:64:ILE:HG22	85:TB:85:LEU:HD23	1.59	0.82
32:A:3203:A:H1'	69:E:303:LYS:CE	2.09	0.82
1:AA:1465:C:OP1	16:A2:39:GLU:HB2	1.78	0.82
85:TA:85:LEU:HA	85:TA:88:LYS:CG	2.10	0.82
70:5:255:PHE:CD1	70:5:258:ILE:O	2.33	0.82
1:AA:764:A:N6	18:AL:213:PHE:CD2	2.48	0.82
32:A:2493:C:C4	32:A:2540:C:C4	2.68	0.82
1:AA:1368:U:OP2	30:AF:197:GLN:HG2	1.79	0.81
37:K:155:LEU:CB	37:K:158:TYR:CE2	2.60	0.81
70:5:255:PHE:HE1	70:5:258:ILE:O	1.61	0.81
1:AA:740:G:O3'	21:AU:86:ARG:NH2	2.13	0.81
81:p:81:TYR:OH	81:p:147:LEU:CD1	2.28	0.81
55:e:243:PHE:CZ	55:e:246:ALA:HA	2.10	0.81
32:A:2155:A:N3	60:o:26:PHE:CG	2.49	0.81
32:A:2389:C:OP1	70:5:300:PRO:HB2	1.80	0.81
79:k:58:ASP:OD2	85:TA:56:ALA:HB3	1.81	0.81
83:Q:73:ARG:HH12	83:Q:215:VAL:HG12	1.46	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1731:A:C6	57:i:118:TYR:CG	2.69	0.81
32:A:3199:U:C5'	32:A:3201:A:C5	2.64	0.80
69:E:269:TYR:CE1	69:E:303:LYS:CE	2.61	0.80
85:TA:68:VAL:HG11	85:TB:85:LEU:HG	1.62	0.80
12:AQ:77:ARG:NH1	14:AW:149:LEU:CD1	2.43	0.80
32:A:2009:G:OP1	57:i:112:LYS:HD3	1.80	0.80
85:TA:68:VAL:HG21	85:TB:85:LEU:HB3	1.64	0.80
85:TA:85:LEU:HA	85:TA:88:LYS:HG3	1.61	0.80
32:A:2170:G:O2'	63:J:87:VAL:HG21	1.80	0.80
32:A:3157:C:O2'	83:Q:85:GLY:HA2	1.82	0.80
64:I:185:ILE:CG2	85:TA:51:ALA:HB1	2.11	0.80
36:H:99:THR:HA	36:H:108:ARG:NE	1.97	0.80
32:A:3157:C:N4	40:O:14:VAL:HB	1.97	0.80
85:TB:74:LEU:HD23	85:TB:79:ILE:HG12	1.62	0.80
32:A:1751:A:H4'	39:M:64:ARG:NE	1.98	0.79
82:s:351:VAL:HG12	82:s:353:ARG:H	1.46	0.79
1:AA:762:G:OP1	18:AL:205:LYS:NZ	2.16	0.79
32:A:2131:A:C6	62:r:168:ARG:NE	2.36	0.79
1:AA:764:A:O4'	1:AA:765:C:C2	2.35	0.79
26:A0:171:ARG:NH1	26:A0:188:GLU:OE1	2.15	0.79
32:A:3169:C:H6	32:A:3201:A:H61	1.29	0.79
1:AA:1429:C:H4'	1:AA:1430:A:O5'	1.80	0.79
64:I:185:ILE:HB	85:TA:51:ALA:HB2	1.64	0.79
32:A:2379:C:C4	73:9:48:TRP:CZ2	2.71	0.79
32:A:1832:A:H62	54:b:4:ARG:CZ	1.97	0.78
32:A:2373:A:N1	82:s:274:PHE:CB	2.46	0.78
1:AA:1252:G:H5''	7:AK:30:VAL:HG12	1.65	0.78
85:TA:61:PRO:HB2	85:TA:64:ILE:HD13	1.64	0.78
81:p:81:TYR:HE1	81:p:99:ALA:HB2	1.43	0.78
30:AF:123:PHE:CE2	30:AF:139:ARG:HD3	2.18	0.78
1:AA:676:G:OP1	6:AJ:129:LYS:NZ	2.16	0.78
1:AA:812:A:OP1	38:L:43:ASN:ND2	2.17	0.78
32:A:1769:C:C4	35:F:108:ARG:HD2	2.19	0.78
1:AA:892:A:OP1	6:AJ:77:ASN:O	1.99	0.78
32:A:3203:A:H1'	69:E:303:LYS:HZ3	0.95	0.78
32:A:2094:G:OP1	39:M:57:ARG:HD3	1.83	0.78
32:A:2745:A:H4'	45:X:102:LYS:O	1.83	0.78
32:A:3189:C:C2	62:r:154:TRP:CE3	2.71	0.78
32:A:2082:G:OP1	60:o:66:ARG:NH2	2.17	0.77
32:A:2172:A:H2'	63:J:23:ILE:HG12	1.65	0.77
32:A:1751:A:H5''	39:M:64:ARG:HE	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2214:A:H5'	80:l:126:ILE:CD1	2.14	0.77
64:I:197:LEU:CD1	85:TB:80:SER:OG	2.33	0.77
85:TA:81:ASP:CB	85:TB:64:ILE:HD13	2.15	0.77
1:AA:1452:U:OP1	31:AG:380:LYS:O	2.02	0.77
32:A:2094:G:P	39:M:57:ARG:HD3	2.24	0.77
32:A:2171:U:H4'	32:A:2172:A:H3'	1.66	0.77
1:AA:1115:U:H4'	1:AA:1116:A:OP2	1.83	0.77
32:A:2065:A:OP1	77:f:48:TYR:N	2.18	0.77
32:A:1832:A:N6	54:b:4:ARG:CZ	2.48	0.77
32:A:2501:C:H41	50:2:49:ARG:CB	1.96	0.77
32:A:2212:C:H2'	32:A:2213:A:H8	1.49	0.77
32:A:2170:G:O2'	63:J:87:VAL:CG2	2.32	0.77
32:A:2961:C:C4	32:A:2962:C:N4	2.53	0.77
1:AA:1116:A:N3	1:AA:1116:A:H2'	1.98	0.77
1:AA:1401:G:O2'	7:AK:85:VAL:HG21	1.85	0.77
12:AQ:77:ARG:HH22	14:AW:149:LEU:HD13	1.48	0.77
1:AA:1539:C:N4	38:L:52:HIS:HD2	1.83	0.76
1:AA:736:C:OP2	21:AU:68:ARG:NH2	2.18	0.76
3:AC:113:ARG:HB2	17:AH:166:GLU:HG3	1.68	0.76
32:A:1731:A:N6	57:i:118:TYR:HD1	1.82	0.76
32:A:2373:A:C2	82:s:274:PHE:CD2	2.73	0.76
81:p:81:TYR:CD1	81:p:99:ALA:CB	2.68	0.76
1:AA:1146:C:OP1	27:A3:161:ARG:NH2	2.18	0.76
32:A:2897:A:C2	32:A:2898:U:C5	2.73	0.76
32:A:3011:A:O2'	32:A:3173:G:N2	2.18	0.76
1:AA:764:A:N6	18:AL:213:PHE:CE2	2.53	0.76
32:A:1805:A:H5'	68:V:96:ARG:HD3	1.68	0.76
1:AA:699:A:C5	21:AU:28:LYS:HE2	2.20	0.76
1:AA:773:U:H2'	1:AA:774:G:H8	1.50	0.76
1:AA:1025:A:C8	18:AL:153:ARG:CZ	2.69	0.76
32:A:2155:A:C2	60:o:26:PHE:CG	2.73	0.76
32:A:2373:A:C2	82:s:274:PHE:CB	2.68	0.76
32:A:2510:U:O2'	34:D:260:ALA:HB2	1.86	0.76
36:H:99:THR:HA	36:H:108:ARG:CZ	2.15	0.76
1:AA:1016:U:O2'	11:AP:90:CYS:HB3	1.86	0.76
32:A:1902:C:O2	57:i:127:PHE:CE2	2.39	0.76
1:AA:1526:U:O2	26:A0:99:ARG:HA	1.86	0.75
1:AA:826:A:N1	6:AJ:56:PRO:HG3	2.00	0.75
32:A:2198:A:N3	32:A:2198:A:H2'	2.01	0.75
1:AA:1332:A:H1'	7:AK:109:ILE:HG21	1.68	0.75
32:A:2559:U:H1'	32:A:2560:G:OP2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2060:A:C2	32:A:2061:C:C5	2.74	0.75
1:AA:975:A:H2	5:AI:183:HIS:HB2	1.51	0.75
12:AQ:77:ARG:HH12	14:AW:149:LEU:CD1	1.98	0.75
37:K:155:LEU:CA	37:K:158:TYR:HE2	1.77	0.75
32:A:2897:A:N1	32:A:2898:U:C5	2.56	0.74
85:TA:76:LEU:HA	85:TA:79:ILE:HD12	1.68	0.74
1:AA:1115:U:C2	20:AS:53:TYR:HB2	2.21	0.74
1:AA:1558:A:OP2	6:AJ:72:LYS:NZ	2.20	0.74
1:AA:1332:A:C4	7:AK:109:ILE:HG12	2.22	0.74
1:AA:1502:A:N3	32:A:2622:G:H1'	2.02	0.74
32:A:1713:A:N6	70:5:68:PRO:HB3	2.02	0.74
85:TA:85:LEU:CB	85:TA:88:LYS:CE	2.65	0.74
85:TA:85:LEU:HD13	85:TB:65:GLN:HA	1.70	0.74
82:s:351:VAL:CG1	82:s:353:ARG:H	2.01	0.74
83:Q:73:ARG:O	83:Q:74:ARG:HB3	1.87	0.74
85:TA:85:LEU:CD2	85:TB:64:ILE:C	2.57	0.74
32:A:2678:A:N1	48:0:81:PRO:HD3	2.02	0.73
85:TA:68:VAL:HG21	85:TB:85:LEU:CB	2.18	0.73
15:AX:133:GLY:HA3	89:AX:500:GDP:HN22	1.53	0.73
32:A:2379:C:C6	73:9:48:TRP:NE1	2.56	0.73
32:A:2615:A:N6	38:L:58:ILE:CG2	2.51	0.73
1:AA:1233:C:H42	1:AA:1444:A:H61	1.36	0.73
32:A:2961:C:C5	32:A:2962:C:C4	2.76	0.73
1:AA:1382:A:H5'	15:AX:166:ARG:NH1	2.03	0.73
32:A:1738:U:O4	32:A:1760:G:N2	2.21	0.73
32:A:2388:A:H61	34:D:127:ILE:CG2	2.01	0.73
32:A:3203:A:N1	32:A:3204:C:C2	2.56	0.73
32:A:1677:C:H5''	75:c:31:VAL:HG12	1.70	0.73
65:N:50:LEU:H	65:N:110:ASN:HD21	1.37	0.73
70:5:255:PHE:HE1	70:5:258:ILE:C	1.95	0.73
82:s:351:VAL:HG12	82:s:353:ARG:N	2.03	0.73
32:A:1690:C:O2	46:Y:213:ARG:NE	2.20	0.73
17:AH:97:LEU:O	17:AH:101:GLU:HB2	1.89	0.73
32:A:2025:C:OP2	42:S:182:LYS:NZ	2.21	0.73
32:A:2373:A:C2	82:s:274:PHE:HB2	2.22	0.72
32:A:1939:G:H22	32:A:2495:U:C1'	1.93	0.72
32:A:2493:C:C4	32:A:2540:C:C5	2.77	0.72
1:AA:918:A:OP1	10:AO:92:LYS:HB2	1.89	0.72
15:AX:348:TYR:HB2	15:AX:386:ALA:HB1	1.70	0.72
30:AF:126:TYR:CD1	30:AF:139:ARG:NE	2.57	0.72
32:A:2325:U:OP2	82:s:55:SER:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2279:U:OP2	57:i:46:ARG:NH2	2.23	0.72
32:A:3082:G:N2	32:A:3085:A:OP2	2.22	0.72
70:5:255:PHE:CD1	70:5:258:ILE:HB	2.25	0.72
1:AA:1249:U:C4	24:AZ:56:HIS:CE1	2.78	0.72
1:AA:1444:A:H5'	24:AZ:42:LEU:HD11	1.72	0.72
55:e:243:PHE:CE2	55:e:246:ALA:CB	2.73	0.72
85:TA:85:LEU:CA	85:TA:88:LYS:CE	2.57	0.72
1:AA:1526:U:H5	22:AV:102:TRP:CD2	2.07	0.72
1:AA:1320:G:OP1	3:AC:41:ARG:NH1	2.23	0.72
1:AA:1341:C:OP1	24:AZ:99:GLY:CA	2.37	0.72
32:A:2389:C:OP1	70:5:300:PRO:CB	2.38	0.72
1:AA:1526:U:H5	22:AV:102:TRP:CE3	2.06	0.72
32:A:3203:A:H1'	69:E:303:LYS:HZ2	0.91	0.72
32:A:1939:G:H21	32:A:2495:U:C1'	1.89	0.71
1:AA:1442:G:OP1	7:AK:102:ARG:HB3	1.91	0.71
32:A:2379:C:C4	73:9:48:TRP:CE2	2.78	0.71
32:A:3157:C:O2'	83:Q:84:ARG:C	2.34	0.71
1:AA:1225:C:HO2'	1:AA:1449:G:HO2'	1.32	0.71
22:AV:250:ILE:HG22	22:AV:252:LYS:H	1.56	0.71
25:A1:266:LEU:HD13	25:A1:283:LEU:HB3	1.73	0.71
32:A:2388:A:C2	34:D:128:GLN:OE1	2.43	0.71
1:AA:1380:G:H1'	15:AX:164:ASN:HD21	1.53	0.71
22:AV:52:ASP:HB2	83:Q:67:ARG:NH1	2.01	0.71
32:A:2213:A:H4'	80:l:129:HIS:CD2	2.25	0.71
85:TA:64:ILE:O	85:TB:85:LEU:HD23	1.89	0.71
1:AA:1380:G:O2'	15:AX:164:ASN:CG	2.34	0.71
32:A:1787:G:N2	32:A:1790:A:OP2	2.21	0.71
1:AA:1115:U:N3	20:AS:53:TYR:CB	2.51	0.71
85:TA:68:VAL:HG21	85:TB:85:LEU:HG	1.70	0.71
1:AA:1115:U:C6	20:AS:53:TYR:O	2.43	0.71
32:A:2067:C:H4'	77:f:60:LYS:HB2	1.72	0.71
6:AJ:66:PHE:HE2	6:AJ:82:ARG:NE	1.87	0.71
32:A:1833:C:H4'	43:T:209:VAL:HG23	1.72	0.71
85:TA:68:VAL:CG2	85:TB:85:LEU:HD23	2.20	0.71
1:AA:1126:A:C2	20:AS:53:TYR:CE2	2.78	0.70
32:A:1678:C:O2	68:V:42:ARG:NE	2.18	0.70
32:A:2493:C:C4	32:A:2540:C:C2	2.78	0.70
1:AA:769:G:N2	1:AA:772:A:OP2	2.23	0.70
3:AC:158:VAL:HG11	3:AC:162:VAL:HG22	1.72	0.70
79:k:58:ASP:H	85:TA:53:LEU:HD11	1.54	0.70
1:AA:1126:A:N1	20:AS:53:TYR:CD2	2.59	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1002:C:H2'	1:AA:1003:A:H8	1.55	0.70
1:AA:699:A:N7	21:AU:28:LYS:CE	2.53	0.70
32:A:2175:C:OP1	63:J:99:LYS:CE	2.39	0.70
32:A:2753:A:H1'	36:H:88:HIS:HE1	1.51	0.70
32:A:3199:U:H5'	32:A:3201:A:C5	2.26	0.70
1:AA:826:A:H61	6:AJ:56:PRO:CD	1.88	0.70
32:A:1767:G:N7	46:Y:228:ARG:NH1	2.39	0.70
22:AV:288:LYS:HB2	22:AV:327:LEU:HD13	1.74	0.70
1:AA:1200:G:N2	1:AA:1418:G:O2'	2.25	0.70
32:A:2852:C:HO2'	49:1:45:HIS:HD1	0.70	0.70
64:I:185:ILE:CG2	85:TA:51:ALA:CB	2.70	0.70
24:AZ:69:GLY:HA3	29:AD:135:GLY:HA2	1.73	0.70
32:A:2103:A:OP2	64:I:38:ARG:NH2	2.24	0.70
1:AA:797:C:OP1	8:AM:46:ARG:HD3	1.92	0.69
32:A:1832:A:C6	54:b:4:ARG:NH1	2.58	0.69
32:A:3068:G:N2	32:A:3068:G:OP2	2.25	0.69
1:AA:705:C:C5	26:A0:58:VAL:HG12	2.28	0.69
6:AJ:66:PHE:CE2	6:AJ:82:ARG:HG3	2.27	0.69
32:A:1689:C:H41	45:X:14:LEU:HB3	1.55	0.69
1:AA:1432:U:H4'	31:AG:388:ARG:HG3	1.75	0.69
1:AA:1525:C:H5''	22:AV:103:TYR:HE1	1.57	0.69
32:A:1751:A:C5'	39:M:64:ARG:HE	2.05	0.69
32:A:1834:U:O4	43:T:206:ARG:HB2	1.89	0.69
32:A:2395:A:OP1	70:5:172:ARG:NH2	2.25	0.69
81:p:81:TYR:CE1	81:p:99:ALA:HB1	2.27	0.69
32:A:2065:A:C8	44:W:74:ARG:CG	2.76	0.69
1:AA:649:A:C2	29:AD:422:TRP:CE3	2.80	0.69
1:AA:917:C:OP1	10:AO:91:ARG:HB3	1.92	0.69
32:A:3205:C:OP1	69:E:265:TYR:CE1	2.46	0.69
27:A3:140:HIS:NE2	27:A3:144:ARG:HD2	2.08	0.69
1:AA:1115:U:C4	20:AS:53:TYR:CB	2.76	0.69
9:AN:98:LYS:HE2	9:AN:109:PRO:HA	1.75	0.69
32:A:1834:U:N3	43:T:205:SER:O	2.25	0.69
32:A:1906:G:O2'	35:F:137:ARG:HD3	1.92	0.68
32:A:2373:A:N1	82:s:274:PHE:CG	2.61	0.68
32:A:2530:A:O2'	34:D:229:PRO:HB2	1.94	0.68
32:A:2524:A:C6	34:D:92:ARG:CZ	2.76	0.68
32:A:2961:C:N4	32:A:2962:C:C4	2.61	0.68
25:A1:250:GLU:HG2	25:A1:301:ASN:HD21	1.58	0.68
32:A:2155:A:C2	60:o:26:PHE:CD2	2.81	0.68
54:b:27:GLN:HG2	75:c:78:ARG:HH12	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AM:21:LEU:HD22	8:AM:32:TYR:HB3	1.75	0.68
10:AO:199:TRP:HZ2	26:A0:171:ARG:NE	1.88	0.68
19:AR:172:ILE:HD13	19:AR:189:ARG:HG3	1.75	0.68
32:A:1882:A:OP1	56:g:93:ASN:ND2	2.24	0.68
1:AA:1380:G:O2'	15:AX:164:ASN:ND2	2.26	0.68
1:AA:1444:A:N6	7:AK:85:VAL:HG13	2.09	0.68
32:A:1847:U:OP1	39:M:47:ARG:NE	2.27	0.68
32:A:1902:C:C2	57:i:127:PHE:HD2	2.11	0.68
32:A:2615:A:H1'	38:L:81:LYS:HD3	1.75	0.68
32:A:3205:C:OP1	69:E:265:TYR:CD1	2.47	0.68
16:A2:36:ARG:HH12	16:A2:38:ARG:HD2	1.57	0.68
32:A:1713:A:N6	70:5:68:PRO:CB	2.56	0.68
21:AU:169:THR:H	21:AU:172:ASN:HB2	1.59	0.68
32:A:2241:A:H61	62:r:82:ASN:CG	2.02	0.68
32:A:2615:A:N1	38:L:58:ILE:HB	2.08	0.68
83:Q:76:LEU:HB2	83:Q:283:TRP:HZ3	1.59	0.68
32:A:2702:G:OP1	37:K:114:LYS:HE3	1.93	0.68
56:g:142:GLU:HB3	60:o:88:ILE:HG13	1.74	0.68
1:AA:1382:A:H5''	15:AX:166:ARG:NH1	2.08	0.68
32:A:2155:A:C4	60:o:26:PHE:CD2	2.81	0.68
15:AX:56:PRO:HD2	15:AX:147:LYS:HD3	1.75	0.68
32:A:1820:A:O4'	74:a:128:ARG:NH2	2.27	0.68
32:A:2493:C:C5	32:A:2540:C:C5	2.80	0.68
32:A:2869:A:OP1	51:3:127:ALA:N	2.23	0.68
3:AC:128:SER:HB3	3:AC:131:LYS:HG3	1.75	0.67
32:A:1939:G:H3'	32:A:1939:G:N3	2.08	0.67
32:A:2187:C:H4'	63:J:106:LYS:NZ	2.09	0.67
36:H:53:THR:N	36:H:86:THR:HG1	1.92	0.67
85:TA:84:GLU:O	85:TA:88:LYS:HG3	1.93	0.67
16:A2:38:ARG:HG2	16:A2:39:GLU:H	1.58	0.67
32:A:2678:A:N1	48:0:81:PRO:CD	2.56	0.67
32:A:2160:A:H5'	52:4:88:TRP:CZ2	2.28	0.67
32:A:2355:A:H3'	32:A:2356:A:H4'	1.76	0.67
1:AA:662:U:O2'	1:AA:939:A:N6	2.24	0.67
32:A:2139:U:OP1	47:Z:73:LYS:HA	1.94	0.67
85:TA:81:ASP:HB3	85:TB:64:ILE:HD13	1.73	0.67
32:A:2388:A:C5	34:D:141:LEU:CD2	2.77	0.67
1:AA:996:A:N6	1:AA:1085:C:O2'	2.27	0.67
32:A:1939:G:C2	32:A:2495:U:C1'	2.51	0.67
36:H:70:LYS:HE2	36:H:72:ARG:HH12	1.59	0.67
45:X:223:PRO:HD2	46:Y:160:GLN:HE21	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:I:185:ILE:HB	85:TA:51:ALA:CB	2.23	0.67
32:A:2144:A:OP1	41:R:57:ARG:NH1	2.27	0.67
32:A:2373:A:N1	82:s:274:PHE:HB3	2.10	0.67
55:e:173:LEU:HD12	55:e:174:PRO:HD2	1.76	0.67
32:A:2191:A:N6	32:A:2198:A:OP2	2.28	0.67
32:A:2472:A:N3	32:A:2474:C:N4	2.42	0.67
28:A4:81:ASP:HB3	28:A4:84:ALA:HB2	1.77	0.66
32:A:2167:A:N6	32:A:2212:C:OP2	2.27	0.66
36:H:99:THR:C	36:H:108:ARG:NE	2.52	0.66
1:AA:1115:U:C4	20:AS:53:TYR:HB2	2.30	0.66
1:AA:1332:A:O2'	7:AK:96:ARG:HD3	1.94	0.66
32:A:2389:C:H5''	70:5:300:PRO:HB3	1.77	0.66
32:A:1834:U:O4	43:T:206:ARG:HB3	1.91	0.66
32:A:2655:G:N2	32:A:2659:C:O2'	2.28	0.66
32:A:3089:A:N6	86:z:232:ARG:HD2	2.11	0.66
85:TA:81:ASP:CG	85:TB:64:ILE:CD1	2.61	0.66
22:AV:69:SER:HA	22:AV:72:ILE:HD12	1.77	0.66
32:A:2145:G:N1	32:A:2256:U:O4	2.29	0.66
85:TA:64:ILE:O	85:TB:85:LEU:CD2	2.44	0.66
1:AA:699:A:C8	21:AU:28:LYS:CE	2.79	0.66
32:A:2198:A:H61	63:J:150:SER:HB2	0.55	0.66
1:AA:702:C:O2'	1:AA:842:C:O2	2.14	0.66
32:A:1735:A:N7	36:H:69:ARG:HD3	2.11	0.66
32:A:2559:U:C1'	32:A:2560:G:OP2	2.43	0.66
64:I:197:LEU:HD13	85:TB:80:SER:OG	1.96	0.66
1:AA:917:C:O2'	1:AA:921:U:OP1	2.13	0.66
29:AD:99:TRP:O	29:AD:103:LEU:HB2	1.95	0.66
32:A:2796:G:H21	36:H:88:HIS:CE1	2.13	0.66
37:K:61:ASN:HD21	37:K:131:GLU:HG2	1.60	0.66
1:AA:807:A:C8	26:A0:11:ILE:HG21	2.30	0.66
15:AX:123:ARG:HG2	15:AX:306:ILE:HD11	1.78	0.66
32:A:2421:G:H5''	73:9:24:LYS:HG2	1.76	0.66
81:p:81:TYR:OH	81:p:147:LEU:HD12	1.96	0.66
32:A:1751:A:C5'	39:M:64:ARG:NE	2.59	0.65
32:A:1883:G:C5'	56:g:91:MET:HE3	2.26	0.65
32:A:2493:C:C4	32:A:2540:C:C6	2.83	0.65
32:A:2065:A:C8	44:W:74:ARG:HG3	2.32	0.65
32:A:3203:A:C2'	69:E:303:LYS:HZ3	2.10	0.65
85:TA:85:LEU:CD2	85:TB:64:ILE:CD1	2.62	0.65
25:A1:212:CYS:O	25:A1:218:ASN:ND2	2.30	0.65
26:A0:30:ASP:HA	26:A0:33:LEU:HB3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1794:A:OP1	35:F:142:ARG:NH2	2.29	0.65
32:A:1832:A:N6	54:b:4:ARG:NH2	2.44	0.65
32:A:1834:U:H3	43:T:206:ARG:HA	1.58	0.65
85:TA:68:VAL:HB	85:TB:85:LEU:CD2	2.26	0.65
32:A:2157:U:H5'	62:r:182:ARG:NH1	2.11	0.65
32:A:2395:A:C8	70:5:384:HIS:ND1	2.64	0.65
1:AA:821:U:H2'	1:AA:822:G:H8	1.61	0.65
1:AA:1233:C:OP2	1:AA:1236:C:N4	2.30	0.65
32:A:2842:C:OP2	44:W:41:ASN:OD1	2.15	0.65
32:A:3089:A:C6	86:z:232:ARG:HD2	2.32	0.65
32:A:2230:A:N7	32:A:2975:G:O2'	2.30	0.65
32:A:2615:A:C6	38:L:58:ILE:CG2	2.80	0.65
32:A:2065:A:C8	44:W:74:ARG:HB2	2.32	0.65
32:A:2236:C:N4	32:A:2688:C:O2	2.30	0.65
32:A:1814:A:N3	32:A:1862:U:O2'	2.29	0.65
32:A:2945:A:O2'	32:A:2947:U:O4	2.15	0.65
12:AQ:77:ARG:NH1	14:AW:149:LEU:HB3	2.09	0.64
32:A:1884:G:H1'	32:A:1895:C:H1'	1.77	0.64
1:AA:826:A:C6	6:AJ:56:PRO:HG2	2.32	0.64
32:A:1817:C:OP1	48:0:87:ILE:HD13	1.97	0.64
36:H:98:LEU:O	36:H:108:ARG:NH1	2.30	0.64
63:J:166:ALA:O	63:J:170:GLU:HB2	1.97	0.64
32:A:2897:A:C2	32:A:2898:U:C6	2.86	0.64
32:A:2940:A:N1	32:A:2986:C:N4	2.46	0.64
32:A:3157:C:O2'	83:Q:85:GLY:CA	2.45	0.64
59:m:59:GLN:NE2	59:m:77:MET:O	2.31	0.64
29:AD:141:TRP:HB2	29:AD:145:ASN:H	1.63	0.64
32:A:2373:A:C6	82:s:274:PHE:CD1	2.85	0.64
32:A:3200:U:H3	37:K:97:LEU:HB3	1.61	0.64
1:AA:649:A:N6	29:AD:422:TRP:CE2	2.66	0.64
1:AA:1442:G:OP1	7:AK:102:ARG:CB	2.46	0.64
25:A1:251:TYR:HB2	25:A1:300:LYS:HD2	1.79	0.64
32:A:1809:U:O2	43:T:53:LYS:NZ	2.26	0.64
32:A:2493:C:O2'	32:A:2494:C:H5'	1.98	0.64
32:A:2898:U:O2'	51:3:113:ARG:NH2	2.31	0.64
32:A:2950:U:H2'	32:A:2951:A:H8	1.63	0.64
1:AA:699:A:C8	21:AU:28:LYS:HE3	2.33	0.64
1:AA:996:A:OP2	5:AI:119:ASN:ND2	2.31	0.64
1:AA:1526:U:C6	22:AV:102:TRP:CE3	2.85	0.64
32:A:2111:C:H2'	32:A:2112:A:C8	2.33	0.64
32:A:2995:G:H1	32:A:3067:U:H3	1.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:9:129:GLN:HG2	73:9:134:ASN:HB2	1.78	0.64
85:TA:85:LEU:HB3	85:TA:88:LYS:HE3	1.79	0.64
1:AA:674:U:O2'	1:AA:826:A:N3	2.29	0.64
14:AW:84:LEU:HA	14:AW:87:SER:HB2	1.80	0.64
15:AX:214:GLU:HG3	15:AX:232:ARG:HH12	1.62	0.64
19:AR:141:VAL:HA	19:AR:182:ARG:HA	1.79	0.64
32:A:2060:A:N1	32:A:2061:C:C5	2.66	0.64
1:AA:1522:U:H1'	22:AV:65:LEU:HD22	1.80	0.64
2:AB:223:VAL:HG21	2:AB:229:PRO:HB3	1.79	0.64
64:I:207:LEU:O	85:TA:86:LEU:HD11	1.98	0.64
1:AA:1234:C:C6	7:AK:86:ARG:NE	2.66	0.63
32:A:2172:A:C8	63:J:23:ILE:HG12	2.33	0.63
32:A:2615:A:C5	38:L:58:ILE:HG21	2.33	0.63
63:J:159:LEU:O	63:J:163:GLU:N	2.29	0.63
32:A:2214:A:C5'	80:I:126:ILE:HD11	2.26	0.63
32:A:2388:A:H2	34:D:128:GLN:CD	2.06	0.63
15:AX:74:ASP:OD1	15:AX:143:HIS:NE2	2.32	0.63
32:A:1834:U:N3	43:T:206:ARG:CA	2.51	0.63
32:A:1939:G:O2'	32:A:1973:G:H4'	1.98	0.63
32:A:2814:G:N2	65:N:141:GLY:CA	2.62	0.63
46:Y:128:SER:HB3	46:Y:131:ARG:HH11	1.64	0.63
85:TA:85:LEU:CD2	85:TB:64:ILE:CB	2.74	0.63
1:AA:1402:A:H5'	7:AK:75:ILE:HG12	1.81	0.63
1:AA:1464:G:N3	1:AA:1466:C:N4	2.46	0.63
37:K:155:LEU:O	37:K:158:TYR:CD2	2.51	0.63
64:I:204:GLN:HG3	85:TA:90:LEU:HD13	1.79	0.63
81:p:81:TYR:CE1	81:p:143:GLN:HB2	2.33	0.63
85:TA:57:PRO:O	85:TA:58:LYS:HD3	1.98	0.63
32:A:1762:A:N7	61:q:33:ARG:HG3	2.14	0.63
32:A:1939:G:C8	34:D:259:LYS:HD2	2.33	0.63
70:5:255:PHE:CE1	70:5:258:ILE:C	2.71	0.63
5:AI:140:LYS:HZ1	5:AI:145:ILE:H	1.47	0.63
32:A:3122:U:OP1	32:A:3124:U:H1'	1.98	0.63
1:AA:1234:C:H6	7:AK:86:ARG:HE	1.45	0.63
1:AA:1539:C:N4	38:L:52:HIS:CD2	2.66	0.63
8:AM:23:LEU:HB2	8:AM:43:ARG:HH22	1.63	0.63
15:AX:329:LEU:HB3	15:AX:333:GLY:HA3	1.81	0.63
32:A:1744:A:OP1	39:M:87:HIS:HE1	1.81	0.63
70:5:114:GLU:H	70:5:118:GLN:HE21	1.47	0.63
1:AA:1103:A:N7	1:AA:1574:G:O2'	2.27	0.63
32:A:2257:C:P	58:j:61:LYS:HB2	2.38	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2308:A:OP1	48:O:93:ARG:NH2	2.32	0.63
32:A:2586:U:H2'	32:A:2587:G:H8	1.62	0.63
85:TB:75:THR:O	85:TB:79:ILE:HG13	1.98	0.63
1:AA:735:A:O2'	21:AU:72:MET:SD	2.53	0.62
32:A:2373:A:N3	82:s:274:PHE:CD2	2.66	0.62
32:A:3157:C:H41	40:O:14:VAL:HB	1.63	0.62
35:F:59:ARG:NH1	35:F:88:ALA:O	2.32	0.62
43:T:94:ILE:HD11	43:T:106:LEU:HD11	1.81	0.62
79:k:58:ASP:N	85:TA:53:LEU:HD11	2.14	0.62
85:TA:85:LEU:CA	85:TA:88:LYS:CD	2.75	0.62
1:AA:1116:A:O2'	1:AA:1117:A:OP2	2.17	0.62
32:A:2065:A:N9	44:W:74:ARG:HG3	2.14	0.62
32:A:2365:U:H2'	32:A:2366:G:H8	1.63	0.62
32:A:2661:U:H2'	32:A:2662:A:H8	1.64	0.62
18:AL:68:PRO:HA	18:AL:94:LEU:HD12	1.81	0.62
32:A:2027:A:O2'	32:A:2048:U:OP1	2.17	0.62
32:A:2961:C:C4	32:A:2962:C:C5	2.86	0.62
64:I:204:GLN:HG3	85:TA:90:LEU:CD1	2.28	0.62
32:A:1777:A:H4'	35:F:115:LYS:HE3	1.81	0.62
32:A:2420:U:H1'	73:9:32:GLY:HA2	1.80	0.62
34:D:194:ASN:HD22	34:D:247:VAL:HG22	1.64	0.62
1:AA:918:A:H4'	1:AA:920:G:H4'	1.80	0.62
1:AA:929:A:OP2	29:AD:419:ARG:NH1	2.31	0.62
10:AO:199:TRP:CZ2	26:A0:171:ARG:NE	2.65	0.62
32:A:2530:A:H4'	32:A:2531:U:H5'	1.82	0.62
64:I:185:ILE:HG22	85:TA:51:ALA:HB1	1.80	0.62
19:AR:110:GLN:HE22	29:AD:395:PRO:HB3	1.65	0.62
23:AY:326:SER:O	25:A1:217:GLN:NE2	2.33	0.62
1:AA:736:C:P	21:AU:68:ARG:HH21	2.23	0.62
1:AA:826:A:C6	6:AJ:56:PRO:CG	2.69	0.62
1:AA:964:C:N3	11:AP:102:LYS:NZ	2.47	0.62
32:A:2694:A:N3	32:A:2942:C:O2'	2.33	0.62
32:A:3203:A:C5	32:A:3204:C:O2	2.53	0.62
36:H:99:THR:CA	36:H:108:ARG:NE	2.63	0.62
39:M:104:LEU:HD22	39:M:109:ARG:HD2	1.80	0.62
32:A:2474:C:O2	69:E:231:HIS:NE2	2.29	0.62
1:AA:764:A:C6	18:AL:213:PHE:CD2	2.88	0.62
1:AA:892:A:OP2	6:AJ:76:ALA:CB	2.42	0.62
10:AO:227:GLU:HB3	21:AU:50:PRO:HD2	1.81	0.62
19:AR:202:ARG:HG3	19:AR:234:GLN:HA	1.81	0.62
32:A:2529:U:OP2	34:D:208:ARG:CZ	2.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:TB:70:ASP:OD1	85:TB:71:ILE:HD12	2.00	0.62
86:z:190:ARG:NH1	86:z:260:LEU:O	2.32	0.62
1:AA:812:A:P	38:L:43:ASN:ND2	2.69	0.61
32:A:1974:A:H5'	34:D:261:GLY:HA2	1.81	0.61
32:A:2389:C:C5'	70:5:300:PRO:HB3	2.30	0.61
37:K:4:PHE:HB3	37:K:9:GLN:HB2	1.81	0.61
19:AR:295:ASP:O	19:AR:299:ASN:ND2	2.32	0.61
32:A:1777:A:N6	32:A:1780:U:OP2	2.33	0.61
32:A:3199:U:H4'	32:A:3201:A:C5	2.35	0.61
71:6:155:TYR:O	71:6:267:ARG:NH1	2.33	0.61
79:k:63:CYS:HA	79:k:77:ARG:HA	1.81	0.61
32:A:2065:A:C5	44:W:74:ARG:HD2	2.35	0.61
32:A:2068:C:H5'	32:A:2069:U:OP2	2.00	0.61
32:A:2560:G:OP2	32:A:2560:G:H8	1.82	0.61
32:A:1713:A:C6	70:5:68:PRO:CB	2.83	0.61
74:a:68:PRO:HG2	74:a:71:HIS:HD2	1.65	0.61
15:AX:93:THR:HG21	30:AF:120:ARG:HD3	1.80	0.61
32:A:2275:U:H1'	41:R:12:ASN:HB3	1.82	0.61
1:AA:1589:C:H2'	1:AA:1590:A:H8	1.66	0.61
15:AX:154:HIS:HA	15:AX:261:ALA:HB3	1.82	0.61
25:A1:133:TRP:NE1	25:A1:137:LEU:O	2.34	0.61
32:A:1698:C:O2'	32:A:1702:A:N3	2.33	0.61
1:AA:1382:A:H5''	15:AX:166:ARG:HH12	1.64	0.61
32:A:1823:A:C8	74:a:125:PRO:O	2.54	0.61
32:A:2131:A:N6	62:r:168:ARG:NE	2.47	0.61
32:A:2388:A:H2	34:D:128:GLN:OE1	1.82	0.61
17:AH:75:ARG:HH22	17:AH:77:SER:HB2	1.66	0.61
64:I:185:ILE:HG21	85:TA:51:ALA:CB	2.30	0.61
1:AA:649:A:C6	29:AD:422:TRP:CD2	2.88	0.61
3:AC:148:LYS:HD3	28:A4:140:LEU:HD12	1.83	0.61
5:AI:158:ARG:NH1	12:AQ:23:TYR:OH	2.34	0.61
6:AJ:66:PHE:HE2	6:AJ:82:ARG:HE	1.49	0.61
15:AX:56:PRO:HA	15:AX:59:HIS:HD2	1.65	0.61
32:A:3115:U:H2'	32:A:3116:C:H6	1.66	0.61
1:AA:780:C:C4	18:AL:194:TYR:CE2	2.88	0.61
1:AA:1278:C:OP1	29:AD:269:ARG:NH1	2.34	0.61
1:AA:1428:G:O2'	1:AA:1432:U:O2'	2.19	0.61
2:AB:96:GLY:O	14:AW:152:ARG:NH2	2.33	0.61
15:AX:177:ARG:HB2	15:AX:288:ALA:HB2	1.83	0.61
82:s:351:VAL:CG1	82:s:353:ARG:O	2.49	0.61
1:AA:1315:G:H21	30:AF:36:ARG:HH12	1.47	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2536:G:H2'	32:A:2537:G:H8	1.66	0.60
32:A:3206:C:N3	69:E:178:ILE:HG13	2.16	0.60
1:AA:710:U:O2	21:AU:30:ARG:NH2	2.33	0.60
1:AA:850:U:H1'	21:AU:27:ARG:NH2	2.16	0.60
1:AA:1560:U:O2'	32:A:2582:A:H2	1.74	0.60
32:A:2172:A:C2'	63:J:23:ILE:CG1	2.62	0.60
32:A:2852:C:O2'	49:1:45:HIS:ND1	2.11	0.60
32:A:3089:A:N6	86:z:232:ARG:CD	2.64	0.60
32:A:3150:U:N3	69:E:118:VAL:HG21	2.15	0.60
44:W:100:THR:HG1	44:W:132:HIS:HE2	1.48	0.60
83:Q:118:ARG:HE	83:Q:134:LEU:HD12	1.66	0.60
1:AA:1388:C:H2'	1:AA:1389:G:N3	2.17	0.60
4:AE:105:CYS:O	11:AP:64:LYS:NZ	2.35	0.60
7:AK:56:SER:O	7:AK:60:ASN:ND2	2.34	0.60
32:A:3157:C:N4	40:O:14:VAL:CB	2.64	0.60
48:0:177:ARG:HH12	48:0:179:ARG:HD3	1.66	0.60
8:AM:29:ARG:NH1	13:AT:147:VAL:O	2.34	0.60
26:A0:78:ARG:NH2	26:A0:142:VAL:O	2.34	0.60
32:A:2606:U:C5	86:z:209:ARG:NH2	2.68	0.60
37:K:153:LYS:O	37:K:158:TYR:CE1	2.55	0.60
64:I:207:LEU:CD2	85:TB:82:LEU:HD21	2.31	0.60
1:AA:1292:A:C2	31:AG:216:LEU:HD12	2.36	0.60
1:AA:1473:C:H4'	16:A2:32:ARG:HH12	1.65	0.60
10:AO:79:ARG:HH12	10:AO:87:PRO:HD2	1.66	0.60
32:A:2325:U:P	82:s:55:SER:HB2	2.42	0.60
32:A:2377:G:H21	73:9:32:GLY:CA	2.14	0.60
32:A:2961:C:C2	32:A:2962:C:C5	2.89	0.60
32:A:3199:U:H4'	32:A:3201:A:C8	2.36	0.60
1:AA:752:C:O2'	1:AA:793:C:N4	2.34	0.60
1:AA:1144:U:H2'	1:AA:1145:A:H8	1.66	0.60
15:AX:248:LYS:NZ	15:AX:296:MET:SD	2.74	0.60
25:A1:299:LEU:HD11	25:A1:304:GLU:HG3	1.83	0.60
32:A:1936:A:OP1	32:A:1938:A:N6	2.34	0.60
32:A:2158:U:O2'	62:r:153:ARG:NH2	2.33	0.60
32:A:2822:C:O2'	32:A:2915:C:OP2	2.19	0.60
32:A:3175:A:OP2	32:A:3187:C:N4	2.33	0.60
32:A:3210:C:N4	69:E:156:ARG:C	2.58	0.60
39:M:75:TYR:O	51:3:113:ARG:NH1	2.35	0.60
55:e:85:SER:HG	59:m:50:ARG:H	1.50	0.60
55:e:146:ARG:HA	55:e:151:ARG:HD2	1.83	0.60
1:AA:953:U:O2'	1:AA:954:C:OP2	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AO:169:GLN:HG2	19:AR:229:ASN:HD21	1.66	0.60
29:AD:266:ASP:HB2	29:AD:269:ARG:HH21	1.67	0.60
32:A:2395:A:N7	70:5:384:HIS:CE1	2.69	0.60
32:A:3110:C:O2'	69:E:266:ARG:NH1	2.35	0.60
83:Q:73:ARG:HG3	83:Q:74:ARG:N	2.17	0.60
31:AG:126:LYS:H	31:AG:131:ILE:HD11	1.67	0.60
32:A:2524:A:N6	34:D:92:ARG:CZ	2.65	0.60
64:I:185:ILE:CB	85:TA:51:ALA:HB2	2.32	0.60
70:5:107:HIS:HD2	70:5:109:ARG:H	1.49	0.60
32:A:3189:C:O2'	62:r:155:ALA:N	2.30	0.60
70:5:296:ALA:HB3	70:5:302:ARG:HG3	1.81	0.60
1:AA:1439:A:H2'	1:AA:1440:G:H8	1.65	0.60
11:AP:94:ARG:HH12	11:AP:101:GLY:HA2	1.67	0.60
26:A0:135:MET:SD	26:A0:135:MET:N	2.71	0.60
32:A:2241:A:N6	62:r:82:ASN:OD1	2.33	0.60
3:AC:89:ASP:OD1	3:AC:112:ARG:NH2	2.35	0.59
17:AH:116:GLU:HB3	17:AH:136:MET:HB3	1.83	0.59
22:AV:241:ARG:NH2	26:A0:60:ARG:O	2.34	0.59
26:A0:63:ARG:HB3	26:A0:137:HIS:HD2	1.67	0.59
32:A:2379:C:C5	73:9:48:TRP:CZ2	2.86	0.59
32:A:2814:G:N2	65:N:141:GLY:HA3	2.17	0.59
1:AA:702:C:H5'	1:AA:848:U:H1'	1.83	0.59
1:AA:1382:A:H5'	15:AX:166:ARG:HH11	1.66	0.59
4:AE:44:GLU:HA	4:AE:62:GLY:HA2	1.83	0.59
19:AR:106:MET:HE2	29:AD:371:VAL:HG11	1.84	0.59
32:A:2235:C:C5	37:K:78:SER:CB	2.81	0.59
35:F:282:PRO:O	35:F:290:TYR:OH	2.17	0.59
1:AA:1292:A:N3	31:AG:216:LEU:HD12	2.16	0.59
15:AX:339:PRO:HG2	25:A1:262:ILE:HD13	1.83	0.59
32:A:2379:C:C5	73:9:48:TRP:CD2	2.90	0.59
1:AA:892:A:P	6:AJ:77:ASN:H	2.24	0.59
1:AA:1340:C:H4'	24:AZ:100:LYS:HE3	1.84	0.59
1:AA:1411:G:H2'	1:AA:1412:G:H8	1.67	0.59
4:AE:6:LEU:HB3	4:AE:66:VAL:HB	1.84	0.59
11:AP:54:MET:HE2	11:AP:57:PRO:HD3	1.84	0.59
29:AD:423:SER:OG	29:AD:424:ASN:N	2.35	0.59
32:A:2665:U:OP2	40:O:17:ARG:HD2	2.01	0.59
66:P:90:VAL:HG11	66:P:125:CYS:HB3	1.85	0.59
70:5:255:PHE:CE1	70:5:258:ILE:HB	2.36	0.59
86:z:140:SER:HB2	86:z:143:LEU:HB3	1.83	0.59
1:AA:1025:A:N7	18:AL:153:ARG:CZ	2.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1438:A:H2'	1:AA:1439:A:H8	1.66	0.59
32:A:2388:A:C6	34:D:141:LEU:HD23	2.37	0.59
32:A:2906:C:H42	49:1:19:ARG:HH22	1.49	0.59
64:I:143:LEU:HD12	64:I:146:LEU:HD13	1.84	0.59
76:d:165:THR:HG23	76:d:167:HIS:H	1.68	0.59
79:k:58:ASP:OD1	85:TA:53:LEU:HD21	2.01	0.59
1:AA:1166:A:H4'	1:AA:1167:A:O5'	2.03	0.59
15:AX:370:LYS:HD3	30:AF:85:VAL:HG21	1.84	0.59
32:A:2060:A:C8	32:A:2079:C:N4	2.67	0.59
32:A:2829:C:OP2	32:A:2830:A:O2'	2.18	0.59
1:AA:856:A:OP1	13:AT:162:LYS:N	2.36	0.59
29:AD:325:ARG:NH2	29:AD:430:THR:OXT	2.34	0.59
32:A:2493:C:C4	32:A:2540:C:N3	2.71	0.59
32:A:2537:G:O2'	32:A:2634:U:OP2	2.20	0.59
32:A:3044:A:H2'	32:A:3045:A:C8	2.36	0.59
40:O:45:PRO:HG2	40:O:48:ARG:HD2	1.84	0.59
43:T:137:ARG:NH2	72:7:95:LEU:O	2.34	0.59
15:AX:93:THR:O	30:AF:127:HIS:NE2	2.33	0.59
15:AX:120:PRO:HA	15:AX:302:HIS:HA	1.85	0.59
24:AZ:53:PRO:HD2	24:AZ:55:HIS:HE1	1.68	0.59
32:A:1672:C:OP1	43:T:51:TRP:HB2	2.03	0.59
32:A:1688:A:OP2	45:X:5:LYS:NZ	2.35	0.59
32:A:1823:A:HO2'	74:a:126:HIS:CE1	2.21	0.59
32:A:2661:U:H2'	32:A:2662:A:C8	2.38	0.59
37:K:155:LEU:CG	37:K:158:TYR:HE2	2.16	0.59
85:TA:82:LEU:CD2	85:TB:67:LEU:HD13	2.28	0.59
16:A2:38:ARG:HG2	16:A2:39:GLU:N	2.17	0.59
29:AD:323:ILE:HD11	29:AD:349:LEU:HD23	1.84	0.59
32:A:1731:A:N1	57:i:118:TYR:CG	2.71	0.59
32:A:2740:A:H2'	32:A:2741:A:H8	1.68	0.59
32:A:3089:A:N1	86:z:232:ARG:HD2	2.17	0.59
64:I:93:ASN:ND2	64:I:95:MET:O	2.36	0.59
1:AA:764:A:C6	18:AL:213:PHE:CG	2.91	0.59
19:AR:266:ARG:NH2	19:AR:267:TYR:OH	2.36	0.59
1:AA:668:U:N3	29:AD:422:TRP:CH2	2.71	0.58
1:AA:1138:G:H2'	1:AA:1139:A:H8	1.67	0.58
7:AK:90:ARG:HG2	7:AK:97:PRO:HA	1.85	0.58
26:A0:104:TYR:CE2	26:A0:105:THR:CG2	2.85	0.58
31:AG:253:LYS:HB3	31:AG:365:ARG:HH22	1.68	0.58
32:A:2615:A:N6	38:L:58:ILE:HG22	2.18	0.58
35:F:113:LYS:HG3	35:F:157:GLY:H	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:b:65:VAL:HB	78:h:154:ILE:HG22	1.85	0.58
1:AA:1342:C:OP2	24:AZ:96:LYS:HA	2.02	0.58
1:AA:1380:G:O2'	15:AX:164:ASN:CB	2.51	0.58
21:AU:198:VAL:HG13	21:AU:202:ARG:HH11	1.69	0.58
32:A:2961:C:C2	32:A:2962:C:C6	2.91	0.58
40:O:77:ASP:O	40:O:83:LYS:NZ	2.37	0.58
62:r:36:ARG:NH1	79:k:80:HIS:O	2.36	0.58
22:AV:30:LEU:O	22:AV:34:TYR:N	2.35	0.58
32:A:1689:C:N4	45:X:14:LEU:HB3	2.19	0.58
32:A:1823:A:O2'	74:a:126:HIS:CE1	2.56	0.58
75:c:227:GLU:OE2	75:c:302:ARG:NH1	2.36	0.58
85:TA:68:VAL:CG1	85:TB:85:LEU:HG	2.32	0.58
1:AA:1162:A:N3	1:AA:1497:C:O2'	2.37	0.58
20:AS:78:TYR:OH	20:AS:134:ARG:NH2	2.36	0.58
32:A:1751:A:H5'	39:M:64:ARG:HH21	1.68	0.58
57:i:94:LYS:NZ	57:i:102:MET:SD	2.76	0.58
32:A:3224:G:H2'	32:A:3225:G:H8	1.68	0.58
68:V:33:ARG:NH2	76:d:61:ARG:O	2.36	0.58
83:Q:76:LEU:HB2	83:Q:283:TRP:CZ3	2.37	0.58
32:A:1887:A:O4'	35:F:285:PRO:HD3	2.04	0.58
83:Q:73:ARG:HG3	83:Q:74:ARG:H	1.68	0.58
26:A0:83:LYS:NZ	26:A0:138:ASP:OD1	2.36	0.58
32:A:1705:A:N6	73:9:40:GLY:O	2.37	0.58
32:A:3199:U:C4'	32:A:3201:A:C8	2.87	0.58
42:S:142:THR:OG1	74:a:60:CYS:SG	2.61	0.58
75:c:105:ARG:HD2	75:c:112:LYS:HB2	1.86	0.58
1:AA:1526:U:C5	22:AV:102:TRP:CG	2.92	0.58
7:AK:54:ILE:HG21	7:AK:75:ILE:HB	1.85	0.58
32:A:1831:G:OP2	54:b:4:ARG:HG3	2.04	0.58
32:A:2652:G:N7	32:A:2653:C:N4	2.51	0.58
32:A:2961:C:N4	32:A:2962:C:N3	2.52	0.58
85:TA:62:PRO:O	85:TA:65:GLN:HB2	2.04	0.58
32:A:1813:C:C5	57:i:36:LEU:HD11	2.38	0.58
32:A:1832:A:H62	54:b:4:ARG:NH1	1.90	0.58
32:A:1861:U:OP1	41:R:40:ARG:NH1	2.37	0.58
32:A:2052:A:H5''	56:g:150:LYS:HE3	1.84	0.58
32:A:2060:A:C2	32:A:2061:C:C6	2.92	0.58
32:A:2678:A:H2	48:0:80:ALA:CB	2.17	0.58
1:AA:922:C:H2'	1:AA:923:A:H8	1.67	0.57
1:AA:996:A:H3'	1:AA:997:A:H8	1.69	0.57
2:AB:197:HIS:NE2	2:AB:240:ASP:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AV:91:TYR:HA	22:AV:94:LYS:HZ3	1.69	0.57
25:A1:134:PRO:HG2	25:A1:137:LEU:HD12	1.86	0.57
31:AG:198:ARG:NH1	31:AG:199:TRP:O	2.37	0.57
32:A:1744:A:OP1	39:M:87:HIS:CE1	2.57	0.57
10:AO:105:CYS:HB2	10:AO:108:CYS:H	1.70	0.57
32:A:1805:A:H5'	68:V:96:ARG:CD	2.33	0.57
32:A:2339:G:H4'	50:2:55:PRO:HG2	1.86	0.57
1:AA:700:A:OP2	21:AU:27:ARG:NH1	2.36	0.57
1:AA:1502:A:C2	32:A:2622:G:H1'	2.39	0.57
7:AK:108:ARG:HH12	17:AH:124:VAL:HA	1.68	0.57
15:AX:268:LEU:O	15:AX:294:ARG:NH1	2.36	0.57
32:A:1837:C:OP1	54:b:4:ARG:NH2	2.37	0.57
32:A:2174:G:O2'	63:J:100:GLY:HA3	2.04	0.57
32:A:2372:U:C6	67:U:96:TYR:CE1	2.91	0.57
37:K:153:LYS:O	37:K:158:TYR:HE1	1.86	0.57
72:7:185:LEU:HB3	72:7:189:LEU:HD12	1.85	0.57
1:AA:658:G:H5'	29:AD:229:PHE:HB2	1.87	0.57
1:AA:826:A:N6	6:AJ:55:ARG:HA	2.19	0.57
2:AB:210:ARG:NH2	2:AB:211:ASP:OD1	2.37	0.57
32:A:3002:G:H2'	32:A:3003:A:H8	1.69	0.57
54:b:30:SER:HB2	54:b:76:VAL:HB	1.85	0.57
82:s:188:LEU:HD11	82:s:422:VAL:HG23	1.86	0.57
1:AA:711:U:C6	8:AM:13:ARG:HG3	2.39	0.57
1:AA:1253:C:OP1	7:AK:30:VAL:HB	2.04	0.57
9:AN:18:ILE:HD11	9:AN:29:ARG:HE	1.69	0.57
15:AX:246:GLU:OE1	15:AX:249:ARG:NH2	2.38	0.57
16:A2:38:ARG:CG	16:A2:39:GLU:H	2.17	0.57
32:A:1755:A:O2'	36:H:63:PRO:O	2.23	0.57
32:A:1821:A:OP2	48:0:95:ARG:NH1	2.37	0.57
32:A:2157:U:H5'	62:r:182:ARG:HH12	1.69	0.57
48:0:140:GLN:HG3	48:0:177:ARG:HG2	1.85	0.57
85:TB:83:ASN:HA	85:TB:86:LEU:CD2	2.34	0.57
1:AA:1038:C:O2'	18:AL:154:TYR:CZ	2.57	0.57
1:AA:1389:G:H21	1:AA:1418:G:H1	1.51	0.57
1:AA:1452:U:H2'	1:AA:1453:A:H8	1.69	0.57
3:AC:115:ASN:HD22	23:AY:310:LEU:HA	1.69	0.57
9:AN:31:THR:OG1	13:AT:65:MET:SD	2.63	0.57
16:A2:38:ARG:HH22	16:A2:88:SER:HA	1.70	0.57
19:AR:323:GLU:O	19:AR:327:LEU:N	2.37	0.57
32:A:2187:C:H4'	63:J:106:LYS:HZ1	1.69	0.57
37:K:155:LEU:CA	37:K:158:TYR:CZ	2.57	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:q:48:PRO:HG2	61:q:51:GLN:HG3	1.85	0.57
64:I:204:GLN:CG	85:TA:90:LEU:CD1	2.82	0.57
83:Q:74:ARG:O	83:Q:75:PHE:HB2	2.03	0.57
7:AK:61:THR:OG1	24:AZ:27:ASN:ND2	2.38	0.57
32:A:1713:A:C6	70:5:68:PRO:HB2	2.39	0.57
32:A:1813:C:H5	57:i:36:LEU:HD21	1.68	0.57
32:A:1994:A:O2'	32:A:1995:A:OP2	2.22	0.57
32:A:2145:G:H1'	42:S:104:ARG:NH1	2.19	0.57
32:A:3198:A:H2'	32:A:3201:A:H62	1.68	0.57
34:D:232:ARG:HH11	34:D:293:LYS:HB2	1.70	0.57
46:Y:72:LYS:O	46:Y:76:GLN:NE2	2.38	0.57
83:Q:73:ARG:O	83:Q:74:ARG:CB	2.51	0.57
85:TA:85:LEU:CB	85:TA:88:LYS:NZ	2.67	0.57
32:A:1800:G:N1	32:A:1803:A:OP2	2.37	0.57
32:A:2349:G:O2'	32:A:2351:U:O4	2.23	0.57
34:D:198:SER:HB3	34:D:206:TYR:HE2	1.68	0.57
40:O:143:THR:OG1	40:O:146:ASN:ND2	2.38	0.57
46:Y:115:LEU:HD21	46:Y:127:PRO:HD2	1.87	0.57
51:3:163:THR:HG23	51:3:165:PHE:H	1.70	0.57
81:p:156:ASP:HA	81:p:159:THR:HG22	1.86	0.57
15:AX:382:PHE:O	31:AG:300:TYR:OH	2.22	0.57
19:AR:103:TYR:OH	29:AD:307:LYS:NZ	2.38	0.57
22:AV:81:SER:OG	22:AV:83:GLU:OE1	2.22	0.57
32:A:1828:A:H4'	32:A:1829:A:C8	2.40	0.57
32:A:2094:G:P	39:M:57:ARG:HH21	2.28	0.57
32:A:2615:A:N1	38:L:58:ILE:HD12	2.20	0.57
36:H:99:THR:O	36:H:108:ARG:HD3	2.05	0.57
46:Y:156:LEU:HD12	73:9:91:LEU:HD23	1.87	0.57
83:Q:73:ARG:HH11	83:Q:215:VAL:CG1	1.96	0.57
1:AA:1332:A:C5	7:AK:109:ILE:HG12	2.40	0.56
22:AV:49:CYS:SG	22:AV:50:LEU:N	2.77	0.56
45:X:160:ASP:OD2	45:X:163:ARG:NH1	2.38	0.56
47:Z:75:THR:HB	47:Z:83:LYS:HG2	1.87	0.56
64:I:207:LEU:HD23	85:TB:82:LEU:HD21	1.87	0.56
1:AA:1143:C:OP2	27:A3:136:ARG:HG2	2.05	0.56
17:AH:75:ARG:HG3	17:AH:146:GLU:HG2	1.87	0.56
22:AV:43:ARG:NH2	22:AV:375:TYR:OH	2.37	0.56
22:AV:110:HIS:HA	22:AV:113:ILE:HD12	1.86	0.56
32:A:1683:C:H41	46:Y:225:ASN:HD21	1.52	0.56
1:AA:761:A:OP2	18:AL:199:HIS:HE1	1.88	0.56
1:AA:1431:G:H3'	31:AG:377:ARG:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1515:G:N2	1:AA:1535:U:O2	2.38	0.56
1:AA:1528:A:H4'	26:A0:101:ARG:HD2	1.88	0.56
12:AQ:77:ARG:NH1	14:AW:149:LEU:CB	2.60	0.56
32:A:1751:A:C4'	39:M:64:ARG:NE	2.66	0.56
32:A:1881:A:OP2	56:g:111:ARG:NH2	2.33	0.56
32:A:2132:A:H62	60:o:16:GLN:HE22	1.54	0.56
32:A:2155:A:N3	60:o:26:PHE:CD2	2.71	0.56
32:A:2240:C:C4	62:r:196:HIS:HB2	2.40	0.56
32:A:2606:U:H4'	32:A:2607:U:H3'	1.87	0.56
32:A:3199:U:C4'	32:A:3201:A:C5	2.89	0.56
32:A:3199:U:C4'	32:A:3201:A:N7	2.63	0.56
35:F:63:GLN:HA	35:F:81:ASP:HA	1.88	0.56
37:K:155:LEU:HG	37:K:158:TYR:CE2	2.40	0.56
53:8:97:LYS:HA	53:8:99:ARG:HH21	1.70	0.56
55:e:131:PHE:HB3	59:m:74:MET:HE3	1.88	0.56
63:J:170:GLU:HA	63:J:173:ILE:HG12	1.88	0.56
64:I:139:LYS:O	85:TA:48:LEU:HG	2.04	0.56
72:7:159:LYS:HB2	74:a:88:HIS:HA	1.86	0.56
81:p:81:TYR:OH	81:p:147:LEU:HD13	2.03	0.56
82:s:239:ASN:HB2	82:s:299:PHE:HB2	1.86	0.56
26:A0:171:ARG:CZ	26:A0:188:GLU:OE2	2.54	0.56
32:A:2060:A:C6	32:A:2061:C:N4	2.74	0.56
32:A:3181:U:OP1	62:r:101:PRO:HD3	2.05	0.56
76:d:208:VAL:HG23	76:d:252:LEU:HB2	1.87	0.56
1:AA:684:U:H5'	13:AT:150:PRO:HB2	1.88	0.56
25:A1:190:LEU:HG	25:A1:233:SER:HB3	1.88	0.56
32:A:1877:U:O3'	39:M:30:ASN:ND2	2.38	0.56
32:A:2379:C:H5	73:9:48:TRP:CE2	2.18	0.56
32:A:2529:U:OP2	34:D:208:ARG:NH2	2.37	0.56
32:A:2678:A:C2	48:0:80:ALA:HA	2.40	0.56
32:A:3089:A:C5	86:z:232:ARG:CZ	2.83	0.56
32:A:3203:A:C6	32:A:3204:C:N3	2.73	0.56
85:TB:74:LEU:CD2	85:TB:79:ILE:HG12	2.35	0.56
1:AA:1126:A:OP2	4:AE:119:SER:HB3	2.05	0.56
1:AA:1577:U:H2'	1:AA:1578:A:H8	1.71	0.56
32:A:2148:A:OP1	41:R:99:ARG:HG2	2.06	0.56
32:A:2235:C:C6	37:K:78:SER:HB2	2.40	0.56
32:A:2493:C:C6	32:A:2540:C:C5	2.93	0.56
1:AA:922:C:H2'	1:AA:923:A:C8	2.40	0.56
1:AA:1169:G:H2'	1:AA:1170:G:H8	1.70	0.56
1:AA:1225:C:OP2	1:AA:1360:G:N2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1526:U:O2	26:A0:99:ARG:HG2	2.05	0.56
1:AA:1597:C:OP1	16:A2:25:LYS:NZ	2.37	0.56
2:AB:264:ARG:NH2	2:AB:268:GLU:OE2	2.39	0.56
31:AG:245:ARG:O	31:AG:246:ARG:NH1	2.39	0.56
32:A:2372:U:H6	67:U:96:TYR:CD1	2.21	0.56
32:A:2930:U:H2'	32:A:2931:A:H8	1.70	0.56
20:AS:94:SER:OG	20:AS:96:CYS:SG	2.61	0.56
34:D:228:LEU:HD11	34:D:234:MET:HE3	1.88	0.56
82:s:138:ASP:N	82:s:138:ASP:OD1	2.39	0.56
10:AO:171:GLU:O	19:AR:199:LYS:NZ	2.38	0.56
13:AT:126:PRO:O	13:AT:137:ARG:NH2	2.39	0.56
32:A:1677:C:C5'	75:c:31:VAL:HG12	2.34	0.56
32:A:3201:A:H2'	32:A:3201:A:N3	2.19	0.56
36:H:99:THR:O	36:H:108:ARG:NE	2.39	0.56
37:K:80:HIS:ND1	37:K:81:THR:O	2.37	0.56
85:TA:74:LEU:CD1	85:TA:78:GLU:HB3	2.32	0.56
1:AA:663:A:H2'	1:AA:664:G:H8	1.71	0.56
1:AA:696:U:H2'	1:AA:697:G:C8	2.41	0.56
1:AA:1438:A:H2'	1:AA:1439:A:C8	2.41	0.56
32:A:1823:A:O2'	74:a:126:HIS:ND1	2.35	0.56
32:A:1881:A:OP1	56:g:90:ARG:HG2	2.05	0.56
32:A:2185:G:N1	32:A:2186:C:N4	2.54	0.56
32:A:2186:C:H2'	32:A:2187:C:C6	2.40	0.56
32:A:2372:U:O2	32:A:2372:U:H2'	2.06	0.56
32:A:2372:U:C5	67:U:96:TYR:CD1	2.93	0.56
66:P:175:PRO:HG3	81:p:177:ARG:HD3	1.88	0.56
71:6:184:LEU:HD13	81:p:191:LYS:HD3	1.88	0.56
1:AA:1341:C:C5	24:AZ:94:PRO:HD2	2.41	0.55
32:A:2085:A:H2'	32:A:2086:A:H8	1.69	0.55
32:A:2139:U:OP2	47:Z:74:SER:HB3	2.06	0.55
32:A:2524:A:N6	34:D:92:ARG:NH1	2.53	0.55
32:A:2926:A:O2'	32:A:3087:C:OP1	2.22	0.55
63:J:163:GLU:HA	63:J:166:ALA:HB3	1.88	0.55
1:AA:1530:A:OP1	26:A0:29:ARG:NH2	2.39	0.55
19:AR:75:VAL:HG13	19:AR:303:LEU:HD11	1.88	0.55
32:A:2085:A:H2'	32:A:2086:A:C8	2.41	0.55
32:A:2261:C:C2	42:S:184:ARG:HD2	2.41	0.55
37:K:27:PRO:HG2	37:K:30:LYS:HB2	1.88	0.55
86:z:148:MET:HG3	86:z:155:THR:HG22	1.86	0.55
1:AA:1061:A:H5''	34:D:254:LYS:HZ1	1.71	0.55
1:AA:1289:G:O2'	1:AA:1297:G:OP2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AH:161:GLN:NE2	17:AH:170:MET:SD	2.71	0.55
32:A:1804:A:C6	76:d:68:PRO:HB3	2.41	0.55
32:A:2084:A:N6	60:o:71:PHE:HB2	2.21	0.55
32:A:2559:U:H4'	32:A:2560:G:O5'	2.05	0.55
45:X:143:PHE:O	45:X:147:LYS:HB2	2.06	0.55
55:e:151:ARG:HH22	55:e:259:GLU:HG3	1.71	0.55
17:AH:99:ALA:HA	17:AH:104:ILE:HD12	1.88	0.55
31:AG:253:LYS:O	31:AG:365:ARG:NH1	2.35	0.55
32:A:1823:A:C8	74:a:126:HIS:HA	2.41	0.55
32:A:2135:A:H2'	32:A:2135:A:N3	2.21	0.55
32:A:2385:U:OP1	34:D:71:LYS:HE2	2.05	0.55
83:Q:71:PRO:C	83:Q:212:ASN:ND2	2.64	0.55
1:AA:931:C:C6	6:AJ:42:PRO:HG3	2.42	0.55
1:AA:1055:U:H2'	1:AA:1056:A:H8	1.71	0.55
1:AA:1161:A:H2'	1:AA:1162:A:H8	1.72	0.55
1:AA:1221:A:H5''	1:AA:1222:A:H2'	1.87	0.55
1:AA:1310:C:H5''	17:AH:113:ARG:HH22	1.72	0.55
9:AN:14:VAL:HA	9:AN:65:LEU:HA	1.88	0.55
22:AV:82:ARG:NH1	22:AV:119:TYR:O	2.39	0.55
31:AG:293:ILE:HG23	31:AG:328:VAL:HG23	1.88	0.55
32:A:2545:U:H5''	32:A:2546:G:H5'	1.87	0.55
32:A:3203:A:C6	32:A:3204:C:C2	2.94	0.55
39:M:164:ILE:HG12	39:M:174:VAL:HG11	1.87	0.55
79:k:36:THR:HG21	79:k:87:LEU:HD11	1.87	0.55
1:AA:1121:A:H4'	29:AD:299:LYS:HD2	1.88	0.55
12:AQ:38:ASP:OD1	12:AQ:42:ARG:NH2	2.38	0.55
16:A2:33:VAL:HG21	16:A2:104:LEU:HB3	1.88	0.55
23:AY:361:ASN:ND2	24:AZ:37:PHE:O	2.39	0.55
32:A:2131:A:N6	62:r:168:ARG:HB2	2.22	0.55
82:s:212:ARG:HD3	82:s:379:LEU:HB3	1.89	0.55
85:TA:88:LYS:HZ2	85:TB:65:GLN:HB3	1.71	0.55
22:AV:117:LEU:HD11	22:AV:146:LEU:HD21	1.87	0.55
32:A:1811:A:H61	75:c:49:ARG:CZ	2.09	0.55
32:A:2439:U:H2'	32:A:2440:G:H8	1.72	0.55
32:A:2527:A:C6	70:5:33:TRP:HE3	2.25	0.55
83:Q:73:ARG:NH1	83:Q:215:VAL:HG11	2.14	0.55
85:TA:85:LEU:O	85:TA:88:LYS:HD2	2.06	0.55
1:AA:1488:C:H2'	1:AA:1489:G:H8	1.72	0.55
10:AO:173:ARG:NH2	19:AR:190:ASP:OD1	2.40	0.55
23:AY:280:VAL:HG12	23:AY:284:LYS:HE3	1.88	0.55
32:A:2003:A:OP2	32:A:2734:A:O2'	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2683:C:OP1	48:O:86:THR:HG22	2.06	0.55
32:A:3157:C:N4	40:O:14:VAL:CG2	2.70	0.55
32:A:3204:C:C4	32:A:3205:C:N3	2.75	0.55
47:Z:104:PRO:HA	47:Z:107:ASN:HB2	1.88	0.55
1:AA:1115:U:C5	20:AS:53:TYR:C	2.85	0.55
5:AI:182:PRO:HB2	5:AI:185:GLY:H	1.72	0.55
14:AW:104:ILE:HG13	14:AW:112:LEU:HD23	1.89	0.55
20:AS:114:GLU:HA	20:AS:117:LEU:HD12	1.88	0.55
22:AV:79:ILE:HG23	22:AV:84:GLU:HB2	1.88	0.55
25:A1:169:ARG:HD2	25:A1:213:PRO:HA	1.87	0.55
32:A:1702:A:C8	50:2:66:TRP:CG	2.95	0.55
32:A:1977:U:H2'	32:A:1978:A:H8	1.71	0.55
35:F:252:SER:O	35:F:256:HIS:ND1	2.39	0.55
45:X:175:GLN:H	45:X:184:ARG:HD3	1.72	0.55
85:TB:83:ASN:O	85:TB:86:LEU:HD23	2.06	0.55
1:AA:649:A:C5	29:AD:422:TRP:CD1	2.94	0.55
1:AA:1148:A:OP2	27:A3:165:LYS:HE3	2.07	0.55
1:AA:1285:G:H4'	29:AD:242:ARG:HH12	1.71	0.55
32:A:2402:A:C8	34:D:131:TYR:CE2	2.95	0.55
32:A:2734:A:H2'	32:A:2735:G:H8	1.72	0.55
65:N:81:GLU:O	65:N:123:ARG:NH2	2.40	0.55
82:s:266:CYS:SG	82:s:267:LYS:N	2.80	0.55
85:TA:85:LEU:HD22	85:TB:64:ILE:CG1	2.01	0.55
1:AA:992:U:O2'	1:AA:994:A:OP2	2.24	0.54
15:AX:299:ASN:ND2	15:AX:338:ASP:OD1	2.38	0.54
25:A1:86:ARG:NH1	25:A1:96:PRO:O	2.40	0.54
32:A:1731:A:N6	57:i:118:TYR:CG	2.65	0.54
32:A:2170:G:O2'	63:J:87:VAL:HG23	2.06	0.54
32:A:3115:U:H2'	32:A:3116:C:C6	2.42	0.54
36:H:53:THR:N	36:H:86:THR:OG1	2.39	0.54
1:AA:881:A:H61	10:AO:82:LYS:HG3	1.67	0.54
15:AX:180:GLN:HB2	15:AX:289:LEU:HD22	1.89	0.54
32:A:2615:A:N3	38:L:58:ILE:HD12	2.19	0.54
32:A:2933:G:N2	32:A:2936:U:O2	2.36	0.54
56:g:107:MET:SD	56:g:148:ARG:NH1	2.81	0.54
70:5:214:ARG:NH1	70:5:363:LEU:O	2.39	0.54
81:p:81:TYR:HE1	81:p:99:ALA:CB	2.06	0.54
83:Q:71:PRO:O	83:Q:212:ASN:CG	2.48	0.54
1:AA:1589:C:H2'	1:AA:1590:A:C8	2.43	0.54
12:AQ:77:ARG:HH12	14:AW:149:LEU:CG	2.20	0.54
13:AT:78:PHE:HB2	13:AT:86:VAL:HB	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AX:155:ILE:HD12	15:AX:262:VAL:HB	1.90	0.54
32:A:3024:U:H2'	32:A:3025:A:H8	1.71	0.54
56:g:110:ILE:HD11	56:g:157:LEU:HD13	1.88	0.54
85:TA:85:LEU:HB2	85:TA:88:LYS:HZ2	1.73	0.54
1:AA:1213:A:H2'	1:AA:1214:A:C4	2.43	0.54
10:AO:199:TRP:NE1	26:A0:166:TYR:O	2.33	0.54
32:A:1677:C:O2'	68:V:42:ARG:NH2	2.40	0.54
32:A:1751:A:H5''	39:M:64:ARG:NE	2.17	0.54
32:A:3189:C:OP2	62:r:158:SER:HB3	2.07	0.54
78:h:85:ASN:HB3	78:h:88:ASP:HB2	1.89	0.54
85:TA:68:VAL:CG2	85:TB:85:LEU:CD2	2.86	0.54
9:AN:18:ILE:HD11	9:AN:29:ARG:HB3	1.89	0.54
22:AV:52:ASP:H	83:Q:67:ARG:HH22	1.55	0.54
22:AV:105:ARG:HB2	22:AV:108:THR:HG23	1.90	0.54
22:AV:246:ASN:O	26:A0:70:ARG:NH2	2.38	0.54
27:A3:190:GLN:HE22	27:A3:192:PRO:HB3	1.72	0.54
28:A4:291:VAL:O	28:A4:295:ASN:CB	2.56	0.54
54:b:21:ARG:NH1	75:c:79:LEU:O	2.41	0.54
66:P:160:ARG:HH12	71:6:126:ARG:HB3	1.71	0.54
1:AA:684:U:H4'	13:AT:150:PRO:HG2	1.90	0.54
48:0:136:GLU:OE2	48:0:139:ARG:NH1	2.40	0.54
62:r:173:ARG:HD3	62:r:195:TYR:O	2.07	0.54
1:AA:844:A:N3	26:A0:201:TRP:NE1	2.56	0.54
1:AA:1210:U:H2'	1:AA:1211:G:C8	2.42	0.54
1:AA:1470:A:H2'	1:AA:1471:A:H8	1.73	0.54
7:AK:74:GLU:OE1	23:AY:383:LYS:NZ	2.40	0.54
17:AH:184:ILE:HG12	25:A1:230:TYR:HD2	1.73	0.54
32:A:3189:C:OP1	52:4:85:ARG:N	2.25	0.54
35:F:293:PHE:HB2	56:g:55:THR:HG21	1.89	0.54
1:AA:1211:G:O6	1:AA:1354:A:N6	2.40	0.54
1:AA:1452:U:OP2	31:AG:380:LYS:HD3	2.07	0.54
11:AP:92:TYR:OH	11:AP:140:TYR:OH	2.25	0.54
19:AR:258:LYS:HB3	19:AR:261:LEU:HD12	1.88	0.54
28:A4:125:PRO:O	28:A4:129:GLN:NE2	2.40	0.54
32:A:1760:G:OP2	61:q:59:LYS:NZ	2.39	0.54
63:J:24:VAL:HG11	63:J:35:LEU:HD21	1.89	0.54
85:TA:74:LEU:HD22	85:TA:78:GLU:OE1	2.08	0.54
1:AA:1511:C:H3'	1:AA:1512:A:H5''	1.89	0.54
1:AA:1545:U:H2'	1:AA:1546:A:H8	1.72	0.54
3:AC:113:ARG:HH21	17:AH:164:LEU:HB2	1.73	0.54
32:A:1914:A:H5'	50:2:74:ALA:CB	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2508:C:H2'	32:A:2509:A:C8	2.42	0.54
32:A:3127:G:N2	32:A:3130:A:OP2	2.41	0.54
65:N:172:VAL:O	65:N:176:LEU:HB2	2.07	0.54
79:k:46:ASN:ND2	79:k:49:CYS:SG	2.80	0.54
79:k:57:HIS:CE1	85:TA:53:LEU:N	2.76	0.54
1:AA:1066:C:H2'	1:AA:1067:A:C8	2.42	0.54
1:AA:1491:C:H2'	1:AA:1492:A:H8	1.73	0.54
1:AA:1600:A:N1	16:A2:98:SER:HB3	2.23	0.54
32:A:1811:A:H61	75:c:49:ARG:CD	2.20	0.54
32:A:1813:C:C5	57:i:36:LEU:HD21	2.42	0.54
32:A:1935:A:H3'	32:A:1936:A:H5''	1.89	0.54
32:A:2278:A:OP1	57:i:51:ARG:NH1	2.40	0.54
32:A:2930:U:H2'	32:A:2931:A:C8	2.44	0.54
32:A:3009:C:O2'	32:A:3115:U:OP1	2.23	0.54
32:A:3157:C:Cl'	83:Q:84:ARG:HB3	2.38	0.54
1:AA:751:A:OP1	9:AN:47:LYS:NZ	2.39	0.53
1:AA:1216:C:H2'	1:AA:1217:G:C8	2.44	0.53
1:AA:1488:C:H2'	1:AA:1489:G:C8	2.43	0.53
2:AB:198:THR:OG1	2:AB:227:CYS:SG	2.65	0.53
17:AH:76:LEU:HG	17:AH:145:LEU:HB2	1.90	0.53
20:AS:105:GLU:HA	20:AS:108:LYS:HD2	1.89	0.53
22:AV:262:VAL:HA	22:AV:265:LYS:HB2	1.90	0.53
32:A:1902:C:O2'	57:i:126:LYS:HB2	2.08	0.53
32:A:3124:U:O2	32:A:3124:U:H2'	2.07	0.53
32:A:3199:U:H4'	32:A:3201:A:C4	2.43	0.53
35:F:103:GLN:HE22	35:F:249:ASN:HB2	1.73	0.53
69:E:210:THR:OG1	69:E:262:GLY:O	2.26	0.53
81:p:100:GLU:HG3	81:p:136:THR:HG22	1.89	0.53
82:s:67:GLN:O	82:s:71:HIS:ND1	2.40	0.53
85:TA:85:LEU:CA	85:TA:88:LYS:HG3	2.36	0.53
1:AA:1115:U:C4	20:AS:53:TYR:HB3	2.42	0.53
1:AA:1400:U:H2'	1:AA:1401:G:C8	2.43	0.53
1:AA:1456:U:O2	30:AF:102:GLY:HA3	2.07	0.53
7:AK:41:ARG:NH1	24:AZ:48:THR:O	2.40	0.53
15:AX:222:LEU:HD12	15:AX:225:VAL:HB	1.90	0.53
32:A:2155:A:C6	60:o:26:PHE:CZ	2.81	0.53
32:A:2257:C:OP1	58:j:61:LYS:N	2.42	0.53
32:A:3150:U:C4	69:E:118:VAL:HG21	2.42	0.53
50:2:89:SER:O	50:2:89:SER:OG	2.26	0.53
76:d:79:ALA:HB1	76:d:251:GLN:HE22	1.72	0.53
85:TB:74:LEU:HD12	85:TB:78:GLU:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:661:C:H2'	1:AA:662:U:H6	1.71	0.53
1:AA:1173:C:H2'	1:AA:1174:U:C6	2.43	0.53
2:AB:63:LEU:HD13	2:AB:138:ARG:HH22	1.74	0.53
17:AH:106:ILE:HD12	17:AH:143:LEU:HD22	1.91	0.53
32:A:3018:A:N3	32:A:3126:C:O2'	2.35	0.53
71:6:224:HIS:HD2	71:6:226:LEU:H	1.55	0.53
72:7:159:LYS:HE3	72:7:161:GLU:HB2	1.89	0.53
76:d:192:SER:OG	76:d:215:ARG:O	2.26	0.53
79:k:14:LYS:HE3	79:k:69:GLY:HA2	1.90	0.53
85:TA:68:VAL:CG2	85:TB:85:LEU:HG	2.38	0.53
85:TA:81:ASP:CA	85:TB:64:ILE:CD1	2.86	0.53
86:z:109:ILE:HG23	86:z:193:LEU:HD12	1.90	0.53
86:z:146:VAL:HB	86:z:178:ILE:HB	1.89	0.53
1:AA:1315:G:N2	30:AF:36:ARG:HH12	2.06	0.53
1:AA:1320:G:P	3:AC:37:ASN:HD21	2.31	0.53
1:AA:1429:C:O2	1:AA:1429:C:H2'	2.08	0.53
1:AA:1577:U:H2'	1:AA:1578:A:C8	2.43	0.53
19:AR:187:GLU:OE1	19:AR:191:ARG:NH1	2.41	0.53
25:A1:65:ASP:OD1	25:A1:65:ASP:N	2.40	0.53
32:A:1740:A:H5''	39:M:133:LYS:NZ	2.23	0.53
32:A:2103:A:P	64:I:38:ARG:HH22	2.31	0.53
32:A:2818:C:O2	86:z:227:SER:CB	2.55	0.53
44:W:115:ASP:OD2	44:W:119:ARG:NH2	2.42	0.53
55:e:183:THR:HG23	55:e:186:GLY:H	1.73	0.53
63:J:159:LEU:HG	63:J:163:GLU:HB3	1.90	0.53
81:p:79:ILE:HG12	81:p:101:VAL:HG12	1.89	0.53
19:AR:194:GLN:NE2	19:AR:202:ARG:O	2.41	0.53
29:AD:219:ASP:HB3	29:AD:326:LEU:HD11	1.88	0.53
32:A:1713:A:O2'	32:A:1714:C:OP1	2.24	0.53
32:A:2082:G:N2	47:Z:88:MET:SD	2.81	0.53
32:A:2818:C:O2'	86:z:227:SER:HA	2.09	0.53
34:D:223:THR:HG21	34:D:235:GLN:HE21	1.74	0.53
72:7:45:ASN:HD21	72:7:259:ASP:HA	1.73	0.53
85:TA:88:LYS:HD2	85:TB:68:VAL:HG21	1.90	0.53
1:AA:1309:A:H5'	31:AG:117:PHE:CD2	2.43	0.53
12:AQ:78:LYS:NZ	14:AW:164:GLU:OE2	2.41	0.53
20:AS:89:ASN:HD22	20:AS:92:PHE:HD1	1.55	0.53
22:AV:328:PRO:HA	22:AV:331:LEU:HD12	1.91	0.53
32:A:1703:C:O2'	32:A:1704:U:OP2	2.20	0.53
32:A:1943:A:H2'	32:A:1944:C:H5''	1.91	0.53
32:A:2599:U:OP2	32:A:2625:C:N4	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:3065:U:OP2	69:E:239:ARG:NH1	2.41	0.53
47:Z:39:SER:OG	65:N:222:ASN:ND2	2.41	0.53
1:AA:707:C:O2	1:AA:707:C:H2'	2.08	0.53
1:AA:780:C:C4	18:AL:194:TYR:HE2	2.25	0.53
1:AA:1529:A:H5'	26:A0:104:TYR:HE1	1.73	0.53
2:AB:93:HIS:NE2	2:AB:224:ASP:OD2	2.36	0.53
19:AR:167:HIS:O	19:AR:189:ARG:NH2	2.40	0.53
32:A:1672:C:O2'	43:T:149:ARG:O	2.20	0.53
32:A:2259:C:O2'	32:A:2261:C:OP2	2.16	0.53
32:A:2279:U:OP2	57:i:46:ARG:HD2	2.08	0.53
32:A:3102:U:H2'	32:A:3103:C:H6	1.73	0.53
32:A:3204:C:C5	32:A:3205:C:C2	2.96	0.53
36:H:84:GLU:OE1	45:X:44:ARG:NH2	2.39	0.53
43:T:71:ALA:H	43:T:180:GLU:HG2	1.74	0.53
71:6:236:LEU:HB3	71:6:252:CYS:HB3	1.91	0.53
82:s:237:PRO:HG2	82:s:240:GLN:HE21	1.73	0.53
1:AA:1139:A:H2'	1:AA:1140:A:C8	2.44	0.53
25:A1:175:VAL:HG13	25:A1:205:LEU:HB3	1.91	0.53
26:A0:192:ASN:HD21	26:A0:194:GLN:HB2	1.74	0.53
32:A:1713:A:C6	70:5:68:PRO:HB3	2.43	0.53
32:A:1846:C:P	42:S:177:ARG:H	2.32	0.53
32:A:2523:C:H6	70:5:37:SER:HG	1.55	0.53
33:B:1607:U:O4	33:B:1664:G:O6	2.27	0.53
34:D:125:LYS:HD3	70:5:258:ILE:HD11	1.91	0.53
47:Z:138:CYS:SG	47:Z:139:LEU:N	2.80	0.53
64:I:185:ILE:CB	85:TA:51:ALA:CB	2.86	0.53
72:7:247:ASN:ND2	72:7:251:ILE:O	2.39	0.53
77:f:171:LEU:HA	77:f:174:ILE:HG22	1.91	0.53
1:AA:706:C:OP1	26:A0:43:ARG:NH1	2.42	0.53
1:AA:1361:G:H2'	1:AA:1362:G:H8	1.73	0.53
1:AA:1444:A:C5	7:AK:85:VAL:HG22	2.43	0.53
1:AA:1572:A:H2'	1:AA:1573:A:C8	2.43	0.53
6:AJ:67:THR:HG22	6:AJ:79:LYS:HG3	1.90	0.53
19:AR:202:ARG:NH1	19:AR:234:GLN:O	2.41	0.53
22:AV:187:PHE:O	22:AV:191:ALA:HB3	2.08	0.53
32:A:1673:U:C4	32:A:1674:A:H1'	2.44	0.53
32:A:1867:A:N1	32:A:2019:G:O2'	2.38	0.53
32:A:2198:A:H62	63:J:150:SER:HB3	1.71	0.53
32:A:2302:U:H2'	32:A:2303:A:H8	1.74	0.53
32:A:2383:U:O2'	70:5:92:LEU:HD11	2.08	0.53
32:A:3204:C:C5	32:A:3205:C:N3	2.77	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:s:178:ASP:HA	82:s:181:VAL:HG12	1.90	0.53
1:AA:944:U:H2'	1:AA:945:G:H8	1.73	0.53
15:AX:310:LEU:HD21	15:AX:328:LEU:HD12	1.91	0.53
32:A:1677:C:H5''	75:c:31:VAL:CG1	2.37	0.53
32:A:1851:G:O4'	32:A:2134:A:N6	2.41	0.53
32:A:2493:C:N4	32:A:2540:C:N1	2.57	0.53
32:A:2493:C:C2'	32:A:2494:C:H5'	2.39	0.53
32:A:2606:U:H5	86:z:209:ARG:NE	2.05	0.53
32:A:2661:U:OP2	69:E:238:ARG:NH2	2.41	0.53
36:H:58:ARG:NH2	45:X:66:PRO:O	2.41	0.53
38:L:49:SER:HG	38:L:78:LYS:HZ1	1.57	0.53
46:Y:95:ASN:OD1	46:Y:149:ARG:NH1	2.42	0.53
1:AA:1401:G:HO2'	7:AK:85:VAL:HG21	1.74	0.52
1:AA:1444:A:C6	7:AK:85:VAL:HG13	2.43	0.52
1:AA:1539:C:C5	38:L:52:HIS:HB3	2.43	0.52
3:AC:70:SER:HB2	3:AC:93:ARG:HH21	1.74	0.52
32:A:2961:C:O2	32:A:2961:C:H2'	2.08	0.52
32:A:3018:A:H61	32:A:3130:A:H61	1.57	0.52
35:F:103:GLN:HE22	35:F:249:ASN:HD22	1.57	0.52
63:J:56:ARG:NH2	63:J:80:ILE:O	2.41	0.52
67:U:120:GLY:HA3	67:U:124:ASP:HB3	1.90	0.52
4:AE:41:ASN:O	21:AU:185:LYS:N	2.40	0.52
32:A:1731:A:N3	51:3:99:ALA:CB	2.73	0.52
32:A:2362:A:N6	32:A:2432:A:O4'	2.42	0.52
32:A:2365:U:H2'	32:A:2366:G:C8	2.44	0.52
32:A:2439:U:H2'	32:A:2440:G:C8	2.44	0.52
32:A:3181:U:OP1	62:r:94:ARG:NH2	2.42	0.52
38:L:60:VAL:HA	38:L:73:ILE:HG22	1.91	0.52
48:0:119:LYS:O	48:0:120:HIS:ND1	2.42	0.52
61:q:40:PRO:HG3	61:q:51:GLN:HB3	1.91	0.52
72:7:158:PHE:O	74:a:90:GLN:NE2	2.42	0.52
1:AA:1126:A:N1	20:AS:53:TYR:CG	2.78	0.52
22:AV:235:GLU:HG3	22:AV:243:VAL:HG11	1.91	0.52
32:A:2174:G:H1	32:A:2187:C:H42	1.57	0.52
35:F:141:ILE:HG13	35:F:142:ARG:HG2	1.90	0.52
79:k:57:HIS:CG	85:TA:53:LEU:CB	2.60	0.52
86:z:186:THR:HA	86:z:190:ARG:HE	1.75	0.52
1:AA:1089:U:H2'	1:AA:1090:A:H8	1.72	0.52
32:A:1732:C:O2	32:A:1732:C:H2'	2.08	0.52
32:A:2196:A:H4'	32:A:2213:A:H2	1.74	0.52
32:A:3203:A:C6	32:A:3204:C:O2	2.62	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AJ:103:GLN:OE1	86:z:181:PRO:HG3	2.03	0.52
32:A:1731:A:N3	51:3:99:ALA:HB1	2.25	0.52
32:A:1939:G:N3	32:A:1939:G:C2'	2.73	0.52
32:A:2037:U:H4'	32:A:2040:G:C6	2.43	0.52
32:A:2306:A:O2'	48:0:84:ARG:NH2	2.39	0.52
32:A:2672:A:OP1	43:T:111:LYS:HE2	2.10	0.52
54:b:72:VAL:HG13	54:b:90:HIS:HB2	1.91	0.52
16:A2:33:VAL:HG11	16:A2:104:LEU:HD13	1.91	0.52
32:A:1998:U:O2	50:2:52:GLU:HB3	2.10	0.52
32:A:2470:G:H4'	38:L:36:THR:OG1	2.10	0.52
32:A:2479:C:H2'	32:A:2479:C:O2	2.08	0.52
32:A:2868:C:O2'	39:M:77:ARG:NH1	2.42	0.52
85:TA:64:ILE:HD12	85:TA:64:ILE:H	1.73	0.52
1:AA:818:C:H1'	1:AA:851:A:H1'	1.90	0.52
1:AA:881:A:C6	10:AO:82:LYS:HA	2.45	0.52
1:AA:1431:G:O6	31:AG:276:ARG:NH2	2.43	0.52
3:AC:88:GLU:O	3:AC:92:LEU:HB2	2.09	0.52
22:AV:67:VAL:HG13	22:AV:72:ILE:HD11	1.92	0.52
32:A:2060:A:C6	32:A:2061:C:C4	2.98	0.52
32:A:2155:A:C5	60:o:26:PHE:CE2	2.97	0.52
32:A:2850:U:H2'	32:A:2851:A:N3	2.24	0.52
40:O:32:LEU:HB3	40:O:52:MET:HE2	1.92	0.52
45:X:124:THR:O	70:5:48:ARG:NH2	2.38	0.52
85:TA:68:VAL:CG2	85:TB:85:LEU:CG	2.85	0.52
1:AA:840:A:H2'	1:AA:841:A:C8	2.45	0.52
1:AA:1229:U:H1'	1:AA:1441:A:N3	2.24	0.52
3:AC:125:ARG:HB2	3:AC:159:PRO:HA	1.91	0.52
15:AX:155:ILE:HB	15:AX:262:VAL:HA	1.92	0.52
30:AF:114:THR:HG21	30:AF:205:LEU:HD23	1.92	0.52
31:AG:271:LYS:HG2	31:AG:284:ILE:HG12	1.92	0.52
31:AG:363:TRP:HA	31:AG:366:GLN:HE21	1.74	0.52
32:A:1826:G:H4'	32:A:1828:A:H2	1.74	0.52
32:A:2055:U:H2'	32:A:2056:G:H8	1.75	0.52
32:A:2241:A:O2'	62:r:193:LYS:N	2.43	0.52
32:A:2347:C:H2'	32:A:2348:A:C8	2.44	0.52
32:A:2431:C:OP2	32:A:2433:C:N4	2.42	0.52
32:A:2501:C:H41	50:2:49:ARG:CG	2.23	0.52
34:D:111:ARG:HH22	34:D:163:ILE:HD12	1.74	0.52
47:Z:138:CYS:HA	58:j:70:ARG:HD3	1.92	0.52
55:e:243:PHE:CZ	55:e:252:HIS:CE1	2.97	0.52
64:I:47:LEU:HD22	65:N:226:ILE:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:TA:57:PRO:C	85:TA:58:LYS:HD3	2.35	0.52
1:AA:873:G:H1'	1:AA:921:U:H1'	1.91	0.52
1:AA:1175:G:H2'	1:AA:1176:G:H8	1.74	0.52
25:A1:182:LEU:HD13	25:A1:187:LYS:HG3	1.92	0.52
26:A0:172:ALA:HA	26:A0:175:ILE:HG22	1.92	0.52
31:AG:178:HIS:HA	31:AG:181:ALA:HB3	1.92	0.52
32:A:2341:C:OP1	73:9:16:ASP:OD2	2.27	0.52
34:D:142:VAL:HG11	34:D:163:ILE:HD11	1.91	0.52
40:O:129:CYS:HG	48:0:156:THR:HG1	1.51	0.52
49:1:35:ASN:HB3	49:1:38:ARG:HG2	1.92	0.52
72:7:276:PHE:HB2	72:7:304:VAL:HG22	1.92	0.52
82:s:96:GLN:HG2	82:s:303:PRO:HD3	1.92	0.52
85:TA:85:LEU:HB3	85:TA:88:LYS:CE	2.38	0.52
1:AA:881:A:N6	10:AO:82:LYS:HA	2.24	0.52
1:AA:970:A:H2'	1:AA:971:A:H8	1.75	0.52
1:AA:1265:C:H5'	17:AH:122:GLN:HE21	1.75	0.52
5:AI:119:ASN:O	5:AI:121:LYS:N	2.43	0.52
22:AV:106:ASN:HA	22:AV:109:ILE:HD12	1.92	0.52
28:A4:281:GLU:O	28:A4:285:ASN:CB	2.58	0.52
32:A:1689:C:C5	45:X:14:LEU:HD13	2.45	0.52
32:A:1832:A:N6	54:b:4:ARG:HH22	2.08	0.52
32:A:2501:C:N4	50:2:49:ARG:HG2	2.24	0.52
32:A:2532:U:H2'	32:A:2533:A:H8	1.74	0.52
32:A:3144:A:H2'	32:A:3145:A:H8	1.75	0.52
32:A:3205:C:H5'	69:E:265:TYR:CD2	2.45	0.52
1:AA:649:A:C5	29:AD:422:TRP:CG	2.98	0.51
1:AA:1109:A:H2'	1:AA:1110:A:H8	1.75	0.51
3:AC:75:ASN:ND2	7:AK:121:SER:O	2.38	0.51
9:AN:6:SER:OG	9:AN:7:SER:N	2.43	0.51
32:A:2213:A:C4'	80:l:129:HIS:CD2	2.92	0.51
1:AA:704:U:N3	26:A0:57:ASP:OD2	2.31	0.51
1:AA:740:G:H2'	1:AA:741:A:H8	1.75	0.51
1:AA:1239:C:H2'	1:AA:1240:A:H8	1.75	0.51
1:AA:1535:U:O2'	1:AA:1536:A:OP1	2.26	0.51
1:AA:1562:G:H1'	1:AA:1583:A:H2	1.75	0.51
2:AB:156:GLU:OE2	2:AB:169:ARG:NE	2.42	0.51
19:AR:162:SER:O	19:AR:170:ARG:NH2	2.42	0.51
22:AV:316:GLN:HE22	22:AV:322:THR:HA	1.74	0.51
29:AD:298:PHE:HE1	29:AD:351:ARG:HH21	1.58	0.51
32:A:1760:G:P	61:q:59:LYS:NZ	2.83	0.51
32:A:1892:A:C2	51:3:169:ARG:CZ	2.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1893:A:H1'	32:A:1894:G:C8	2.46	0.51
32:A:2379:C:C5	73:9:48:TRP:CD1	2.95	0.51
32:A:3169:C:C6	32:A:3201:A:N6	2.75	0.51
75:c:59:ARG:HH22	75:c:182:GLU:HA	1.75	0.51
1:AA:826:A:C2	6:AJ:56:PRO:HG3	2.41	0.51
1:AA:1580:U:H2'	1:AA:1581:G:C8	2.45	0.51
6:AJ:67:THR:HG23	86:z:163:ARG:HH22	1.75	0.51
14:AW:88:PRO:HA	14:AW:91:GLN:HB2	1.93	0.51
15:AX:60:GLY:H	15:AX:63:HIS:HD2	1.58	0.51
17:AH:123:SER:OG	17:AH:124:VAL:N	2.41	0.51
22:AV:274:LYS:HD2	22:AV:341:LEU:HB3	1.92	0.51
32:A:2673:G:H2'	32:A:2674:U:H6	1.76	0.51
39:M:264:GLN:NE2	39:M:267:PHE:O	2.43	0.51
55:e:58:VAL:HB	55:e:153:LEU:HD12	1.93	0.51
65:N:135:SER:HB2	86:z:74:ILE:HD12	1.92	0.51
1:AA:798:C:H2'	1:AA:799:A:C8	2.46	0.51
1:AA:844:A:N3	26:A0:201:TRP:CD1	2.79	0.51
1:AA:1007:G:H2'	1:AA:1008:A:C8	2.45	0.51
2:AB:60:ASP:O	2:AB:64:ASN:ND2	2.42	0.51
10:AO:76:ASP:OD1	10:AO:76:ASP:N	2.41	0.51
22:AV:52:ASP:CB	83:Q:67:ARG:NH1	2.64	0.51
29:AD:307:LYS:O	29:AD:308:GLN:NE2	2.41	0.51
32:A:1808:A:N3	32:A:1809:U:O2'	2.43	0.51
32:A:2137:C:H4'	64:I:43:GLN:HE21	1.75	0.51
32:A:2615:A:C4	38:L:58:ILE:HD12	2.46	0.51
32:A:3122:U:H4'	32:A:3123:G:H4'	1.92	0.51
51:3:188:VAL:HB	56:g:104:ASN:HD22	1.76	0.51
66:P:138:GLU:OE2	71:6:136:ARG:NH1	2.44	0.51
76:d:124:ARG:NH1	76:d:201:SER:OG	2.43	0.51
79:k:18:VAL:HG12	79:k:64:VAL:HG22	1.92	0.51
1:AA:686:A:H2'	1:AA:687:G:C8	2.45	0.51
1:AA:872:G:H2'	1:AA:873:G:C8	2.45	0.51
1:AA:944:U:H2'	1:AA:945:G:C8	2.45	0.51
1:AA:992:U:N3	5:AI:120:ALA:HB2	2.26	0.51
1:AA:1471:A:H2'	1:AA:1472:G:C8	2.46	0.51
13:AT:51:ASN:ND2	13:AT:95:ASN:OD1	2.43	0.51
31:AG:114:SER:O	31:AG:122:ARG:NH2	2.44	0.51
32:A:2135:A:N3	32:A:2135:A:C2'	2.73	0.51
32:A:2241:A:H61	62:r:82:ASN:ND2	2.09	0.51
35:F:241:ASN:OD1	35:F:256:HIS:NE2	2.40	0.51
40:O:129:CYS:SG	48:0:156:THR:OG1	2.65	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:705:C:H2'	26:A0:136:TYR:CZ	2.45	0.51
4:AE:121:LYS:O	4:AE:123:ARG:NH1	2.44	0.51
19:AR:113:GLU:OE1	19:AR:116:ARG:NH2	2.43	0.51
19:AR:251:GLU:OE1	19:AR:280:LYS:NZ	2.44	0.51
22:AV:89:GLU:O	22:AV:93:TYR:HB2	2.11	0.51
24:AZ:33:VAL:HA	24:AZ:36:LEU:HG	1.93	0.51
26:A0:148:GLU:HA	26:A0:151:THR:HG22	1.93	0.51
32:A:1733:C:O2	36:H:72:ARG:HB3	2.10	0.51
32:A:1852:C:O2'	32:A:1854:U:OP2	2.29	0.51
32:A:2182:G:O2'	32:A:2183:C:OP1	2.28	0.51
32:A:2185:G:C2	32:A:2186:C:C4	2.99	0.51
32:A:2187:C:O4'	63:J:103:GLN:OE1	2.29	0.51
32:A:2536:G:H2'	32:A:2537:G:C8	2.45	0.51
32:A:3089:A:H61	86:z:232:ARG:HD2	1.76	0.51
32:A:3210:C:N3	69:E:156:ARG:HA	2.26	0.51
35:F:263:LEU:HA	35:F:266:VAL:HG12	1.92	0.51
1:AA:1430:A:H3'	30:AF:35:SER:O	2.11	0.51
8:AM:100:HIS:H	8:AM:103:MET:HE2	1.74	0.51
15:AX:222:LEU:HD11	15:AX:243:VAL:HG13	1.93	0.51
25:A1:56:ARG:HH11	28:A4:83:THR:HG23	1.75	0.51
32:A:1759:U:H2'	32:A:1760:G:C8	2.46	0.51
32:A:1818:A:OP1	48:0:95:ARG:NH2	2.44	0.51
32:A:1939:G:N3	32:A:1939:G:C3'	2.73	0.51
32:A:1964:U:H2'	32:A:1965:A:H8	1.76	0.51
32:A:2294:A:OP2	39:M:39:ARG:NH2	2.43	0.51
32:A:2507:A:O2'	32:A:2508:C:OP1	2.23	0.51
32:A:2678:A:N1	48:0:81:PRO:HD2	2.25	0.51
32:A:3151:A:C8	69:E:116:LYS:NZ	2.73	0.51
32:A:3201:A:N3	32:A:3201:A:C2'	2.73	0.51
37:K:155:LEU:CA	37:K:158:TYR:CD2	2.74	0.51
46:Y:198:ARG:NH2	50:2:70:LEU:O	2.43	0.51
64:I:110:LEU:HA	64:I:113:ARG:HB2	1.93	0.51
71:6:42:LEU:HD21	77:f:61:HIS:HD2	1.75	0.51
75:c:108:LEU:HG	75:c:110:ILE:HG13	1.93	0.51
75:c:138:THR:O	75:c:142:GLU:HB2	2.11	0.51
1:AA:649:A:N1	29:AD:422:TRP:CD2	2.79	0.51
8:AM:54:TYR:HD1	8:AM:66:VAL:HG22	1.76	0.51
15:AX:119:TYR:OH	25:A1:321:ASN:ND2	2.38	0.51
26:A0:171:ARG:NH2	26:A0:188:GLU:OE2	2.44	0.51
32:A:1759:U:H5''	39:M:196:ARG:HD3	1.92	0.51
32:A:1802:A:N7	32:A:1805:A:N6	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:3157:C:H1'	83:Q:84:ARG:HB3	1.92	0.51
37:K:51:SER:O	43:T:206:ARG:NH1	2.44	0.51
55:e:257:LYS:HE2	55:e:273:ARG:HB2	1.93	0.51
64:I:133:PRO:HA	64:I:136:GLU:HG2	1.92	0.51
70:5:112:LEU:HD12	70:5:310:ALA:HB1	1.92	0.51
1:AA:663:A:H2'	1:AA:664:G:C8	2.45	0.51
1:AA:953:U:N3	13:AT:36:THR:HG21	2.25	0.51
1:AA:1174:U:H2'	1:AA:1175:G:H8	1.74	0.51
17:AH:182:GLU:O	17:AH:185:LYS:NZ	2.43	0.51
22:AV:129:LEU:HB2	22:AV:137:ILE:HD11	1.93	0.51
22:AV:288:LYS:HD2	22:AV:327:LEU:HD22	1.92	0.51
26:A0:104:TYR:CE2	26:A0:105:THR:HG23	2.46	0.51
32:A:2395:A:H1'	70:5:384:HIS:HB2	1.92	0.51
32:A:2469:A:H2	38:L:33:GLN:HE22	1.58	0.51
34:D:164:LEU:H	34:D:180:ASP:HB3	1.75	0.51
2:AB:112:ASP:O	2:AB:113:HIS:ND1	2.44	0.51
25:A1:79:SER:HB3	28:A4:93:PRO:HD3	1.92	0.51
32:A:1863:A:H2'	32:A:1864:A:H8	1.76	0.51
32:A:2094:G:O2'	32:A:2265:A:N3	2.40	0.51
39:M:44:ARG:HG3	39:M:45:ARG:HG3	1.93	0.51
70:5:136:LEU:O	70:5:140:ASP:HB2	2.11	0.51
71:6:293:LEU:HD11	71:6:335:LEU:HD13	1.91	0.51
85:TB:77:LEU:O	85:TB:77:LEU:HD23	2.11	0.51
1:AA:913:A:H2'	1:AA:914:A:H8	1.74	0.50
1:AA:1308:U:H1'	3:AC:64:HIS:ND1	2.25	0.50
1:AA:1451:U:H5''	31:AG:380:LYS:NZ	2.27	0.50
10:AO:80:ASN:OD1	29:AD:191:ARG:NH2	2.44	0.50
25:A1:56:ARG:HH22	28:A4:85:VAL:H	1.58	0.50
25:A1:169:ARG:NE	25:A1:210:ASP:OD2	2.43	0.50
30:AF:126:TYR:CE1	30:AF:139:ARG:NE	2.80	0.50
32:A:1894:G:H2'	32:A:1895:C:H6	1.75	0.50
32:A:2192:A:H2'	32:A:2193:U:C6	2.46	0.50
54:b:35:ARG:HG2	60:o:101:TRP:HD1	1.76	0.50
56:g:94:ILE:HD12	56:g:95:PRO:HD2	1.92	0.50
57:i:125:GLY:O	57:i:128:ARG:NH1	2.43	0.50
62:r:149:ARG:HD3	62:r:152:THR:HG21	1.93	0.50
64:I:203:VAL:O	85:TB:79:ILE:HG21	2.11	0.50
68:V:55:TYR:O	68:V:145:ARG:NH1	2.44	0.50
79:k:15:GLN:NE2	79:k:50:SER:O	2.44	0.50
1:AA:1138:G:H2'	1:AA:1139:A:C8	2.46	0.50
14:AW:95:ALA:HB1	14:AW:144:LEU:HG	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:384:LYS:NZ	23:AY:394:PHE:O	2.43	0.50
25:A1:266:LEU:HD11	25:A1:289:ILE:HG12	1.93	0.50
31:AG:217:ASP:N	31:AG:217:ASP:OD1	2.43	0.50
32:A:2810:G:H2'	32:A:2811:G:H8	1.76	0.50
32:A:3202:U:C2	32:A:3203:A:C8	2.99	0.50
39:M:68:GLU:OE1	39:M:71:GLN:NE2	2.45	0.50
71:6:186:PRO:O	71:6:191:ASN:ND2	2.44	0.50
85:TA:76:LEU:H	85:TA:76:LEU:HD12	1.76	0.50
1:AA:1173:C:H2'	1:AA:1174:U:H6	1.77	0.50
1:AA:1190:C:H2'	1:AA:1191:C:H6	1.76	0.50
15:AX:346:SER:OG	15:AX:347:ASN:N	2.45	0.50
17:AH:78:VAL:HG22	17:AH:172:VAL:HG22	1.92	0.50
19:AR:208:ILE:O	19:AR:214:ASN:ND2	2.43	0.50
22:AV:157:TYR:O	22:AV:184:TYR:OH	2.28	0.50
32:A:1812:C:O2	75:c:45:LEU:HD13	2.10	0.50
32:A:2173:G:N3	63:J:150:SER:OG	2.44	0.50
32:A:2520:C:O2	32:A:2528:G:N2	2.34	0.50
38:L:73:ILE:HG13	38:L:84:ALA:HB3	1.93	0.50
62:r:132:ARG:HD3	62:r:133:PRO:HD2	1.94	0.50
66:P:68:TRP:O	66:P:70:THR:N	2.43	0.50
69:E:269:TYR:CZ	69:E:303:LYS:HE2	2.41	0.50
83:Q:83:ARG:HD3	83:Q:143:ARG:HE	1.76	0.50
85:TA:53:LEU:HD23	85:TA:53:LEU:H	1.76	0.50
1:AA:668:U:C4	29:AD:422:TRP:CH2	2.98	0.50
1:AA:1406:U:H1'	1:AA:1407:U:H5'	1.93	0.50
5:AI:91:SER:OG	5:AI:92:HIS:N	2.43	0.50
29:AD:150:LYS:N	29:AD:153:ALA:O	2.38	0.50
32:A:1749:C:OP2	32:A:2899:C:O2'	2.22	0.50
32:A:1829:A:H2'	32:A:1830:G:H8	1.76	0.50
32:A:2740:A:H2'	32:A:2741:A:C8	2.45	0.50
32:A:2752:C:H2'	32:A:2753:A:H8	1.77	0.50
42:S:133:VAL:HG21	42:S:154:VAL:HB	1.92	0.50
53:8:172:GLU:OE1	77:f:183:ARG:NH1	2.40	0.50
81:p:81:TYR:CD1	81:p:143:GLN:HB2	2.46	0.50
1:AA:807:A:H8	1:AA:808:C:H41	1.56	0.50
1:AA:928:A:N3	29:AD:421:VAL:HG11	2.26	0.50
1:AA:1084:C:H2'	1:AA:1085:C:H6	1.77	0.50
9:AN:11:ARG:HA	9:AN:68:ALA:HB2	1.92	0.50
17:AH:170:MET:HE2	25:A1:157:VAL:HB	1.92	0.50
32:A:1731:A:N1	57:i:118:TYR:CB	2.74	0.50
32:A:2081:U:H2'	32:A:2082:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2608:G:H4'	86:z:209:ARG:HH22	1.75	0.50
32:A:2668:A:H2'	32:A:2669:A:H8	1.77	0.50
33:B:1628:C:H2'	33:B:1629:A:H8	1.77	0.50
35:F:168:LYS:HD3	56:g:90:ARG:HH12	1.77	0.50
53:8:178:TYR:CZ	77:f:180:GLU:HG2	2.46	0.50
83:Q:244:ARG:HE	83:Q:247:LEU:HD13	1.75	0.50
1:AA:798:C:H2'	1:AA:799:A:H8	1.76	0.50
1:AA:826:A:H62	6:AJ:55:ARG:HG2	1.75	0.50
1:AA:861:U:H2'	1:AA:862:A:H8	1.75	0.50
1:AA:1429:C:C5	1:AA:1461:A:C4	2.99	0.50
1:AA:1456:U:H2'	1:AA:1457:G:O4'	2.12	0.50
22:AV:132:LYS:HG2	22:AV:136:GLY:HA2	1.94	0.50
25:A1:211:ARG:NH1	25:A1:221:TYR:OH	2.44	0.50
31:AG:281:ALA:HB2	31:AG:332:VAL:HG23	1.94	0.50
32:A:2746:U:H2'	32:A:2747:U:C6	2.46	0.50
32:A:3200:U:O4	37:K:97:LEU:HD22	2.12	0.50
64:I:189:GLN:HA	64:I:192:ILE:HG22	1.94	0.50
1:AA:1411:G:H2'	1:AA:1412:G:C8	2.46	0.50
3:AC:100:PHE:HB3	3:AC:103:CYS:HB2	1.94	0.50
10:AO:73:VAL:O	10:AO:109:ARG:NH2	2.45	0.50
30:AF:126:TYR:CE1	30:AF:139:ARG:CZ	2.78	0.50
32:A:1713:A:HO2'	32:A:1714:C:P	2.34	0.50
32:A:3200:U:N3	37:K:97:LEU:HB3	2.27	0.50
43:T:154:LYS:O	43:T:155:ARG:NH1	2.42	0.50
85:TA:68:VAL:CB	85:TB:85:LEU:HG	2.42	0.50
1:AA:696:U:H2'	1:AA:697:G:H8	1.77	0.50
1:AA:857:G:OP1	13:AT:162:LYS:NZ	2.29	0.50
1:AA:982:A:N6	1:AA:1007:G:O6	2.45	0.50
32:A:1752:U:H2'	32:A:1753:A:H8	1.77	0.50
32:A:1788:C:O2	50:2:64:HIS:NE2	2.42	0.50
32:A:1863:A:H2'	32:A:1864:A:C8	2.47	0.50
32:A:1912:A:H2'	32:A:1913:G:C8	2.47	0.50
32:A:2897:A:N1	32:A:2898:U:C4	2.79	0.50
32:A:3200:U:H4'	32:A:3201:A:H5''	1.94	0.50
32:A:3204:C:O2'	69:E:207:THR:HG21	2.11	0.50
44:W:100:THR:OG1	44:W:132:HIS:NE2	2.37	0.50
46:Y:191:ASN:ND2	68:V:216:TYR:OH	2.45	0.50
66:P:82:ARG:NH1	66:P:95:GLU:OE2	2.44	0.50
68:V:59:GLY:H	68:V:76:VAL:HG13	1.77	0.50
85:TA:85:LEU:HD21	85:TB:64:ILE:O	2.11	0.50
86:z:117:ASP:OD1	86:z:117:ASP:N	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:699:A:H61	21:AU:32:ASP:CG	2.20	0.50
1:AA:1263:G:H1	1:AA:1329:U:H3	1.59	0.50
2:AB:98:ARG:HD2	20:AS:60:ILE:HD12	1.93	0.50
20:AS:80:SER:O	20:AS:133:ARG:NH2	2.44	0.50
30:AF:126:TYR:CD1	30:AF:139:ARG:CZ	2.84	0.50
32:A:1812:C:N3	75:c:45:LEU:HD13	2.26	0.50
32:A:1832:A:H5'	54:b:114:ARG:NH2	2.26	0.50
32:A:2060:A:O2'	32:A:2061:C:H5''	2.12	0.50
32:A:2590:A:H2'	32:A:2591:A:C8	2.47	0.50
32:A:3165:C:H2'	32:A:3166:U:C6	2.46	0.50
85:TA:85:LEU:HD21	85:TB:64:ILE:CG1	2.30	0.50
1:AA:918:A:P	10:AO:92:LYS:HB2	2.52	0.49
1:AA:1116:A:HO2'	1:AA:1117:A:P	2.35	0.49
9:AN:99:PRO:HB2	9:AN:106:LEU:HB2	1.94	0.49
11:AP:134:LYS:O	21:AU:193:ARG:NE	2.45	0.49
32:A:2470:G:O2'	38:L:36:THR:HB	2.12	0.49
32:A:2961:C:C4	32:A:2962:C:N3	2.75	0.49
32:A:2961:C:N3	32:A:2962:C:C4	2.78	0.49
36:H:56:VAL:HG12	36:H:82:LEU:HA	1.93	0.49
36:H:67:GLU:HB3	45:X:61:ARG:HH12	1.77	0.49
37:K:154:ARG:C	37:K:158:TYR:CZ	2.90	0.49
71:6:41:ASP:OD1	71:6:41:ASP:N	2.39	0.49
83:Q:76:LEU:HD11	83:Q:80:PHE:CB	2.42	0.49
85:TA:85:LEU:HB2	85:TA:88:LYS:NZ	2.27	0.49
86:z:158:ALA:O	86:z:162:ILE:HG22	2.11	0.49
1:AA:1539:C:H41	38:L:52:HIS:HD2	1.57	0.49
15:AX:203:LYS:O	15:AX:205:GLN:NE2	2.39	0.49
20:AS:9:VAL:HB	20:AS:15:ARG:HD3	1.94	0.49
23:AY:382:GLU:HG3	23:AY:383:LYS:HG3	1.93	0.49
32:A:2093:U:O2	32:A:2266:U:O2'	2.29	0.49
43:T:105:GLN:NE2	48:0:104:LYS:O	2.36	0.49
65:N:218:ILE:HG23	65:N:223:MET:HB2	1.92	0.49
65:N:240:LYS:NZ	65:N:251:VAL:O	2.44	0.49
72:7:115:MET:HB3	72:7:270:PRO:HB3	1.94	0.49
76:d:216:MET:HE3	76:d:217:HIS:H	1.77	0.49
1:AA:1041:A:H4'	1:AA:1042:U:H5'	1.95	0.49
1:AA:1395:C:N4	1:AA:1412:G:O6	2.45	0.49
32:A:1937:A:O2'	32:A:1938:A:O4'	2.31	0.49
32:A:2372:U:O4	82:s:270:LYS:HD2	2.12	0.49
32:A:3173:G:H2'	32:A:3174:U:O4'	2.12	0.49
40:O:41:ARG:NH2	40:O:131:PRO:O	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S:54:THR:H	42:S:57:SER:HB3	1.78	0.49
42:S:146:LYS:HE3	74:a:58:ILE:HD11	1.94	0.49
54:b:27:GLN:HE21	54:b:80:LEU:HD23	1.76	0.49
68:V:52:GLU:O	68:V:143:ARG:NH2	2.45	0.49
82:s:105:TRP:HZ3	82:s:268:PRO:HA	1.77	0.49
1:AA:1116:A:N3	1:AA:1116:A:C2'	2.73	0.49
1:AA:1239:C:H2'	1:AA:1240:A:C8	2.46	0.49
1:AA:1410:G:C2	1:AA:1411:G:N7	2.81	0.49
15:AX:102:ARG:NH1	15:AX:346:SER:O	2.39	0.49
32:A:1778:U:OP1	35:F:120:VAL:HG23	2.13	0.49
32:A:2132:A:H62	60:o:16:GLN:NE2	2.09	0.49
32:A:2134:A:C4	32:A:2135:A:N7	2.80	0.49
32:A:2674:U:H2'	32:A:2675:G:O4'	2.11	0.49
64:I:114:HIS:HA	64:I:117:ARG:HG2	1.95	0.49
71:6:240:ILE:HD13	71:6:248:GLY:HA3	1.93	0.49
1:AA:1383:A:N1	30:AF:198:ARG:HG2	2.28	0.49
10:AO:215:ARG:HD3	26:A0:88:GLN:HA	1.93	0.49
23:AY:317:ASN:ND2	25:A1:155:ASP:OD2	2.46	0.49
28:A4:246:ARG:O	28:A4:250:LEU:CB	2.60	0.49
32:A:2176:C:OP2	63:J:99:LYS:CE	2.59	0.49
32:A:2341:C:N4	73:9:24:LYS:O	2.46	0.49
32:A:2953:U:H5''	52:4:71:VAL:HG12	1.95	0.49
51:3:116:ARG:NH2	51:3:159:ASP:OD1	2.46	0.49
1:AA:1197:G:H1	1:AA:1425:U:H3	1.59	0.49
1:AA:1432:U:OP2	31:AG:377:ARG:HG3	2.13	0.49
1:AA:1450:C:H2'	1:AA:1451:U:C6	2.47	0.49
1:AA:1552:G:H2'	1:AA:1553:A:C8	2.47	0.49
12:AQ:77:ARG:HH22	14:AW:149:LEU:CD1	2.22	0.49
32:A:1731:A:OP1	36:H:74:HIS:NE2	2.45	0.49
32:A:2961:C:N4	32:A:2962:C:N4	2.60	0.49
32:A:3203:A:N9	69:E:303:LYS:NZ	2.60	0.49
42:S:107:LYS:HD2	43:T:212:LEU:HD21	1.95	0.49
45:X:180:ASP:OD2	45:X:180:ASP:N	2.44	0.49
60:o:54:MET:O	60:o:58:GLN:NE2	2.45	0.49
65:N:204:GLU:OE2	65:N:208:ASN:ND2	2.45	0.49
68:V:23:MET:HE2	68:V:114:PRO:HD3	1.94	0.49
85:TA:81:ASP:OD1	85:TB:64:ILE:HD13	2.12	0.49
1:AA:1148:A:P	27:A3:165:LYS:HE3	2.53	0.49
1:AA:1525:C:C6	22:AV:105:ARG:CZ	2.96	0.49
15:AX:269:TRP:HB3	15:AX:332:GLU:HB2	1.94	0.49
32:A:1740:A:H5''	39:M:133:LYS:HZ2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2010:U:O4'	32:A:2012:A:H5'	2.12	0.49
32:A:2615:A:H62	38:L:58:ILE:HG22	1.77	0.49
32:A:3174:U:H2'	32:A:3175:A:H8	1.77	0.49
63:J:28:LEU:O	80:l:67:GLN:NE2	2.46	0.49
70:5:349:ARG:NH1	70:5:383:GLN:O	2.45	0.49
71:6:220:SER:HB2	71:6:268:LEU:HG	1.93	0.49
2:AB:80:SER:OG	2:AB:81:VAL:N	2.46	0.49
14:AW:130:ASP:HB3	14:AW:133:LYS:HB3	1.93	0.49
32:A:2123:C:H2'	32:A:2124:A:C8	2.48	0.49
32:A:2198:A:C6	63:J:150:SER:CB	2.75	0.49
32:A:2322:C:OP1	48:0:139:ARG:NE	2.42	0.49
36:H:53:THR:HG21	45:X:130:ARG:HD2	1.94	0.49
55:e:122:ASP:O	55:e:126:GLN:NE2	2.45	0.49
63:J:137:LEU:HA	63:J:140:VAL:HG12	1.95	0.49
75:c:97:TYR:HB2	75:c:181:SER:HA	1.94	0.49
82:s:332:LEU:HD21	82:s:359:ALA:HB2	1.94	0.49
1:AA:900:C:H41	6:AJ:74:ASN:ND2	2.11	0.49
1:AA:1471:A:H2'	1:AA:1472:G:H8	1.76	0.49
1:AA:1498:C:H2'	1:AA:1499:U:H6	1.78	0.49
1:AA:1551:G:H2'	1:AA:1552:G:H8	1.78	0.49
1:AA:1595:G:H2'	1:AA:1596:A:C8	2.48	0.49
26:A0:92:PRO:O	26:A0:122:GLY:N	2.46	0.49
32:A:2274:A:OP1	75:c:36:ARG:CD	2.52	0.49
32:A:2355:A:OP1	43:T:169:LYS:NZ	2.44	0.49
32:A:2366:G:H2'	32:A:2367:A:H8	1.78	0.49
32:A:2552:U:C2	32:A:2553:G:C8	3.01	0.49
37:K:155:LEU:CG	37:K:158:TYR:CE2	2.94	0.49
46:Y:169:ARG:HH12	46:Y:181:PHE:HE1	1.60	0.49
48:0:90:ASN:OD1	48:0:93:ARG:NH2	2.45	0.49
82:s:351:VAL:HG12	82:s:352:THR:N	2.28	0.49
1:AA:1439:A:H2'	1:AA:1440:G:C8	2.46	0.49
14:AW:150:THR:HG22	14:AW:161:THR:HA	1.94	0.49
15:AX:383:LEU:HG	31:AG:310:ARG:HB3	1.94	0.49
15:AX:398:LEU:HD21	30:AF:86:PHE:HD2	1.78	0.49
25:A1:102:ASN:OD1	25:A1:105:LEU:N	2.43	0.49
25:A1:198:TYR:HA	25:A1:205:LEU:HA	1.94	0.49
32:A:1884:G:N3	32:A:1895:C:O2'	2.44	0.49
32:A:2172:A:H8	63:J:23:ILE:HG12	1.78	0.49
32:A:2198:A:N3	32:A:2198:A:C2'	2.73	0.49
32:A:2302:U:H2'	32:A:2303:A:C8	2.48	0.49
32:A:2342:U:C5	67:U:74:HIS:CE1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:3174:U:H2'	32:A:3175:A:C8	2.48	0.49
37:K:105:LYS:HG3	37:K:122:MET:HE1	1.95	0.49
45:X:149:SER:OG	45:X:150:GLY:N	2.45	0.49
85:TA:85:LEU:HD11	85:TB:67:LEU:HD12	1.94	0.49
1:AA:1037:A:OP2	18:AL:100:LYS:NZ	2.34	0.48
32:A:2065:A:H1'	44:W:74:ARG:O	2.12	0.48
32:A:2898:U:O2	32:A:2898:U:H3'	2.12	0.48
32:A:3210:C:H42	69:E:156:ARG:C	2.18	0.48
35:F:48:LEU:HD11	78:h:95:ARG:HB2	1.95	0.48
57:i:57:TYR:OH	61:q:28:ARG:O	2.29	0.48
69:E:206:VAL:HG11	69:E:289:VAL:HG22	1.95	0.48
81:p:182:ASN:OD1	81:p:185:ARG:NH1	2.44	0.48
1:AA:658:G:O2'	1:AA:1286:A:O2'	2.30	0.48
1:AA:1174:U:H2'	1:AA:1175:G:C8	2.48	0.48
1:AA:1216:C:H2'	1:AA:1217:G:H8	1.76	0.48
18:AL:66:PRO:HD2	18:AL:102:MET:HE3	1.94	0.48
26:A0:104:TYR:CE2	26:A0:105:THR:HG22	2.48	0.48
31:AG:250:LEU:HB2	31:AG:252:SER:HB3	1.94	0.48
34:D:180:ASP:OD1	34:D:180:ASP:N	2.46	0.48
38:L:55:PRO:HB3	38:L:77:ILE:HG12	1.93	0.48
48:0:86:THR:O	48:0:90:ASN:ND2	2.46	0.48
72:7:49:ASN:OD1	72:7:256:ARG:NH1	2.46	0.48
76:d:66:VAL:HG12	76:d:69:PRO:HD2	1.96	0.48
77:f:166:PHE:HA	77:f:169:ILE:HG22	1.95	0.48
14:AW:114:ILE:HG21	14:AW:142:LEU:HD21	1.95	0.48
25:A1:85:VAL:HG22	31:AG:125:MET:HB2	1.93	0.48
32:A:1763:A:H5'	61:q:34:ARG:CZ	2.42	0.48
32:A:1807:U:O2'	32:A:1808:A:O5'	2.31	0.48
32:A:1850:U:H2'	32:A:2134:A:H61	1.78	0.48
32:A:2388:A:C5	34:D:141:LEU:HD23	2.49	0.48
32:A:2409:A:H2'	32:A:2410:U:C6	2.48	0.48
41:R:57:ARG:HE	42:S:169:ARG:HH21	1.61	0.48
75:c:102:GLU:HG2	75:c:105:ARG:HE	1.77	0.48
76:d:85:PHE:O	76:d:86:ASP:OD1	2.32	0.48
1:AA:1115:U:C4'	1:AA:1116:A:OP2	2.58	0.48
3:AC:140:GLU:HG3	3:AC:153:LEU:HD13	1.94	0.48
6:AJ:103:GLN:CD	86:z:181:PRO:HB2	2.31	0.48
32:A:1713:A:N6	70:5:68:PRO:HB2	2.27	0.48
32:A:1735:A:OP2	45:X:9:TRP:NE1	2.46	0.48
32:A:2068:C:H5'	32:A:2069:U:P	2.54	0.48
32:A:2069:U:H3'	32:A:2069:U:O2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2155:A:N3	60:o:26:PHE:CD1	2.69	0.48
32:A:2275:U:H2'	32:A:2276:C:C6	2.48	0.48
32:A:2347:C:H2'	32:A:2348:A:H8	1.79	0.48
32:A:2499:U:O2	32:A:2499:U:H3'	2.13	0.48
37:K:22:ASP:HB3	37:K:147:GLN:HE21	1.79	0.48
53:8:150:LEU:HB2	55:e:212:HIS:HE1	1.77	0.48
82:s:298:GLN:OE1	82:s:300:HIS:NE2	2.37	0.48
1:AA:799:A:H2'	1:AA:800:C:C6	2.48	0.48
2:AB:267:VAL:HG23	2:AB:270:LEU:HD23	1.96	0.48
6:AJ:103:GLN:OE1	86:z:181:PRO:HG2	2.09	0.48
32:A:1935:A:H2'	32:A:1938:A:H61	1.77	0.48
32:A:2310:G:N2	32:A:2676:A:OP2	2.35	0.48
32:A:2493:C:N3	32:A:2540:C:C6	2.81	0.48
32:A:2635:G:H2'	32:A:2636:G:H8	1.79	0.48
32:A:2810:G:H2'	32:A:2811:G:C8	2.49	0.48
32:A:3189:C:C5	52:4:83:LYS:HE2	2.48	0.48
50:2:57:ASN:OD1	50:2:60:ARG:NH2	2.44	0.48
72:7:78:VAL:HG13	76:d:282:ILE:HB	1.95	0.48
85:TA:81:ASP:O	85:TA:85:LEU:HG	2.12	0.48
1:AA:664:G:H4'	1:AA:1138:G:C8	2.49	0.48
1:AA:740:G:H2'	1:AA:741:A:C8	2.48	0.48
1:AA:757:A:H62	1:AA:783:A:H1'	1.78	0.48
2:AB:90:HIS:HB3	2:AB:118:LEU:HD11	1.96	0.48
2:AB:156:GLU:OE1	2:AB:169:ARG:NH2	2.46	0.48
2:AB:208:ALA:HA	2:AB:211:ASP:HB2	1.96	0.48
17:AH:109:HIS:CD2	17:AH:142:CYS:HB3	2.49	0.48
22:AV:129:LEU:HD11	22:AV:144:PHE:HE1	1.79	0.48
32:A:2298:A:N6	35:F:145:LEU:HD22	2.29	0.48
32:A:2642:C:H2'	32:A:2643:G:C8	2.48	0.48
32:A:2787:A:H2'	32:A:2788:C:C6	2.48	0.48
32:A:2961:C:N3	32:A:2962:C:C5	2.81	0.48
32:A:3157:C:O4'	83:Q:84:ARG:HB3	2.14	0.48
32:A:3218:A:OP2	69:E:212:GLY:N	2.46	0.48
35:F:62:VAL:HG13	78:h:118:HIS:HB2	1.96	0.48
53:8:163:LYS:HA	77:f:86:TYR:HB2	1.95	0.48
81:p:119:ILE:HD11	81:p:157:MET:HB3	1.96	0.48
1:AA:761:A:OP1	18:AL:201:ARG:NH2	2.46	0.48
1:AA:856:A:H5'	13:AT:162:LYS:HB2	1.96	0.48
1:AA:1527:A:H2'	1:AA:1528:A:O4'	2.13	0.48
12:AQ:77:ARG:HH22	14:AW:149:LEU:HD22	1.78	0.48
30:AF:123:PHE:CE1	30:AF:139:ARG:HD3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1824:U:C4	74:a:121:HIS:CG	3.02	0.48
43:T:191:THR:OG1	43:T:192:ALA:N	2.46	0.48
68:V:69:ASP:N	68:V:69:ASP:OD1	2.45	0.48
71:6:307:HIS:HB2	71:6:311:MET:HE2	1.96	0.48
1:AA:661:C:H2'	1:AA:662:U:C6	2.48	0.48
1:AA:896:A:H2'	1:AA:897:C:C6	2.49	0.48
1:AA:1382:A:C5'	15:AX:166:ARG:HH12	2.19	0.48
8:AM:29:ARG:HH21	13:AT:140:ILE:HG13	1.79	0.48
10:AO:67:ARG:NH1	10:AO:110:ASP:OD2	2.43	0.48
25:A1:112:LEU:HD23	31:AG:111:LEU:HD22	1.95	0.48
32:A:2015:G:C6	32:A:2731:U:H5''	2.48	0.48
35:F:116:THR:OG1	35:F:117:ARG:N	2.47	0.48
64:I:207:LEU:HD22	85:TB:86:LEU:HD13	1.96	0.48
77:f:82:LEU:HD13	77:f:85:ASP:HB3	1.95	0.48
1:AA:910:A:H2'	1:AA:911:U:H6	1.79	0.48
1:AA:1116:A:H4'	1:AA:1116:A:OP1	2.13	0.48
1:AA:1229:U:O2	1:AA:1229:U:H3'	2.13	0.48
1:AA:1462:G:H2'	1:AA:1463:G:H8	1.79	0.48
4:AE:5:GLU:OE1	11:AP:75:LYS:NZ	2.47	0.48
5:AI:139:ALA:HB1	5:AI:144:VAL:HG21	1.96	0.48
8:AM:29:ARG:HB2	13:AT:155:LEU:HD11	1.95	0.48
9:AN:91:VAL:HG13	9:AN:100:CYS:HB3	1.96	0.48
31:AG:197:SER:HB2	31:AG:245:ARG:HH21	1.79	0.48
32:A:1867:A:H62	32:A:2295:C:H5	1.62	0.48
32:A:1925:A:H2'	32:A:1926:A:C8	2.49	0.48
32:A:2060:A:C4	32:A:2079:C:C4	3.02	0.48
32:A:2531:U:O2	34:D:253:ASN:N	2.43	0.48
64:I:101:ASN:H	64:I:151:ASN:HA	1.79	0.48
86:z:145:LEU:HD11	86:z:177:LEU:HB3	1.96	0.48
1:AA:1053:A:N6	1:AA:1100:C:O2'	2.45	0.48
1:AA:1308:U:H2'	1:AA:1309:A:C8	2.49	0.48
2:AB:135:MET:HG3	2:AB:140:GLY:HA3	1.96	0.48
15:AX:145:CYS:HB3	15:AX:150:TRP:HB2	1.96	0.48
18:AL:78:VAL:HG23	18:AL:81:ILE:HD11	1.95	0.48
32:A:2213:A:H4'	80:l:129:HIS:NE2	2.29	0.48
32:A:3144:A:H2'	32:A:3145:A:C8	2.49	0.48
36:H:99:THR:CA	36:H:108:ARG:CD	2.92	0.48
70:5:255:PHE:HZ	70:5:260:PRO:HA	1.79	0.48
76:d:91:PRO:HG2	76:d:94:ASP:HB2	1.96	0.48
85:TA:85:LEU:HB3	85:TA:88:LYS:NZ	2.28	0.48
85:TA:88:LYS:NZ	85:TB:65:GLN:HB3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:833:A:H2'	1:AA:834:G:C8	2.49	0.47
1:AA:970:A:H2'	1:AA:971:A:C8	2.49	0.47
1:AA:1504:U:H2'	1:AA:1505:A:C8	2.49	0.47
5:AI:154:LEU:HA	5:AI:158:ARG:HD2	1.96	0.47
22:AV:246:ASN:HB3	26:A0:70:ARG:HH12	1.79	0.47
32:A:2373:A:C6	82:s:274:PHE:CG	3.02	0.47
58:j:45:GLU:OE2	58:j:70:ARG:NH2	2.39	0.47
69:E:134:SER:OG	69:E:135:LYS:N	2.47	0.47
70:5:276:THR:HG23	70:5:278:PHE:H	1.79	0.47
72:7:189:LEU:HD22	72:7:192:TRP:HE1	1.79	0.47
1:AA:807:A:H1'	1:AA:808:C:H5	1.79	0.47
1:AA:826:A:N6	6:AJ:55:ARG:CG	2.65	0.47
1:AA:991:G:H21	1:AA:996:A:H2	1.60	0.47
1:AA:1564:A:H2'	1:AA:1565:A:H8	1.78	0.47
12:AQ:78:LYS:HB3	16:A2:110:ARG:HH12	1.79	0.47
22:AV:171:GLU:OE2	26:A0:78:ARG:NH1	2.47	0.47
31:AG:303:TYR:OH	31:AG:340:GLN:OE1	2.32	0.47
32:A:1800:G:H22	32:A:1803:A:H5'	1.79	0.47
32:A:2532:U:H2'	32:A:2533:A:C8	2.49	0.47
55:e:243:PHE:CD2	55:e:246:ALA:HB2	2.49	0.47
68:V:102:MET:SD	68:V:102:MET:N	2.86	0.47
1:AA:1025:A:C8	18:AL:153:ARG:NH2	2.82	0.47
9:AN:6:SER:OG	9:AN:69:LEU:O	2.24	0.47
9:AN:110:LEU:HD21	21:AU:125:ARG:HG2	1.96	0.47
13:AT:80:LEU:HD12	13:AT:84:GLU:HB2	1.97	0.47
22:AV:164:VAL:HA	22:AV:167:VAL:HG12	1.96	0.47
22:AV:208:LEU:O	22:AV:212:GLY:N	2.47	0.47
27:A3:140:HIS:CD2	27:A3:144:ARG:HD2	2.49	0.47
32:A:1812:C:C2	75:c:45:LEU:HD13	2.49	0.47
32:A:1924:U:H2'	32:A:1925:A:H8	1.79	0.47
32:A:2170:G:H2'	32:A:2171:U:C2	2.49	0.47
32:A:3189:C:C6	52:4:86:GLY:HA2	2.49	0.47
75:c:86:ASP:N	75:c:86:ASP:OD1	2.45	0.47
76:d:203:MET:HE3	76:d:206:GLY:HA2	1.96	0.47
1:AA:1089:U:H2'	1:AA:1090:A:C8	2.49	0.47
1:AA:1228:A:C5	7:AK:98:ARG:CZ	2.97	0.47
1:AA:1444:A:C6	7:AK:85:VAL:HG22	2.49	0.47
1:AA:1560:U:O2'	32:A:2582:A:C2	2.58	0.47
2:AB:141:ILE:HB	2:AB:190:PRO:HA	1.96	0.47
4:AE:47:LEU:HD23	4:AE:48:PRO:HD2	1.95	0.47
7:AK:55:ASN:HA	7:AK:58:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A1:189:LYS:NZ	25:A1:235:ASN:O	2.44	0.47
32:A:2041:U:H2'	32:A:2042:U:C6	2.49	0.47
32:A:2070:C:H3'	32:A:2070:C:O2	2.15	0.47
32:A:2678:A:H2	48:O:80:ALA:HA	1.78	0.47
32:A:2796:G:H21	36:H:88:HIS:HE1	1.61	0.47
32:A:3002:G:H2'	32:A:3003:A:C8	2.50	0.47
32:A:3131:G:H2'	32:A:3132:G:O4'	2.14	0.47
36:H:100:GLN:CA	36:H:108:ARG:HD3	2.44	0.47
51:3:148:VAL:CG1	71:6:360:ARG:HA	2.45	0.47
53:8:97:LYS:HD2	53:8:99:ARG:HH21	1.79	0.47
1:AA:1234:C:O2'	1:AA:1235:U:OP1	2.30	0.47
1:AA:1284:U:O2'	29:AD:347:GLN:OE1	2.32	0.47
8:AM:121:ALA:HA	8:AM:124:LYS:HD2	1.96	0.47
16:A2:48:GLU:HA	16:A2:51:VAL:HG22	1.97	0.47
32:A:2176:C:P	63:J:99:LYS:HZ3	2.31	0.47
32:A:2620:G:H2'	32:A:2621:G:C8	2.50	0.47
32:A:3008:C:O2'	32:A:3009:C:H5'	2.15	0.47
34:D:154:THR:HG22	34:D:157:MET:HE2	1.95	0.47
35:F:208:HIS:HE1	78:h:55:LEU:HD11	1.80	0.47
82:s:163:VAL:HG21	82:s:171:VAL:HG11	1.94	0.47
1:AA:1180:U:H2'	1:AA:1181:G:H8	1.80	0.47
1:AA:1440:G:H2'	1:AA:1441:A:C8	2.49	0.47
10:AO:218:ARG:NH2	26:A0:87:TRP:O	2.47	0.47
16:A2:70:ILE:HD11	30:AF:155:MET:HG3	1.96	0.47
32:A:2395:A:N9	70:5:384:HIS:ND1	2.62	0.47
32:A:2528:G:H3'	34:D:208:ARG:HH21	1.77	0.47
32:A:2586:U:H2'	32:A:2587:G:C8	2.48	0.47
32:A:3203:A:N1	32:A:3204:C:O2	2.40	0.47
78:h:62:PRO:HD3	78:h:133:PRO:HB3	1.96	0.47
83:Q:71:PRO:C	83:Q:212:ASN:CG	2.82	0.47
1:AA:708:C:H2'	1:AA:709:G:C8	2.50	0.47
1:AA:1526:U:C6	22:AV:102:TRP:CZ3	3.03	0.47
7:AK:65:LYS:HG3	7:AK:66:ILE:HG13	1.97	0.47
8:AM:20:ARG:NH2	8:AM:38:HIS:O	2.47	0.47
22:AV:40:TRP:HE3	22:AV:43:ARG:HD2	1.79	0.47
24:AZ:42:LEU:HA	24:AZ:45:LYS:HE3	1.95	0.47
26:A0:38:TYR:O	26:A0:59:ARG:NH2	2.48	0.47
31:AG:378:GLU:OE2	31:AG:388:ARG:NE	2.48	0.47
32:A:1813:C:O2	32:A:1813:C:H3'	2.14	0.47
32:A:1817:C:H5'	48:O:87:ILE:HD11	1.96	0.47
32:A:1847:U:H2'	32:A:1848:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2390:A:H5'	70:5:299:ARG:HB3	1.96	0.47
32:A:2514:C:H2'	32:A:2515:U:H6	1.78	0.47
32:A:2620:G:H2'	32:A:2621:G:H8	1.80	0.47
32:A:2961:C:C5	32:A:2962:C:C5	3.02	0.47
32:A:2962:C:H42	32:A:3016:G:H22	1.62	0.47
32:A:3191:A:C2	62:r:133:PRO:HB3	2.49	0.47
39:M:109:ARG:HH22	56:g:91:MET:HG3	1.79	0.47
43:T:63:LEU:HD23	43:T:65:GLY:H	1.80	0.47
46:Y:119:ALA:HA	67:U:111:PHE:HZ	1.78	0.47
51:3:183:ARG:HD3	51:3:186:LEU:HD11	1.97	0.47
83:Q:73:ARG:CG	83:Q:74:ARG:H	2.26	0.47
85:TA:85:LEU:CD1	85:TB:64:ILE:O	2.63	0.47
1:AA:1017:A:N1	11:AP:112:LYS:NZ	2.61	0.47
1:AA:1175:G:H2'	1:AA:1176:G:C8	2.49	0.47
1:AA:1366:C:O3'	1:AA:1419:G:N2	2.41	0.47
3:AC:134:PHE:HB2	28:A4:109:ALA:HB1	1.95	0.47
15:AX:121:ALA:HB3	15:AX:299:ASN:HA	1.97	0.47
20:AS:4:SER:OG	20:AS:15:ARG:NH1	2.47	0.47
32:A:2124:A:OP1	32:A:2125:C:H3'	2.15	0.47
32:A:2139:U:P	47:Z:74:SER:H	2.38	0.47
32:A:2143:G:H2'	32:A:2144:A:H8	1.78	0.47
32:A:3155:C:H2'	32:A:3156:A:C8	2.50	0.47
42:S:196:ASN:ND2	54:b:18:GLY:O	2.47	0.47
49:1:23:GLU:HB2	61:q:128:MET:HE1	1.97	0.47
56:g:140:VAL:H	60:o:85:HIS:CD2	2.33	0.47
59:m:34:ASP:OD1	59:m:34:ASP:N	2.45	0.47
62:r:71:PRO:HD2	62:r:107:LEU:HD23	1.96	0.47
67:U:144:ARG:HB3	67:U:147:VAL:HG22	1.97	0.47
1:AA:844:A:H2'	1:AA:845:A:C8	2.50	0.47
1:AA:1302:C:OP1	3:AC:165:LYS:NZ	2.37	0.47
1:AA:1478:A:N7	27:A3:128:LYS:N	2.63	0.47
1:AA:1489:G:H21	1:AA:1583:A:H1'	1.79	0.47
2:AB:194:ILE:HG12	2:AB:220:VAL:HG13	1.97	0.47
9:AN:13:ILE:HG23	9:AN:66:LEU:HB2	1.97	0.47
13:AT:2:PRO:HA	29:AD:408:TRP:HB2	1.96	0.47
16:A2:6:LEU:HA	16:A2:9:ARG:HD3	1.97	0.47
22:AV:122:GLN:HE22	22:AV:151:PHE:HA	1.80	0.47
32:A:2125:C:OP2	42:S:178:LYS:HG2	2.15	0.47
32:A:2185:G:C2	32:A:2186:C:N4	2.83	0.47
37:K:171:THR:HG22	62:r:59:GLU:H	1.79	0.47
54:b:66:ASN:HD22	54:b:68:ARG:HH11	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:r:39:VAL:HG23	62:r:50:GLU:HB2	1.96	0.47
63:J:114:LEU:HD21	80:l:96:LEU:HB3	1.96	0.47
70:5:278:PHE:HA	82:s:156:TYR:HE2	1.80	0.47
83:Q:92:PHE:O	83:Q:96:ARG:HB2	2.14	0.47
1:AA:963:C:H2'	1:AA:964:C:C5	2.49	0.47
1:AA:1195:U:H2'	1:AA:1196:A:C8	2.49	0.47
1:AA:1217:G:H2'	1:AA:1218:A:H8	1.80	0.47
1:AA:1581:G:H2'	1:AA:1583:A:OP2	2.15	0.47
1:AA:1593:U:OP1	16:A2:22:LYS:HD3	2.14	0.47
2:AB:124:HIS:HB3	2:AB:236:VAL:HG12	1.97	0.47
15:AX:46:ARG:N	15:AX:358:GLN:OE1	2.48	0.47
15:AX:226:VAL:HG22	15:AX:243:VAL:HG11	1.97	0.47
22:AV:66:PRO:HB3	22:AV:99:PRO:HB2	1.97	0.47
32:A:2379:C:N4	73:9:48:TRP:HZ2	2.00	0.47
32:A:2524:A:C2	34:D:92:ARG:HD3	2.51	0.47
32:A:2814:G:N2	65:N:141:GLY:HA2	2.30	0.47
46:Y:143:ASP:OD2	73:9:137:ARG:NH2	2.45	0.47
55:e:143:LYS:O	55:e:146:ARG:NH2	2.48	0.47
66:P:122:VAL:HG23	66:P:157:SER:HA	1.96	0.47
78:h:71:GLU:HA	78:h:74:VAL:HG12	1.97	0.47
83:Q:112:TYR:O	83:Q:115:SER:OG	2.28	0.47
1:AA:1491:C:H2'	1:AA:1492:A:C8	2.50	0.46
9:AN:13:ILE:HD11	9:AN:30:VAL:HG11	1.97	0.46
15:AX:118:ALA:O	15:AX:302:HIS:ND1	2.47	0.46
17:AH:81:LYS:HG3	17:AH:169:ALA:HB3	1.97	0.46
17:AH:176:GLN:HG2	25:A1:151:ILE:HB	1.97	0.46
31:AG:161:LEU:HD11	31:AG:244:PHE:HZ	1.80	0.46
32:A:1699:C:H5	46:Y:172:ILE:HD12	1.81	0.46
32:A:1751:A:H5'	39:M:64:ARG:NH2	2.30	0.46
32:A:1902:C:O2	57:i:127:PHE:HD2	1.84	0.46
32:A:2051:A:H5'	56:g:105:ARG:NH1	2.29	0.46
32:A:2160:A:H5'	52:4:88:TRP:CE2	2.50	0.46
32:A:2228:A:N6	52:4:102:GLN:HE21	2.12	0.46
32:A:3092:U:H2'	32:A:3093:C:C6	2.51	0.46
32:A:3189:C:C2	62:r:154:TRP:CD2	2.90	0.46
67:U:144:ARG:HA	67:U:144:ARG:HD2	1.74	0.46
70:5:243:GLU:O	70:5:247:THR:OG1	2.32	0.46
76:d:194:VAL:HG22	76:d:214:VAL:HG22	1.98	0.46
85:TA:68:VAL:CB	85:TB:85:LEU:CD2	2.92	0.46
1:AA:994:A:H1'	30:AF:166:ARG:HH11	1.80	0.46
1:AA:1177:C:H2'	1:AA:1178:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1409:A:H2'	1:AA:1410:G:H8	1.79	0.46
1:AA:1525:C:H5''	22:AV:103:TYR:CE1	2.45	0.46
2:AB:138:ARG:HB2	20:AS:30:LEU:HD21	1.96	0.46
26:A0:64:LEU:HD23	26:A0:134:VAL:HG13	1.97	0.46
32:A:1892:A:C1'	71:6:378:GLY:HA3	2.45	0.46
32:A:1952:U:H2'	32:A:1953:A:H8	1.80	0.46
32:A:2170:G:HO2'	63:J:87:VAL:HG21	1.77	0.46
32:A:2209:G:C2'	32:A:2210:C:OP1	2.62	0.46
32:A:2245:A:H4'	32:A:2246:A:OP1	2.14	0.46
32:A:3212:C:H4'	48:0:106:ASN:OD1	2.14	0.46
64:I:80:ARG:NH1	80:I:113:GLU:OE2	2.48	0.46
66:P:52:ASN:HD21	71:6:320:GLN:HE22	1.63	0.46
1:AA:649:A:C2	29:AD:422:TRP:CD2	3.03	0.46
1:AA:686:A:H2'	1:AA:687:G:H8	1.80	0.46
1:AA:851:A:H5'	1:AA:853:C:N4	2.29	0.46
1:AA:969:A:H2'	1:AA:970:A:H8	1.80	0.46
1:AA:1059:U:H2'	1:AA:1060:A:C8	2.51	0.46
10:AO:131:THR:HG23	19:AR:97:GLU:HA	1.96	0.46
13:AT:117:GLU:HA	13:AT:120:LYS:HG2	1.97	0.46
30:AF:110:LEU:HD13	30:AF:201:MET:HG3	1.96	0.46
30:AF:123:PHE:CZ	30:AF:139:ARG:CD	2.76	0.46
32:A:1745:U:O4	51:3:108:LYS:NZ	2.47	0.46
32:A:1965:A:H2'	32:A:1966:G:H8	1.81	0.46
32:A:2342:U:C5	67:U:74:HIS:ND1	2.83	0.46
32:A:2383:U:O4	32:A:2384:A:N6	2.47	0.46
32:A:2840:C:OP2	65:N:143:GLY:N	2.46	0.46
38:L:93:GLY:O	38:L:95:ARG:NH1	2.48	0.46
44:W:49:ARG:HB3	44:W:51:GLN:HG3	1.98	0.46
86:z:162:ILE:HG23	86:z:171:PRO:HG3	1.97	0.46
1:AA:1233:C:H42	1:AA:1444:A:N6	2.09	0.46
1:AA:1245:U:H1'	1:AA:1247:G:H1'	1.97	0.46
17:AH:69:PRO:HA	28:A4:61:LYS:HA	1.96	0.46
25:A1:56:ARG:HH12	28:A4:84:ALA:HA	1.80	0.46
32:A:1739:A:O2'	32:A:1888:G:H1'	2.16	0.46
32:A:1836:A:C2	74:a:130:HIS:HB3	2.50	0.46
32:A:1884:G:N7	35:F:281:ARG:HD2	2.31	0.46
32:A:1911:C:H2'	32:A:1912:A:C8	2.51	0.46
32:A:2142:A:O2'	32:A:2262:C:OP1	2.27	0.46
32:A:2167:A:H62	32:A:2211:U:H5''	1.80	0.46
32:A:2675:G:OP1	43:T:81:LYS:NZ	2.47	0.46
32:A:3076:A:H2'	32:A:3077:C:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:3195:A:OP2	32:A:3196:G:O2'	2.32	0.46
32:A:3199:U:O3'	32:A:3201:A:H5''	2.16	0.46
63:J:164:LEU:HD22	80:l:77:ILE:HD12	1.97	0.46
1:AA:708:C:H1'	1:AA:842:C:H5''	1.97	0.46
1:AA:911:U:H2'	1:AA:912:U:C6	2.50	0.46
1:AA:1559:G:H2'	1:AA:1560:U:C6	2.51	0.46
4:AE:47:LEU:HD13	4:AE:51:ILE:HG12	1.97	0.46
8:AM:23:LEU:HB2	8:AM:43:ARG:HH12	1.81	0.46
12:AQ:63:ILE:HG12	16:A2:4:PRO:HG2	1.96	0.46
21:AU:100:ALA:HA	21:AU:103:ARG:HD2	1.98	0.46
22:AV:340:LYS:O	22:AV:344:LEU:N	2.33	0.46
32:A:1693:C:H3'	32:A:1693:C:O2	2.14	0.46
32:A:1914:A:H5'	50:2:74:ALA:HB1	1.97	0.46
32:A:2615:A:C6	38:L:58:ILE:HG21	2.50	0.46
32:A:2673:G:H2'	32:A:2674:U:C6	2.51	0.46
33:B:1629:A:H2'	33:B:1630:A:H8	1.81	0.46
39:M:222:TYR:HE2	39:M:262:PRO:HB3	1.80	0.46
70:5:145:HIS:HD2	70:5:149:GLN:HE22	1.64	0.46
72:7:253:LYS:HD2	72:7:266:GLY:H	1.79	0.46
81:p:111:ILE:O	81:p:116:ARG:NH2	2.48	0.46
1:AA:914:A:H2'	1:AA:915:C:H6	1.81	0.46
1:AA:1249:U:N3	24:AZ:56:HIS:CE1	2.84	0.46
1:AA:1465:C:OP1	16:A2:39:GLU:CB	2.59	0.46
1:AA:1578:A:H2'	1:AA:1579:C:H6	1.81	0.46
6:AJ:57:GLN:HG2	6:AJ:109:LEU:HD21	1.98	0.46
6:AJ:66:PHE:CE2	6:AJ:82:ARG:NE	2.74	0.46
11:AP:75:LYS:HG3	11:AP:119:PHE:HE2	1.80	0.46
15:AX:119:TYR:HE2	25:A1:321:ASN:HB2	1.80	0.46
15:AX:141:VAL:HG21	15:AX:307:VAL:HG11	1.97	0.46
16:A2:38:ARG:CG	16:A2:39:GLU:N	2.78	0.46
23:AY:295:GLN:N	23:AY:299:GLU:OE1	2.48	0.46
24:AZ:81:GLU:OE2	29:AD:124:LYS:NZ	2.37	0.46
36:H:99:THR:O	36:H:108:ARG:CD	2.62	0.46
64:I:106:ALA:HA	64:I:109:LYS:HB2	1.98	0.46
82:s:351:VAL:HG13	82:s:353:ARG:O	2.15	0.46
1:AA:991:G:H1	5:AI:119:ASN:CG	2.24	0.46
1:AA:1210:U:H2'	1:AA:1211:G:H8	1.80	0.46
1:AA:1462:G:H2'	1:AA:1463:G:C8	2.51	0.46
8:AM:16:HIS:CE1	8:AM:39:ASN:HD22	2.34	0.46
19:AR:170:ARG:H	19:AR:189:ARG:HH22	1.63	0.46
31:AG:72:ASP:OD1	31:AG:72:ASP:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1834:U:C4	43:T:207:THR:N	2.83	0.46
32:A:1837:C:O2	32:A:1837:C:H3'	2.14	0.46
32:A:2190:C:O2'	63:J:146:GLY:CA	2.64	0.46
51:3:129:TYR:HA	51:3:144:LEU:HD13	1.98	0.46
71:6:275:GLN:HA	71:6:311:MET:HA	1.98	0.46
81:p:41:SER:N	81:p:44:SER:OG	2.44	0.46
2:AB:172:ARG:HH21	31:AG:155:LYS:HE3	1.80	0.46
4:AE:117:LEU:HD22	16:A2:10:LEU:HD12	1.97	0.46
13:AT:36:THR:HA	13:AT:45:ARG:HD3	1.98	0.46
30:AF:133:GLU:HA	30:AF:136:THR:HG22	1.98	0.46
32:A:2377:G:H21	73:9:32:GLY:HA3	1.80	0.46
32:A:2389:C:OP1	70:5:300:PRO:HB3	2.16	0.46
32:A:2524:A:C4	34:D:92:ARG:HD3	2.50	0.46
32:A:2746:U:H2'	32:A:2747:U:H6	1.81	0.46
32:A:2894:U:H5''	32:A:2895:U:O4'	2.16	0.46
32:A:3108:U:O2	69:E:264:ILE:HD13	2.15	0.46
63:J:119:GLU:HA	63:J:122:ARG:HE	1.80	0.46
1:AA:948:U:H2'	1:AA:949:U:C6	2.50	0.46
1:AA:1087:A:H2'	1:AA:1088:C:H6	1.81	0.46
1:AA:1190:C:H2'	1:AA:1191:C:C6	2.50	0.46
1:AA:1249:U:H3'	7:AK:28:HIS:CE1	2.51	0.46
1:AA:1255:U:H2'	1:AA:1256:A:C8	2.51	0.46
1:AA:1523:A:H2'	1:AA:1524:A:C8	2.51	0.46
2:AB:192:LEU:HD11	2:AB:220:VAL:HG12	1.97	0.46
26:A0:71:LEU:HD13	26:A0:78:ARG:HG3	1.97	0.46
32:A:1924:U:H2'	32:A:1925:A:C8	2.50	0.46
32:A:1939:G:C2	32:A:2495:U:N1	2.84	0.46
32:A:2155:A:O2'	32:A:2156:A:O4'	2.33	0.46
32:A:2293:A:N6	39:M:37:GLU:OE1	2.49	0.46
32:A:3056:C:H2'	32:A:3057:C:C6	2.51	0.46
36:H:65:ALA:HB3	36:H:71:PRO:HA	1.98	0.46
66:P:51:ARG:NH2	71:6:160:ASP:OD1	2.49	0.46
83:Q:74:ARG:O	83:Q:75:PHE:CB	2.62	0.46
85:TA:85:LEU:CD2	85:TB:64:ILE:HD12	2.45	0.46
1:AA:649:A:N1	29:AD:422:TRP:CE2	2.84	0.46
1:AA:893:G:O5'	6:AJ:98:GLU:HA	2.16	0.46
1:AA:1005:U:OP1	5:AI:152:LYS:HE3	2.15	0.46
1:AA:1401:G:N2	1:AA:1404:A:OP2	2.43	0.46
2:AB:81:VAL:HG22	14:AW:83:MET:HE1	1.97	0.46
20:AS:97:GLN:HA	20:AS:100:VAL:HG12	1.98	0.46
29:AD:222:ILE:HA	29:AD:245:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1680:A:C5	32:A:1681:G:H1'	2.51	0.46
32:A:1728:U:O2	45:X:96:LYS:NZ	2.49	0.46
32:A:1887:A:O4'	35:F:284:TYR:HA	2.16	0.46
32:A:1924:U:OP1	34:D:98:GLY:N	2.48	0.46
32:A:2800:U:H2'	32:A:2801:A:C8	2.52	0.46
32:A:2847:C:H2'	32:A:2848:A:O4'	2.16	0.46
55:e:55:ARG:HD3	55:e:157:LEU:HB2	1.96	0.46
82:s:168:GLU:HG2	82:s:172:ILE:HD12	1.98	0.46
85:TA:68:VAL:HB	85:TB:85:LEU:HD21	1.96	0.46
1:AA:1234:C:C5	7:AK:86:ARG:HD2	2.52	0.45
4:AE:9:ILE:HD12	4:AE:90:ARG:HG2	1.97	0.45
23:AY:391:ASN:HD22	84:u:615:UNK:C	2.29	0.45
26:A0:61:GLU:HG3	26:A0:62:SER:H	1.81	0.45
32:A:2180:A:O2'	32:A:2206:C:O3'	2.33	0.45
32:A:2197:G:O4'	80:l:126:ILE:HG21	2.16	0.45
32:A:2550:A:C8	32:A:2590:A:C4	3.04	0.45
32:A:2584:C:H2'	32:A:2585:G:H8	1.80	0.45
32:A:2678:A:C2	48:0:80:ALA:CB	2.97	0.45
50:2:82:ARG:NH1	50:2:89:SER:O	2.49	0.45
56:g:84:TYR:OH	56:g:164:LYS:NZ	2.40	0.45
66:P:54:ARG:NH1	71:6:155:TYR:OH	2.49	0.45
67:U:129:MET:HG2	76:d:82:ALA:HB2	1.98	0.45
80:l:76:ASN:H	80:l:79:LYS:HB2	1.80	0.45
82:s:351:VAL:HG21	82:s:375:ASN:O	2.16	0.45
1:AA:1576:G:H2'	1:AA:1577:U:C6	2.52	0.45
5:AI:84:PRO:HB3	5:AI:101:SER:HA	1.97	0.45
21:AU:179:ALA:O	21:AU:183:SER:OG	2.25	0.45
22:AV:79:ILE:HD13	22:AV:85:ILE:HD13	1.97	0.45
32:A:1817:C:H2'	32:A:1818:A:C8	2.50	0.45
32:A:1869:A:N7	57:i:120:HIS:NE2	2.63	0.45
32:A:2035:U:O2'	39:M:70:GLY:HA3	2.17	0.45
32:A:2379:C:C4	73:9:48:TRP:NE1	2.82	0.45
32:A:2664:U:H2'	32:A:2665:U:H6	1.80	0.45
32:A:2796:G:N2	36:H:88:HIS:CE1	2.81	0.45
40:O:108:LEU:HD13	48:0:122:LEU:HD21	1.97	0.45
42:S:94:ARG:HA	42:S:94:ARG:HD3	1.77	0.45
42:S:129:ARG:NH2	42:S:151:LYS:O	2.49	0.45
63:J:60:ILE:HG22	63:J:62:GLU:H	1.80	0.45
69:E:82:ASP:OD1	69:E:188:LYS:NZ	2.47	0.45
72:7:88:PRO:HG2	72:7:115:MET:HA	1.98	0.45
72:7:170:PRO:HG2	72:7:180:CYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:TB:75:THR:CG2	85:TB:78:GLU:HB2	2.27	0.45
1:AA:649:A:N6	29:AD:422:TRP:CZ2	2.84	0.45
1:AA:1265:C:H5''	3:AC:37:ASN:HA	1.99	0.45
1:AA:1333:G:H2'	1:AA:1334:G:C8	2.50	0.45
1:AA:1413:U:H2'	1:AA:1414:C:C6	2.51	0.45
1:AA:1595:G:H2'	1:AA:1596:A:H8	1.79	0.45
22:AV:200:GLU:HA	22:AV:203:ASN:HD22	1.80	0.45
25:A1:263:LEU:HD21	25:A1:280:LYS:HD3	1.98	0.45
32:A:1693:C:H6	46:Y:178:TRP:CD1	2.34	0.45
32:A:1953:A:O2'	32:A:2463:A:OP1	2.34	0.45
32:A:2524:A:C6	34:D:92:ARG:NE	2.84	0.45
66:P:101:VAL:HG13	71:6:150:ARG:HD2	1.97	0.45
71:6:286:ARG:NH1	71:6:295:GLN:O	2.50	0.45
75:c:213:LEU:HD22	75:c:216:ARG:HH21	1.81	0.45
1:AA:1296:A:OP1	2:AB:207:VAL:HG11	2.16	0.45
1:AA:1455:U:H2'	1:AA:1456:U:H6	1.82	0.45
1:AA:1578:A:H2'	1:AA:1579:C:C6	2.50	0.45
3:AC:148:LYS:NZ	28:A4:128:PHE:O	2.40	0.45
5:AI:86:ALA:HA	5:AI:99:VAL:HA	1.98	0.45
5:AI:140:LYS:HZ1	5:AI:145:ILE:N	2.12	0.45
12:AQ:77:ARG:HH12	14:AW:149:LEU:HD13	1.58	0.45
18:AL:129:ILE:HD13	18:AL:184:LEU:HD11	1.98	0.45
19:AR:202:ARG:NH2	19:AR:236:GLU:OE2	2.49	0.45
21:AU:112:GLU:OE2	21:AU:115:ARG:NH2	2.49	0.45
25:A1:103:LEU:HD23	25:A1:106:LEU:HD12	1.96	0.45
31:AG:116:LEU:HA	31:AG:116:LEU:HD23	1.77	0.45
32:A:1789:A:H2	32:A:1916:G:H1'	1.82	0.45
32:A:1890:C:OP1	51:3:168:ARG:NH2	2.49	0.45
32:A:2336:U:C2	32:A:2337:A:C8	3.04	0.45
32:A:2388:A:N3	34:D:128:GLN:OE1	2.49	0.45
32:A:2471:G:O2'	32:A:2654:U:O4	2.31	0.45
32:A:2493:C:C2	32:A:2540:C:C5	3.05	0.45
35:F:221:LEU:HG	35:F:222:THR:HG23	1.99	0.45
61:q:137:GLN:HA	61:q:140:ARG:HD2	1.98	0.45
70:5:128:ILE:HD11	70:5:372:LEU:HD22	1.99	0.45
71:6:233:LEU:HD11	71:6:236:LEU:HB2	1.98	0.45
75:c:160:LEU:HD21	75:c:223:MET:HG3	1.99	0.45
81:p:56:ASP:OD2	81:p:60:ARG:NH2	2.49	0.45
1:AA:1208:U:O4	1:AA:1358:A:N6	2.49	0.45
1:AA:1369:U:H1'	30:AF:106:LEU:HD21	1.98	0.45
7:AK:45:TYR:HA	24:AZ:43:ALA:HB1	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AX:262:VAL:HG21	15:AX:268:LEU:HD11	1.99	0.45
19:AR:193:ILE:O	19:AR:197:PHE:N	2.43	0.45
19:AR:208:ILE:HA	19:AR:211:LYS:HZ3	1.81	0.45
31:AG:275:LYS:H	31:AG:346:LEU:HD23	1.81	0.45
32:A:1942:C:H2'	32:A:1943:A:O4'	2.16	0.45
32:A:2721:G:C2	32:A:3098:U:O2	2.70	0.45
35:F:291:SER:HB3	56:g:52:LEU:HB2	1.98	0.45
40:O:49:VAL:HG21	40:O:121:ALA:HB3	1.97	0.45
63:J:92:LYS:HE3	63:J:151:LEU:HD11	1.99	0.45
72:7:94:HIS:NE2	76:d:279:THR:OG1	2.42	0.45
1:AA:845:A:H5''	21:AU:60:TYR:HE2	1.81	0.45
1:AA:1402:A:H5'	7:AK:75:ILE:CD1	2.47	0.45
4:AE:92:ASN:HB2	11:AP:117:MET:HE3	1.98	0.45
8:AM:20:ARG:NH1	8:AM:42:PRO:O	2.49	0.45
16:A2:60:GLU:HG3	16:A2:62:ARG:HD3	1.99	0.45
17:AH:153:ALA:O	17:AH:157:LEU:HB2	2.16	0.45
17:AH:161:GLN:HA	17:AH:164:LEU:HG	1.98	0.45
31:AG:380:LYS:HG3	31:AG:386:GLY:HA2	1.98	0.45
32:A:1841:U:H2'	32:A:1842:A:C8	2.52	0.45
32:A:2461:A:OP1	69:E:238:ARG:N	2.47	0.45
32:A:2864:U:O5'	44:W:50:ARG:NE	2.50	0.45
32:A:2962:C:H42	32:A:3016:G:N2	2.15	0.45
79:k:57:HIS:CE1	85:TA:53:LEU:H	2.35	0.45
82:s:240:GLN:HG2	82:s:298:GLN:HG2	1.97	0.45
1:AA:768:A:H4'	9:AN:24:LYS:HB2	1.99	0.45
1:AA:824:U:H2'	1:AA:825:U:C6	2.51	0.45
1:AA:941:G:H4'	1:AA:942:A:H5''	1.98	0.45
1:AA:1006:U:H2'	1:AA:1007:G:C8	2.52	0.45
32:A:1812:C:O2	75:c:45:LEU:CD2	2.51	0.45
32:A:2239:A:O2'	37:K:29:GLY:HA3	2.17	0.45
59:m:42:ARG:O	59:m:44:HIS:ND1	2.49	0.45
64:I:204:GLN:CG	85:TA:90:LEU:HD13	2.44	0.45
1:AA:741:A:P	21:AU:86:ARG:NH2	2.89	0.45
21:AU:80:ARG:HA	21:AU:83:HIS:HB3	1.98	0.45
23:AY:307:GLU:HB3	23:AY:309:LYS:HG3	1.99	0.45
32:A:1964:U:H2'	32:A:1965:A:C8	2.51	0.45
32:A:2020:U:O4	39:M:58:GLN:NE2	2.50	0.45
32:A:2235:C:H5	37:K:78:SER:HB2	1.71	0.45
32:A:2261:C:O2	42:S:184:ARG:HD2	2.16	0.45
68:V:100:LYS:HA	68:V:105:ARG:HB3	1.98	0.45
72:7:317:LEU:O	72:7:320:SER:OG	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:k:94:ILE:HD12	79:k:94:ILE:HA	1.87	0.45
1:AA:1249:U:C5	24:AZ:56:HIS:CE1	3.05	0.45
1:AA:1440:G:H2'	1:AA:1441:A:H8	1.82	0.45
23:AY:391:ASN:ND2	84:u:615:UNK:C	2.80	0.45
32:A:2042:U:H2'	32:A:2043:C:C6	2.52	0.45
32:A:2187:C:H4'	63:J:106:LYS:HZ3	1.79	0.45
32:A:2383:U:O2'	70:5:92:LEU:CD1	2.65	0.45
32:A:2523:C:O2	34:D:87:HIS:HB3	2.17	0.45
56:g:144:THR:O	56:g:146:THR:N	2.49	0.45
82:s:401:LEU:HA	82:s:417:VAL:HG21	1.99	0.45
1:AA:1194:C:P	30:AF:178:ARG:HH22	2.40	0.45
1:AA:1382:A:C5'	15:AX:166:ARG:HH11	2.23	0.45
1:AA:1402:A:H5'	7:AK:75:ILE:CG1	2.47	0.45
3:AC:69:LEU:HD12	7:AK:119:GLN:HE21	1.82	0.45
13:AT:15:TYR:OH	13:AT:50:PHE:O	2.24	0.45
15:AX:60:GLY:H	15:AX:63:HIS:CD2	2.34	0.45
17:AH:75:ARG:HH12	17:AH:77:SER:HB2	1.82	0.45
32:A:1829:A:H2'	32:A:1830:G:C8	2.52	0.45
32:A:1939:G:C2	32:A:2495:U:C2	3.05	0.45
32:A:2006:C:H2'	32:A:2007:U:C6	2.52	0.45
32:A:2045:A:H2'	32:A:2046:C:C6	2.52	0.45
32:A:2971:A:O2'	65:N:104:MET:HE2	2.16	0.45
32:A:3089:A:C6	86:z:232:ARG:CD	3.00	0.45
32:A:3143:U:O4	32:A:3144:A:N6	2.50	0.45
34:D:64:VAL:HG13	34:D:80:ARG:HH12	1.81	0.45
35:F:167:MET:HE3	57:i:62:ILE:HG12	1.98	0.45
40:O:132:PRO:HD3	48:0:185:PHE:HD1	1.82	0.45
49:1:44:LEU:HD22	49:1:53:ARG:HB3	1.99	0.45
53:8:155:PRO:O	53:8:158:HIS:NE2	2.50	0.45
68:V:80:ILE:HB	68:V:85:TRP:HB2	1.99	0.45
74:a:49:LEU:HD23	74:a:60:CYS:HB3	1.99	0.45
82:s:184:LEU:HD23	82:s:184:LEU:HA	1.87	0.45
1:AA:769:G:OP2	9:AN:73:ARG:NH2	2.50	0.44
1:AA:948:U:H4'	18:AL:191:PRO:CG	2.48	0.44
1:AA:1169:G:H2'	1:AA:1170:G:C8	2.52	0.44
1:AA:1284:U:HO2'	29:AD:347:GLN:CD	2.26	0.44
1:AA:1452:U:OP2	31:AG:380:LYS:CD	2.64	0.44
1:AA:1495:C:H2'	1:AA:1496:U:C6	2.52	0.44
3:AC:72:HIS:HB3	3:AC:112:ARG:HD2	1.99	0.44
8:AM:100:HIS:HB3	8:AM:103:MET:HG3	1.98	0.44
14:AW:134:TYR:HE1	14:AW:172:ILE:HG12	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:282:PHE:HE1	28:A4:408:LYS:HA	1.82	0.44
28:A4:633:LEU:HA	28:A4:636:ALA:HB3	1.98	0.44
32:A:1836:A:N3	74:a:130:HIS:HB3	2.32	0.44
32:A:1851:G:H2'	32:A:2693:A:N7	2.32	0.44
32:A:1902:C:H2'	57:i:126:LYS:H	1.83	0.44
32:A:2235:C:H3'	32:A:2235:C:O2	2.16	0.44
32:A:2385:U:P	34:D:71:LYS:HE2	2.57	0.44
32:A:2473:A:H8	38:L:35:MET:HB2	1.81	0.44
32:A:2493:C:C4	32:A:2540:C:N1	2.85	0.44
41:R:111:LYS:HD2	54:b:127:GLN:HB3	2.00	0.44
67:U:112:PRO:HA	67:U:113:GLU:HA	1.65	0.44
85:TB:86:LEU:HA	85:TB:89:THR:OG1	2.17	0.44
1:AA:939:A:H3'	1:AA:939:A:OP2	2.16	0.44
1:AA:1219:U:H5''	1:AA:1220:A:OP1	2.18	0.44
1:AA:1258:A:N7	1:AA:1330:C:H5''	2.32	0.44
1:AA:1354:A:O2'	1:AA:1355:G:H5''	2.17	0.44
1:AA:1552:G:H2'	1:AA:1553:A:H8	1.82	0.44
10:AO:119:ASN:OD1	10:AO:119:ASN:N	2.49	0.44
23:AY:387:LEU:O	23:AY:390:SER:OG	2.32	0.44
29:AD:286:GLU:HB2	29:AD:288:HIS:CE1	2.52	0.44
29:AD:370:VAL:HB	29:AD:385:ALA:H	1.81	0.44
30:AF:130:SER:H	30:AF:133:GLU:HB2	1.82	0.44
32:A:1952:U:H2'	32:A:1953:A:C8	2.53	0.44
32:A:2065:A:N7	44:W:74:ARG:HB2	2.31	0.44
32:A:2507:A:HO2'	32:A:2508:C:P	2.38	0.44
45:X:192:LYS:HE3	45:X:192:LYS:HB2	1.77	0.44
53:8:181:PRO:HB3	59:m:60:ASP:HB3	1.98	0.44
55:e:82:SER:OG	55:e:83:LEU:N	2.50	0.44
62:r:135:LEU:HD11	62:r:139:VAL:HG22	1.98	0.44
65:N:191:SER:OG	65:N:192:ARG:N	2.50	0.44
1:AA:800:C:H2'	1:AA:801:A:C8	2.52	0.44
1:AA:1419:G:H4'	1:AA:1420:U:H5''	1.99	0.44
3:AC:94:LYS:NZ	29:AD:92:LYS:O	2.39	0.44
3:AC:165:LYS:HD3	3:AC:167:LEU:HD22	2.00	0.44
29:AD:394:ASP:OD1	29:AD:394:ASP:N	2.43	0.44
32:A:1690:C:N3	46:Y:213:ARG:NH2	2.56	0.44
32:A:2004:G:H2'	32:A:2005:C:C6	2.52	0.44
32:A:2075:U:O2'	32:A:2833:A:N7	2.39	0.44
32:A:2190:C:O2'	63:J:146:GLY:HA2	2.18	0.44
32:A:2796:G:N2	36:H:88:HIS:HE1	2.14	0.44
35:F:181:LYS:HD3	35:F:181:LYS:HA	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Y:235:LEU:HD23	46:Y:235:LEU:HA	1.87	0.44
75:c:105:ARG:HH11	75:c:112:LYS:H	1.66	0.44
82:s:117:GLY:N	82:s:395:GLY:O	2.50	0.44
83:Q:76:LEU:HD11	83:Q:80:PHE:HB2	2.00	0.44
85:TA:68:VAL:HG21	85:TB:85:LEU:CD2	2.43	0.44
1:AA:717:G:H4'	1:AA:718:A:O5'	2.18	0.44
1:AA:1399:A:H2	1:AA:1445:G:O2'	2.01	0.44
1:AA:1455:U:H2'	1:AA:1456:U:C6	2.52	0.44
4:AE:4:TYR:O	4:AE:96:HIS:ND1	2.47	0.44
16:A2:59:ASN:ND2	16:A2:66:CYS:SG	2.90	0.44
30:AF:176:ASP:HA	30:AF:179:ARG:HE	1.82	0.44
32:A:2372:U:C5	67:U:96:TYR:CG	3.05	0.44
32:A:2517:U:H2'	32:A:2518:A:C8	2.52	0.44
32:A:3009:C:O2	32:A:3009:C:H3'	2.17	0.44
37:K:155:LEU:C	37:K:158:TYR:CD2	2.96	0.44
46:Y:111:MET:O	46:Y:114:THR:OG1	2.35	0.44
55:e:176:ALA:HB2	55:e:191:THR:HG21	1.99	0.44
64:I:101:ASN:HB2	64:I:152:MET:HB2	2.00	0.44
66:P:52:ASN:HB3	66:P:55:ASN:HB2	2.00	0.44
71:6:274:LYS:O	71:6:312:THR:OG1	2.33	0.44
73:9:64:ASP:OD1	73:9:64:ASP:N	2.48	0.44
75:c:240:LEU:HB3	75:c:301:LEU:HD11	2.00	0.44
1:AA:1007:G:H2'	1:AA:1008:A:H8	1.82	0.44
13:AT:76:LEU:HB2	13:AT:88:VAL:HG13	1.99	0.44
15:AX:338:ASP:H	25:A1:261:ASN:HD22	1.66	0.44
25:A1:187:LYS:O	25:A1:191:ILE:HG12	2.18	0.44
27:A3:142:LYS:HD2	27:A3:142:LYS:HA	1.82	0.44
32:A:1828:A:H62	32:A:2683:C:H1'	1.83	0.44
32:A:1881:A:C6	56:g:97:TYR:CD2	3.06	0.44
32:A:2366:G:H2'	32:A:2367:A:C8	2.53	0.44
32:A:2863:U:O2	32:A:2869:A:N6	2.46	0.44
60:o:80:SER:O	60:o:80:SER:OG	2.35	0.44
69:E:227:GLN:NE2	69:E:236:THR:OG1	2.51	0.44
70:5:386:TRP:NE1	70:5:398:GLU:OE1	2.50	0.44
75:c:265:THR:OG1	75:c:266:ALA:N	2.51	0.44
81:p:140:SER:OG	81:p:141:ARG:N	2.51	0.44
85:TA:85:LEU:CA	85:TA:88:LYS:HD2	2.48	0.44
1:AA:881:A:N6	10:AO:82:LYS:CG	2.75	0.44
1:AA:1349:U:H2'	1:AA:1350:G:C8	2.52	0.44
3:AC:38:ARG:HB3	3:AC:43:ARG:HH21	1.83	0.44
4:AE:15:ARG:NH1	21:AU:178:GLU:OE1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AW:100:VAL:HG21	14:AW:144:LEU:HD22	1.98	0.44
15:AX:105:ALA:O	15:AX:140:HIS:ND1	2.50	0.44
24:AZ:39:GLU:CD	24:AZ:40:LEU:H	2.26	0.44
28:A4:633:LEU:O	28:A4:637:PHE:N	2.45	0.44
31:AG:157:SER:HB2	31:AG:209:LEU:HD22	1.99	0.44
32:A:1806:U:H1'	32:A:1807:U:OP2	2.18	0.44
32:A:1827:C:O2'	41:R:48:ARG:NH1	2.51	0.44
32:A:2121:G:H2'	32:A:2122:A:H8	1.82	0.44
32:A:2125:C:O4'	32:A:2263:C:H1'	2.18	0.44
32:A:2160:A:OP2	52:4:83:LYS:NZ	2.49	0.44
32:A:2409:A:H5''	70:5:222:ARG:HH21	1.83	0.44
32:A:2963:A:H2'	32:A:2964:U:O4'	2.17	0.44
32:A:3009:C:C5	32:A:3031:G:N1	2.86	0.44
34:D:124:GLU:HB2	34:D:163:ILE:HG13	2.00	0.44
43:T:149:ARG:NH2	43:T:152:CYS:SG	2.91	0.44
55:e:100:LYS:HE2	55:e:100:LYS:HB3	1.76	0.44
58:j:91:TRP:CD2	60:o:58:GLN:HG2	2.53	0.44
64:I:204:GLN:CG	85:TA:90:LEU:HD11	2.46	0.44
82:s:90:LYS:NZ	82:s:232:GLN:OE1	2.51	0.44
82:s:381:THR:O	82:s:385:GLN:NE2	2.50	0.44
86:z:107:LEU:HD23	86:z:107:LEU:H	1.83	0.44
1:AA:773:U:H2'	1:AA:774:G:C8	2.40	0.44
1:AA:844:A:C4	26:A0:201:TRP:CD1	3.06	0.44
1:AA:1204:C:O2'	1:AA:1225:C:N4	2.51	0.44
1:AA:1529:A:O2'	22:AV:64:LYS:O	2.18	0.44
24:AZ:66:ARG:HD2	24:AZ:73:ASP:HB3	1.99	0.44
26:A0:85:TRP:HB3	26:A0:93:CYS:HB2	1.99	0.44
26:A0:132:GLU:HA	26:A0:207:GLN:HE21	1.83	0.44
31:AG:365:ARG:HB2	31:AG:370:LEU:HD12	2.00	0.44
32:A:1683:C:N4	46:Y:225:ASN:HD21	2.15	0.44
32:A:1965:A:H2'	32:A:1966:G:C8	2.53	0.44
32:A:2819:G:O4'	86:z:227:SER:HB2	2.18	0.44
32:A:3000:A:H2'	32:A:3001:G:C8	2.53	0.44
42:S:115:LEU:HB3	54:b:118:PRO:HB2	2.00	0.44
44:W:101:LYS:HD3	77:f:56:ILE:HG21	1.98	0.44
46:Y:199:PHE:HB2	70:5:65:HIS:CD2	2.53	0.44
47:Z:69:VAL:HG23	47:Z:91:LEU:HD21	2.00	0.44
55:e:50:ALA:N	55:e:232:PHE:O	2.51	0.44
67:U:68:VAL:HG13	67:U:97:VAL:HG12	1.99	0.44
74:a:67:ILE:O	75:c:275:TYR:OH	2.33	0.44
75:c:72:ILE:HD13	75:c:178:LEU:HD13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:c:163:GLU:HG2	75:c:188:PRO:HB2	1.99	0.44
75:c:179:THR:HG23	75:c:194:THR:HG21	1.99	0.44
76:d:180:THR:HG23	76:d:225:TYR:HB2	2.00	0.44
76:d:247:VAL:HG13	76:d:262:HIS:HB3	2.00	0.44
76:d:250:LYS:HE2	76:d:252:LEU:HA	2.00	0.44
1:AA:650:U:C4	29:AD:427:ARG:HD3	2.52	0.44
1:AA:661:C:H5'	29:AD:300:ARG:HG3	2.00	0.44
1:AA:872:G:H2'	1:AA:873:G:H8	1.81	0.44
1:AA:1002:C:H2'	1:AA:1003:A:C8	2.44	0.44
1:AA:1177:C:H2'	1:AA:1178:G:C8	2.53	0.44
15:AX:88:VAL:O	15:AX:92:LYS:NZ	2.49	0.44
26:A0:101:ARG:HB3	26:A0:113:LYS:HB3	2.00	0.44
30:AF:172:VAL:HG12	30:AF:240:ARG:HD3	2.00	0.44
32:A:2692:G:N1	32:A:2696:A:OP2	2.37	0.44
37:K:155:LEU:N	37:K:158:TYR:CZ	2.86	0.44
77:f:134:VAL:HG23	77:f:148:SER:HB2	2.00	0.44
1:AA:1361:G:H2'	1:AA:1362:G:C8	2.52	0.44
4:AE:35:ILE:HD11	18:AL:90:ARG:HH11	1.82	0.44
8:AM:32:TYR:HB2	8:AM:54:TYR:HB3	2.00	0.44
19:AR:334:THR:OG1	19:AR:335:GLU:N	2.51	0.44
25:A1:182:LEU:HD11	25:A1:190:LEU:HD12	2.00	0.44
32:A:1756:A:C2	32:A:1757:A:C8	3.06	0.44
32:A:1822:U:O2	32:A:2707:A:O2'	2.33	0.44
32:A:1911:C:H2'	32:A:1912:A:H8	1.82	0.44
32:A:2100:C:O2'	32:A:2135:A:O2'	2.34	0.44
32:A:2321:A:N7	48:0:142:GLY:HA3	2.33	0.44
32:A:2339:G:H21	32:A:2427:C:H5'	1.82	0.44
32:A:2523:C:O2	34:D:87:HIS:CG	2.71	0.44
32:A:2640:C:C2	32:A:2641:A:C8	3.06	0.44
32:A:3076:A:N1	32:A:3093:C:N4	2.66	0.44
39:M:133:LYS:HG2	51:3:168:ARG:NH2	2.32	0.44
44:W:62:HIS:ND1	44:W:94:GLU:OE2	2.47	0.44
61:q:138:GLN:O	61:q:142:ASN:ND2	2.50	0.44
71:6:184:LEU:HD22	81:p:191:LYS:HB2	1.99	0.44
78:h:127:LEU:O	78:h:131:ASN:ND2	2.47	0.44
85:TA:62:PRO:HA	85:TA:65:GLN:CG	2.48	0.44
5:AI:101:SER:OG	5:AI:105:GLU:N	2.47	0.43
5:AI:152:LYS:HB2	5:AI:152:LYS:HE2	1.86	0.43
15:AX:387:ASN:HD22	15:AX:390:LEU:H	1.66	0.43
28:A4:116:VAL:HG11	29:AD:141:TRP:HZ3	1.83	0.43
31:AG:334:GLY:O	31:AG:340:GLN:NE2	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2167:A:N6	32:A:2211:U:H5''	2.33	0.43
32:A:2501:C:N4	50:2:49:ARG:CG	2.81	0.43
32:A:2511:C:O2'	34:D:258:GLY:N	2.51	0.43
32:A:2688:C:H2'	32:A:2689:C:C6	2.53	0.43
32:A:3041:U:O2'	32:A:3042:U:O5'	2.36	0.43
32:A:3157:C:N4	40:O:14:VAL:HG21	2.33	0.43
40:O:96:ARG:NH1	40:O:126:LYS:O	2.49	0.43
45:X:20:ILE:HG13	45:X:23:ARG:HH22	1.83	0.43
71:6:187:VAL:HG23	71:6:319:PHE:HB3	1.99	0.43
71:6:261:ARG:HE	71:6:261:ARG:HB3	1.70	0.43
82:s:103:ASP:OD1	82:s:103:ASP:N	2.51	0.43
83:Q:183:LEU:HD21	83:Q:219:GLU:HG2	2.00	0.43
1:AA:881:A:H62	10:AO:82:LYS:HG3	1.80	0.43
1:AA:932:C:O3'	13:AT:4:LYS:NZ	2.51	0.43
1:AA:1524:A:N7	22:AV:396:GLN:NE2	2.66	0.43
25:A1:166:PRO:O	25:A1:169:ARG:NH1	2.51	0.43
30:AF:58:LEU:HA	30:AF:61:GLU:HB3	2.00	0.43
32:A:2051:A:H2'	32:A:2052:A:C8	2.53	0.43
32:A:2277:U:H2'	32:A:2278:A:H8	1.83	0.43
32:A:2298:A:H61	35:F:145:LEU:HD22	1.83	0.43
32:A:2728:C:H2'	32:A:2729:U:H6	1.82	0.43
32:A:3113:A:H2'	32:A:3114:U:C6	2.53	0.43
35:F:63:GLN:HG2	35:F:81:ASP:HB3	1.99	0.43
35:F:262:THR:HG22	35:F:264:PRO:HD2	2.00	0.43
41:R:107:ILE:HD12	43:T:211:THR:HG21	2.00	0.43
70:5:200:ARG:HG2	70:5:231:THR:HG22	1.99	0.43
70:5:203:VAL:HG11	70:5:278:PHE:HZ	1.83	0.43
77:f:162:LEU:HD12	77:f:167:ALA:HA	2.00	0.43
85:TA:68:VAL:HG21	85:TB:85:LEU:HD23	1.99	0.43
1:AA:764:A:N1	18:AL:213:PHE:CG	2.85	0.43
1:AA:915:C:H2'	1:AA:916:C:C6	2.52	0.43
1:AA:1023:C:H2'	1:AA:1024:G:C8	2.53	0.43
1:AA:1231:A:O2'	1:AA:1236:C:N4	2.50	0.43
1:AA:1304:C:H2'	1:AA:1305:A:O4'	2.17	0.43
1:AA:1456:U:OP2	31:AG:277:LYS:HE2	2.18	0.43
11:AP:139:ARG:NE	11:AP:139:ARG:O	2.51	0.43
15:AX:86:ARG:HD2	15:AX:86:ARG:HA	1.84	0.43
15:AX:392:GLU:O	15:AX:396:ALA:N	2.51	0.43
19:AR:68:PRO:HG2	19:AR:307:LEU:HA	2.01	0.43
22:AV:152:ILE:HA	22:AV:155:GLU:HA	2.00	0.43
22:AV:196:PHE:HB3	22:AV:201:GLU:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A4:556:LYS:O	28:A4:560:GLU:CB	2.67	0.43
30:AF:123:PHE:CE1	30:AF:139:ARG:NH1	2.86	0.43
32:A:2801:A:H2'	32:A:2802:A:C8	2.53	0.43
32:A:2950:U:H2'	32:A:2951:A:C8	2.48	0.43
32:A:3169:C:H3'	32:A:3169:C:O2	2.19	0.43
37:K:155:LEU:HG	37:K:158:TYR:HE2	1.80	0.43
55:e:243:PHE:CD2	55:e:246:ALA:CB	3.01	0.43
81:p:80:SER:OG	81:p:82:CYS:SG	2.75	0.43
1:AA:737:C:H3'	1:AA:737:C:O2	2.19	0.43
1:AA:914:A:H2'	1:AA:915:C:C6	2.53	0.43
1:AA:1429:C:H1'	1:AA:1430:A:OP2	2.19	0.43
1:AA:1485:G:H2'	1:AA:1486:C:O4'	2.19	0.43
7:AK:128:TRP:CD2	31:AG:379:ARG:HD2	2.54	0.43
18:AL:67:PRO:HA	18:AL:68:PRO:HD3	1.81	0.43
23:AY:353:LEU:HD12	24:AZ:22:VAL:HG11	2.01	0.43
26:A0:71:LEU:HD23	26:A0:71:LEU:HA	1.89	0.43
31:AG:162:MET:HB3	31:AG:162:MET:HE3	1.82	0.43
31:AG:315:PHE:HD2	31:AG:345:ARG:HD2	1.84	0.43
32:A:1769:C:N4	35:F:108:ARG:HD2	2.31	0.43
32:A:1881:A:H62	56:g:111:ARG:HD3	1.84	0.43
32:A:2286:A:H2'	32:A:2287:U:C6	2.53	0.43
32:A:2326:C:OP2	82:s:55:SER:OG	2.26	0.43
32:A:2832:A:C8	77:f:49:LYS:HB3	2.53	0.43
34:D:121:PRO:HB3	34:D:166:SER:HA	2.00	0.43
34:D:123:GLU:HG3	70:5:256:TYR:HE2	1.83	0.43
35:F:86:VAL:HG13	35:F:175:LYS:HG2	2.00	0.43
39:M:233:ARG:HB3	39:M:244:LEU:HD11	2.01	0.43
42:S:109:THR:OG1	42:S:110:SER:N	2.51	0.43
42:S:162:GLU:HG3	54:b:107:GLN:HA	2.00	0.43
64:I:102:VAL:HG11	64:I:173:PHE:HD1	1.83	0.43
64:I:143:LEU:HG	64:I:147:PHE:HE2	1.83	0.43
64:I:189:GLN:HG2	85:TA:55:ASN:HD21	1.50	0.43
64:I:194:TYR:HD1	85:TB:77:LEU:HD12	1.84	0.43
67:U:124:ASP:O	67:U:128:SER:OG	2.34	0.43
70:5:306:ASP:OD1	70:5:309:ARG:NH1	2.51	0.43
71:6:277:GLN:HE22	71:6:279:ILE:HB	1.83	0.43
81:p:81:TYR:HH	81:p:147:LEU:HB2	1.72	0.43
1:AA:1260:A:N6	1:AA:1330:C:O2	2.51	0.43
1:AA:1294:A:C6	2:AB:170:TYR:CD2	3.05	0.43
1:AA:1444:A:C4	7:AK:85:VAL:HG22	2.54	0.43
1:AA:1588:G:H2'	1:AA:1589:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AE:5:GLU:CD	4:AE:97:PRO:HD3	2.44	0.43
10:AO:113:LEU:HD23	10:AO:113:LEU:HA	1.86	0.43
19:AR:146:LYS:HA	19:AR:146:LYS:HD3	1.87	0.43
23:AY:328:PHE:O	23:AY:332:ILE:HG12	2.19	0.43
25:A1:266:LEU:HD21	25:A1:289:ILE:HD11	2.00	0.43
31:AG:364:MET:HE3	31:AG:369:LEU:HD22	2.01	0.43
32:A:1762:A:H62	61:q:33:ARG:HD2	1.83	0.43
32:A:1763:A:H5'	61:q:34:ARG:NE	2.34	0.43
32:A:1811:A:H62	75:c:49:ARG:CZ	2.29	0.43
32:A:1834:U:H3	43:T:206:ARG:CA	2.26	0.43
32:A:1894:G:H2'	32:A:1895:C:C6	2.52	0.43
32:A:2628:U:H4'	32:A:2629:A:O5'	2.16	0.43
64:I:189:GLN:CB	85:TA:55:ASN:HD21	2.29	0.43
64:I:207:LEU:HD22	85:TB:82:LEU:HD21	1.98	0.43
68:V:133:ILE:HD11	68:V:145:ARG:HB3	2.01	0.43
69:E:145:LEU:HD23	69:E:145:LEU:HA	1.90	0.43
82:s:375:ASN:ND2	82:s:390:LYS:O	2.52	0.43
83:Q:79:GLU:OE2	83:Q:103:ARG:NH2	2.51	0.43
1:AA:838:U:H2'	1:AA:839:A:C8	2.53	0.43
1:AA:1357:A:H2'	1:AA:1358:A:C8	2.53	0.43
5:AI:99:VAL:N	5:AI:108:ALA:O	2.50	0.43
13:AT:7:PHE:HA	13:AT:8:PRO:HD3	1.86	0.43
15:AX:283:ALA:HB3	15:AX:286:GLU:HG2	2.00	0.43
15:AX:336:ALA:HA	25:A1:261:ASN:HD21	1.84	0.43
22:AV:97:HIS:NE2	26:A0:107:GLN:O	2.48	0.43
22:AV:387:VAL:HG22	22:AV:391:GLN:HE21	1.84	0.43
26:A0:100:VAL:HG12	26:A0:102:PRO:HD3	2.00	0.43
32:A:1892:A:N1	51:3:169:ARG:NH1	2.67	0.43
32:A:1975:U:H2'	32:A:1976:U:C6	2.54	0.43
32:A:2108:G:N7	65:N:67:LYS:NZ	2.66	0.43
32:A:2152:A:OP1	60:o:34:ASN:HB3	2.19	0.43
32:A:2220:A:H2'	32:A:2221:C:C6	2.54	0.43
32:A:2379:C:O2	32:A:2379:C:H3'	2.19	0.43
32:A:2584:C:H2'	32:A:2585:G:C8	2.54	0.43
32:A:2906:C:H42	49:1:19:ARG:NH2	2.15	0.43
32:A:3014:G:H5''	52:4:96:PRO:HB2	2.01	0.43
32:A:3122:U:H5'	32:A:3124:U:O4'	2.19	0.43
37:K:155:LEU:HG	37:K:158:TYR:CD2	2.53	0.43
69:E:309:ASP:OD1	69:E:309:ASP:N	2.50	0.43
70:5:211:THR:OG1	70:5:274:ASN:ND2	2.46	0.43
76:d:187:GLU:O	76:d:218:THR:OG1	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:s:206:VAL:HG13	82:s:235:ASP:HB3	2.00	0.43
1:AA:649:A:C6	29:AD:422:TRP:NE1	2.85	0.43
1:AA:669:U:C6	29:AD:422:TRP:CH2	3.06	0.43
1:AA:765:C:O2	1:AA:765:C:H3'	2.18	0.43
1:AA:1230:C:N4	1:AA:1446:A:O2'	2.47	0.43
1:AA:1309:A:O2'	17:AH:137:ARG:NH2	2.50	0.43
1:AA:1470:A:H2'	1:AA:1471:A:C8	2.53	0.43
2:AB:103:GLU:HA	20:AS:60:ILE:HD11	2.00	0.43
7:AK:48:ALA:HB3	24:AZ:44:LYS:HE3	2.00	0.43
14:AW:110:ASN:HB3	14:AW:125:ARG:HH21	1.83	0.43
25:A1:56:ARG:HA	25:A1:59:LYS:HB2	1.99	0.43
25:A1:267:LEU:HD11	25:A1:280:LYS:HE3	2.00	0.43
27:A3:151:ARG:HE	27:A3:151:ARG:HB3	1.58	0.43
32:A:1734:C:H42	57:i:107:LEU:CD2	2.31	0.43
32:A:2060:A:C4	32:A:2079:C:N4	2.86	0.43
32:A:2238:A:N3	37:K:111:MET:HG2	2.33	0.43
32:A:2299:U:H5''	32:A:2300:G:H5''	2.01	0.43
32:A:2333:G:N1	32:A:2442:U:O4	2.52	0.43
32:A:2511:C:O2	32:A:2511:C:H3'	2.19	0.43
32:A:2511:C:O3'	34:D:257:ILE:HB	2.19	0.43
32:A:2549:C:H4'	32:A:2550:A:H5'	2.01	0.43
32:A:2577:C:O2	32:A:2577:C:H3'	2.18	0.43
39:M:28:LYS:HD3	60:o:94:HIS:CE1	2.53	0.43
63:J:156:VAL:HA	80:l:101:LEU:HD13	2.00	0.43
64:I:82:LEU:HD23	64:I:82:LEU:HA	1.88	0.43
69:E:208:ALA:HB2	69:E:297:VAL:HG12	1.99	0.43
81:p:79:ILE:HD13	81:p:147:LEU:HD11	2.01	0.43
81:p:81:TYR:CD1	81:p:99:ALA:HA	2.53	0.43
1:AA:789:U:H2'	1:AA:790:A:C8	2.53	0.43
1:AA:1016:U:O2	11:AP:90:CYS:HA	2.19	0.43
1:AA:1551:G:H2'	1:AA:1552:G:C8	2.53	0.43
2:AB:88:ARG:HH11	14:AW:117:GLY:HA2	1.84	0.43
11:AP:85:SER:OG	11:AP:89:GLY:N	2.52	0.43
16:A2:99:LEU:HD23	16:A2:103:LYS:HE3	1.99	0.43
20:AS:89:ASN:HB3	20:AS:92:PHE:HB2	2.00	0.43
32:A:1783:U:H5''	50:2:88:LYS:HD3	2.01	0.43
32:A:1832:A:H61	54:b:4:ARG:HH22	1.65	0.43
32:A:1939:G:N3	32:A:1939:G:H2'	2.33	0.43
32:A:2170:G:HO2'	63:J:87:VAL:CG2	2.30	0.43
32:A:2196:A:H4'	32:A:2213:A:C2	2.53	0.43
32:A:2240:C:P	37:K:71:LYS:NZ	2.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:2293:A:C6	39:M:39:ARG:HD2	2.54	0.43
32:A:2484:C:H3'	32:A:2484:C:O2	2.19	0.43
32:A:3139:G:H2'	32:A:3140:A:C8	2.53	0.43
34:D:137:ALA:HB2	34:D:210:ALA:HA	2.01	0.43
39:M:127:VAL:HG21	39:M:138:VAL:HG21	2.01	0.43
52:4:77:LYS:HB3	52:4:77:LYS:HE3	1.88	0.43
54:b:78:GLU:HG2	54:b:84:VAL:HG22	2.00	0.43
56:g:140:VAL:HB	60:o:85:HIS:HD2	1.84	0.43
85:TA:64:ILE:C	85:TB:85:LEU:CD2	2.92	0.43
85:TA:71:ILE:O	85:TA:74:LEU:HG	2.18	0.43
1:AA:953:U:H1'	1:AA:954:C:H5''	2.01	0.43
1:AA:1006:U:H2'	1:AA:1007:G:H8	1.83	0.43
13:AT:4:LYS:O	13:AT:11:ARG:NH2	2.52	0.43
25:A1:92:LYS:H	25:A1:92:LYS:HG3	1.60	0.43
25:A1:262:ILE:HD12	25:A1:265:THR:HB	2.00	0.43
32:A:1834:U:O2	43:T:205:SER:HB3	2.18	0.43
32:A:2664:U:H2'	32:A:2665:U:C6	2.54	0.43
32:A:2685:U:O4'	32:A:2697:G:N2	2.51	0.43
32:A:3018:A:C2	32:A:3019:G:C8	3.06	0.43
32:A:3206:C:O2	32:A:3206:C:H3'	2.19	0.43
33:B:1622:A:H2'	33:B:1623:G:C8	2.54	0.43
39:M:97:SER:HB2	39:M:143:GLU:HB3	2.01	0.43
39:M:116:ILE:HB	39:M:154:ILE:HG13	2.01	0.43
40:O:62:TYR:OH	83:Q:272:GLU:OE1	2.37	0.43
43:T:190:LYS:NZ	43:T:198:GLU:OE1	2.40	0.43
48:O:163:GLU:OE2	48:O:181:ARG:NH1	2.51	0.43
61:q:153:ARG:HH12	61:q:173:ALA:HA	1.83	0.43
1:AA:651:A:H5'	29:AD:317:HIS:ND1	2.34	0.43
1:AA:839:A:H2'	1:AA:840:A:C8	2.54	0.43
1:AA:1119:U:O4	29:AD:355:ARG:NH2	2.46	0.43
1:AA:1195:U:OP1	30:AF:185:LYS:NZ	2.50	0.43
1:AA:1498:C:H2'	1:AA:1499:U:C6	2.54	0.43
1:AA:1516:G:P	18:AL:223:ARG:HH11	2.42	0.43
10:AO:235:MET:HE3	10:AO:236:PRO:HD2	2.00	0.43
15:AX:151:LEU:HD23	15:AX:257:HIS:H	1.84	0.43
17:AH:128:LYS:HB2	17:AH:128:LYS:HE3	1.64	0.43
31:AG:311:GLU:HA	31:AG:314:MET:HG2	2.01	0.43
32:A:1818:A:H5''	48:O:95:ARG:HH21	1.84	0.43
32:A:2123:C:OP1	47:Z:76:ARG:NH2	2.51	0.43
32:A:2253:U:H2'	32:A:2254:C:C6	2.53	0.43
32:A:2622:G:C2	32:A:2623:A:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:3196:G:O2'	32:A:3197:U:OP2	2.37	0.43
43:T:180:GLU:OE2	76:d:230:ARG:NH1	2.46	0.43
46:Y:69:ASP:OD1	46:Y:69:ASP:N	2.52	0.43
54:b:49:ARG:HG3	54:b:50:GLU:HG3	2.01	0.43
64:I:162:LYS:HG3	64:I:195:SER:HB2	2.01	0.43
67:U:109:ASP:HB2	67:U:112:PRO:HD2	2.01	0.43
71:6:99:ARG:O	71:6:103:LEU:HB2	2.19	0.43
77:f:111:HIS:O	77:f:115:ASN:HB2	2.18	0.43
79:k:65:ASP:N	79:k:65:ASP:OD1	2.52	0.43
1:AA:1025:A:C8	18:AL:153:ARG:NH1	2.87	0.42
15:AX:149:ASP:HA	15:AX:197:ARG:HH12	1.84	0.42
21:AU:189:TRP:HA	21:AU:200:PRO:HD3	2.00	0.42
24:AZ:72:ARG:NH2	29:AD:127:ASN:OD1	2.52	0.42
29:AD:336:VAL:HG21	29:AD:345:LEU:HD13	2.00	0.42
32:A:2523:C:O2	34:D:87:HIS:ND1	2.52	0.42
32:A:3008:C:O2'	32:A:3051:A:N3	2.39	0.42
40:O:80:LEU:HD12	40:O:86:ILE:HG12	2.00	0.42
45:X:64:ASP:OD1	45:X:64:ASP:N	2.51	0.42
62:r:144:LYS:HA	62:r:144:LYS:HD3	1.70	0.42
68:V:101:THR:OG1	68:V:104:TYR:O	2.33	0.42
69:E:45:SER:O	72:7:307:ARG:NH2	2.52	0.42
69:E:197:HIS:HD2	69:E:318:THR:HG23	1.83	0.42
74:a:104:GLU:HG2	74:a:107:PRO:HD2	2.01	0.42
1:AA:894:C:N4	6:AJ:117:ASP:OD2	2.51	0.42
1:AA:1132:U:H2'	1:AA:1133:C:C6	2.54	0.42
1:AA:1146:C:C2	1:AA:1147:G:C8	3.07	0.42
1:AA:1188:A:C2	1:AA:1429:C:N3	2.87	0.42
1:AA:1497:C:H2'	1:AA:1498:C:C6	2.54	0.42
15:AX:56:PRO:HA	15:AX:59:HIS:CD2	2.50	0.42
17:AH:89:ASP:O	17:AH:92:GLU:HG2	2.19	0.42
22:AV:127:TYR:HA	22:AV:130:VAL:HG12	2.01	0.42
23:AY:359:SER:HB3	25:A1:211:ARG:NH2	2.34	0.42
25:A1:163:VAL:H	28:A4:134:GLU:HG3	1.85	0.42
32:A:1795:A:H5''	35:F:147:ARG:NH2	2.35	0.42
32:A:2013:U:H2'	32:A:2014:A:C8	2.54	0.42
32:A:2144:A:N6	32:A:2257:C:H42	2.18	0.42
32:A:2493:C:H3'	32:A:2493:C:O2	2.19	0.42
32:A:3089:A:N7	86:z:232:ARG:NH1	2.67	0.42
32:A:3104:U:C2	32:A:3105:A:C8	3.07	0.42
53:8:107:THR:OG1	53:8:108:PHE:N	2.52	0.42
67:U:19:VAL:HB	73:9:136:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:k:40:GLU:O	79:k:44:SER:CB	2.67	0.42
85:TA:64:ILE:CG2	85:TB:85:LEU:HD23	2.42	0.42
1:AA:848:U:H2'	1:AA:849:U:C6	2.53	0.42
1:AA:974:U:O2'	1:AA:975:A:N7	2.50	0.42
2:AB:202:ILE:HG23	2:AB:204:GLU:HG2	2.01	0.42
10:AO:146:GLN:O	10:AO:150:LEU:N	2.44	0.42
15:AX:93:THR:HG21	30:AF:120:ARG:HH11	1.84	0.42
15:AX:279:LYS:HA	15:AX:279:LYS:HD3	1.76	0.42
15:AX:368:HIS:HB3	15:AX:371:ALA:HB2	2.00	0.42
19:AR:225:VAL:HG22	19:AR:262:LEU:HD23	2.01	0.42
22:AV:244:TYR:HA	22:AV:249:LEU:HB2	2.00	0.42
26:A0:78:ARG:HE	26:A0:78:ARG:HB3	1.68	0.42
30:AF:195:LYS:HD2	30:AF:204:LYS:HE3	2.01	0.42
32:A:2060:A:C5	32:A:2061:C:C4	3.07	0.42
32:A:2240:C:P	37:K:71:LYS:HZ2	2.41	0.42
32:A:2446:A:H3'	32:A:2447:A:H5''	2.01	0.42
32:A:2852:C:H3'	49:1:44:LEU:O	2.19	0.42
36:H:108:ARG:NH2	36:H:140:PHE:CE1	2.78	0.42
64:I:139:LYS:O	85:TA:48:LEU:CG	2.67	0.42
71:6:261:ARG:HG2	71:6:323:TRP:CE2	2.54	0.42
79:k:57:HIS:CD2	85:TA:53:LEU:HB3	2.49	0.42
85:TA:85:LEU:HD22	85:TB:64:ILE:CA	2.45	0.42
1:AA:867:C:O2'	1:AA:869:C:N4	2.46	0.42
1:AA:1320:G:OP2	3:AC:37:ASN:ND2	2.47	0.42
1:AA:1380:G:C1'	15:AX:164:ASN:ND2	2.71	0.42
4:AE:39:LEU:HD21	4:AE:64:PHE:HD1	1.85	0.42
15:AX:111:TYR:O	15:AX:115:THR:OG1	2.24	0.42
17:AH:93:TYR:HA	17:AH:96:VAL:HG12	2.01	0.42
20:AS:95:THR:O	20:AS:99:PHE:HB2	2.20	0.42
24:AZ:6:GLU:HA	24:AZ:9:PHE:HB3	2.02	0.42
28:A4:83:THR:O	28:A4:83:THR:OG1	2.36	0.42
32:A:1907:A:N3	32:A:2930:U:O2'	2.47	0.42
32:A:2140:G:N3	47:Z:76:ARG:HD2	2.35	0.42
32:A:2182:G:N2	32:A:2199:A:O2'	2.50	0.42
32:A:2408:U:H2'	32:A:2409:A:H8	1.83	0.42
32:A:2517:U:H2'	32:A:2518:A:H8	1.84	0.42
32:A:2646:G:H4'	32:A:3093:C:H4'	2.01	0.42
32:A:2699:C:H2'	32:A:2700:G:H8	1.84	0.42
32:A:2803:A:H2'	32:A:2804:A:O4'	2.19	0.42
32:A:3123:G:H2'	32:A:3124:U:OP2	2.20	0.42
32:A:3203:A:H1'	69:E:303:LYS:CD	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:O:42:ILE:HD13	40:O:42:ILE:HA	1.91	0.42
47:Z:71:ARG:NH1	47:Z:92:GLU:O	2.52	0.42
66:P:165:MET:HG3	66:P:170:VAL:HG13	2.01	0.42
73:9:128:PHE:HB3	73:9:135:PHE:HD2	1.84	0.42
1:AA:1279:C:O2'	1:AA:1296:A:N1	2.51	0.42
1:AA:1284:U:O2'	29:AD:347:GLN:CD	2.63	0.42
1:AA:1400:U:H3	1:AA:1404:A:H62	1.67	0.42
15:AX:123:ARG:HD3	15:AX:297:MET:HE2	2.01	0.42
29:AD:392:ARG:HB3	29:AD:394:ASP:OD1	2.18	0.42
32:A:2672:A:H4'	43:T:110:ASP:O	2.20	0.42
32:A:2961:C:C6	32:A:2962:C:C5	3.08	0.42
32:A:3041:U:H4'	32:A:3042:U:OP1	2.19	0.42
36:H:110:ASP:OD1	36:H:110:ASP:N	2.43	0.42
38:L:107:LEU:HD23	38:L:107:LEU:HA	1.91	0.42
55:e:128:PHE:HB2	59:m:73:ARG:HB2	2.02	0.42
82:s:343:GLN:HG3	82:s:355:PHE:HZ	1.85	0.42
85:TA:54:ASP:O	85:TA:57:PRO:HB3	2.19	0.42
1:AA:715:G:H2'	1:AA:716:U:C6	2.55	0.42
1:AA:849:U:H2'	1:AA:850:U:C6	2.54	0.42
1:AA:877:G:H2'	1:AA:878:G:C8	2.54	0.42
1:AA:1017:A:N3	11:AP:108:THR:OG1	2.52	0.42
1:AA:1144:U:H2'	1:AA:1145:A:C8	2.51	0.42
1:AA:1597:C:P	16:A2:25:LYS:HZ1	2.41	0.42
2:AB:242:SER:OG	14:AW:119:LYS:O	2.36	0.42
15:AX:151:LEU:HD21	15:AX:256:PHE:HD1	1.85	0.42
15:AX:168:LEU:HA	15:AX:180:GLN:HE22	1.85	0.42
16:A2:88:SER:O	16:A2:92:THR:OG1	2.32	0.42
18:AL:191:PRO:HA	18:AL:192:PRO:HD3	1.96	0.42
19:AR:329:LYS:HG2	19:AR:346:LEU:HD11	2.02	0.42
23:AY:356:CYS:O	23:AY:360:LYS:NZ	2.49	0.42
32:A:1756:A:H5''	36:H:66:GLY:H	1.85	0.42
32:A:1762:A:N7	61:q:33:ARG:CG	2.83	0.42
32:A:1856:A:H2'	32:A:1857:U:C6	2.54	0.42
32:A:2253:U:H2'	32:A:2254:C:H6	1.85	0.42
32:A:2388:A:C2	34:D:128:GLN:HB2	2.54	0.42
32:A:2461:A:H2'	32:A:2462:A:H8	1.85	0.42
32:A:3078:C:H2'	32:A:3079:G:H8	1.85	0.42
32:A:3161:G:O2'	32:A:3162:C:H2'	2.19	0.42
35:F:126:LYS:NZ	35:F:138:HIS:O	2.50	0.42
40:O:153:ARG:HE	40:O:157:ARG:HH21	1.68	0.42
43:T:75:HIS:HD2	43:T:120:VAL:HG13	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:V:28:SER:HB3	76:d:67:ILE:HD11	2.01	0.42
85:TA:62:PRO:HA	85:TA:65:GLN:CD	2.44	0.42
85:TA:67:LEU:O	85:TA:70:ASP:HB3	2.19	0.42
1:AA:948:U:H4'	18:AL:191:PRO:HG2	2.00	0.42
1:AA:1109:A:H2'	1:AA:1110:A:C8	2.55	0.42
1:AA:1278:C:O2'	2:AB:178:ASN:OD1	2.36	0.42
1:AA:1308:U:H2'	1:AA:1309:A:H8	1.85	0.42
1:AA:1355:G:N2	1:AA:1356:A:N7	2.67	0.42
1:AA:1527:A:O5'	26:A0:99:ARG:NH1	2.53	0.42
2:AB:82:ARG:HA	2:AB:82:ARG:HD2	1.82	0.42
7:AK:53:ARG:HE	23:AY:372:HIS:CD2	2.38	0.42
13:AT:105:ILE:HG22	13:AT:106:LEU:HG	2.02	0.42
26:A0:160:SER:OG	26:A0:161:LEU:N	2.52	0.42
30:AF:109:SER:OG	30:AF:113:GLN:NE2	2.53	0.42
32:A:1703:C:OP1	73:9:34:LYS:NZ	2.50	0.42
32:A:1833:C:OP1	54:b:116:ARG:HG3	2.20	0.42
32:A:1845:C:H2'	32:A:1846:C:H6	1.84	0.42
32:A:1893:A:O3'	32:A:1894:G:H8	2.03	0.42
32:A:1912:A:H2'	32:A:1913:G:H8	1.85	0.42
32:A:1993:A:H8	32:A:2498:U:O2'	2.03	0.42
32:A:2562:U:O2'	34:D:284:ARG:N	2.53	0.42
64:I:207:LEU:HD12	64:I:207:LEU:HA	1.94	0.42
71:6:81:LYS:O	71:6:81:LYS:HG2	2.20	0.42
78:h:74:VAL:O	78:h:78:PHE:HB2	2.18	0.42
1:AA:649:A:N6	29:AD:422:TRP:NE1	2.67	0.42
1:AA:659:U:H2'	1:AA:660:C:H6	1.84	0.42
2:AB:167:HIS:CE1	31:AG:153:THR:HA	2.55	0.42
10:AO:188:PRO:HA	10:AO:189:PRO:HD3	1.86	0.42
19:AR:129:PRO:HA	19:AR:130:PRO:HD3	1.94	0.42
32:A:2061:C:O2	32:A:2061:C:H3'	2.19	0.42
32:A:2751:G:H2'	32:A:2752:C:C6	2.54	0.42
32:A:3092:U:O2'	32:A:3093:C:OP1	2.35	0.42
32:A:3170:C:H3'	32:A:3170:C:O2	2.19	0.42
38:L:35:MET:HE3	38:L:35:MET:HB3	1.76	0.42
39:M:284:LYS:HB2	56:g:40:GLU:HB3	2.02	0.42
63:J:56:ARG:HE	63:J:56:ARG:HB2	1.66	0.42
63:J:59:ASP:OD1	63:J:59:ASP:N	2.52	0.42
65:N:108:THR:O	65:N:112:SER:OG	2.31	0.42
69:E:52:HIS:CE1	72:7:131:LYS:HD3	2.54	0.42
1:AA:704:U:OP1	1:AA:845:A:N6	2.48	0.42
1:AA:782:A:N6	1:AA:950:A:H4'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:892:A:OP1	6:AJ:77:ASN:HB2	2.20	0.42
7:AK:65:LYS:HE3	7:AK:65:LYS:HB2	1.95	0.42
11:AP:54:MET:SD	20:AS:69:ARG:NH1	2.93	0.42
23:AY:388:LYS:HE3	23:AY:388:LYS:HB3	1.90	0.42
26:A0:73:LEU:HB3	26:A0:76:LEU:HB2	2.01	0.42
31:AG:378:GLU:OE2	31:AG:388:ARG:CZ	2.68	0.42
32:A:1751:A:O3'	39:M:64:ARG:CD	2.68	0.42
32:A:2385:U:H2'	32:A:2386:C:H6	1.84	0.42
32:A:2523:C:H6	70:5:37:SER:OG	2.03	0.42
32:A:2527:A:C6	70:5:33:TRP:CE3	3.06	0.42
32:A:2678:A:H2	48:0:80:ALA:HB2	1.83	0.42
32:A:3054:G:H2'	32:A:3055:U:C6	2.55	0.42
35:F:89:THR:OG1	35:F:90:ALA:N	2.52	0.42
47:Z:117:ILE:O	60:o:45:ASN:ND2	2.46	0.42
55:e:200:MET:HE3	55:e:200:MET:HB2	1.92	0.42
62:r:63:PRO:HA	62:r:64:PRO:HD3	1.92	0.42
71:6:218:LEU:HB3	71:6:235:TRP:HB3	2.02	0.42
72:7:195:THR:HG23	72:7:197:GLU:H	1.84	0.42
73:9:22:THR:OG1	73:9:23:SER:N	2.52	0.42
76:d:83:GLY:O	76:d:262:HIS:NE2	2.43	0.42
1:AA:782:A:N7	9:AN:46:ARG:NH1	2.65	0.42
1:AA:1044:U:H2'	1:AA:1045:G:O4'	2.20	0.42
1:AA:1059:U:H2'	1:AA:1060:A:H8	1.84	0.42
1:AA:1371:U:H4'	1:AA:1389:G:OP1	2.20	0.42
22:AV:179:GLN:HB3	22:AV:214:LYS:HE3	2.00	0.42
22:AV:219:VAL:HG22	22:AV:356:THR:HG22	2.01	0.42
27:A3:183:LYS:HE2	27:A3:183:LYS:HB2	1.90	0.42
31:AG:284:ILE:HD12	31:AG:329:THR:HG23	2.01	0.42
32:A:2140:G:C2	47:Z:76:ARG:HD2	2.55	0.42
32:A:2511:C:O2'	34:D:258:GLY:C	2.63	0.42
32:A:3051:A:C6	32:A:3115:U:H4'	2.55	0.42
34:D:154:THR:H	34:D:157:MET:HE2	1.84	0.42
62:r:46:THR:HG23	79:k:73:ARG:HB3	2.02	0.42
63:J:162:GLU:O	63:J:166:ALA:CB	2.68	0.42
69:E:248:ILE:HG13	69:E:250:ARG:H	1.85	0.42
72:7:244:ALA:HB1	72:7:250:ARG:HD3	2.02	0.42
77:f:119:ILE:HD12	77:f:159:ILE:HG21	2.02	0.42
82:s:105:TRP:CD2	82:s:271:LEU:HD13	2.55	0.42
82:s:228:ASP:HB2	82:s:230:ARG:HH11	1.84	0.42
83:Q:240:ILE:HG22	83:Q:242:GLY:H	1.85	0.42
85:TA:79:ILE:HA	85:TA:82:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:913:A:H2'	1:AA:914:A:C8	2.54	0.41
1:AA:1481:C:P	29:AD:237:ARG:HH21	2.43	0.41
3:AC:145:TYR:HD1	28:A4:140:LEU:HD13	1.85	0.41
22:AV:52:ASP:HB3	83:Q:67:ARG:HH12	1.78	0.41
32:A:1807:U:HO2'	32:A:1808:A:C5'	2.33	0.41
32:A:2055:U:C4	60:o:71:PHE:CD2	3.08	0.41
32:A:2060:A:N9	32:A:2079:C:N4	2.67	0.41
32:A:2158:U:H2'	62:r:195:TYR:OH	2.20	0.41
32:A:2552:U:H2'	32:A:2553:G:H8	1.85	0.41
32:A:2668:A:H2'	32:A:2669:A:C8	2.54	0.41
34:D:207:ILE:H	34:D:207:ILE:HG13	1.52	0.41
35:F:197:THR:OG1	35:F:198:GLY:N	2.53	0.41
36:H:59:TRP:HD1	36:H:60:TRP:CD1	2.37	0.41
40:O:33:LEU:HD21	40:O:59:LEU:HD22	2.02	0.41
56:g:154:ASP:OD1	56:g:154:ASP:N	2.53	0.41
62:r:99:MET:HE2	62:r:99:MET:HB3	1.75	0.41
64:I:51:THR:HG23	65:N:250:ARG:HH22	1.85	0.41
66:P:137:LEU:HA	66:P:137:LEU:HD23	1.83	0.41
74:a:69:TYR:OH	75:c:256:ARG:NH1	2.53	0.41
1:AA:1032:C:H2'	1:AA:1033:U:C6	2.55	0.41
1:AA:1055:U:H1'	1:AA:1590:A:H1'	2.02	0.41
4:AE:13:MET:HG3	4:AE:17:GLU:HB2	2.01	0.41
12:AQ:77:ARG:O	12:AQ:80:ARG:NE	2.52	0.41
15:AX:364:ASN:O	15:AX:367:GLN:NE2	2.53	0.41
20:AS:25:LEU:HD12	20:AS:25:LEU:HA	1.84	0.41
25:A1:103:LEU:HA	25:A1:106:LEU:HG	2.03	0.41
29:AD:208:PRO:HB3	29:AD:214:THR:HG23	2.01	0.41
30:AF:240:ARG:HG2	30:AF:242:TRP:H	1.85	0.41
31:AG:165:VAL:HG22	31:AG:240:PHE:HE2	1.85	0.41
32:A:2185:G:O5'	32:A:2185:G:H8	2.03	0.41
32:A:2411:U:H2'	32:A:2412:A:H8	1.85	0.41
32:A:2744:U:O2	32:A:2745:A:N6	2.53	0.41
32:A:2802:A:H2'	32:A:2803:A:O4'	2.19	0.41
32:A:3189:C:H1'	62:r:154:TRP:HB3	2.02	0.41
32:A:3228:U:OP2	69:E:49:TRP:NE1	2.52	0.41
45:X:7:PRO:HA	57:i:101:ARG:HB3	2.01	0.41
82:s:375:ASN:H	82:s:391:ASN:HD22	1.66	0.41
85:TA:81:ASP:CA	85:TB:64:ILE:HD11	2.51	0.41
1:AA:702:C:H2'	1:AA:703:A:O4'	2.20	0.41
1:AA:852:A:H3'	1:AA:853:C:C6	2.55	0.41
1:AA:1005:U:H4'	5:AI:87:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1195:U:H2'	1:AA:1196:A:H8	1.86	0.41
1:AA:1209:C:H2'	1:AA:1210:U:C6	2.56	0.41
1:AA:1226:C:H4'	17:AH:128:LYS:NZ	2.35	0.41
1:AA:1369:U:OP2	30:AF:200:LEU:HD13	2.19	0.41
3:AC:69:LEU:HD12	7:AK:119:GLN:HG3	2.01	0.41
7:AK:53:ARG:HE	23:AY:372:HIS:HD2	1.67	0.41
13:AT:138:GLU:N	13:AT:142:GLU:OE2	2.38	0.41
15:AX:365:TRP:NE1	15:AX:395:CYS:O	2.45	0.41
24:AZ:7:TYR:HE1	25:A1:240:GLU:HA	1.84	0.41
32:A:1751:A:C4'	39:M:64:ARG:CZ	2.83	0.41
32:A:1789:A:H5''	73:9:17:ARG:NH2	2.35	0.41
32:A:1834:U:N3	43:T:205:SER:C	2.79	0.41
32:A:2760:A:N1	32:A:2786:U:N3	2.69	0.41
55:e:260:LEU:HD23	55:e:264:LEU:HD23	2.02	0.41
62:r:182:ARG:HH11	62:r:194:LEU:HD12	1.85	0.41
68:V:56:LEU:HB3	68:V:122:LEU:HD11	2.02	0.41
1:AA:1575:U:OP1	27:A3:137:LYS:HB2	2.21	0.41
3:AC:77:ASP:HA	3:AC:78:GLY:HA2	1.81	0.41
5:AI:177:ASP:OD1	5:AI:177:ASP:N	2.52	0.41
6:AJ:66:PHE:CE2	6:AJ:82:ARG:CG	3.01	0.41
11:AP:141:ARG:H	12:AQ:28:ARG:HH12	1.67	0.41
17:AH:75:ARG:NH1	17:AH:76:LEU:O	2.53	0.41
23:AY:296:ASN:HB3	25:A1:71:PRO:HG3	2.02	0.41
25:A1:291:GLU:OE1	25:A1:318:ARG:NH1	2.54	0.41
30:AF:67:GLU:O	30:AF:71:THR:N	2.42	0.41
30:AF:88:ASP:OD2	30:AF:91:ILE:N	2.41	0.41
32:A:1833:C:OP1	54:b:116:ARG:CG	2.68	0.41
32:A:1850:U:C2'	32:A:2134:A:H61	2.33	0.41
32:A:2017:U:OP2	39:M:59:ARG:NH2	2.52	0.41
32:A:2087:U:H2'	32:A:2088:U:C6	2.55	0.41
32:A:2217:C:H4'	64:I:150:HIS:CD2	2.55	0.41
32:A:2456:U:H2'	32:A:2457:A:C8	2.55	0.41
32:A:2678:A:H2	48:0:80:ALA:CA	2.32	0.41
32:A:2819:G:C6	32:A:2820:A:C5	3.08	0.41
32:A:3078:C:H2'	32:A:3079:G:C8	2.55	0.41
32:A:3181:U:P	62:r:94:ARG:HH21	2.43	0.41
60:o:28:SER:OG	60:o:29:LEU:N	2.53	0.41
64:I:86:ILE:HA	64:I:89:VAL:HG22	2.02	0.41
75:c:56:PRO:HA	75:c:57:PRO:HD3	1.88	0.41
85:TA:68:VAL:HB	85:TB:85:LEU:HD23	2.02	0.41
86:z:103:PHE:HA	86:z:107:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:675:A:O3'	6:AJ:129:LYS:HD3	2.21	0.41
1:AA:1087:A:H2'	1:AA:1088:C:C6	2.56	0.41
1:AA:1230:C:N4	1:AA:1446:A:HO2'	2.19	0.41
1:AA:1414:C:H2'	1:AA:1415:G:O4'	2.21	0.41
1:AA:1571:U:O2'	1:AA:1572:A:H5'	2.21	0.41
4:AE:102:LEU:HD21	11:AP:71:HIS:HA	2.03	0.41
8:AM:101:PRO:HA	8:AM:104:ILE:HD12	2.02	0.41
16:A2:55:CYS:O	16:A2:59:ASN:ND2	2.44	0.41
23:AY:285:GLN:HA	23:AY:288:THR:HG22	2.02	0.41
26:A0:113:LYS:HE3	26:A0:113:LYS:HB2	1.94	0.41
29:AD:220:THR:HG22	29:AD:247:VAL:HG23	2.02	0.41
29:AD:359:HIS:HB3	29:AD:370:VAL:HG11	2.03	0.41
30:AF:240:ARG:HD3	30:AF:240:ARG:HH11	1.74	0.41
32:A:1680:A:OP1	68:V:43:PRO:HD2	2.20	0.41
32:A:1689:C:H2'	32:A:1690:C:C5	2.55	0.41
32:A:1798:A:H8	32:A:1798:A:OP2	2.03	0.41
32:A:2515:U:H2'	32:A:2516:C:H6	1.85	0.41
32:A:2605:C:O2	86:z:209:ARG:HG3	2.21	0.41
58:j:53:ASP:OD1	58:j:53:ASP:N	2.45	0.41
61:q:42:PRO:O	61:q:44:ASP:N	2.52	0.41
68:V:49:ILE:HG21	68:V:54:TRP:HE3	1.84	0.41
76:d:251:GLN:H	76:d:251:GLN:HG2	1.65	0.41
1:AA:668:U:O2'	10:AO:83:GLY:HA3	2.19	0.41
1:AA:1560:U:H2'	1:AA:1561:C:C6	2.56	0.41
3:AC:127:LEU:HD12	3:AC:132:TYR:HE1	1.86	0.41
7:AK:36:ARG:HA	7:AK:39:LYS:HD2	2.02	0.41
11:AP:142:GLU:OE2	12:AQ:28:ARG:NH1	2.53	0.41
12:AQ:78:LYS:NZ	14:AW:162:VAL:O	2.52	0.41
15:AX:271:ARG:HA	15:AX:284:PRO:HD3	2.02	0.41
23:AY:387:LEU:C	23:AY:390:SER:HG	2.27	0.41
32:A:2213:A:H2'	80:l:126:ILE:HD12	2.03	0.41
32:A:2370:A:H5''	67:U:71:ARG:NH2	2.35	0.41
32:A:2616:A:O2'	32:A:3046:C:O2	2.33	0.41
32:A:2989:G:H5''	32:A:2990:A:H5'	2.02	0.41
33:B:1642:G:H2'	33:B:1643:A:C8	2.55	0.41
39:M:115:PRO:HD3	39:M:255:MET:HE3	2.02	0.41
39:M:264:GLN:O	39:M:266:PHE:N	2.53	0.41
40:O:57:GLU:HA	40:O:104:TYR:HE2	1.86	0.41
46:Y:209:LEU:HD23	46:Y:209:LEU:HA	1.94	0.41
63:J:111:LEU:HD12	63:J:111:LEU:HA	1.92	0.41
85:TA:75:THR:O	85:TA:79:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:649:A:N1	29:AD:422:TRP:CE3	2.89	0.41
1:AA:659:U:H2'	1:AA:660:C:C6	2.56	0.41
1:AA:892:A:OP1	6:AJ:77:ASN:C	2.64	0.41
1:AA:925:U:H1'	6:AJ:56:PRO:HB3	2.03	0.41
1:AA:1095:U:H2'	1:AA:1096:A:C8	2.55	0.41
1:AA:1442:G:H21	1:AA:1447:G:N2	2.18	0.41
1:AA:1456:U:H4'	31:AG:337:ARG:NH2	2.36	0.41
1:AA:1468:U:C2	1:AA:1469:G:C8	3.09	0.41
15:AX:248:LYS:O	15:AX:251:SER:OG	2.39	0.41
22:AV:187:PHE:O	22:AV:191:ALA:CB	2.69	0.41
26:A0:83:LYS:HA	26:A0:86:LEU:HD12	2.02	0.41
32:A:1734:C:H42	57:i:107:LEU:HD22	1.86	0.41
32:A:2113:G:C6	60:o:15:ARG:HG2	2.56	0.41
32:A:2457:A:H3'	40:O:10:SER:HB3	2.02	0.41
32:A:2974:A:H2'	32:A:2975:G:C8	2.56	0.41
34:D:201:GLY:O	70:5:30:ALA:N	2.54	0.41
48:0:87:ILE:HD12	48:0:87:ILE:HA	1.90	0.41
72:7:114:ASP:OD1	72:7:114:ASP:N	2.51	0.41
72:7:150:MET:HA	72:7:153:VAL:HG12	2.03	0.41
77:f:76:GLU:HG3	77:f:189:HIS:CD2	2.56	0.41
81:p:104:HIS:HD2	81:p:106:ALA:H	1.68	0.41
85:TA:68:VAL:HG23	85:TB:85:LEU:HD23	1.99	0.41
1:AA:1251:A:H2'	1:AA:1252:G:O4'	2.21	0.41
1:AA:1523:A:OP1	22:AV:68:SER:HB3	2.21	0.41
4:AE:42:LEU:HD11	4:AE:65:LEU:HB2	2.02	0.41
5:AI:93:ASN:OD1	5:AI:93:ASN:N	2.53	0.41
13:AT:19:GLY:HA3	13:AT:54:GLN:HB3	2.02	0.41
15:AX:152:ILE:H	15:AX:195:ASN:ND2	2.19	0.41
15:AX:378:LYS:HA	15:AX:381:LEU:HB3	2.03	0.41
19:AR:285:LEU:HD23	19:AR:285:LEU:HA	1.92	0.41
19:AR:294:ILE:H	19:AR:294:ILE:HG12	1.58	0.41
24:AZ:32:LYS:HA	24:AZ:32:LYS:HD2	1.95	0.41
32:A:1824:U:C5	74:a:121:HIS:HB3	2.56	0.41
32:A:2818:C:C2	32:A:2819:G:C8	3.09	0.41
32:A:2842:C:H5''	44:W:41:ASN:HD21	1.86	0.41
32:A:3034:U:H2'	32:A:3035:C:C6	2.56	0.41
32:A:3143:U:H2'	32:A:3144:A:C8	2.56	0.41
35:F:160:SER:HB3	57:i:80:LEU:HD13	2.02	0.41
37:K:158:TYR:OH	62:r:86:VAL:HG21	2.21	0.41
55:e:191:THR:HA	55:e:194:THR:HG22	2.01	0.41
63:J:67:PRO:HD2	63:J:85:PRO:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:I:48:MET:HG3	65:N:250:ARG:HH21	1.86	0.41
67:U:15:PRO:HB3	68:V:206:GLU:HG2	2.03	0.41
82:s:229:LEU:HD23	82:s:229:LEU:HA	1.88	0.41
1:AA:682:A:H2'	1:AA:683:G:H8	1.85	0.41
1:AA:699:A:C5	21:AU:28:LYS:HG2	2.56	0.41
1:AA:1263:G:P	3:AC:38:ARG:HH12	2.44	0.41
1:AA:1597:C:P	16:A2:25:LYS:NZ	2.94	0.41
2:AB:88:ARG:NH1	14:AW:117:GLY:HA2	2.36	0.41
4:AE:51:ILE:HG21	4:AE:89:ILE:HG23	2.02	0.41
5:AI:118:ARG:O	5:AI:122:LYS:HG3	2.21	0.41
5:AI:162:MET:HE2	5:AI:162:MET:HB3	1.83	0.41
19:AR:68:PRO:HB2	19:AR:307:LEU:HD23	2.03	0.41
19:AR:175:ARG:HE	19:AR:181:LEU:HB2	1.86	0.41
23:AY:358:LEU:HD22	23:AY:369:LYS:HG2	2.03	0.41
23:AY:386:ILE:HA	23:AY:389:GLU:HB2	2.02	0.41
24:AZ:96:LYS:HB2	24:AZ:96:LYS:HE3	1.94	0.41
26:A0:76:LEU:HD23	26:A0:76:LEU:HA	1.91	0.41
26:A0:213:ALA:HA	26:A0:214:LYS:HA	1.86	0.41
30:AF:62:GLU:HG3	30:AF:66:ARG:HE	1.86	0.41
32:A:1831:G:OP1	54:b:3:ALA:HB3	2.20	0.41
32:A:1856:A:OP2	32:A:2986:C:O2'	2.32	0.41
32:A:1868:G:H2'	39:M:40:PRO:HG3	2.03	0.41
32:A:1871:A:O2'	32:A:1872:U:OP1	2.37	0.41
32:A:1939:G:N3	32:A:2495:U:H1'	2.25	0.41
32:A:2139:U:OP2	47:Z:74:SER:CB	2.68	0.41
32:A:3145:A:H2'	32:A:3146:G:H8	1.85	0.41
32:A:3198:A:H2'	32:A:3198:A:N3	2.35	0.41
35:F:289:PRO:HG2	39:M:277:MET:HE2	2.03	0.41
39:M:230:PRO:HB2	81:p:62:PRO:HD3	2.03	0.41
69:E:58:VAL:CG1	69:E:62:LYS:HE3	2.50	0.41
69:E:76:LYS:HG3	69:E:170:LEU:HD21	2.02	0.41
70:5:175:TYR:HA	70:5:178:VAL:HG12	2.03	0.41
71:6:67:ALA:HA	71:6:68:PRO:HD3	1.94	0.41
75:c:98:ILE:HG12	75:c:119:LEU:HD13	2.03	0.41
76:d:140:LYS:HB3	76:d:140:LYS:HE2	1.78	0.41
82:s:351:VAL:CG1	82:s:352:THR:N	2.83	0.41
85:TA:85:LEU:HD22	85:TB:64:ILE:CB	2.47	0.41
86:z:172:GLU:HB3	86:z:179:ARG:HB3	2.03	0.41
86:z:220:LYS:HA	86:z:223:LYS:HD3	2.02	0.41
1:AA:715:G:H1'	1:AA:817:G:H5'	2.02	0.41
1:AA:826:A:N7	6:AJ:55:ARG:HG2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1362:G:H2'	1:AA:1363:C:C6	2.56	0.41
3:AC:76:LEU:HD23	3:AC:76:LEU:HA	1.94	0.41
10:AO:167:ILE:HG13	19:AR:226:ASP:HB3	2.02	0.41
15:AX:49:SER:HB3	15:AX:67:HIS:HB2	2.03	0.41
15:AX:266:ASN:OD1	15:AX:266:ASN:N	2.53	0.41
18:AL:166:LEU:HD23	18:AL:166:LEU:HA	1.91	0.41
19:AR:276:VAL:HG11	19:AR:307:LEU:HD13	2.03	0.41
32:A:1731:A:OP1	36:H:74:HIS:CE1	2.74	0.41
32:A:2049:U:H2'	32:A:2050:A:C8	2.56	0.41
32:A:2052:A:H5''	56:g:150:LYS:CE	2.50	0.41
32:A:2067:C:OP1	77:f:58:LYS:HA	2.21	0.41
32:A:2186:C:N3	32:A:2187:C:N4	2.69	0.41
46:Y:155:LEU:HD23	46:Y:155:LEU:HA	1.88	0.41
65:N:176:LEU:HD23	65:N:176:LEU:HA	1.92	0.41
71:6:212:SER:OG	71:6:214:TRP:NE1	2.54	0.41
74:a:88:HIS:HB2	74:a:91:VAL:HB	2.03	0.41
76:d:40:ARG:H	76:d:40:ARG:HG2	1.69	0.41
1:AA:672:A:H2'	1:AA:673:U:C6	2.57	0.40
1:AA:1238:C:H2'	1:AA:1239:C:C6	2.57	0.40
1:AA:1429:C:C6	1:AA:1461:A:C2	3.09	0.40
9:AN:17:VAL:HA	9:AN:28:VAL:HG22	2.03	0.40
19:AR:281:ILE:HD12	19:AR:281:ILE:HG23	1.85	0.40
22:AV:349:SER:OG	22:AV:350:GLU:N	2.55	0.40
26:A0:161:LEU:H	26:A0:161:LEU:HG	1.52	0.40
32:A:1896:U:C2	32:A:1897:A:C8	3.09	0.40
32:A:1982:G:H2'	32:A:1983:U:C6	2.56	0.40
32:A:2727:C:H2'	32:A:2728:C:H6	1.86	0.40
34:D:113:ARG:O	34:D:147:ARG:NH1	2.53	0.40
41:R:122:ARG:NH1	42:S:72:GLU:OE2	2.54	0.40
46:Y:172:ILE:HD11	46:Y:198:ARG:HB2	2.03	0.40
51:3:183:ARG:NH2	71:6:356:ARG:O	2.41	0.40
70:5:125:THR:HB	70:5:371:ASN:HB2	2.03	0.40
83:Q:77:SER:CB	83:Q:103:ARG:HH22	2.32	0.40
85:TB:80:SER:O	85:TB:84:GLU:HG2	2.21	0.40
1:AA:770:C:H5''	1:AA:771:A:C5	2.57	0.40
1:AA:840:A:H2'	1:AA:841:A:H8	1.84	0.40
1:AA:1298:U:H2'	1:AA:1299:A:O4'	2.21	0.40
22:AV:273:ILE:HG13	22:AV:352:LEU:HD13	2.03	0.40
23:AY:332:ILE:HG23	25:A1:211:ARG:HH22	1.87	0.40
25:A1:181:ASN:O	25:A1:230:TYR:OH	2.35	0.40
30:AF:129:ALA:HB1	30:AF:133:GLU:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:A:1984:A:N3	32:A:1984:A:H2'	2.36	0.40
32:A:2081:U:OP2	60:o:67:ARG:HD3	2.21	0.40
32:A:2090:A:H2'	32:A:2091:A:C8	2.56	0.40
32:A:2324:U:H2'	32:A:2325:U:C6	2.56	0.40
47:Z:85:ILE:HD13	47:Z:85:ILE:HA	1.95	0.40
69:E:199:ARG:HA	69:E:199:ARG:HD3	1.81	0.40
75:c:245:LEU:HD22	75:c:250:VAL:HB	2.04	0.40
76:d:213:THR:HG22	76:d:247:VAL:HB	2.02	0.40
1:AA:649:A:C4	29:AD:422:TRP:CG	3.10	0.40
1:AA:1084:C:OP1	5:AI:192:ARG:HB2	2.21	0.40
1:AA:1412:G:C2	1:AA:1413:U:C5	3.09	0.40
10:AO:91:ARG:HH11	10:AO:91:ARG:HD3	1.74	0.40
15:AX:168:LEU:HD21	15:AX:178:PHE:HB3	2.03	0.40
22:AV:105:ARG:HA	22:AV:105:ARG:HD3	1.92	0.40
22:AV:203:ASN:O	22:AV:207:SER:OG	2.33	0.40
22:AV:347:ILE:HD12	22:AV:347:ILE:HA	1.96	0.40
25:A1:209:THR:OG1	25:A1:218:ASN:OD1	2.35	0.40
30:AF:93:LYS:HA	30:AF:93:LYS:HD3	1.90	0.40
30:AF:178:ARG:HA	30:AF:178:ARG:HD2	1.83	0.40
32:A:1805:A:O2'	32:A:1806:U:OP1	2.34	0.40
32:A:1832:A:H62	54:b:4:ARG:NH2	2.11	0.40
32:A:2318:A:H2'	32:A:2319:A:C8	2.57	0.40
32:A:2409:A:OP1	70:5:222:ARG:HD3	2.22	0.40
32:A:2410:U:H2'	32:A:2411:U:C6	2.56	0.40
32:A:2629:A:N3	32:A:3079:G:O2'	2.50	0.40
32:A:2804:A:H2'	32:A:2805:A:C8	2.56	0.40
32:A:3192:C:OP1	62:r:132:ARG:NH1	2.54	0.40
32:A:3224:G:H2'	32:A:3225:G:C8	2.51	0.40
35:F:68:SER:OG	35:F:69:LEU:N	2.55	0.40
42:S:181:LYS:HB3	42:S:181:LYS:HE2	1.86	0.40
57:i:36:LEU:HD13	75:c:41:PHE:HE2	1.87	0.40
83:Q:182:ARG:HD3	83:Q:187:LEU:HD11	2.03	0.40
85:TA:61:PRO:CB	85:TA:64:ILE:HD13	2.45	0.40
1:AA:798:C:C2	1:AA:799:A:C8	3.10	0.40
1:AA:829:C:H1'	1:AA:857:G:H22	1.86	0.40
1:AA:833:A:H2'	1:AA:834:G:H8	1.85	0.40
1:AA:838:U:H2'	1:AA:839:A:H8	1.86	0.40
1:AA:1371:U:H2'	1:AA:1372:C:H6	1.87	0.40
1:AA:1373:U:H2'	1:AA:1374:A:C8	2.56	0.40
4:AE:113:LEU:HD13	4:AE:113:LEU:HA	1.96	0.40
11:AP:60:GLU:HA	11:AP:61:PRO:HD3	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AR:136:VAL:O	19:AR:186:TRP:NE1	2.40	0.40
22:AV:182:SER:HA	22:AV:185:VAL:HG22	2.04	0.40
30:AF:204:LYS:HB2	30:AF:204:LYS:HE2	1.83	0.40
32:A:2086:A:H2'	32:A:2087:U:C6	2.56	0.40
32:A:2120:G:H1'	47:Z:36:PHE:HD2	1.87	0.40
32:A:2208:A:C2	32:A:2209:G:H1'	2.56	0.40
42:S:122:LEU:HD13	42:S:128:ILE:HD11	2.03	0.40
70:5:200:ARG:HD3	70:5:229:LEU:HD21	2.03	0.40
71:6:224:HIS:CD2	71:6:227:GLU:H	2.39	0.40
72:7:95:LEU:HA	76:d:281:MET:HE1	2.02	0.40
79:k:40:GLU:O	79:k:44:SER:HB2	2.22	0.40
1:AA:805:C:H6	1:AA:805:C:H2'	1.69	0.40
3:AC:165:LYS:HB3	3:AC:167:LEU:HB2	2.02	0.40
14:AW:100:VAL:HG22	20:AS:85:PHE:HB2	2.03	0.40
20:AS:6:LEU:HD23	20:AS:6:LEU:HA	1.88	0.40
22:AV:44:GLU:OE2	22:AV:78:ASN:ND2	2.49	0.40
25:A1:108:ILE:HD13	25:A1:108:ILE:HA	1.92	0.40
26:A0:102:PRO:HA	26:A0:112:GLY:HA3	2.03	0.40
32:A:1672:C:H2'	32:A:1673:U:O4'	2.22	0.40
32:A:1731:A:N6	57:i:118:TYR:CE1	2.77	0.40
32:A:1868:G:OP2	39:M:41:ARG:NH1	2.47	0.40
32:A:1992:C:O2'	34:D:274:ARG:HA	2.21	0.40
32:A:2363:A:H3'	32:A:2364:C:H5''	2.03	0.40
32:A:2495:U:O4	32:A:2509:A:H2	2.04	0.40
32:A:2524:A:N3	32:A:2524:A:H2'	2.37	0.40
32:A:2617:A:H1'	32:A:2619:A:N7	2.36	0.40
32:A:2807:U:H2'	32:A:2808:U:C6	2.56	0.40
37:K:62:THR:HG22	37:K:129:PRO:HA	2.02	0.40
42:S:84:ASN:HA	42:S:87:ILE:HG22	2.04	0.40
45:X:67:ILE:HA	45:X:68:PRO:HD3	1.88	0.40
61:q:162:GLU:HA	61:q:163:LEU:HA	1.84	0.40
62:r:96:HIS:CE1	62:r:134:ARG:HB3	2.57	0.40
64:I:146:LEU:HD23	64:I:177:LEU:HB3	2.04	0.40
80:l:81:GLY:HA2	80:l:86:LEU:HD12	2.02	0.40
82:s:316:CYS:HB3	82:s:319:GLN:HG3	2.03	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	
2	AB	218/296 (74%)	204 (94%)	14 (6%)	0	100	100
3	AC	130/167 (78%)	124 (95%)	6 (5%)	0	100	100
4	AE	120/125 (96%)	110 (92%)	8 (7%)	2 (2%)	7	35
5	AI	134/194 (69%)	118 (88%)	13 (10%)	3 (2%)	5	30
6	AJ	106/138 (77%)	87 (82%)	19 (18%)	0	100	100
7	AK	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
8	AM	114/137 (83%)	103 (90%)	11 (10%)	0	100	100
9	AN	105/130 (81%)	90 (86%)	15 (14%)	0	100	100
10	AO	188/258 (73%)	176 (94%)	12 (6%)	0	100	100
11	AP	94/142 (66%)	88 (94%)	6 (6%)	0	100	100
12	AQ	84/87 (97%)	77 (92%)	7 (8%)	0	100	100
13	AT	166/173 (96%)	160 (96%)	6 (4%)	0	100	100
14	AW	95/187 (51%)	82 (86%)	13 (14%)	0	100	100
15	AX	351/398 (88%)	329 (94%)	22 (6%)	0	100	100
16	A2	114/118 (97%)	105 (92%)	9 (8%)	0	100	100
17	AH	120/201 (60%)	109 (91%)	11 (9%)	0	100	100
18	AL	172/257 (67%)	164 (95%)	8 (5%)	0	100	100
19	AR	290/360 (81%)	276 (95%)	14 (5%)	0	100	100
20	AS	133/190 (70%)	127 (96%)	6 (4%)	0	100	100
21	AU	175/205 (85%)	170 (97%)	5 (3%)	0	100	100
22	AV	363/414 (88%)	321 (88%)	42 (12%)	0	100	100
23	AY	118/395 (30%)	111 (94%)	7 (6%)	0	100	100
24	AZ	97/106 (92%)	87 (90%)	10 (10%)	0	100	100
25	A1	273/323 (84%)	257 (94%)	16 (6%)	0	100	100
26	A0	212/218 (97%)	199 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	A3	70/199 (35%)	68 (97%)	2 (3%)	0	100	100
28	A4	541/689 (78%)	502 (93%)	39 (7%)	0	100	100
29	AD	341/430 (79%)	316 (93%)	25 (7%)	0	100	100
30	AF	206/242 (85%)	193 (94%)	13 (6%)	0	100	100
31	AG	311/396 (78%)	294 (94%)	16 (5%)	1 (0%)	36	67
34	D	237/305 (78%)	224 (94%)	12 (5%)	1 (0%)	30	62
35	F	248/311 (80%)	227 (92%)	20 (8%)	1 (0%)	30	62
36	H	96/267 (36%)	88 (92%)	8 (8%)	0	100	100
37	K	175/178 (98%)	157 (90%)	17 (10%)	1 (1%)	21	54
38	L	113/145 (78%)	103 (91%)	10 (9%)	0	100	100
39	M	285/296 (96%)	251 (88%)	32 (11%)	2 (1%)	18	51
40	O	150/175 (86%)	135 (90%)	15 (10%)	0	100	100
41	R	138/149 (93%)	131 (95%)	7 (5%)	0	100	100
42	S	154/205 (75%)	146 (95%)	8 (5%)	0	100	100
43	T	164/212 (77%)	157 (96%)	7 (4%)	0	100	100
44	W	109/148 (74%)	104 (95%)	5 (5%)	0	100	100
45	X	241/256 (94%)	220 (91%)	21 (9%)	0	100	100
46	Y	174/250 (70%)	166 (95%)	7 (4%)	1 (1%)	21	54
47	Z	118/161 (73%)	110 (93%)	8 (7%)	0	100	100
48	0	106/188 (56%)	92 (87%)	14 (13%)	0	100	100
49	1	50/65 (77%)	46 (92%)	4 (8%)	0	100	100
50	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
51	3	93/188 (50%)	90 (97%)	3 (3%)	0	100	100
52	4	36/103 (35%)	36 (100%)	0	0	100	100
53	8	97/206 (47%)	94 (97%)	3 (3%)	0	100	100
54	b	146/155 (94%)	135 (92%)	11 (8%)	0	100	100
55	e	211/279 (76%)	200 (95%)	11 (5%)	0	100	100
56	g	130/166 (78%)	125 (96%)	5 (4%)	0	100	100
57	i	95/128 (74%)	88 (93%)	7 (7%)	0	100	100
58	j	91/123 (74%)	85 (93%)	6 (7%)	0	100	100
59	m	43/128 (34%)	38 (88%)	5 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	o	92/102 (90%)	86 (94%)	6 (6%)	0	100	100
61	q	164/222 (74%)	151 (92%)	10 (6%)	3 (2%)	6	34
62	r	160/196 (82%)	149 (93%)	11 (7%)	0	100	100
63	J	173/192 (90%)	165 (95%)	8 (5%)	0	100	100
64	I	177/261 (68%)	163 (92%)	14 (8%)	0	100	100
65	N	220/251 (88%)	216 (98%)	4 (2%)	0	100	100
66	P	141/179 (79%)	129 (92%)	11 (8%)	1 (1%)	18	51
67	U	150/153 (98%)	144 (96%)	6 (4%)	0	100	100
68	V	204/216 (94%)	195 (96%)	9 (4%)	0	100	100
69	E	304/348 (87%)	286 (94%)	17 (6%)	1 (0%)	36	67
70	5	391/423 (92%)	376 (96%)	15 (4%)	0	100	100
71	6	352/380 (93%)	329 (94%)	23 (6%)	0	100	100
72	7	295/338 (87%)	280 (95%)	14 (5%)	1 (0%)	36	67
73	9	122/137 (89%)	114 (93%)	8 (7%)	0	100	100
74	a	106/142 (75%)	104 (98%)	2 (2%)	0	100	100
75	c	287/332 (86%)	276 (96%)	11 (4%)	0	100	100
76	d	255/306 (83%)	234 (92%)	21 (8%)	0	100	100
77	f	144/194 (74%)	135 (94%)	9 (6%)	0	100	100
78	h	108/158 (68%)	101 (94%)	7 (6%)	0	100	100
79	k	94/112 (84%)	92 (98%)	2 (2%)	0	100	100
80	l	70/138 (51%)	63 (90%)	7 (10%)	0	100	100
81	p	148/206 (72%)	140 (95%)	7 (5%)	1 (1%)	18	51
82	s	391/439 (89%)	362 (93%)	29 (7%)	0	100	100
83	Q	225/292 (77%)	215 (96%)	8 (4%)	2 (1%)	14	47
85	TA	43/198 (22%)	35 (81%)	8 (19%)	0	100	100
85	TB	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
86	z	195/204 (96%)	166 (85%)	23 (12%)	6 (3%)	3	25
All	All	14120/18499 (76%)	13161 (93%)	932 (7%)	27 (0%)	44	74

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AI	120	ALA

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Mol	Chain	Res	Type
66	P	69	ARG
83	Q	74	ARG
37	K	160	GLN
39	M	288	GLU
61	q	43	GLU
69	E	317	PRO
81	p	84	SER
83	Q	75	PHE
86	z	118	LYS
39	M	265	ILE
86	z	117	ASP
4	AE	15	ARG
5	AI	119	ASN
5	AI	145	ILE
61	q	79	PRO
86	z	109	ILE
86	z	113	PRO
86	z	183	PRO
31	AG	210	VAL
35	F	291	SER
86	z	112	SER
34	D	207	ILE
46	Y	203	PRO
61	q	42	PRO
72	7	110	GLY
4	AE	16	PRO

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	
2	AB	193/249 (78%)	191 (99%)	2 (1%)	68	75
3	AC	115/143 (80%)	111 (96%)	4 (4%)	32	57
4	AE	104/107 (97%)	104 (100%)	0	100	100
5	AI	104/147 (71%)	103 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	AJ	93/118 (79%)	93 (100%)	0	100	100
7	AK	91/113 (80%)	89 (98%)	2 (2%)	45	65
8	AM	95/113 (84%)	93 (98%)	2 (2%)	47	66
9	AN	93/115 (81%)	92 (99%)	1 (1%)	65	74
10	AO	171/230 (74%)	170 (99%)	1 (1%)	78	79
11	AP	87/123 (71%)	87 (100%)	0	100	100
12	AQ	78/79 (99%)	78 (100%)	0	100	100
13	AT	153/157 (98%)	152 (99%)	1 (1%)	76	78
14	AW	84/158 (53%)	83 (99%)	1 (1%)	63	73
15	AX	312/351 (89%)	310 (99%)	2 (1%)	78	79
16	A2	99/101 (98%)	98 (99%)	1 (1%)	68	75
17	AH	112/180 (62%)	112 (100%)	0	100	100
18	AL	157/226 (70%)	156 (99%)	1 (1%)	78	79
19	AR	262/318 (82%)	259 (99%)	3 (1%)	65	74
20	AS	116/164 (71%)	116 (100%)	0	100	100
21	AU	153/174 (88%)	149 (97%)	4 (3%)	40	62
22	AV	328/364 (90%)	328 (100%)	0	100	100
23	AY	111/357 (31%)	111 (100%)	0	100	100
24	AZ	89/95 (94%)	88 (99%)	1 (1%)	65	74
25	A1	253/291 (87%)	251 (99%)	2 (1%)	73	77
26	A0	186/190 (98%)	182 (98%)	4 (2%)	45	65
27	A3	66/166 (40%)	66 (100%)	0	100	100
28	A4	83/609 (14%)	83 (100%)	0	100	100
29	AD	286/357 (80%)	282 (99%)	4 (1%)	59	71
30	AF	185/209 (88%)	182 (98%)	3 (2%)	55	70
31	AG	273/342 (80%)	273 (100%)	0	100	100
34	D	193/245 (79%)	190 (98%)	3 (2%)	55	70
35	F	217/262 (83%)	217 (100%)	0	100	100
36	H	88/228 (39%)	87 (99%)	1 (1%)	65	74
37	K	155/156 (99%)	154 (99%)	1 (1%)	78	79
38	L	98/124 (79%)	96 (98%)	2 (2%)	48	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	M	245/249 (98%)	245 (100%)	0	100	100
40	O	133/150 (89%)	132 (99%)	1 (1%)	73	77
41	R	118/126 (94%)	118 (100%)	0	100	100
42	S	141/180 (78%)	141 (100%)	0	100	100
43	T	146/182 (80%)	145 (99%)	1 (1%)	76	78
44	W	91/119 (76%)	90 (99%)	1 (1%)	65	74
45	X	217/227 (96%)	216 (100%)	1 (0%)	81	80
46	Y	159/223 (71%)	159 (100%)	0	100	100
47	Z	111/147 (76%)	111 (100%)	0	100	100
48	0	97/164 (59%)	97 (100%)	0	100	100
49	1	49/60 (82%)	49 (100%)	0	100	100
50	2	40/72 (56%)	40 (100%)	0	100	100
51	3	88/166 (53%)	87 (99%)	1 (1%)	65	74
52	4	37/89 (42%)	37 (100%)	0	100	100
53	8	91/190 (48%)	91 (100%)	0	100	100
54	b	130/135 (96%)	130 (100%)	0	100	100
55	e	188/236 (80%)	188 (100%)	0	100	100
56	g	122/148 (82%)	122 (100%)	0	100	100
57	i	86/110 (78%)	86 (100%)	0	100	100
58	j	74/97 (76%)	74 (100%)	0	100	100
59	m	40/113 (35%)	40 (100%)	0	100	100
60	o	80/87 (92%)	80 (100%)	0	100	100
61	q	113/178 (64%)	113 (100%)	0	100	100
62	r	147/169 (87%)	146 (99%)	1 (1%)	76	78
63	J	138/150 (92%)	137 (99%)	1 (1%)	76	78
64	I	164/232 (71%)	163 (99%)	1 (1%)	78	79
65	N	189/211 (90%)	188 (100%)	1 (0%)	81	80
66	P	125/154 (81%)	125 (100%)	0	100	100
67	U	125/135 (93%)	125 (100%)	0	100	100
68	V	184/191 (96%)	182 (99%)	2 (1%)	65	74
69	E	260/290 (90%)	259 (100%)	1 (0%)	84	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	5	353/368 (96%)	353 (100%)	0	100	100
71	6	313/332 (94%)	309 (99%)	4 (1%)	61	72
72	7	272/303 (90%)	268 (98%)	4 (2%)	57	71
73	9	104/112 (93%)	103 (99%)	1 (1%)	68	75
74	a	101/133 (76%)	101 (100%)	0	100	100
75	c	253/288 (88%)	253 (100%)	0	100	100
76	d	224/274 (82%)	221 (99%)	3 (1%)	61	72
77	f	122/173 (70%)	119 (98%)	3 (2%)	42	63
78	h	104/148 (70%)	104 (100%)	0	100	100
79	k	81/90 (90%)	80 (99%)	1 (1%)	63	73
80	l	67/116 (58%)	66 (98%)	1 (2%)	57	71
81	p	134/181 (74%)	134 (100%)	0	100	100
82	s	336/381 (88%)	336 (100%)	0	100	100
83	Q	209/256 (82%)	207 (99%)	2 (1%)	68	75
85	TA	39/158 (25%)	39 (100%)	0	100	100
85	TB	26/158 (16%)	25 (96%)	1 (4%)	29	55
86	z	175/179 (98%)	173 (99%)	2 (1%)	65	74
All	All	12124/15991 (76%)	12043 (99%)	81 (1%)	73	78

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	189	LEU
2	AB	220	VAL
3	AC	44	VAL
3	AC	122	VAL
3	AC	162	VAL
3	AC	167	LEU
5	AI	95	THR
7	AK	62	ILE
7	AK	109	ILE
8	AM	23	LEU
8	AM	68	LEU
9	AN	64	VAL
10	AO	193	LEU
13	AT	88	VAL

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Mol	Chain	Res	Type
14	AW	107	ILE
15	AX	91	VAL
15	AX	242	ILE
16	A2	33	VAL
18	AL	115	VAL
19	AR	154	THR
19	AR	294	ILE
19	AR	342	ILE
21	AU	29	THR
21	AU	34	LEU
21	AU	42	VAL
21	AU	188	ASN
24	AZ	34	VAL
25	A1	65	ASP
25	A1	175	VAL
26	A0	109	LEU
26	A0	161	LEU
26	A0	193	VAL
26	A0	196	ILE
29	AD	91	THR
29	AD	132	ILE
29	AD	336	VAL
29	AD	421	VAL
30	AF	55	VAL
30	AF	82	THR
30	AF	196	HIS
34	D	220	VAL
34	D	244	VAL
34	D	250	VAL
36	H	130	VAL
37	K	46	VAL
38	L	38	VAL
38	L	105	VAL
40	O	20	LEU
43	T	156	ILE
44	W	126	LEU
45	X	207	THR
51	3	188	VAL
62	r	139	VAL
63	J	135	VAL
64	I	96	ILE
65	N	152	THR

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Mol	Chain	Res	Type
68	V	56	LEU
68	V	144	VAL
69	E	299	VAL
71	6	173	LEU
71	6	179	VAL
71	6	187	VAL
71	6	204	VAL
72	7	70	VAL
72	7	78	VAL
72	7	252	VAL
72	7	324	VAL
73	9	62	VAL
76	d	66	VAL
76	d	67	ILE
76	d	119	GLN
77	f	63	ILE
77	f	75	VAL
77	f	90	VAL
79	k	16	VAL
80	l	68	LEU
83	Q	76	LEU
83	Q	113	VAL
85	TB	71	ILE
86	z	107	LEU
86	z	186	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (245) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	126	GLN
2	AB	134	HIS
3	AC	115	ASN
3	AC	156	GLN
4	AE	14	GLN
4	AE	58	HIS
4	AE	59	ASN
5	AI	129	GLN
5	AI	183	HIS
6	AJ	74	ASN
7	AK	28	HIS
7	AK	55	ASN
8	AM	16	HIS

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Mol	Chain	Res	Type
10	AO	98	ASN
10	AO	103	ASN
10	AO	223	HIS
10	AO	225	GLN
11	AP	95	HIS
11	AP	115	GLN
12	AQ	73	ASN
12	AQ	85	GLN
13	AT	51	ASN
13	AT	56	GLN
13	AT	125	HIS
14	AW	91	GLN
14	AW	110	ASN
14	AW	121	HIS
14	AW	135	GLN
15	AX	59	HIS
15	AX	62	GLN
15	AX	63	HIS
15	AX	81	HIS
15	AX	159	HIS
15	AX	164	ASN
15	AX	180	GLN
15	AX	312	GLN
15	AX	363	ASN
17	AH	122	GLN
17	AH	147	HIS
18	AL	76	GLN
18	AL	107	GLN
18	AL	145	HIS
18	AL	199	HIS
19	AR	76	GLN
19	AR	167	HIS
19	AR	229	ASN
19	AR	277	ASN
19	AR	302	GLN
19	AR	326	ASN
19	AR	350	GLN
20	AS	97	GLN
20	AS	107	GLN
21	AU	79	GLN
21	AU	102	HIS
21	AU	109	ASN

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Mol	Chain	Res	Type
21	AU	117	HIS
21	AU	159	GLN
21	AU	161	GLN
22	AV	122	GLN
22	AV	131	ASN
22	AV	134	GLN
22	AV	156	ASN
22	AV	170	GLN
22	AV	203	ASN
22	AV	261	GLN
22	AV	383	HIS
22	AV	388	GLN
22	AV	391	GLN
22	AV	396	GLN
23	AY	290	ASN
23	AY	381	ASN
23	AY	391	ASN
24	AZ	27	ASN
24	AZ	56	HIS
24	AZ	63	GLN
24	AZ	76	GLN
25	A1	165	ASN
25	A1	235	ASN
25	A1	261	ASN
25	A1	268	GLN
25	A1	301	ASN
26	A0	192	ASN
26	A0	207	GLN
27	A3	129	ASN
28	A4	79	ASN
28	A4	115	ASN
28	A4	122	ASN
29	AD	145	ASN
29	AD	175	GLN
29	AD	292	HIS
29	AD	356	GLN
29	AD	369	HIS
30	AF	113	GLN
30	AF	197	GLN
30	AF	233	ASN
31	AG	87	HIS
31	AG	90	ASN

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Mol	Chain	Res	Type
31	AG	101	GLN
31	AG	148	HIS
31	AG	156	GLN
31	AG	171	ASN
31	AG	288	HIS
31	AG	296	ASN
31	AG	366	GLN
34	D	165	ASN
34	D	235	GLN
35	F	83	HIS
35	F	97	HIS
35	F	103	GLN
35	F	208	HIS
35	F	228	GLN
36	H	121	ASN
37	K	26	GLN
37	K	48	HIS
37	K	61	ASN
37	K	117	HIS
38	L	43	ASN
38	L	52	HIS
38	L	72	GLN
39	M	53	HIS
39	M	87	HIS
39	M	92	GLN
39	M	102	GLN
39	M	130	GLN
39	M	198	GLN
39	M	264	GLN
40	O	39	HIS
40	O	128	ASN
40	O	147	GLN
41	R	125	HIS
42	S	84	ASN
42	S	118	ASN
43	T	75	HIS
43	T	109	ASN
43	T	210	HIS
44	W	41	ASN
44	W	51	GLN
45	X	27	HIS
45	X	76	GLN

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Mol	Chain	Res	Type
45	X	89	GLN
46	Y	73	ASN
46	Y	76	GLN
46	Y	92	ASN
46	Y	99	HIS
46	Y	117	GLN
46	Y	160	GLN
46	Y	183	GLN
46	Y	195	ASN
46	Y	225	ASN
47	Z	98	GLN
51	3	154	GLN
53	8	126	GLN
53	8	143	GLN
53	8	177	HIS
54	b	17	ASN
54	b	24	GLN
54	b	27	GLN
54	b	135	ASN
55	e	67	GLN
55	e	126	GLN
55	e	212	HIS
55	e	252	HIS
56	g	73	GLN
56	g	81	ASN
57	i	89	GLN
58	j	30	GLN
60	o	16	GLN
60	o	58	GLN
60	o	85	HIS
60	o	94	HIS
61	q	139	GLN
61	q	142	ASN
62	r	69	GLN
62	r	96	HIS
62	r	112	HIS
63	J	47	ASN
64	I	41	HIS
64	I	43	GLN
64	I	91	GLN
64	I	100	GLN
64	I	101	ASN

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Mol	Chain	Res	Type
64	I	128	ASN
64	I	204	GLN
65	N	68	ASN
65	N	98	HIS
65	N	110	ASN
65	N	222	ASN
67	U	27	GLN
68	V	84	ASN
69	E	197	HIS
69	E	202	GLN
70	5	65	HIS
70	5	118	GLN
70	5	145	HIS
70	5	155	ASN
70	5	274	ASN
70	5	352	HIS
71	6	37	ASN
71	6	111	GLN
71	6	224	HIS
71	6	239	ASN
71	6	292	GLN
71	6	307	HIS
71	6	320	GLN
71	6	333	GLN
71	6	359	HIS
72	7	45	ASN
72	7	207	HIS
73	9	113	ASN
74	a	44	ASN
74	a	121	HIS
74	a	137	ASN
75	c	42	GLN
75	c	172	ASN
75	c	193	GLN
76	d	153	ASN
76	d	251	GLN
76	d	286	GLN
77	f	61	HIS
77	f	115	ASN
77	f	153	HIS
77	f	158	GLN
79	k	15	GLN

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Mol	Chain	Res	Type
79	k	26	ASN
79	k	35	GLN
79	k	46	ASN
80	l	82	GLN
80	l	100	ASN
80	l	124	GLN
81	p	123	HIS
82	s	87	GLN
82	s	101	ASN
82	s	107	GLN
82	s	154	HIS
82	s	164	HIS
82	s	207	HIS
82	s	238	ASN
82	s	240	GLN
82	s	280	ASN
82	s	327	ASN
82	s	391	ASN
83	Q	139	GLN
86	z	131	ASN
86	z	135	GLN
86	z	202	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	940/954 (98%)	237 (25%)	12 (1%)
32	A	1523/1559 (97%)	349 (22%)	27 (1%)
33	B	51/73 (69%)	14 (27%)	1 (1%)
All	All	2514/2586 (97%)	600 (23%)	40 (1%)

All (600) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	650	U
1	AA	651	A
1	AA	674	U
1	AA	676	G
1	AA	680	U
1	AA	690	U
1	AA	691	A

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Mol	Chain	Res	Type
1	AA	694	C
1	AA	704	U
1	AA	707	C
1	AA	711	U
1	AA	718	A
1	AA	721	U
1	AA	732	A
1	AA	735	A
1	AA	736	C
1	AA	737	C
1	AA	745	A
1	AA	753	A
1	AA	761	A
1	AA	764	A
1	AA	765	C
1	AA	766	G
1	AA	770	C
1	AA	771	A
1	AA	773	U
1	AA	781	A
1	AA	791	G
1	AA	794	U
1	AA	796	G
1	AA	807	A
1	AA	808	C
1	AA	813	A
1	AA	815	C
1	AA	817	G
1	AA	828	C
1	AA	830	U
1	AA	832	U
1	AA	835	C
1	AA	836	A
1	AA	843	G
1	AA	846	A
1	AA	856	A
1	AA	860	A
1	AA	868	C
1	AA	870	C
1	AA	872	G
1	AA	877	G
1	AA	881	A

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Mol	Chain	Res	Type
1	AA	882	A
1	AA	883	U
1	AA	885	U
1	AA	886	C
1	AA	890	C
1	AA	891	C
1	AA	899	G
1	AA	903	U
1	AA	904	C
1	AA	912	U
1	AA	919	A
1	AA	921	U
1	AA	922	C
1	AA	929	A
1	AA	930	G
1	AA	931	C
1	AA	932	C
1	AA	938	A
1	AA	939	A
1	AA	942	A
1	AA	948	U
1	AA	954	C
1	AA	957	C
1	AA	964	C
1	AA	965	C
1	AA	966	A
1	AA	967	A
1	AA	975	A
1	AA	988	G
1	AA	992	U
1	AA	1001	C
1	AA	1009	C
1	AA	1011	C
1	AA	1015	A
1	AA	1016	U
1	AA	1018	G
1	AA	1022	A
1	AA	1028	G
1	AA	1033	U
1	AA	1041	A
1	AA	1042	U
1	AA	1046	A

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Mol	Chain	Res	Type
1	AA	1047	A
1	AA	1049	A
1	AA	1065	C
1	AA	1069	A
1	AA	1081	U
1	AA	1082	A
1	AA	1103	A
1	AA	1105	C
1	AA	1106	C
1	AA	1109	A
1	AA	1116	A
1	AA	1117	A
1	AA	1118	A
1	AA	1119	U
1	AA	1120	C
1	AA	1121	A
1	AA	1125	A
1	AA	1126	A
1	AA	1129	U
1	AA	1138	G
1	AA	1151	C
1	AA	1154	A
1	AA	1167	A
1	AA	1187	U
1	AA	1188	A
1	AA	1189	U
1	AA	1190	C
1	AA	1193	U
1	AA	1200	G
1	AA	1213	A
1	AA	1214	A
1	AA	1215	U
1	AA	1219	U
1	AA	1220	A
1	AA	1223	C
1	AA	1225	C
1	AA	1230	C
1	AA	1231	A
1	AA	1235	U
1	AA	1236	C
1	AA	1237	A
1	AA	1238	C

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Mol	Chain	Res	Type
1	AA	1245	U
1	AA	1246	U
1	AA	1247	G
1	AA	1248	C
1	AA	1249	U
1	AA	1250	C
1	AA	1251	A
1	AA	1258	A
1	AA	1261	C
1	AA	1270	U
1	AA	1271	C
1	AA	1272	A
1	AA	1275	A
1	AA	1282	G
1	AA	1283	A
1	AA	1284	U
1	AA	1285	G
1	AA	1292	A
1	AA	1293	C
1	AA	1295	A
1	AA	1296	A
1	AA	1300	A
1	AA	1309	A
1	AA	1312	C
1	AA	1313	A
1	AA	1314	C
1	AA	1319	A
1	AA	1320	G
1	AA	1326	A
1	AA	1327	G
1	AA	1328	G
1	AA	1330	C
1	AA	1331	A
1	AA	1332	A
1	AA	1333	G
1	AA	1338	A
1	AA	1342	C
1	AA	1343	A
1	AA	1345	G
1	AA	1349	U
1	AA	1353	A
1	AA	1354	A

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Mol	Chain	Res	Type
1	AA	1355	G
1	AA	1356	A
1	AA	1357	A
1	AA	1358	A
1	AA	1365	A
1	AA	1367	A
1	AA	1370	U
1	AA	1374	A
1	AA	1377	C
1	AA	1378	C
1	AA	1379	A
1	AA	1383	A
1	AA	1389	G
1	AA	1390	A
1	AA	1403	A
1	AA	1404	A
1	AA	1405	C
1	AA	1406	U
1	AA	1407	U
1	AA	1415	G
1	AA	1416	A
1	AA	1417	A
1	AA	1420	U
1	AA	1422	G
1	AA	1425	U
1	AA	1430	A
1	AA	1441	A
1	AA	1443	U
1	AA	1447	G
1	AA	1451	U
1	AA	1461	A
1	AA	1466	C
1	AA	1482	A
1	AA	1512	A
1	AA	1517	A
1	AA	1518	C
1	AA	1519	A
1	AA	1520	U
1	AA	1521	U
1	AA	1522	U
1	AA	1524	A
1	AA	1526	U

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Mol	Chain	Res	Type
1	AA	1527	A
1	AA	1529	A
1	AA	1533	C
1	AA	1534	C
1	AA	1535	U
1	AA	1536	A
1	AA	1537	C
1	AA	1539	C
1	AA	1540	A
1	AA	1549	G
1	AA	1557	A
1	AA	1558	A
1	AA	1562	G
1	AA	1564	A
1	AA	1568	U
1	AA	1571	U
1	AA	1582	G
1	AA	1594	G
1	AA	1595	G
1	AA	1599	A
32	A	1672	C
32	A	1674	A
32	A	1678	C
32	A	1679	U
32	A	1681	G
32	A	1689	C
32	A	1690	C
32	A	1693	C
32	A	1700	U
32	A	1704	U
32	A	1708	A
32	A	1709	G
32	A	1711	C
32	A	1713	A
32	A	1714	C
32	A	1715	C
32	A	1716	U
32	A	1717	U
32	A	1724	A
32	A	1727	A
32	A	1728	U
32	A	1732	C

Continued on next page...

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Mol	Chain	Res	Type
32	A	1733	C
32	A	1734	C
32	A	1735	A
32	A	1736	A
32	A	1748	G
32	A	1750	G
32	A	1751	A
32	A	1762	A
32	A	1763	A
32	A	1766	U
32	A	1767	G
32	A	1770	G
32	A	1777	A
32	A	1781	A
32	A	1782	G
32	A	1794	A
32	A	1800	G
32	A	1806	U
32	A	1807	U
32	A	1808	A
32	A	1809	U
32	A	1810	A
32	A	1812	C
32	A	1823	A
32	A	1824	U
32	A	1827	C
32	A	1828	A
32	A	1829	A
32	A	1832	A
32	A	1836	A
32	A	1839	C
32	A	1840	C
32	A	1844	A
32	A	1849	C
32	A	1854	U
32	A	1856	A
32	A	1867	A
32	A	1869	A
32	A	1872	U
32	A	1878	U
32	A	1882	A
32	A	1883	G

Continued on next page...

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Mol	Chain	Res	Type
32	A	1893	A
32	A	1901	C
32	A	1903	C
32	A	1918	G
32	A	1935	A
32	A	1936	A
32	A	1938	A
32	A	1940	A
32	A	1944	C
32	A	1946	C
32	A	1958	G
32	A	1968	G
32	A	1974	A
32	A	1985	G
32	A	1987	G
32	A	1992	C
32	A	1994	A
32	A	1995	A
32	A	2000	C
32	A	2001	C
32	A	2002	G
32	A	2015	G
32	A	2021	U
32	A	2022	G
32	A	2029	A
32	A	2031	A
32	A	2036	C
32	A	2037	U
32	A	2039	A
32	A	2060	A
32	A	2065	A
32	A	2066	C
32	A	2067	C
32	A	2069	U
32	A	2074	A
32	A	2079	C
32	A	2083	U
32	A	2093	U
32	A	2097	A
32	A	2098	G
32	A	2099	U
32	A	2105	G

Continued on next page...

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Mol	Chain	Res	Type
32	A	2113	G
32	A	2125	C
32	A	2126	U
32	A	2134	A
32	A	2135	A
32	A	2142	A
32	A	2147	G
32	A	2154	A
32	A	2160	A
32	A	2163	A
32	A	2166	C
32	A	2168	U
32	A	2169	A
32	A	2172	A
32	A	2173	G
32	A	2174	G
32	A	2180	A
32	A	2181	A
32	A	2183	C
32	A	2186	C
32	A	2187	C
32	A	2189	C
32	A	2190	C
32	A	2193	U
32	A	2194	U
32	A	2197	G
32	A	2198	A
32	A	2200	A
32	A	2204	U
32	A	2210	C
32	A	2211	U
32	A	2218	C
32	A	2219	C
32	A	2220	A
32	A	2224	C
32	A	2227	A
32	A	2228	A
32	A	2229	A
32	A	2230	A
32	A	2233	U
32	A	2237	A
32	A	2239	A

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Mol	Chain	Res	Type
32	A	2241	A
32	A	2245	A
32	A	2246	A
32	A	2250	A
32	A	2262	C
32	A	2263	C
32	A	2284	C
32	A	2297	A
32	A	2300	G
32	A	2315	A
32	A	2322	C
32	A	2324	U
32	A	2332	C
32	A	2345	G
32	A	2350	A
32	A	2351	U
32	A	2356	A
32	A	2357	C
32	A	2360	U
32	A	2361	G
32	A	2362	A
32	A	2364	C
32	A	2365	U
32	A	2371	U
32	A	2373	A
32	A	2379	C
32	A	2381	A
32	A	2390	A
32	A	2393	C
32	A	2396	C
32	A	2404	U
32	A	2407	U
32	A	2414	C
32	A	2415	C
32	A	2434	A
32	A	2443	C
32	A	2444	A
32	A	2445	U
32	A	2447	A
32	A	2458	A
32	A	2478	G
32	A	2484	C

Continued on next page...

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Mol	Chain	Res	Type
32	A	2493	C
32	A	2507	A
32	A	2508	C
32	A	2511	C
32	A	2520	C
32	A	2521	A
32	A	2522	U
32	A	2523	C
32	A	2524	A
32	A	2527	A
32	A	2530	A
32	A	2531	U
32	A	2532	U
32	A	2540	C
32	A	2557	C
32	A	2558	A
32	A	2559	U
32	A	2560	G
32	A	2570	C
32	A	2575	U
32	A	2577	C
32	A	2578	C
32	A	2592	G
32	A	2593	G
32	A	2594	U
32	A	2599	U
32	A	2601	A
32	A	2603	C
32	A	2607	U
32	A	2618	U
32	A	2626	U
32	A	2627	G
32	A	2629	A
32	A	2630	U
32	A	2632	A
32	A	2633	A
32	A	2634	U
32	A	2635	G
32	A	2638	U
32	A	2645	G
32	A	2654	U
32	A	2656	U

Continued on next page...

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Mol	Chain	Res	Type
32	A	2660	U
32	A	2683	C
32	A	2684	C
32	A	2686	G
32	A	2694	A
32	A	2696	A
32	A	2706	A
32	A	2709	A
32	A	2714	A
32	A	2715	A
32	A	2718	C
32	A	2719	G
32	A	2723	A
32	A	2724	G
32	A	2725	A
32	A	2732	G
32	A	2739	U
32	A	2740	A
32	A	2745	A
32	A	2747	U
32	A	2750	U
32	A	2755	A
32	A	2756	C
32	A	2757	A
32	A	2758	G
32	A	2760	A
32	A	2791	A
32	A	2803	A
32	A	2804	A
32	A	2810	G
32	A	2814	G
32	A	2831	G
32	A	2832	A
32	A	2833	A
32	A	2844	G
32	A	2847	C
32	A	2854	U
32	A	2861	A
32	A	2864	U
32	A	2865	C
32	A	2879	A
32	A	2881	C

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Mol	Chain	Res	Type
32	A	2893	A
32	A	2906	C
32	A	2910	A
32	A	2912	C
32	A	2913	A
32	A	2916	G
32	A	2917	G
32	A	2918	A
32	A	2922	A
32	A	2926	A
32	A	2928	C
32	A	2935	A
32	A	2955	U
32	A	2956	A
32	A	2962	C
32	A	2963	A
32	A	2985	C
32	A	2989	G
32	A	2990	A
32	A	2991	U
32	A	2992	G
32	A	2993	U
32	A	2994	U
32	A	3000	A
32	A	3005	A
32	A	3007	C
32	A	3016	G
32	A	3022	G
32	A	3041	U
32	A	3042	U
32	A	3053	A
32	A	3054	G
32	A	3059	A
32	A	3069	A
32	A	3070	G
32	A	3072	U
32	A	3086	U
32	A	3093	C
32	A	3097	U
32	A	3098	U
32	A	3100	U
32	A	3102	U

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Mol	Chain	Res	Type
32	A	3109	U
32	A	3113	A
32	A	3123	G
32	A	3124	U
32	A	3128	A
32	A	3129	A
32	A	3140	A
32	A	3141	A
32	A	3150	U
32	A	3155	C
32	A	3158	A
32	A	3162	C
32	A	3168	C
32	A	3169	C
32	A	3172	C
32	A	3180	A
32	A	3189	C
32	A	3190	A
32	A	3192	C
32	A	3196	G
32	A	3197	U
32	A	3200	U
32	A	3201	A
32	A	3204	C
32	A	3205	C
32	A	3207	A
32	A	3208	C
32	A	3210	C
32	A	3211	C
32	A	3212	C
32	A	3217	A
32	A	3218	A
32	A	3228	U
33	B	1607	U
33	B	1608	G
33	B	1609	U
33	B	1611	G
33	B	1613	U
33	B	1614	U
33	B	1615	A
33	B	1625	A
33	B	1637	C

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Mol	Chain	Res	Type
33	B	1644	G
33	B	1645	A
33	B	1651	A
33	B	1659	U
33	B	1669	G

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	717	G
1	AA	947	U
1	AA	953	U
1	AA	1021	U
1	AA	1115	U
1	AA	1166	A
1	AA	1188	A
1	AA	1234	C
1	AA	1246	U
1	AA	1406	U
1	AA	1429	C
1	AA	1535	U
32	A	1703	C
32	A	1713	A
32	A	1805	A
32	A	1806	U
32	A	1807	U
32	A	1809	U
32	A	1823	A
32	A	1871	A
32	A	1994	A
32	A	2165	C
32	A	2172	A
32	A	2182	G
32	A	2186	C
32	A	2245	A
32	A	2361	G
32	A	2457	A
32	A	2507	A
32	A	2530	A
32	A	2559	U
32	A	2628	U
32	A	2653	C

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Mol	Chain	Res	Type
32	A	2905	A
32	A	2989	G
32	A	3041	U
32	A	3092	U
32	A	3123	G
32	A	3196	G
33	B	1607	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 135 ligands modelled in this entry, 134 are monoatomic - leaving 1 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$
89	GDP	AX	500	15	29,30,30	1.27	2 (6%)	45,47,47	2.03	9 (20%)

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
89	GDP	AX	500	15	-	4/16/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	AX	500	GDP	C5-C4	3.12	1.47	1.38
89	AX	500	GDP	C6-N1	-2.09	1.34	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	AX	500	GDP	C5-C4-N3	-6.57	117.93	128.39
89	AX	500	GDP	N9-C4-N3	5.32	136.59	125.95
89	AX	500	GDP	C2-N3-C4	4.94	120.80	112.30
89	AX	500	GDP	C3'-C2'-C1'	-3.13	95.54	101.46
89	AX	500	GDP	C4-C5-N7	-2.84	106.17	110.67
89	AX	500	GDP	C6-C5-N7	2.67	135.15	130.29
89	AX	500	GDP	O3B-PB-O3A	2.64	113.48	104.64
89	AX	500	GDP	O6-C6-C5	-2.49	119.96	126.53
89	AX	500	GDP	O3'-C3'-C4'	2.29	117.66	111.08

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	AX	500	GDP	C5'-O5'-PA-O3A
89	AX	500	GDP	C5'-O5'-PA-O1A
89	AX	500	GDP	O4'-C1'-N9-C8
89	AX	500	GDP	O4'-C1'-N9-C4

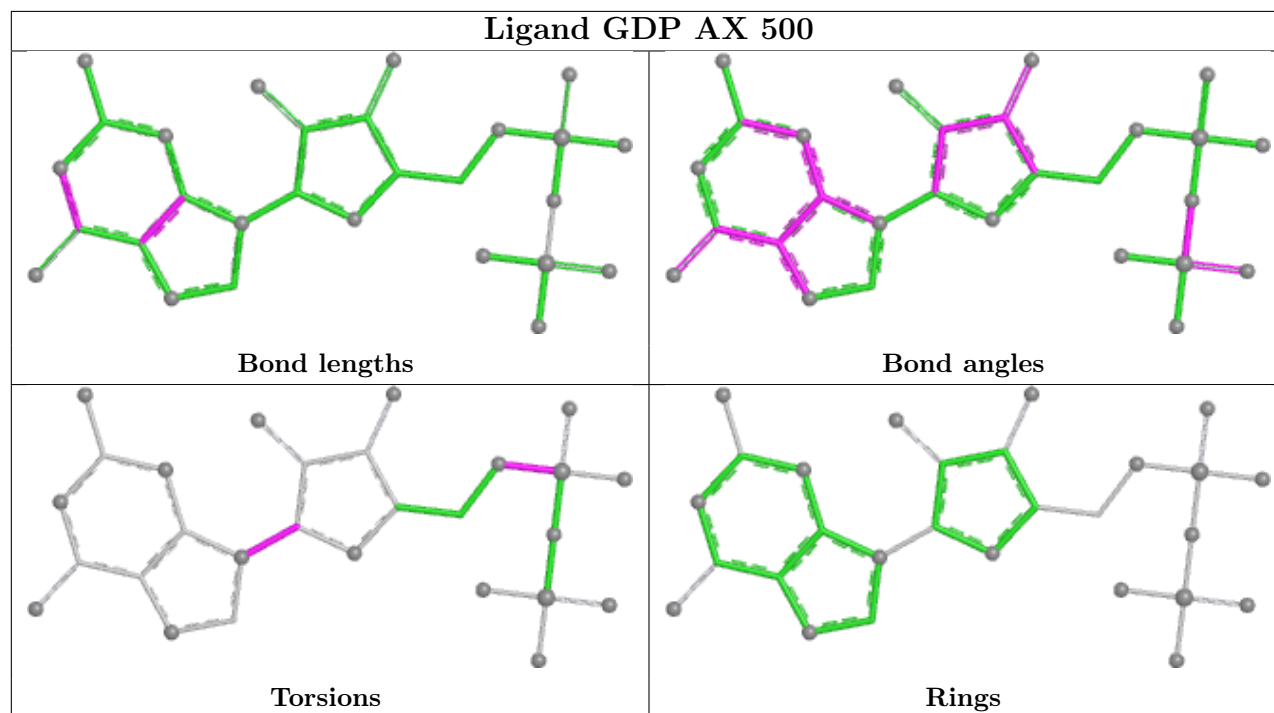
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
89	AX	500	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [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
84	u	4
32	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	414:UNK	C	601:UNK	N	48.75
1	u	106:UNK	C	301:UNK	N	32.31
1	u	315:UNK	C	399:UNK	N	23.19
1	u	615:UNK	C	700:UNK	N	20.56
1	A	2580:U	O3'	2581:A	P	3.48

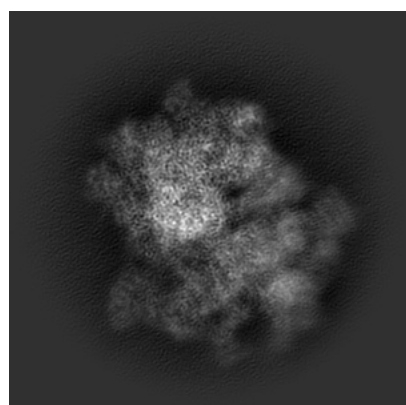
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23096. These allow visual inspection of the internal detail of the map and identification of artifacts.

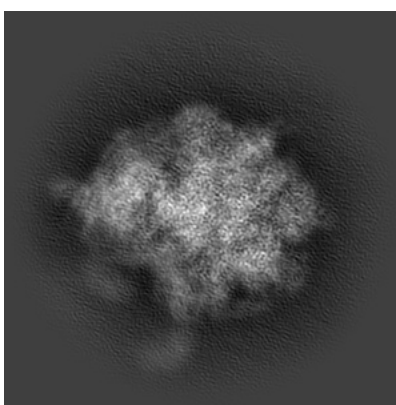
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

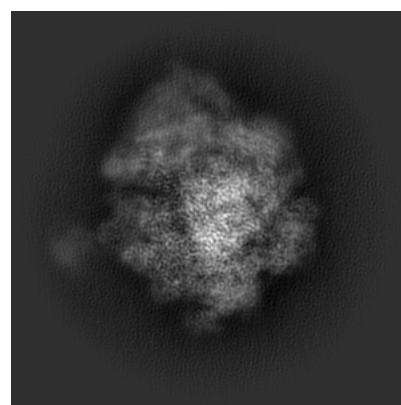
6.1.1 Primary map



X



Y

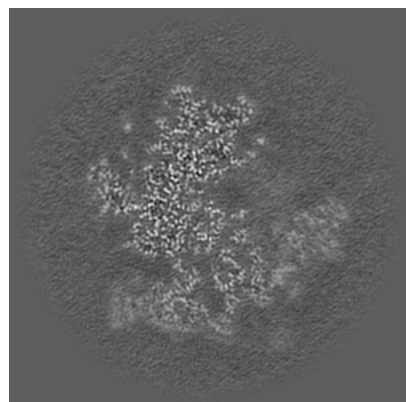


Z

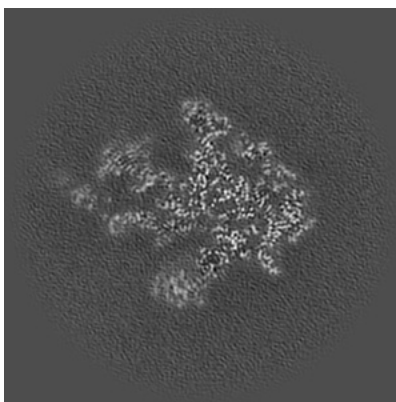
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

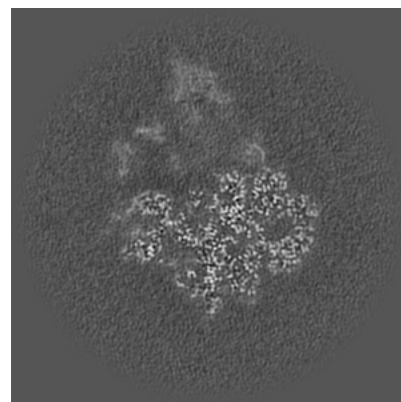
6.2.1 Primary map



X Index: 200



Y Index: 200

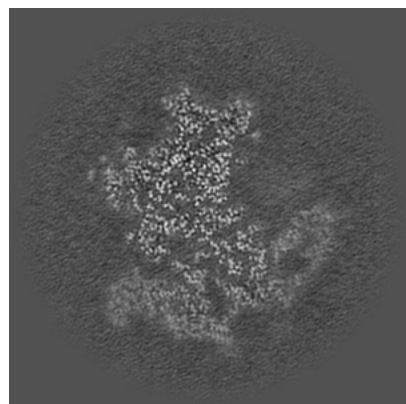


Z Index: 200

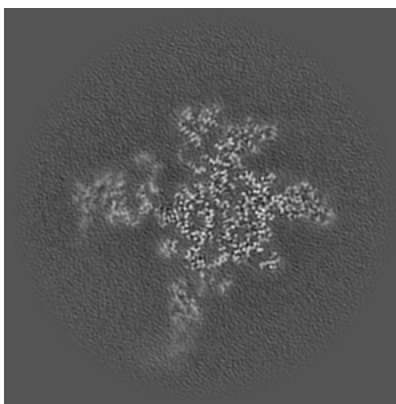
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

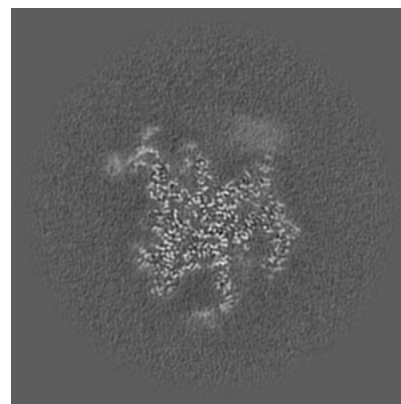
6.3.1 Primary map



X Index: 208



Y Index: 171

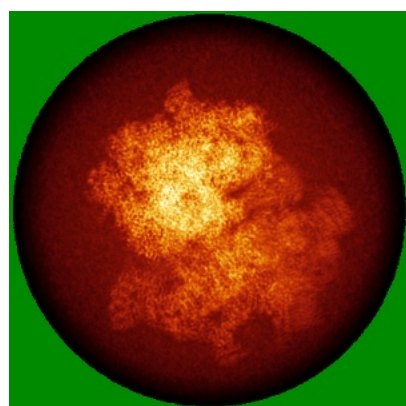


Z Index: 242

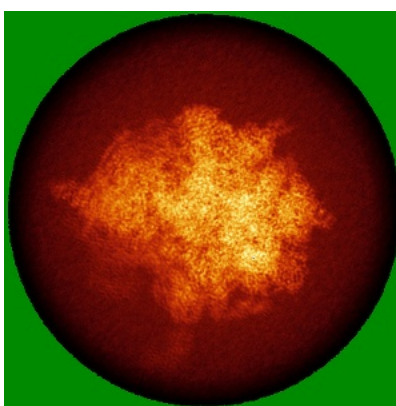
The images above show the largest variance slices of the map in three orthogonal directions.

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

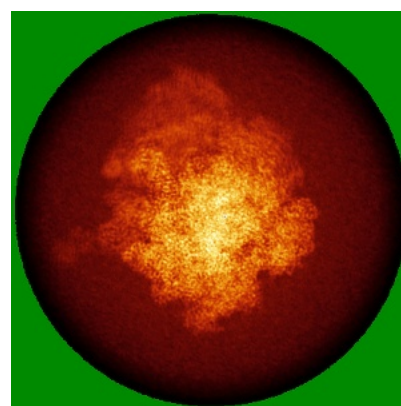
6.4.1 Primary map



X



Y

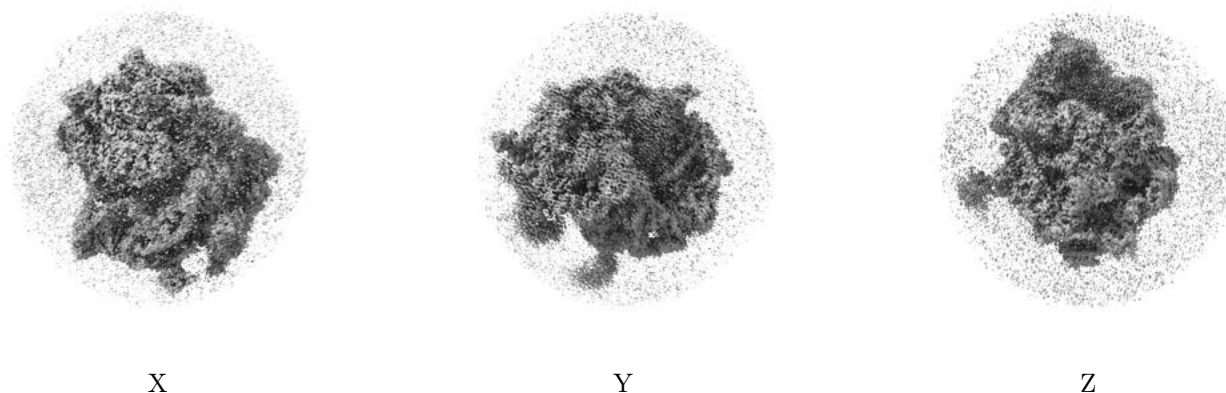


Z

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 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

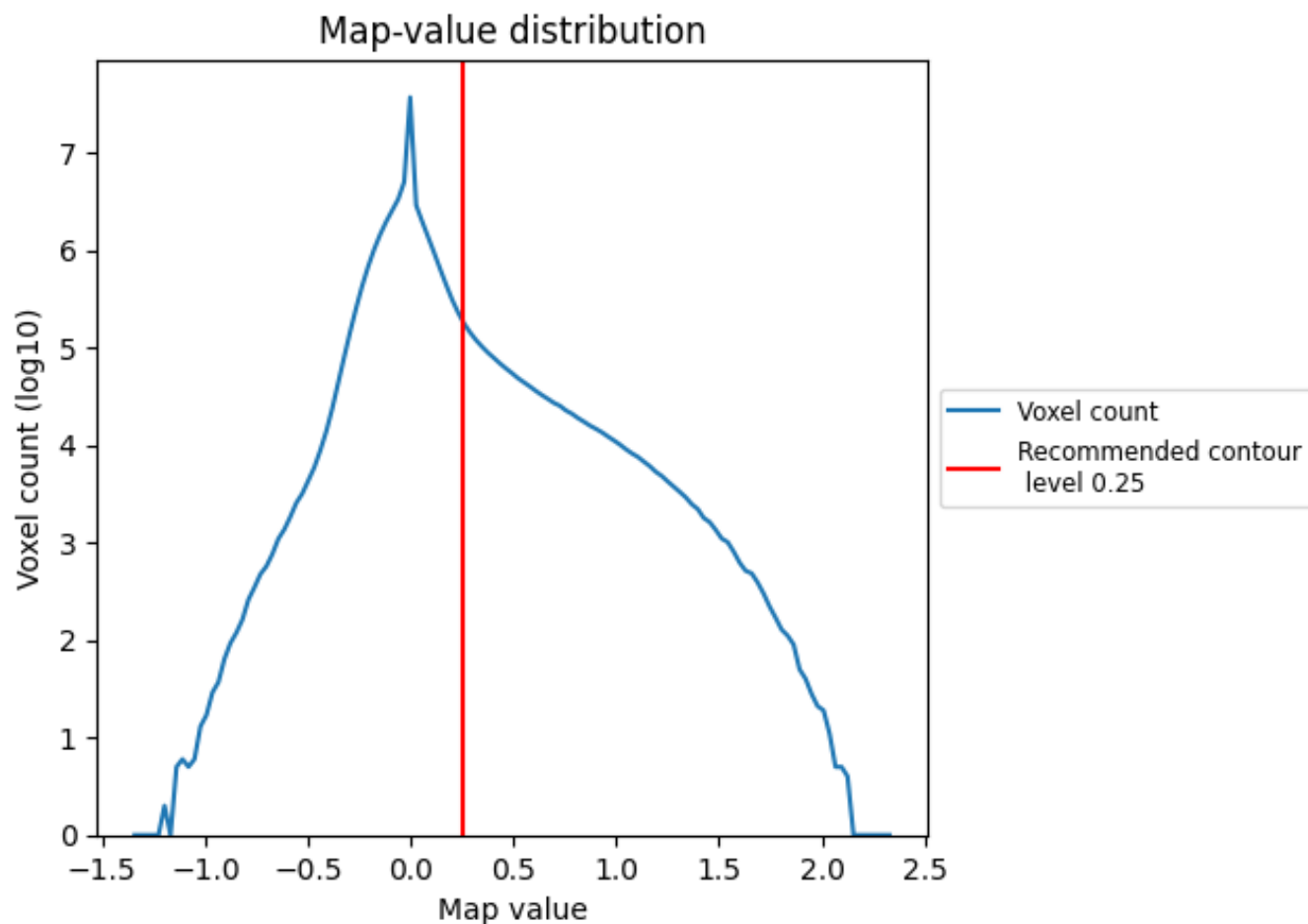
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

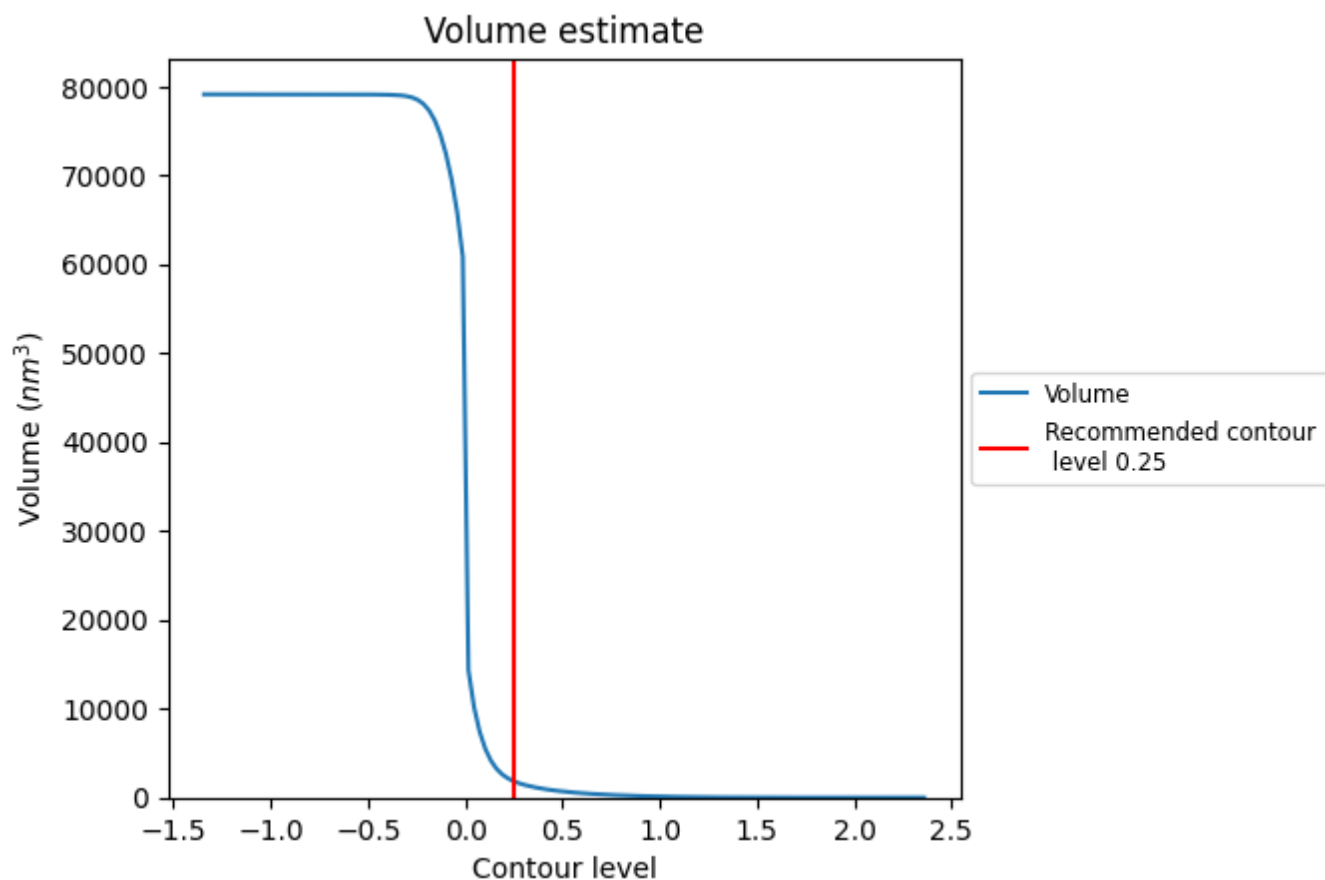
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

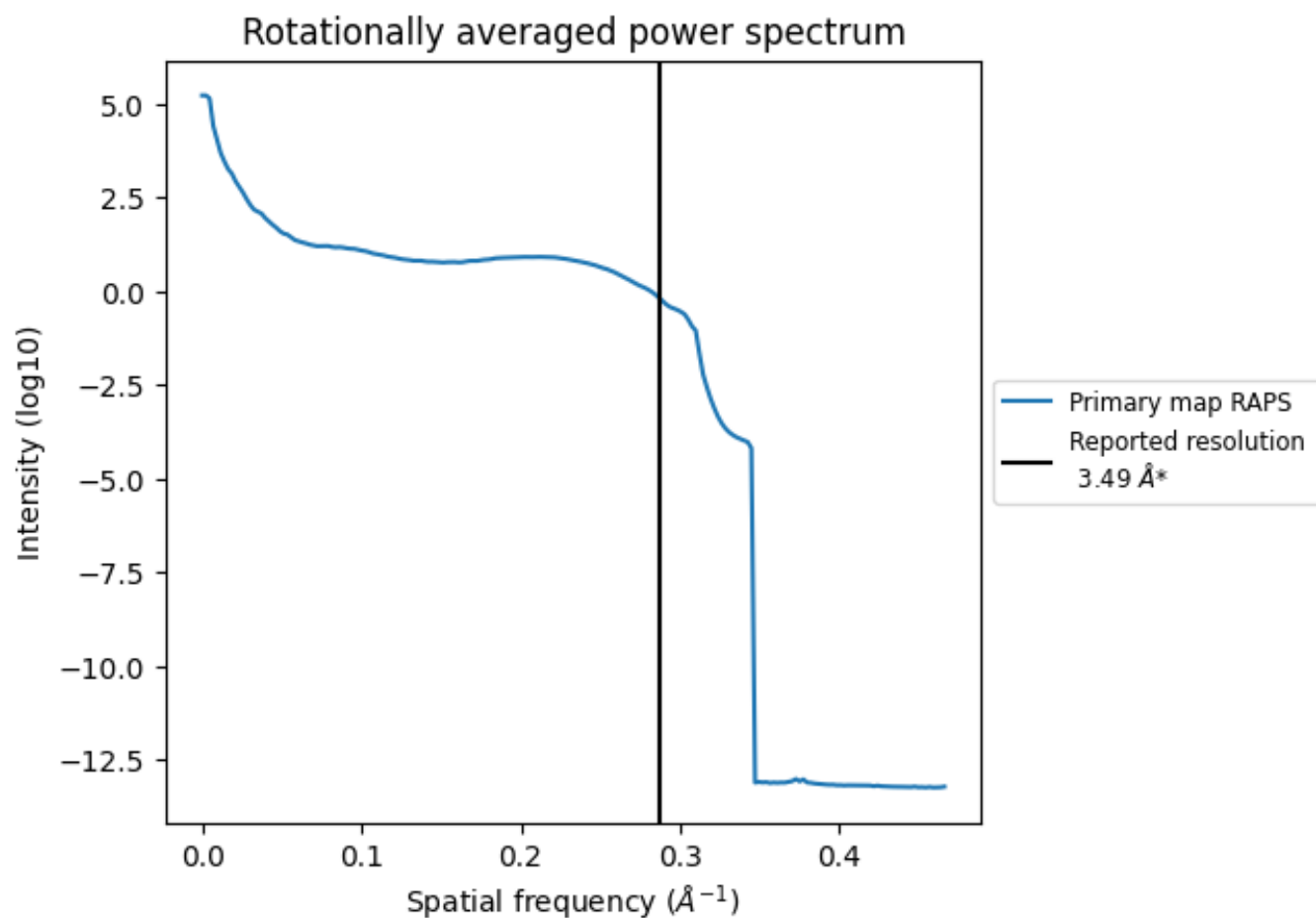
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1834 nm³; this corresponds to an approximate mass of 1656 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 0.287 Å⁻¹

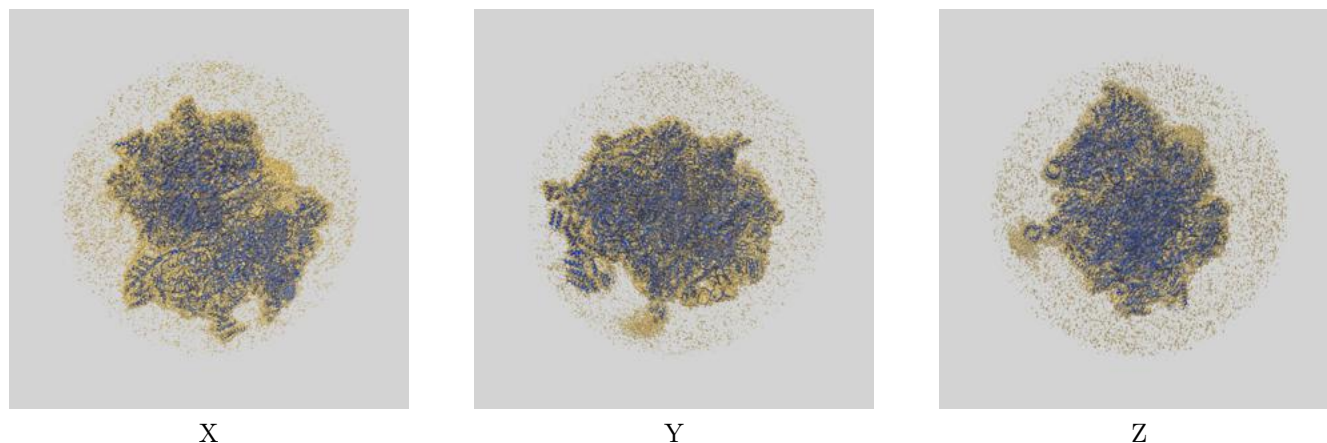
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

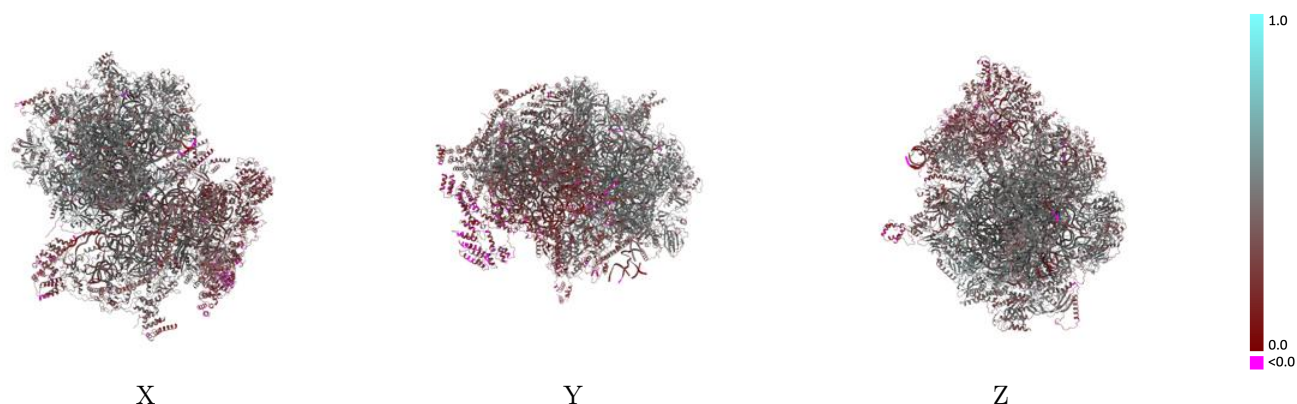
This section contains information regarding the fit between EMDB map EMD-23096 and PDB model 7L08. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



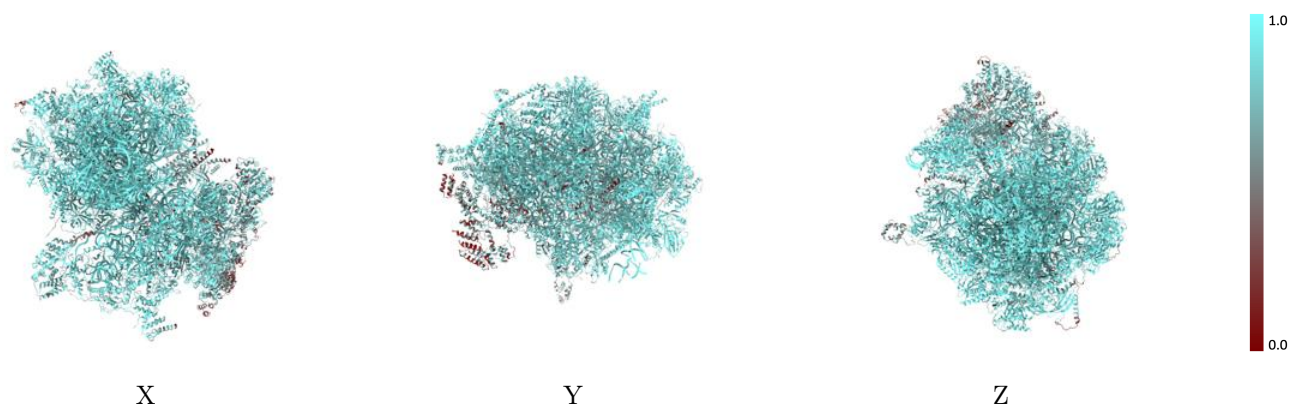
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



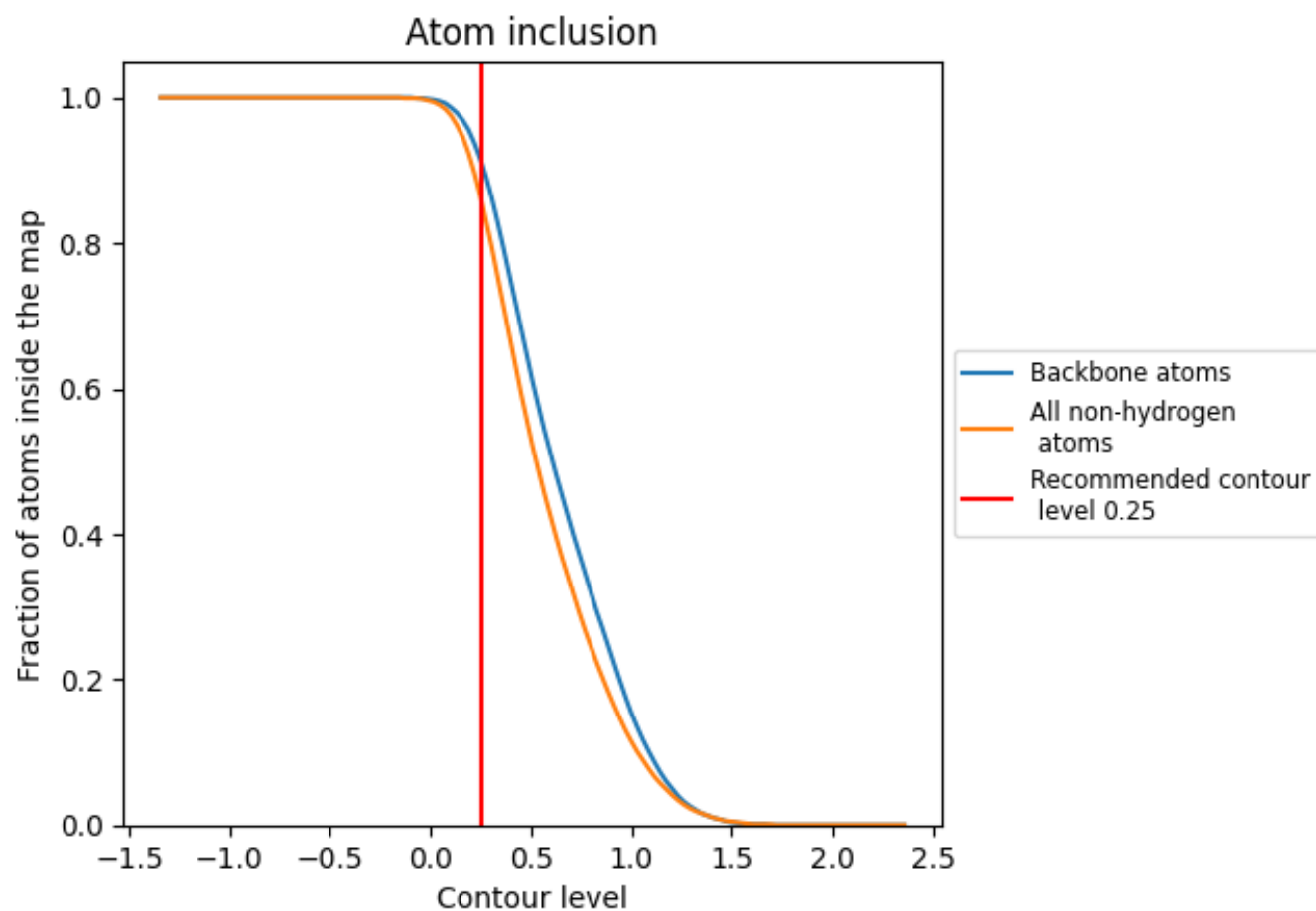
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



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

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8640	 0.4000
0	 0.9130	 0.4790
1	 0.9210	 0.4780
2	 0.9190	 0.5070
3	 0.9160	 0.5120
4	 0.9600	 0.5060
5	 0.9290	 0.4570
6	 0.9160	 0.4360
7	 0.8900	 0.4290
8	 0.7930	 0.3160
9	 0.9040	 0.4420
A	 0.9240	 0.4240
A0	 0.8300	 0.3730
A1	 0.6330	 0.2520
A2	 0.7610	 0.3910
A3	 0.8360	 0.4520
A4	 0.4690	 0.1700
AA	 0.9110	 0.3620
AB	 0.8670	 0.3950
AC	 0.7340	 0.2940
AD	 0.7510	 0.4030
AE	 0.8300	 0.3840
AF	 0.7190	 0.3350
AG	 0.7290	 0.3050
AH	 0.7070	 0.2780
AI	 0.8680	 0.3970
AJ	 0.8630	 0.4870
AK	 0.8300	 0.3300
AL	 0.8200	 0.3930
AM	 0.8580	 0.4200
AN	 0.9290	 0.4590
AO	 0.8660	 0.4010
AP	 0.8660	 0.3950
AQ	 0.8820	 0.4130
AR	 0.8210	 0.3610



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Chain	Atom inclusion	Q-score
AS	 0.8250	 0.3560
AT	 0.8670	 0.4380
AU	 0.8270	 0.3360
AV	 0.7600	 0.2550
AW	 0.8320	 0.3780
AX	 0.7330	 0.2620
AY	 0.6410	 0.2500
AZ	 0.6740	 0.2660
B	 0.9480	 0.3190
D	 0.9220	 0.4950
E	 0.9320	 0.5040
F	 0.9280	 0.4850
H	 0.8990	 0.4370
I	 0.8340	 0.3830
J	 0.7800	 0.2900
K	 0.9440	 0.4980
L	 0.9110	 0.5070
M	 0.9140	 0.4790
N	 0.9190	 0.4960
O	 0.9250	 0.4840
P	 0.9310	 0.4560
Q	 0.8830	 0.4730
R	 0.9110	 0.4940
S	 0.9320	 0.5000
T	 0.9130	 0.5020
TA	 0.5490	 0.1480
TB	 0.6060	 0.2020
U	 0.8960	 0.4540
V	 0.8680	 0.4230
W	 0.9200	 0.5090
X	 0.9050	 0.4650
Y	 0.9150	 0.4550
Z	 0.9250	 0.5080
a	 0.8580	 0.4390
b	 0.9320	 0.4940
c	 0.9120	 0.4580
d	 0.8060	 0.3890
e	 0.7670	 0.2510
f	 0.7770	 0.3610
g	 0.9180	 0.4750
h	 0.8670	 0.3840
i	 0.9130	 0.4900

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Chain	Atom inclusion	Q-score
j	 0.8840	 0.4390
k	 0.8840	 0.4030
l	 0.8090	 0.3270
m	 0.8670	 0.3640
o	 0.9360	 0.5010
p	 0.8370	 0.3880
q	 0.7930	 0.3620
r	 0.9410	 0.4800
s	 0.9150	 0.4620
u	 0.6950	 0.2460
z	 0.6100	 0.3240