



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 02:30 AM UTC

PDB ID : 9BH5 / pdb_00009bh5
EMDB ID : EMD-44533
Title : High-resolution C. elegans 80S ribosome structure - class 1
Authors : Sehgal, E.; Serrao, V.H.B.; Arribere, J.
Deposited on : 2024-04-19
Resolution : 2.63 Å(reported)
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

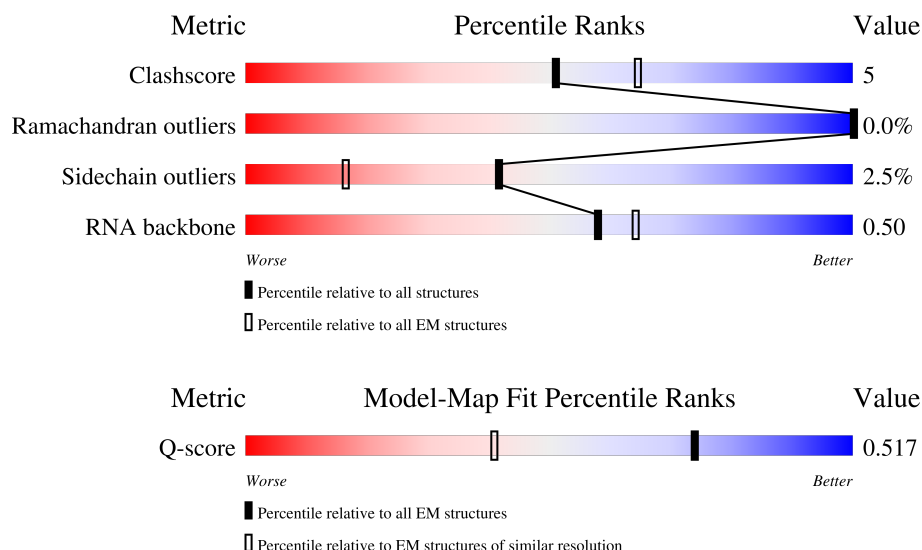
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.63 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.



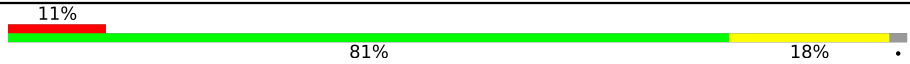
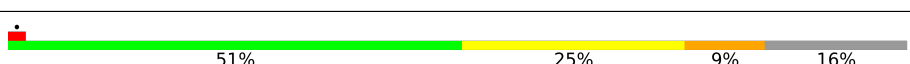
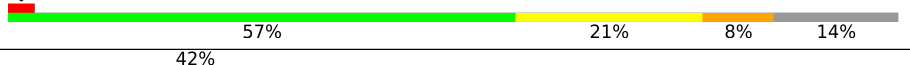
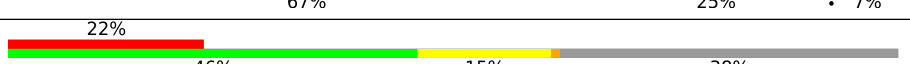
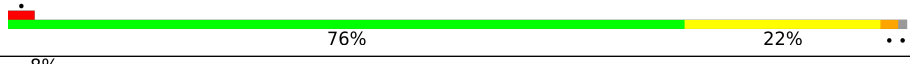
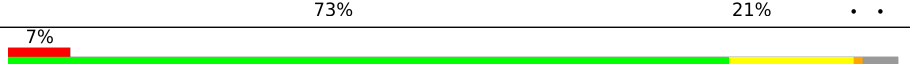
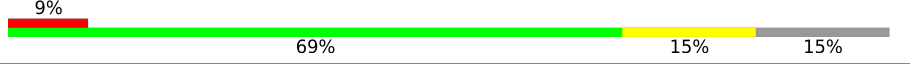
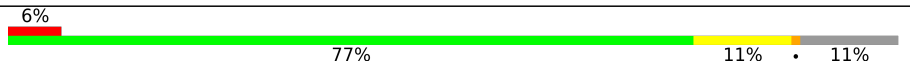
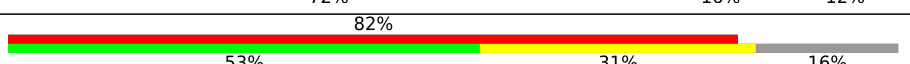
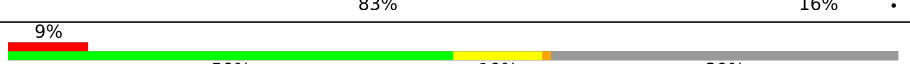
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8888 (2.13 - 3.13)

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	AD	247	25% 70% 15% 15%
2	AB	257	8% 70% 11% 18%
3	AC	272	6% 67% 11% 21%

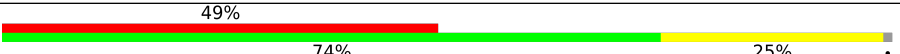
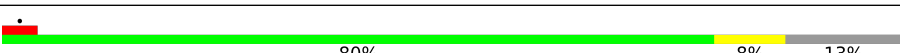
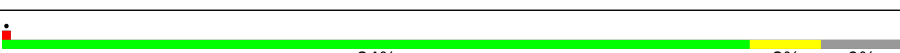
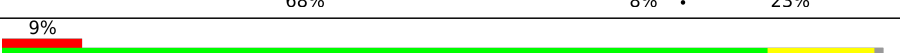
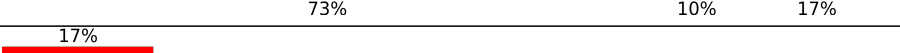
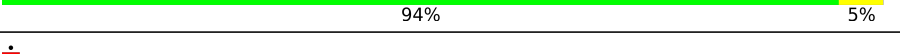
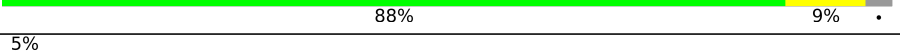
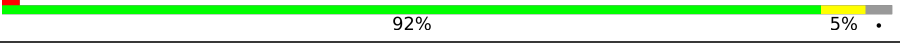
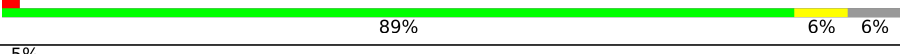
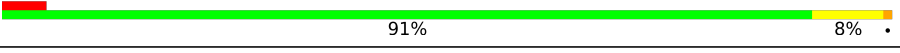
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Mol	Chain	Length	Quality of chain
4	AE	259	
5	A7	119	
6	A8	153	
7	B2	1754	
8	A5	3510	
9	AR	130	
10	AK	149	
11	AW	130	
12	AS	154	
13	AT	146	
14	Aa	117	
15	Af	163	
16	AA	276	
17	AO	152	
18	AI	208	
19	AF	210	
20	AM	140	
21	AV	88	
22	AN	151	
23	AZ	117	
24	Ad	56	
25	AY	131	
26	AU	117	
27	AG	246	
28	Ab	83	

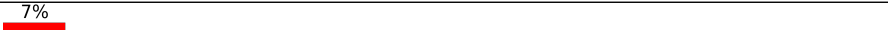
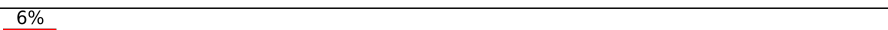
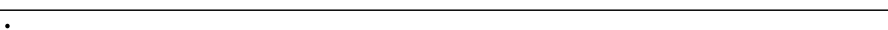
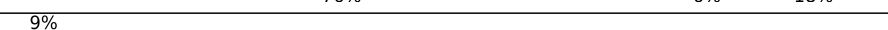
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Mol	Chain	Length	Quality of chain
29	AP	151	
30	Ac	65	
31	Ae	130	
32	AX	143	
33	AL	155	
34	AJ	189	
35	AQ	144	
36	AH	194	
37	CF	244	
38	CS	180	
39	CV	140	
40	CB	401	
41	CU	130	
42	CL	207	
43	CA	260	
44	CG	265	
45	CI	214	
46	CO	202	
47	CC	345	
48	Ch	123	
49	CE	217	
50	Co	105	
51	Cf	124	
52	Ci	104	
53	Cl	51	

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Mol	Chain	Length	Quality of chain
54	CN	204	
55	Ca	145	
56	Cp	91	
57	CM	135	
58	Cc	115	
59	CH	189	
60	CY	142	
61	CR	198	
62	Cb	62	
63	CQ	188	
64	CT	161	
65	CD	293	
66	CZ	136	
67	CP	187	
68	Cn	22	
69	Cg	110	
70	Ck	70	
71	Cm	128	
72	Cd	122	
73	Ce	134	
74	CW	159	
75	Cj	92	
76	CJ	196	
77	CX	146	
78	DA	76	

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Mol	Chain	Length	Quality of chain
78	DB	76	58% 59% 26% 14%
79	DC	10	70% 10% 20%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 332725 atoms, of which 142393 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AD	211	Total	C	H	N	O	S	0	0
			3343	1029	1706	308	291	9		

- Molecule 2 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	210	Total	C	H	N	O	S	0	0
			3453	1071	1769	298	307	8		

- Molecule 3 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AC	215	Total	C	H	N	O	S	0	0
			3389	1062	1735	293	292	7		

- Molecule 4 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AE	255	Total	C	H	N	O	S	0	0
			4120	1277	2107	382	347	7		

- Molecule 5 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	A7	119	Total	C	H	N	O	P	0	0
			3810	1131	1281	447	833	118		

- Molecule 6 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	A8	146	Total	C	H	N	O	P	0	0
			4679	1390	1568	551	1025	145		

- Molecule 7 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B2	1476	Total	C	H	N	O	P	0	0
			47369	14078	15858	5637	10320	1476		

- Molecule 8 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	A5	3022	Total	C	H	N	O	P	0	0
			96979	28814	32467	11522	21154	3022		

- Molecule 9 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	AR	121	Total	C	H	N	O	S	0	0
			1985	604	1009	183	184	5		

- Molecule 10 is a protein called Plectin/S10 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AK	93	Total	C	H	N	O	S	0	0
			1555	509	786	124	135	1		

- Molecule 11 is a protein called Ribosomal Protein, Small subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AW	129	Total	C	H	N	O	S	0	0
			2110	654	1082	193	177	4		

- Molecule 12 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AS	148	Total	C	H	N	O	S	0	0
			2453	754	1248	237	209	5		

- Molecule 13 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AT	140	Total	C	H	N	O	S	0	0
			2260	704	1149	213	193	1		

- Molecule 14 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	Aa	99	Total	C	H	N	O	S	0	0
			1631	496	828	172	129	6		

- Molecule 15 is a protein called Ubiquitin-like protein 1-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	Af	50	Total	C	H	N	O	S	0	0
			789	246	392	77	69	5		

- Molecule 16 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AA	207	Total	C	H	N	O	S	0	0
			3264	1035	1652	281	289	7		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AO	135	Total	C	H	N	O	S	0	0
			2063	624	1049	200	185	5		

- Molecule 18 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AI	207	Total	C	H	N	O	S	0	0
			3391	1044	1723	326	296	2		

- Molecule 19 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	AF	185	Total	C	H	N	O	S	0	0
			2969	914	1515	275	259	6		

- Molecule 20 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AM	117	Total	C	H	N	O	S	0	0
			1808	565	904	162	170	7		

- Molecule 21 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	AV	81	Total	C	H	N	O	S	0	0
			1239	378	622	114	120	5		

- Molecule 22 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AN	151	Total	C	H	N	O	S	0	0
			2514	769	1297	236	206	6		

- Molecule 23 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AZ	71	Total	C	H	N	O	S	0	0
			1165	363	601	100	99	2		

- Molecule 24 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Ad	55	Total	C	H	N	O	S	0	0
			895	284	443	93	71	4		

- Molecule 25 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AY	123	Total	C	H	N	O	S	0	0
			2085	637	1093	188	165	2		

- Molecule 26 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AU	100	Total	C	H	N	O	S	0	0
			1650	500	854	154	138	4		

- Molecule 27 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AG	228	Total	C	H	N	O	S	0	0
			3791	1159	1954	350	321	7		

- Molecule 28 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	Ab	82	Total	C	H	N	O	S	0	0
			1305	404	663	119	111	8		

- Molecule 29 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AP	132	Total	C	H	N	O	S	0	0
			2186	681	1132	194	173	6		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Ac	65	Total	C	H	N	O	S	0	0
			1069	314	549	106	98	2		

- Molecule 31 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Ae	45	Total	C	H	N	O		0	0
			752	219	388	84	61			

- Molecule 32 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AX	140	Total	C	H	N	O	S	0	0
			2242	691	1150	212	186	3		

- Molecule 33 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	AL	143	Total	C	H	N	O	S	0	0
			2380	736	1222	223	194	5		

- Molecule 34 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	AJ	177	Total	C	H	N	O	S	0	0
			3060	936	1592	288	243	1		

- Molecule 35 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	AQ	140	Total	C	H	N	O	S	0	0
			2305	715	1181	215	193	1		

- Molecule 36 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	AH	192	Total	C	H	N	O		0	0
			3187	993	1643	280	271			

- Molecule 37 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	CF	213	Total	C	H	N	O	S	0	0
			3534	1119	1791	320	302	2		

- Molecule 38 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	CS	179	Total	C	H	N	O	S	0	0
			2976	936	1506	278	250	6		

- Molecule 39 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	CV	128	Total	C	H	N	O	S	0	0
			1991	614	1020	182	169	6		

- Molecule 40 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	CB	395	Total	C	H	N	O	S	0	0
			6478	2016	3300	605	547	10		

- Molecule 41 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	CU	100	Total	C	H	N	O	S	0	0
			1692	532	868	147	144	1		

- Molecule 42 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	CL	204	Total	C	H	N	O	S	0	0
			3388	1025	1740	338	283	2		

- Molecule 43 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	CA	249	Total	C	H	N	O	S	0	0
			3875	1178	1980	391	321	5		

- Molecule 44 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	CG	221	Total	C	H	N	O	S	0	0
			3680	1123	1892	354	309	2		

- Molecule 45 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	CI	213	Total	C	H	N	O	S	0	0
			3485	1083	1756	343	290	13		

- Molecule 46 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	CO	201	Total	C	H	N	O	S	0	0
			3328	1031	1714	314	264	5		

- Molecule 47 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CC	335	Total	C	H	N	O	S	0	0
			5420	1675	2769	521	449	6		

- Molecule 48 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	Ch	122	Total	C	H	N	O	S	0	0
			2094	618	1105	201	169	1		

- Molecule 49 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	CE	139	Total	C	H	N	O	S	0	0
			2311	727	1195	203	185	1		

- Molecule 50 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	Co	102	Total	C	H	N	O	S	0	0
			1739	522	902	174	135	6		

- Molecule 51 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	Cf	117	Total	C	H	N	O	S	0	0
			1901	594	971	183	153			

- Molecule 52 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	Ci	104	Total	C	H	N	O	S	0	0
			1754	521	918	176	137	2		

- Molecule 53 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	Cl	50	Total	C	H	N	O	S	0	0
			922	276	487	93	63	3		

- Molecule 54 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	CN	203	Total	C	H	N	O	S	0	0
			3463	1068	1763	358	272	2		

- Molecule 55 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	Ca	144	Total	C	H	N	O	S	0	0
			2299	717	1163	232	183	4		

- Molecule 56 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Cp	88	Total	C	H	N	O	S	0	0
			1404	425	726	134	113	6		

- Molecule 57 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	CM	132	Total	C	H	N	O	S	0	0
			2204	668	1151	205	178	2		

- Molecule 58 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Cc	96	Total	C	H	N	O	S	0	0
			1497	464	762	129	137	5		

- Molecule 59 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	CH	188	Total	C	H	N	O	S	0	0
			3081	954	1577	278	266	6		

- Molecule 60 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	CY	132	Total	C	H	N	O	S	0	0
			2181	651	1131	219	176	4		

- Molecule 61 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	CR	194	Total	C	H	N	O	S	0	0
			3384	1012	1746	349	274	3		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	Cb	52	Total	C	H	N	O	S	0	0
			892	268	460	94	69	1		

- Molecule 63 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	CQ	187	Total	C	H	N	O	S	0	0
			3023	918	1550	299	255	1		

- Molecule 64 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	CT	160	Total	C	H	N	O	S	0	0
			2621	806	1338	256	218	3		

- Molecule 65 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	CD	289	Total	C	H	N	O	S	0	0
			4701	1468	2373	430	428	2		

- Molecule 66 is a protein called Large ribosomal subunit protein eL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	CZ	135	Total	C	H	N	O	S	0	0
			2301	716	1199	200	184	2		

- Molecule 67 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	CP	154	Total	C	H	N	O	S	0	0
			2506	780	1257	249	215	5		

- Molecule 68 is a protein called eL41.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	Cn	22	Total	C	H	N	O	S	0	0
			461	128	252	54	25	2		

- Molecule 69 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	Cg	104	Total	C	H	N	O	S	0	0
			1759	526	922	170	139	2		

- Molecule 70 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	Ck	69	Total	C	H	N	O	S	0	0
			1181	359	622	100	99	1		

- Molecule 71 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	Cm	51	Total	C	H	N	O	S	0	0
			874	258	456	86	69	5		

- Molecule 72 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	Cd	105	Total	C	H	N	O	S	0	0
			1770	544	903	169	151	3		

- Molecule 73 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	Ce	128	Total	C	H	N	O	S	0	0
			2160	652	1119	216	169	4		

- Molecule 74 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	CW	88	Total	C	H	N	O	S	0	0
			1447	442	745	140	118	2		

- Molecule 75 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	Cj	88	Total	C	H	N	O	S	0	0
			1433	431	727	154	117	4		

- Molecule 76 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	CJ	186	Total	C	H	N	O	S	0	0
			3062	952	1555	281	269	5		

- Molecule 77 is a protein called Large ribosomal subunit protein uL23B.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	CX	119	Total	C	H	N	O	S	0	0
			1958	606	1004	181	166	1		

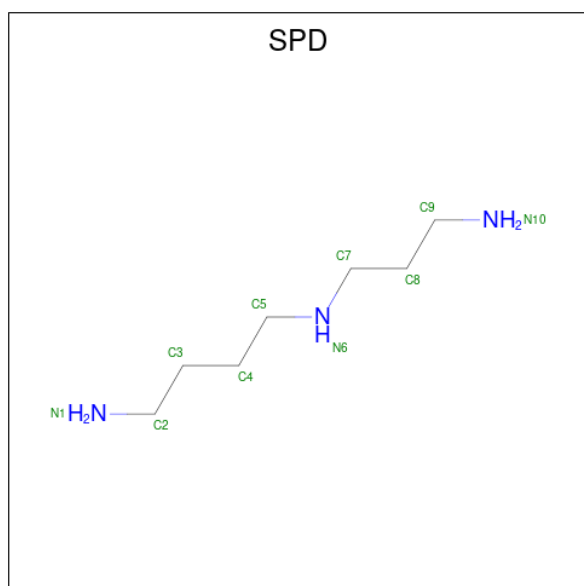
- Molecule 78 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	DA	76	Total	C	H	N	O	P	0	0
			2448	725	821	294	532	76		
78	DB	76	Total	C	H	N	O	P	0	0
			2448	725	821	294	532	76		

- Molecule 79 is a RNA chain called mRNA.

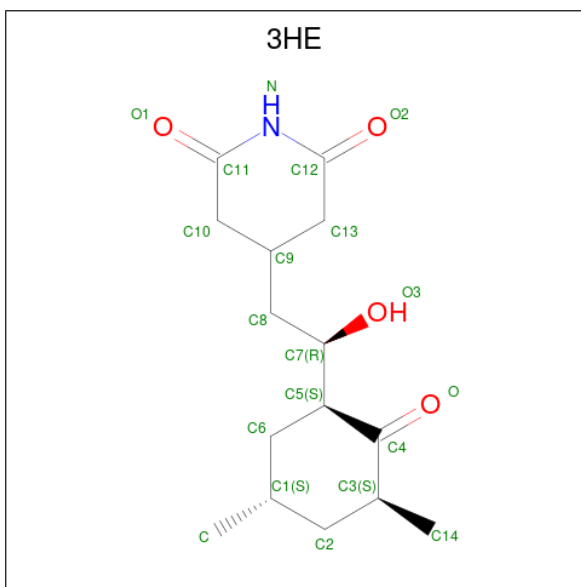
Mol	Chain	Residues	Atoms						AltConf	Trace
79	DC	10	Total	C	H	N	O	P	0	0
			301	90	101	20	80	10		

- Molecule 80 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).

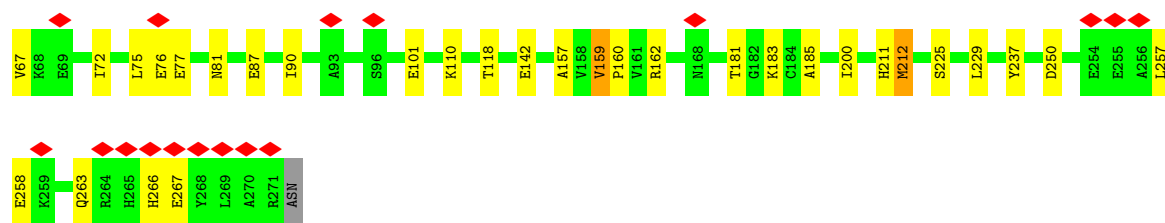


Mol	Chain	Residues	Atoms			AltConf
80	A5	1	Total	C	N	0
			10	7	3	

- Molecule 81 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: $C_{15}H_{23}NO_4$).

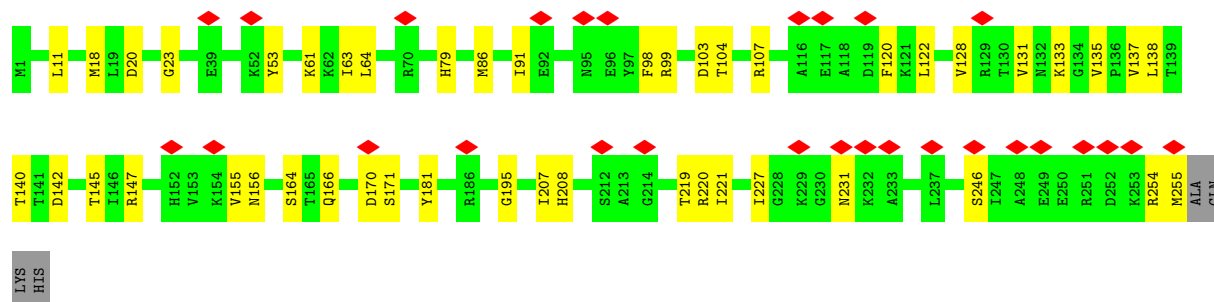


Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
81	A5	1	43	15	23	1	4	0



- Molecule 4: Small ribosomal subunit protein eS4

Chain AE: 11% 81% 18%



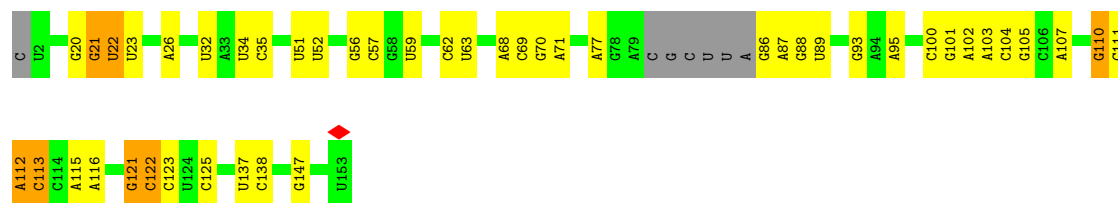
- Molecule 5: 5S rRNA

Chain A7: 80% 18%



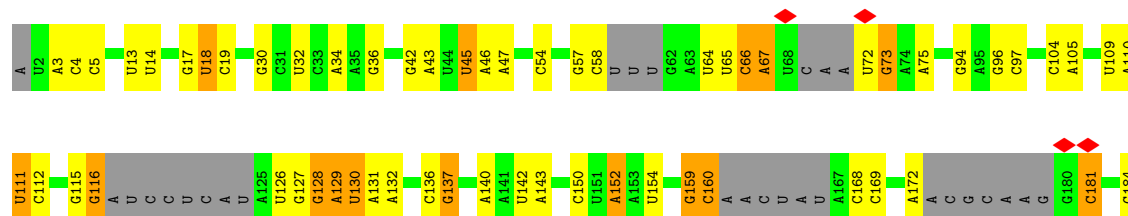
- Molecule 6: 5.8S rRNA

Chain A8: 65% 25% 5% 5%

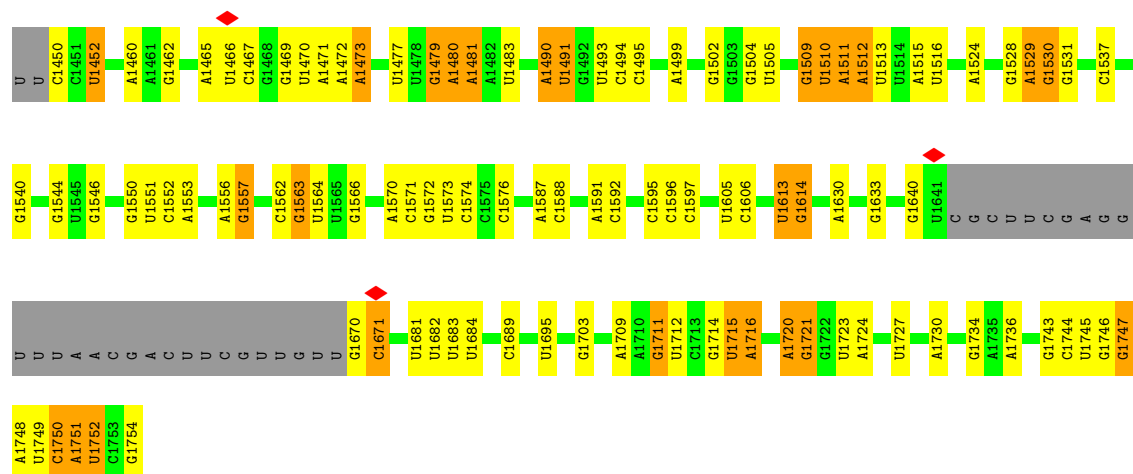


- Molecule 7: 18S rRNA

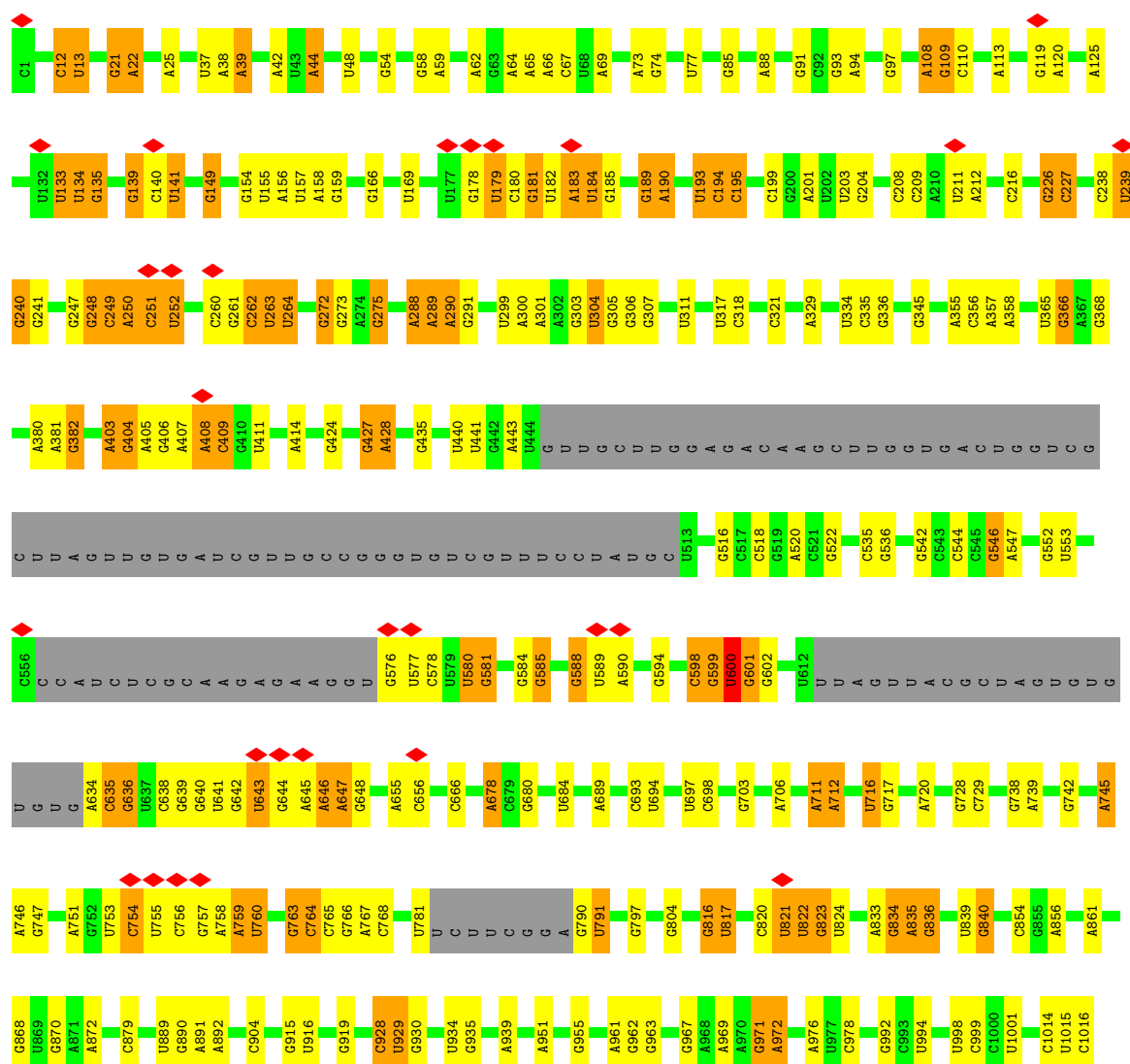
Chain B2: 51% 25% 9% 16%

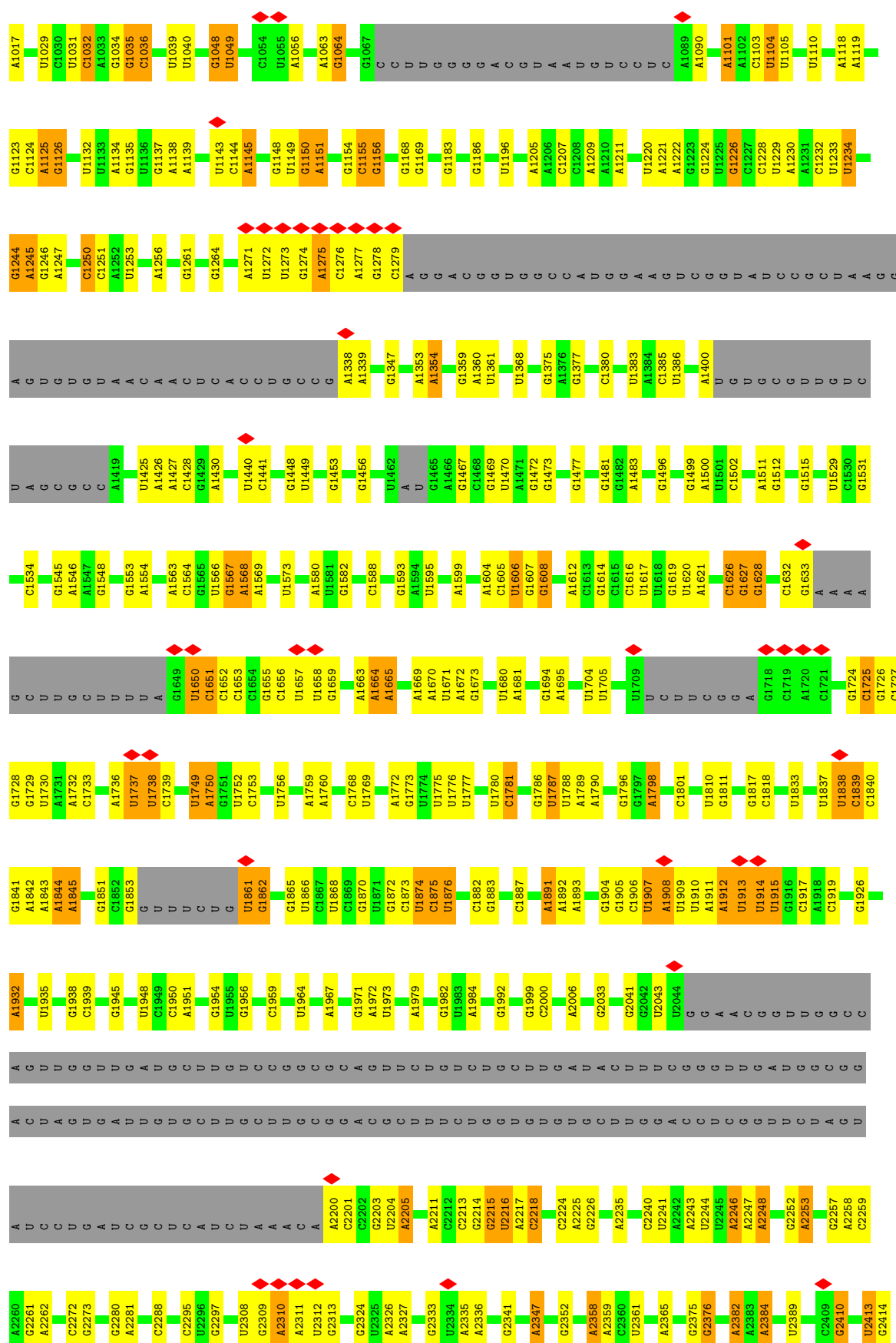


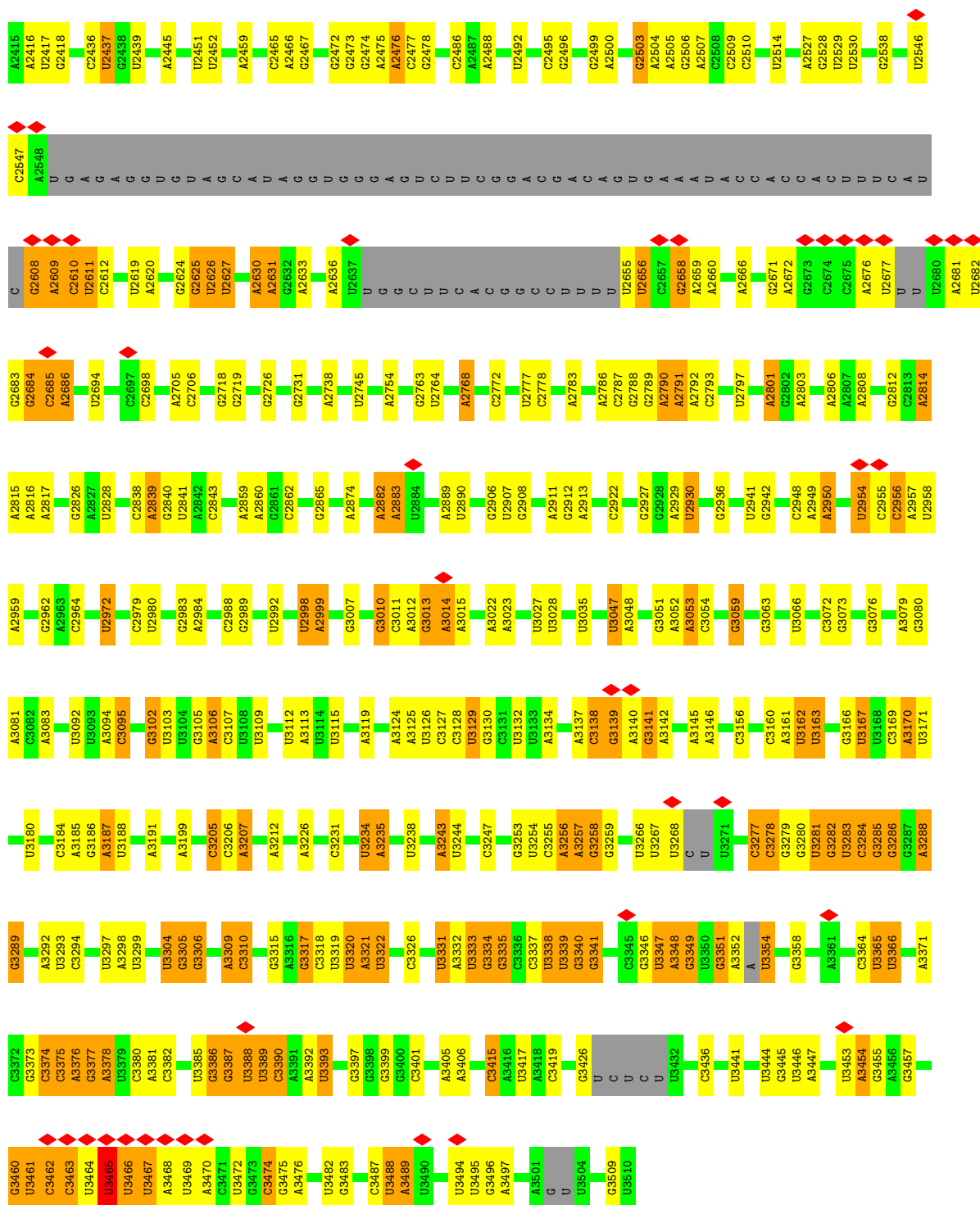




• Molecule 8: 28S rRNA

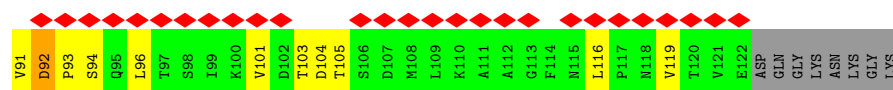




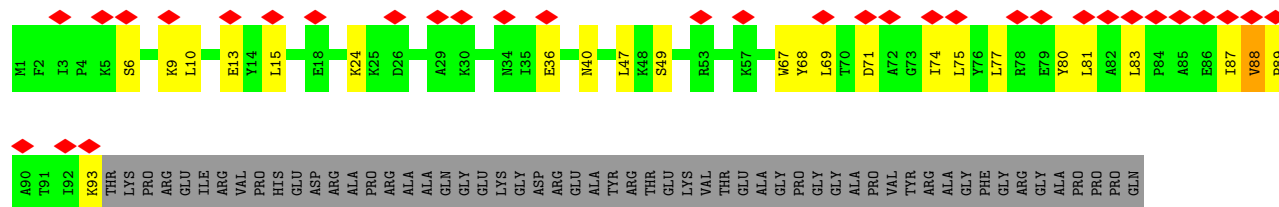


• Molecule 9: Small ribosomal subunit protein eS17

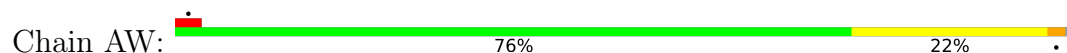




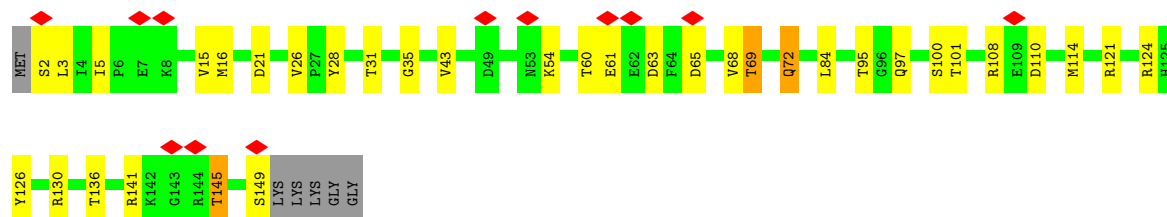
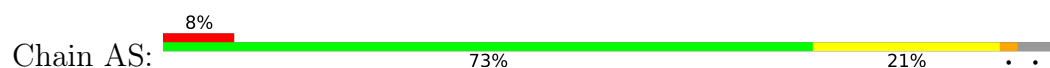
- Molecule 10: Plectin/S10 N-terminal domain-containing protein



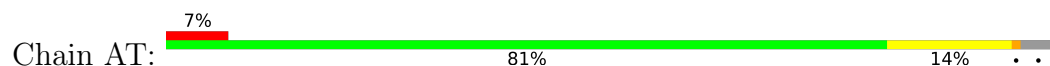
- Molecule 11: Ribosomal Protein, Small subunit



- Molecule 12: Small ribosomal subunit protein uS13

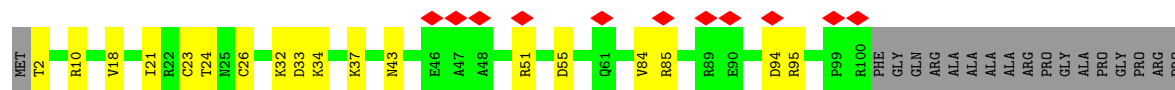


- Molecule 13: Small ribosomal subunit protein eS19

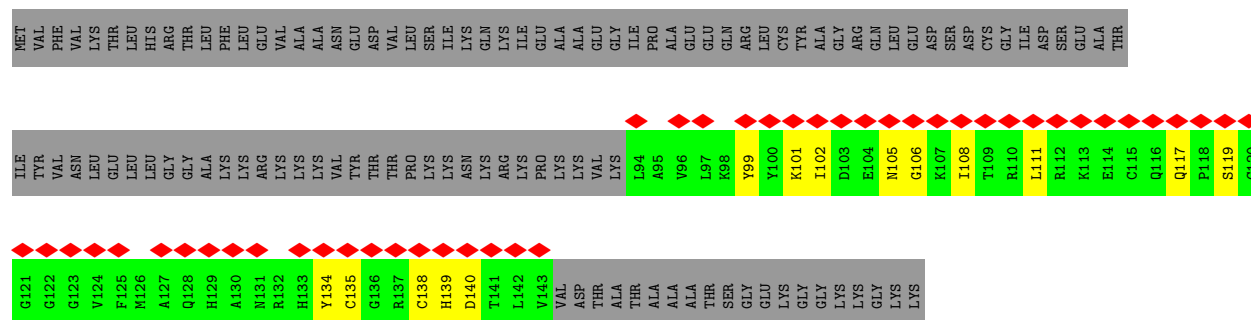


- Molecule 14: Small ribosomal subunit protein eS26

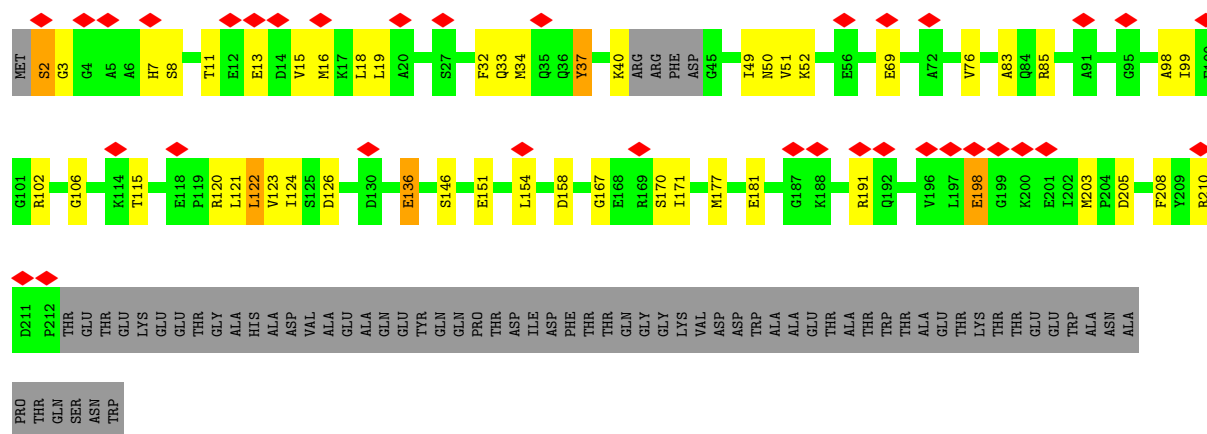




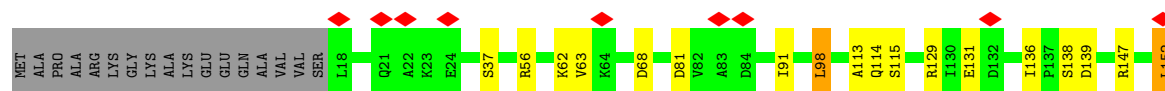
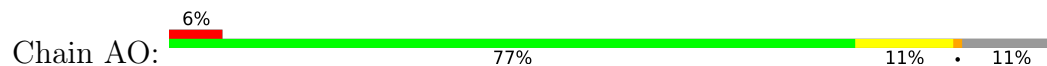
- Molecule 15: Ubiquitin-like protein 1-ribosomal protein eS31 fusion protein



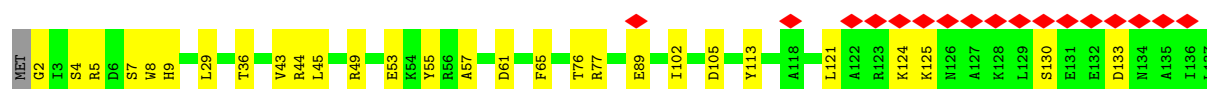
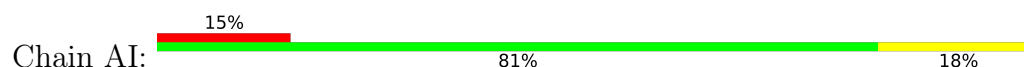
- Molecule 16: Small ribosomal subunit protein uS2

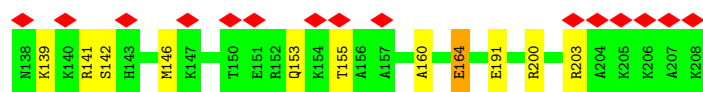


- Molecule 17: Small ribosomal subunit protein uS11

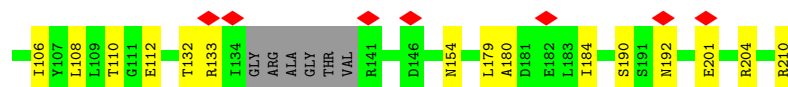
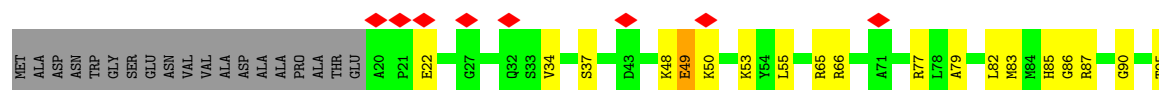
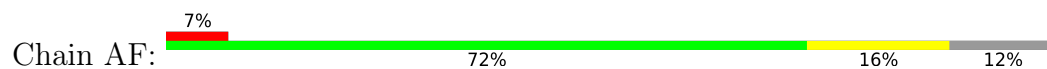


- Molecule 18: Small ribosomal subunit protein eS8

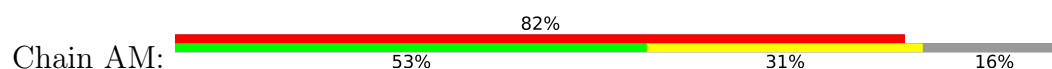




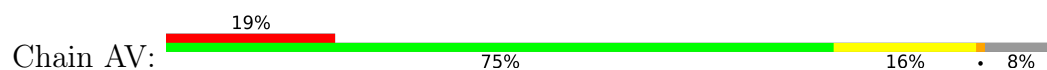
- Molecule 19: Small ribosomal subunit protein uS7



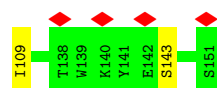
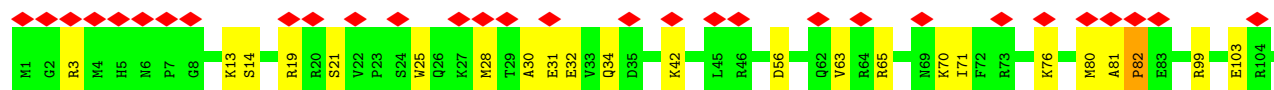
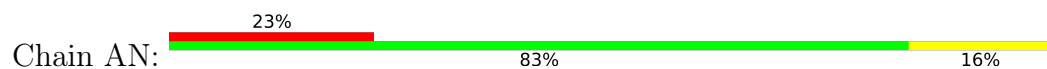
- Molecule 20: Small ribosomal subunit protein eS12



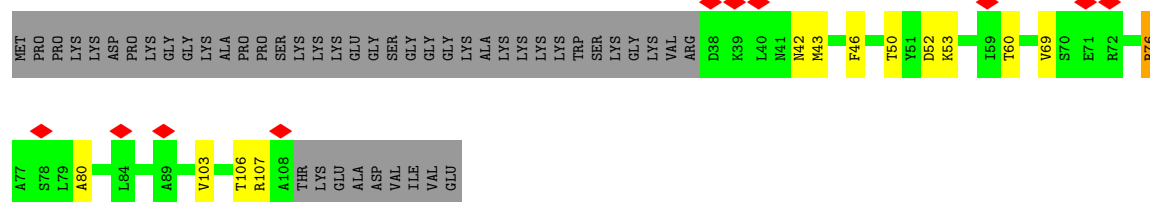
- Molecule 21: Small ribosomal subunit protein eS21



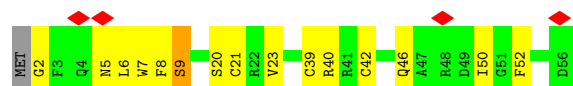
- Molecule 22: Small ribosomal subunit protein uS15



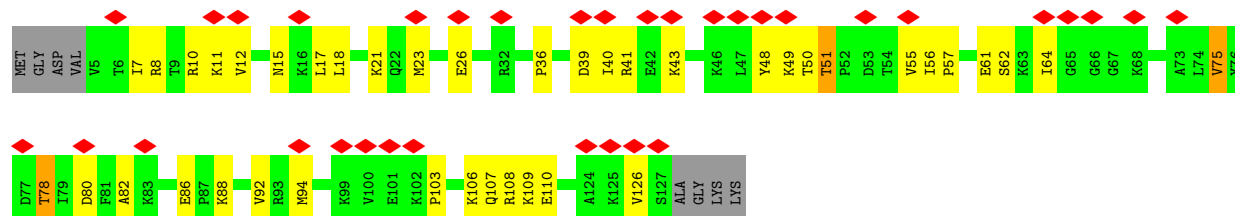
- Molecule 23: Small ribosomal subunit protein eS25



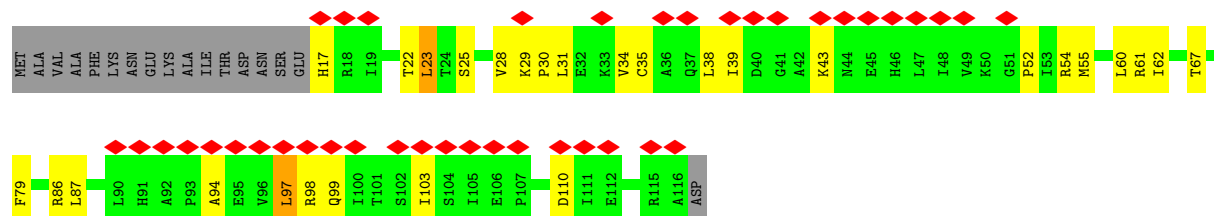
- Molecule 24: Small ribosomal subunit protein uS14



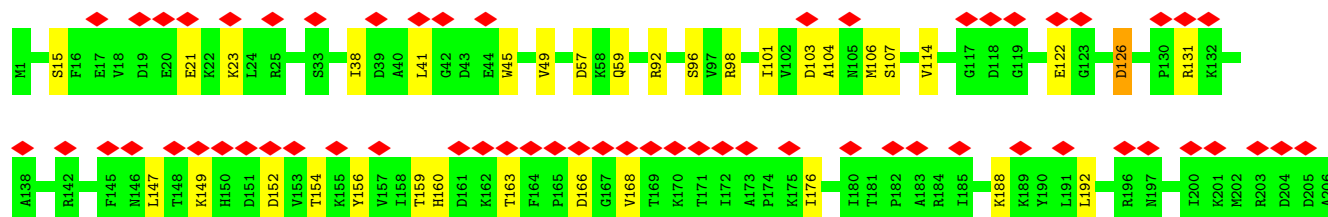
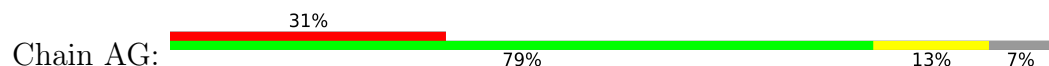
- Molecule 25: Small ribosomal subunit protein eS24

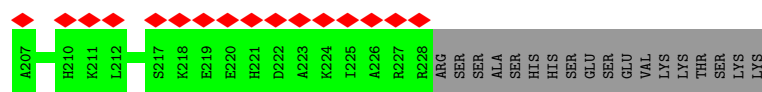


- Molecule 26: Small ribosomal subunit protein uS10

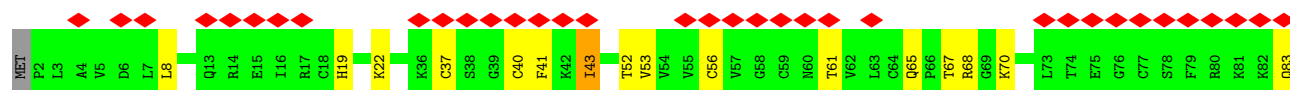
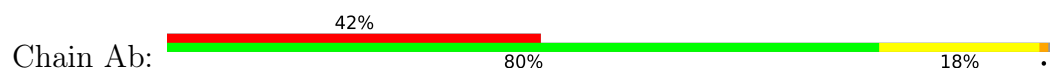


- Molecule 27: Small ribosomal subunit protein eS6

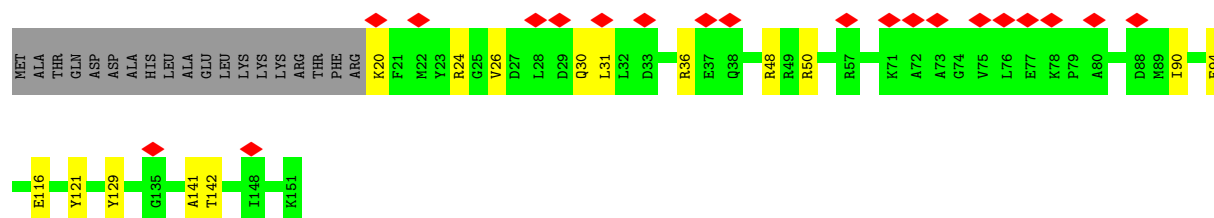
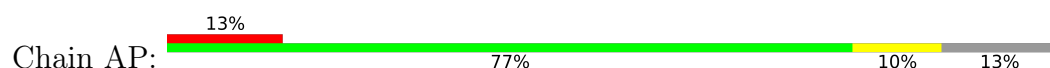




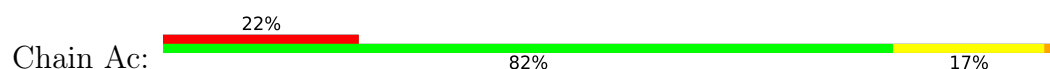
- Molecule 28: Small ribosomal subunit protein eS27



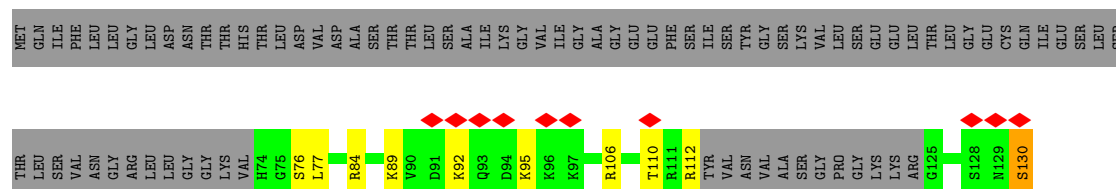
- Molecule 29: Small ribosomal subunit protein uS19



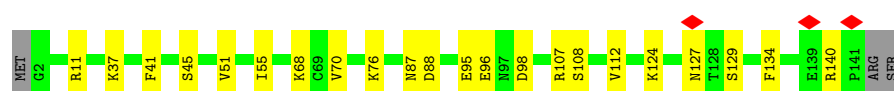
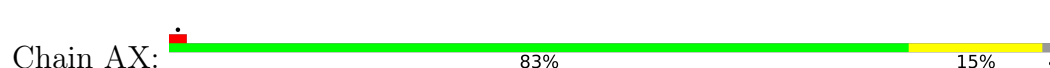
- Molecule 30: Small ribosomal subunit protein eS28



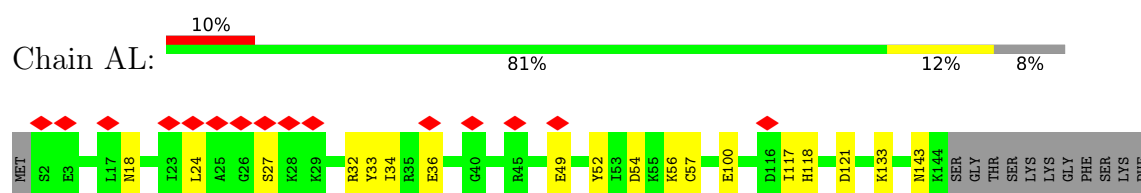
- Molecule 31: Ubiquitin-like domain-containing protein



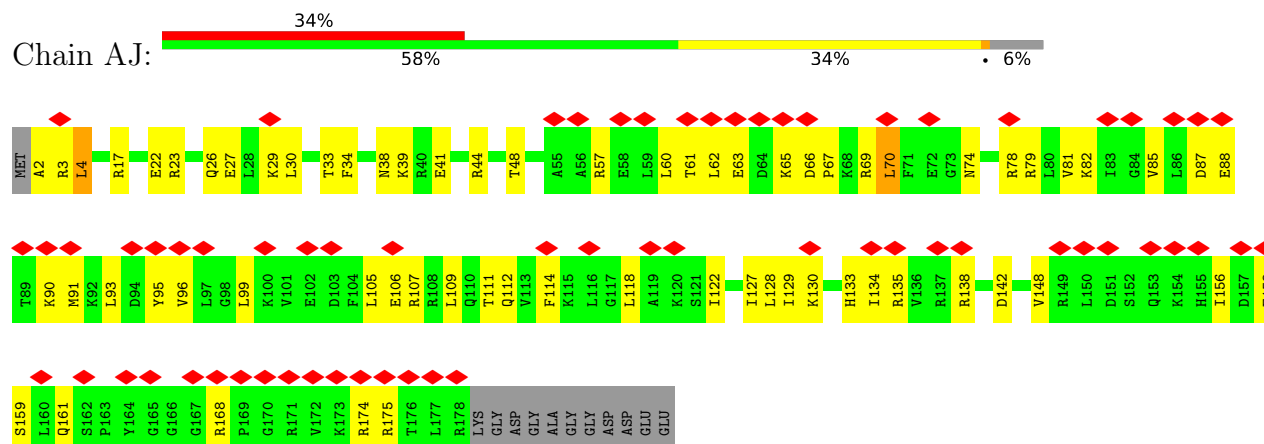
- Molecule 32: Small ribosomal subunit protein uS12



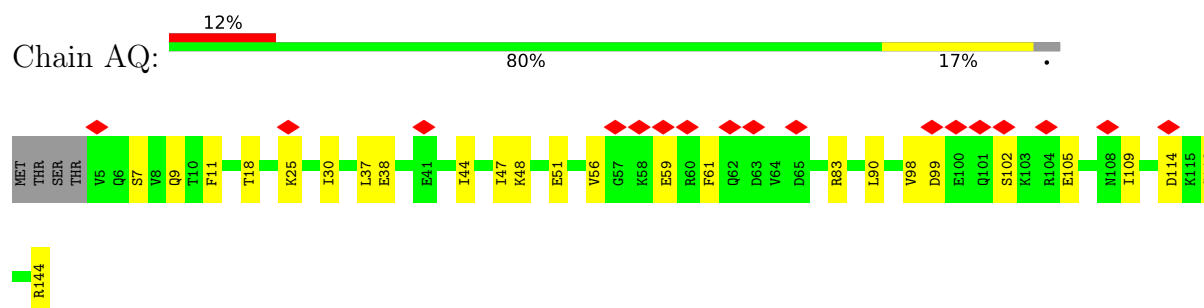
- Molecule 33: Small ribosomal subunit protein uS17



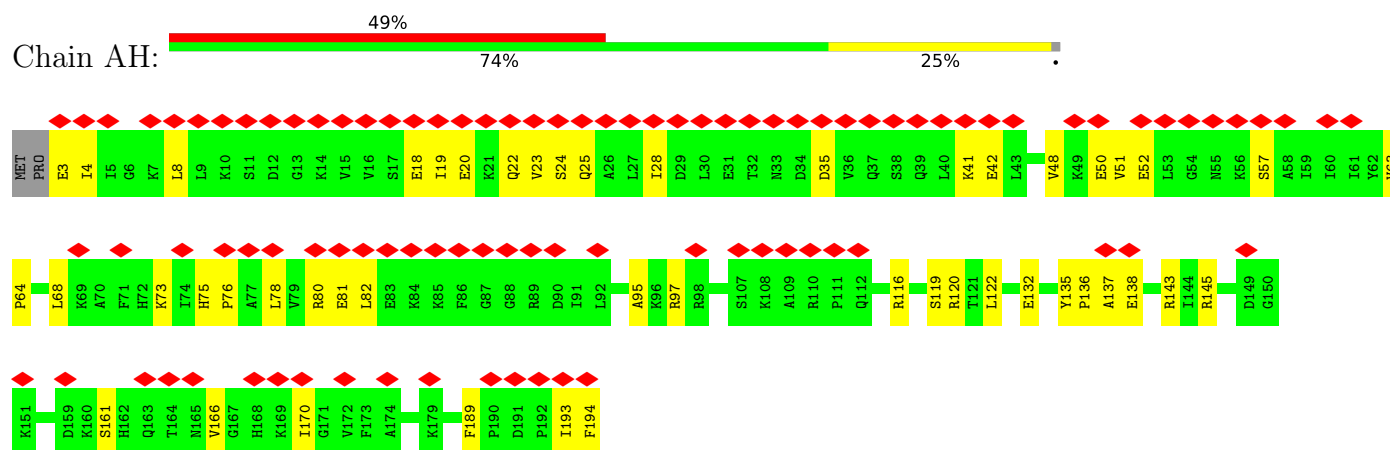
- Molecule 34: Small ribosomal subunit protein uS4



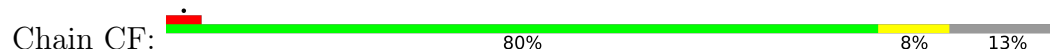
- Molecule 35: Small ribosomal subunit protein uS9

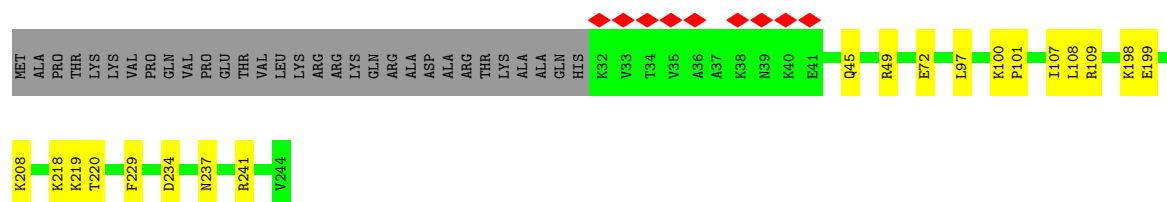


- Molecule 36: Small ribosomal subunit protein eS7

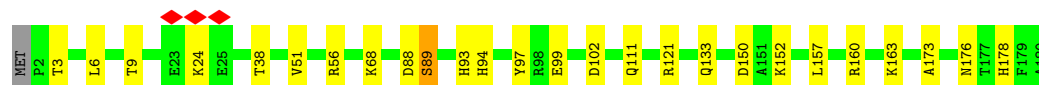
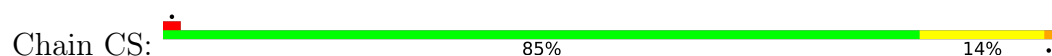


- Molecule 37: Large ribosomal subunit protein uL30

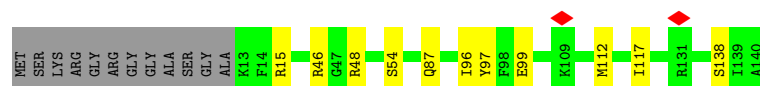
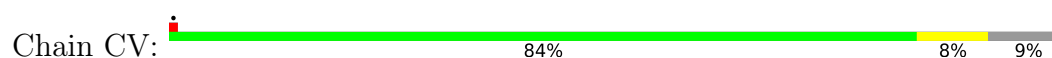




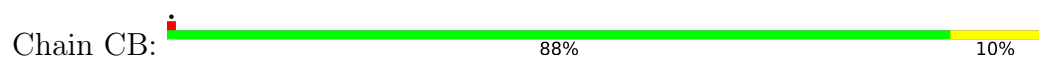
- Molecule 38: Large ribosomal subunit protein eL20



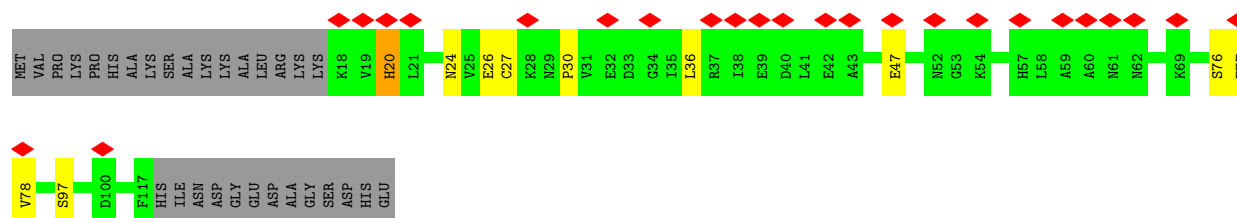
- Molecule 39: Large ribosomal subunit protein uL14



- Molecule 40: Large ribosomal subunit protein uL3

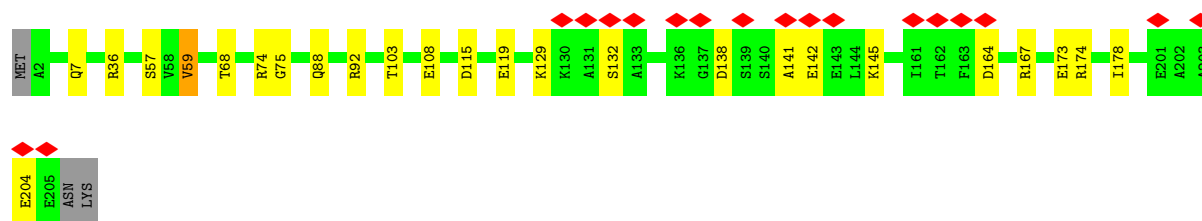


- Molecule 41: Large ribosomal subunit protein eL22



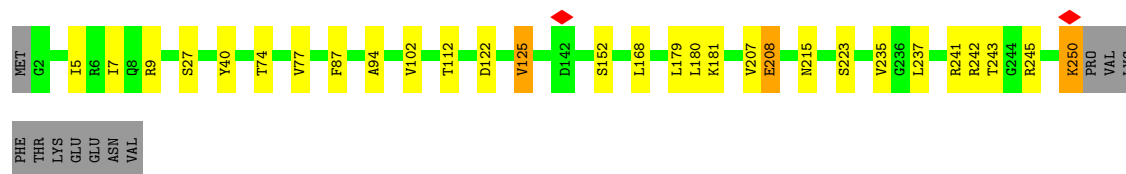
- Molecule 42: Large ribosomal subunit protein eL13





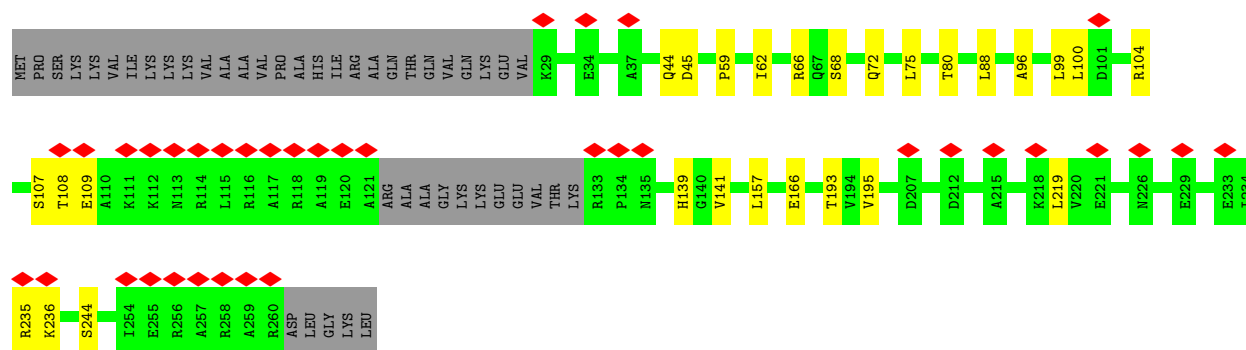
- Molecule 43: Large ribosomal subunit protein uL2

Chain CA: 85% 10% . .



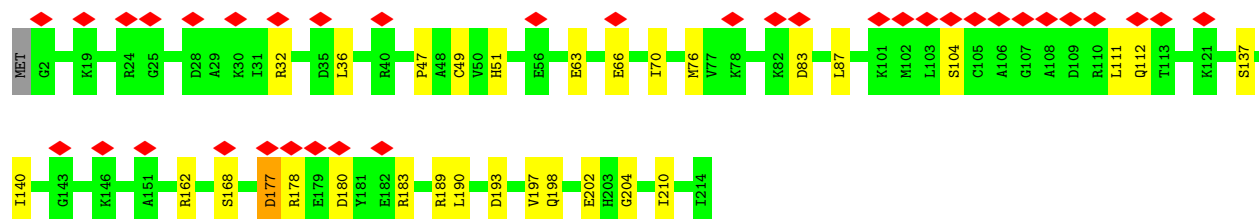
- Molecule 44: Large ribosomal subunit protein eL8

Chain CG: 14% 73% 10% 17%



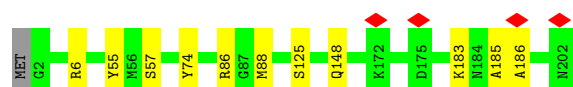
- Molecule 45: Large ribosomal subunit protein uL16

Chain CI: 17% 86% 14%



- Molecule 46: Large ribosomal subunit protein uL13

Chain CO: 94% 5%



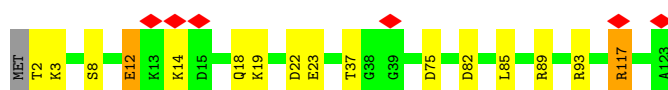
- Molecule 47: Large ribosomal subunit protein uL4

Chain CC:  88% 9% .



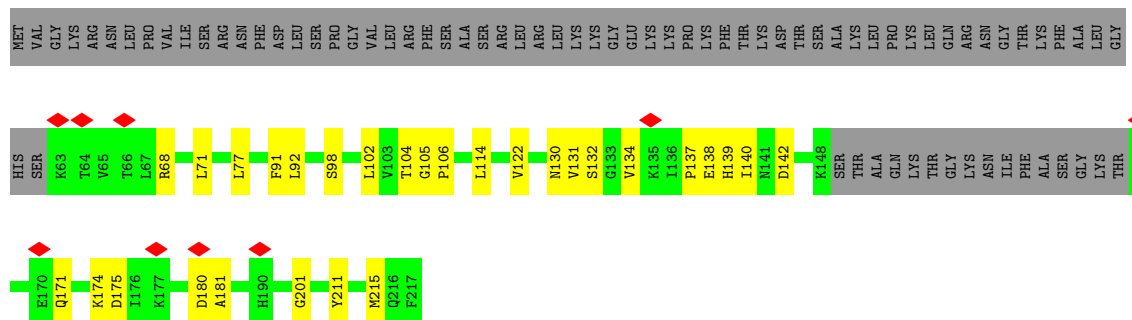
- Molecule 48: Large ribosomal subunit protein uL29

Chain Ch:  86% 11% ..



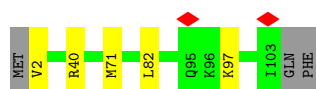
- Molecule 49: Large ribosomal subunit protein eL6

Chain CE:  51% 13% 36%



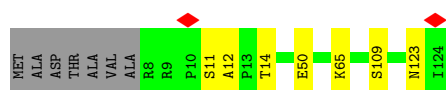
- Molecule 50: Large ribosomal subunit protein eL42

Chain Co:  92% 5% .

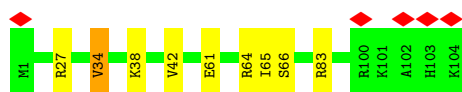


- Molecule 51: Large ribosomal subunit protein eL33

Chain Cf:  89% 6% 6%



- Molecule 52: Large ribosomal subunit protein eL36



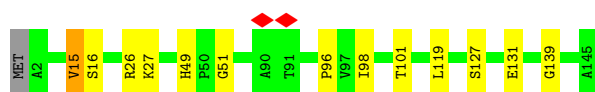
- Molecule 53: Large ribosomal subunit protein eL39



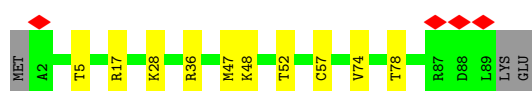
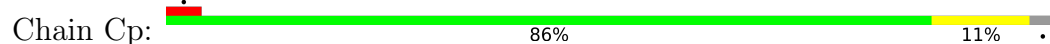
- Molecule 54: Large ribosomal subunit protein eL15



- Molecule 55: Large ribosomal subunit protein uL15



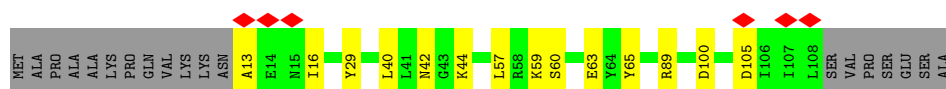
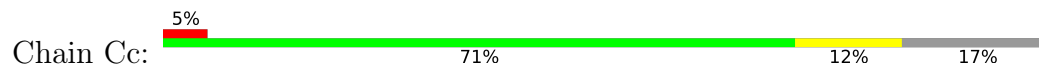
- Molecule 56: Large ribosomal subunit protein eL43



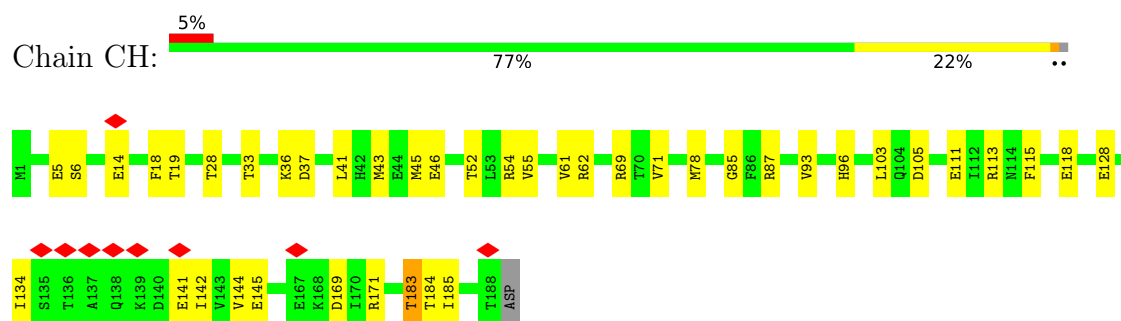
- Molecule 57: Large ribosomal subunit protein eL14



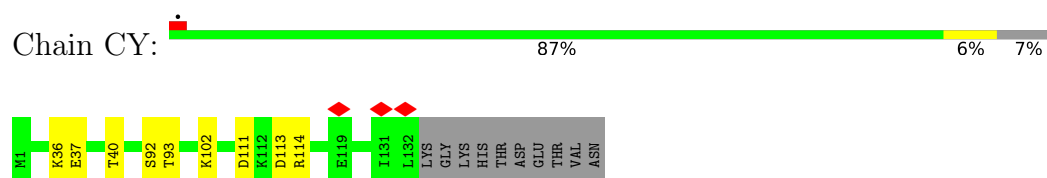
- Molecule 58: Large ribosomal subunit protein eL30



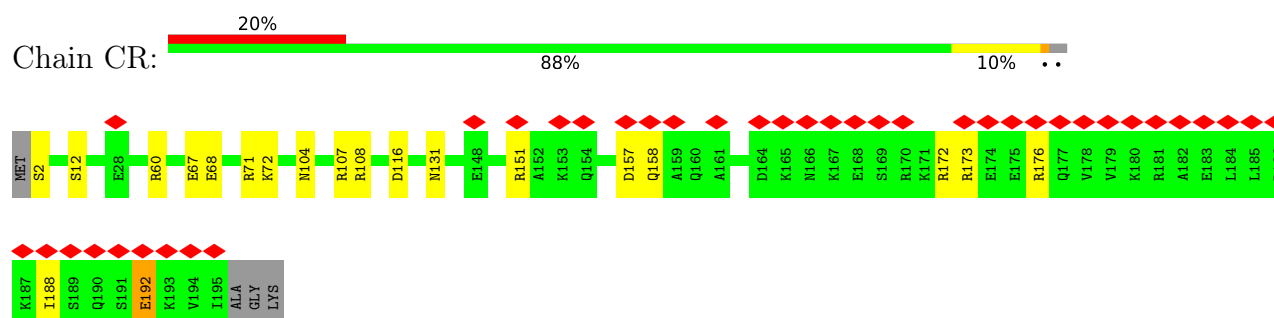
- Molecule 59: Large ribosomal subunit protein uL6



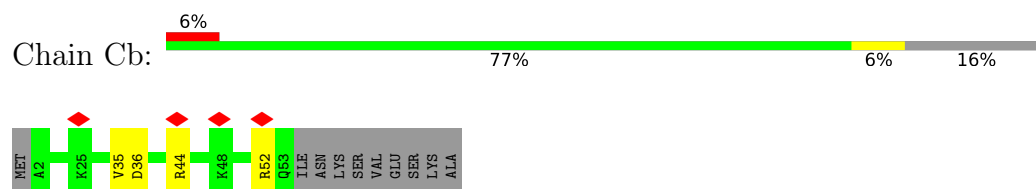
- Molecule 60: Large ribosomal subunit protein uL24



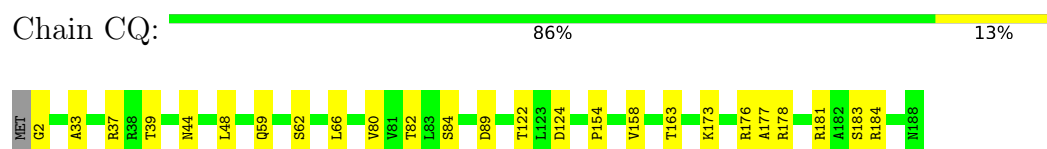
- Molecule 61: Large ribosomal subunit protein eL19



- Molecule 62: 60S ribosomal protein L29

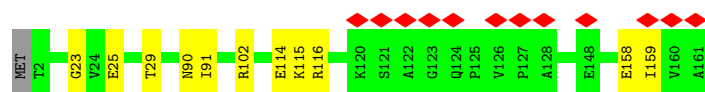


- Molecule 63: Large ribosomal subunit protein eL18

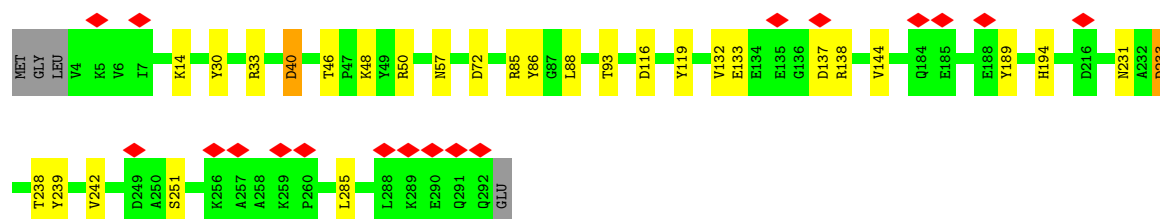
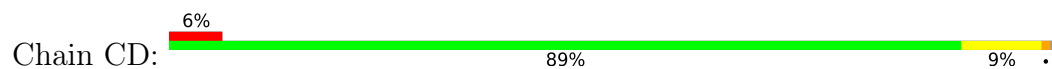


- Molecule 64: Large ribosomal subunit protein eL21

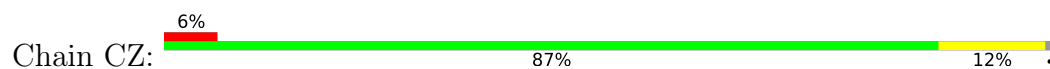




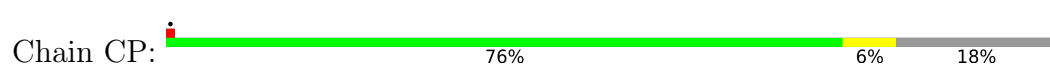
- Molecule 65: Large ribosomal subunit protein uL18



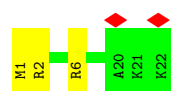
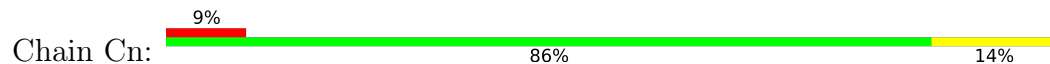
- Molecule 66: Large ribosomal subunit protein eL27



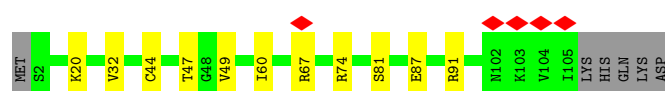
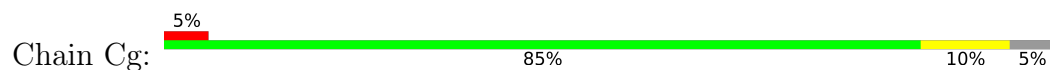
- Molecule 67: Large ribosomal subunit protein uL22



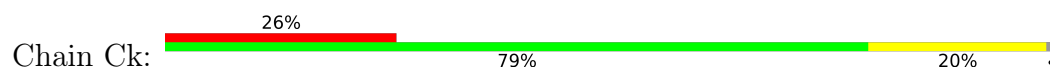
- Molecule 68: eL41

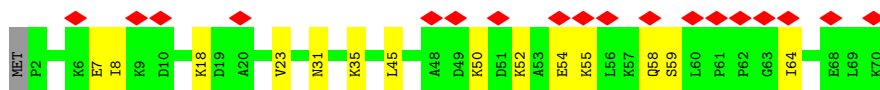


- Molecule 69: Large ribosomal subunit protein eL34

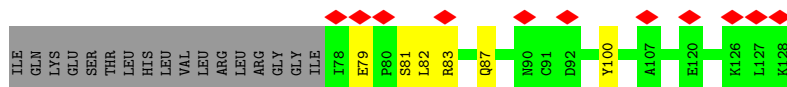
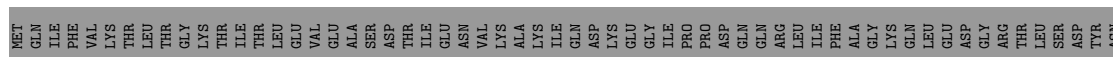
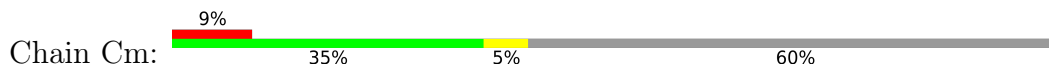


- Molecule 70: Large ribosomal subunit protein eL38

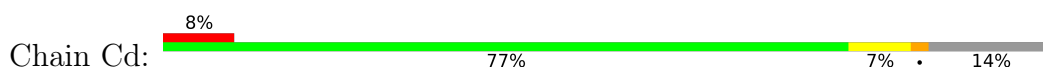




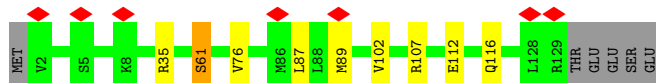
- Molecule 71: Ubiquitin-ribosomal protein eL40 fusion protein



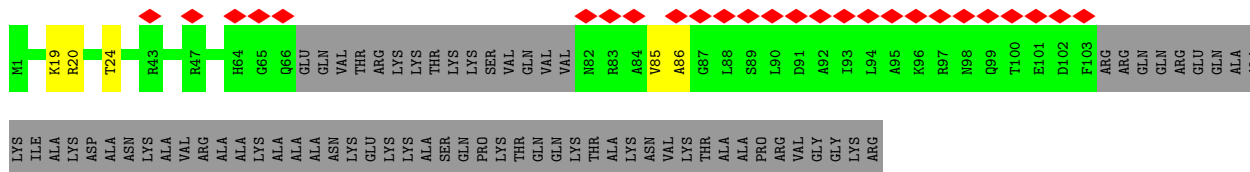
- Molecule 72: Large ribosomal subunit protein eL31



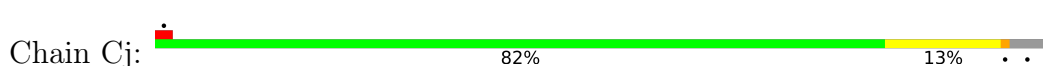
- Molecule 73: Large ribosomal subunit protein eL32



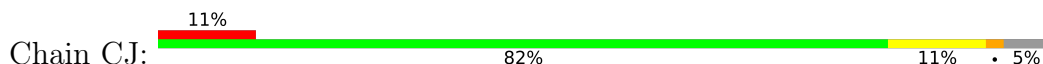
- Molecule 74: Large ribosomal subunit protein eL24

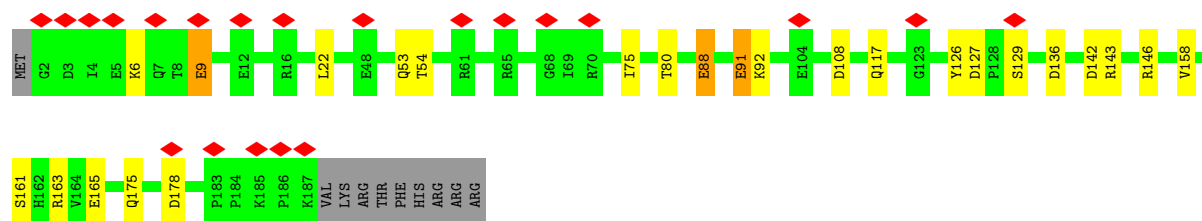


- Molecule 75: Ribosomal protein L37

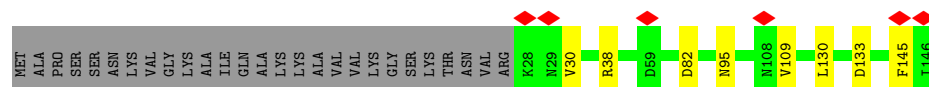
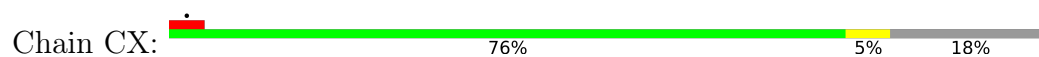


- Molecule 76: Large ribosomal subunit protein uL5B

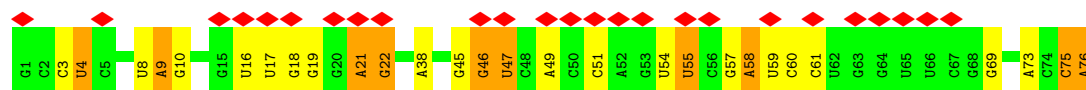




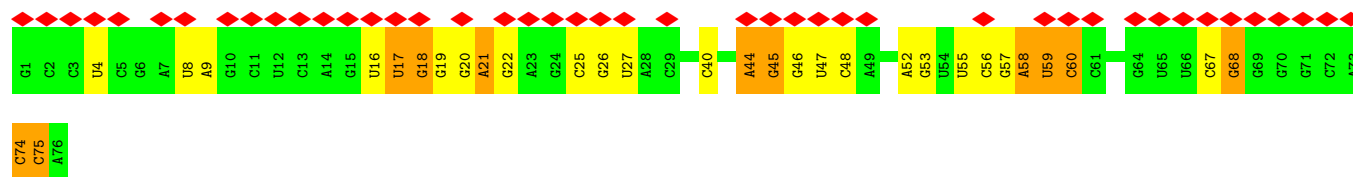
- Molecule 77: Large ribosomal subunit protein uL23B



- Molecule 78: tRNA



- Molecule 78: tRNA



- Molecule 79: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98135	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.94	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	1.866	Depositor
Minimum map value	-1.111	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.182	Depositor
Map size (Å)	441.99997, 441.99997, 441.99997	wwPDB
Map dimensions	680, 680, 680	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.65, 0.65, 0.65	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, 3HE

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	AD	0.19	0/1659	0.30	0/2226
2	AB	0.21	0/1710	0.32	0/2294
3	AC	0.23	0/1689	0.33	0/2289
4	AE	0.21	0/2053	0.33	0/2767
5	A7	0.30	0/2826	0.25	0/4402
6	A8	0.32	0/3477	0.30	0/5416
7	B2	0.30	0/35235	0.30	0/54872
8	A5	0.40	9/72151 (0.0%)	0.33	16/112424 (0.0%)
9	AR	0.19	0/988	0.38	0/1328
10	AK	0.21	0/790	0.38	0/1072
11	AW	0.24	0/1043	0.31	0/1399
12	AS	0.22	0/1225	0.33	0/1641
13	AT	0.21	0/1135	0.33	0/1524
14	Aa	0.24	0/819	0.32	0/1097
15	Af	0.14	0/404	0.37	0/540
16	AA	0.20	0/1645	0.32	0/2230
17	AO	0.23	0/1027	0.35	0/1377
18	AI	0.22	0/1698	0.33	0/2277
19	AF	0.21	0/1475	0.31	0/1986
20	AM	0.14	0/917	0.40	0/1231
21	AV	0.18	0/625	0.31	0/842
22	AN	0.27	0/1240	0.43	1/1658 (0.1%)
23	AZ	0.20	0/572	0.37	0/770
24	Ad	0.24	0/464	0.36	0/615
25	AY	0.21	0/1008	0.37	0/1344
26	AU	0.21	0/808	0.38	0/1090
27	AG	0.18	0/1863	0.32	0/2483
28	Ab	0.17	0/655	0.35	0/880
29	AP	0.20	0/1074	0.34	0/1436
30	Ac	0.19	0/521	0.30	0/695
31	Ae	0.22	0/367	0.48	0/480
32	AX	0.26	0/1112	0.32	0/1487

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AL	0.25	0/1182	0.31	0/1591
34	AJ	0.21	0/1490	0.42	0/1991
35	AQ	0.21	0/1143	0.36	0/1529
36	AH	0.18	0/1572	0.33	0/2114
37	CF	0.28	0/1782	0.31	0/2402
38	CS	0.28	0/1505	0.35	0/2026
39	CV	0.27	0/985	0.30	0/1319
40	CB	0.27	0/3247	0.30	0/4355
41	CU	0.21	0/838	0.36	0/1126
42	CL	0.24	0/1673	0.30	0/2235
43	CA	0.28	0/1932	0.34	0/2593
44	CG	0.23	0/1816	0.30	0/2443
45	CI	0.18	0/1767	0.29	0/2362
46	CO	0.28	0/1645	0.31	0/2198
47	CC	0.26	0/2706	0.30	0/3649
48	Ch	0.22	0/995	0.30	0/1318
49	CE	0.23	0/1140	0.33	0/1530
50	Co	0.27	0/850	0.31	0/1118
51	Cf	0.29	0/953	0.33	0/1283
52	Ci	0.23	0/845	0.28	0/1119
53	Cl	0.26	0/443	0.30	0/582
54	CN	0.30	0/1741	0.34	0/2328
55	Ca	0.29	0/1166	0.31	0/1561
56	Cp	0.27	0/687	0.36	0/915
57	CM	0.24	0/1062	0.30	0/1418
58	Cc	0.25	0/744	0.32	0/1004
59	CH	0.23	0/1528	0.36	0/2058
60	CY	0.23	0/1065	0.30	0/1421
61	CR	0.25	0/1658	0.30	0/2201
62	Cb	0.25	0/439	0.38	0/578
63	CQ	0.28	0/1498	0.30	0/2012
64	CT	0.26	0/1308	0.32	0/1755
65	CD	0.23	0/2368	0.31	0/3179
66	CZ	0.24	0/1123	0.33	0/1497
67	CP	0.28	0/1277	0.32	0/1717
68	Cn	0.23	0/210	0.32	0/266
69	Cg	0.26	0/847	0.32	0/1136
70	Ck	0.21	0/565	0.41	0/748
71	Cm	0.18	0/423	0.32	0/557
72	Cd	0.26	0/881	0.31	0/1184
73	Ce	0.26	0/1057	0.28	0/1407
74	CW	0.21	0/712	0.32	0/949
75	Cj	0.28	0/720	0.33	0/956

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CJ	0.21	0/1533	0.34	0/2052
77	CX	0.24	0/972	0.29	0/1310
78	DA	0.21	0/1819	0.28	0/2833
78	DB	0.18	0/1819	0.26	0/2833
79	DC	0.32	0/218	0.39	0/332
All	All	0.31	9/204224 (0.0%)	0.32	17/299262 (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
11	AW	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A5	3462	C	C1'-N1	37.02	2.04	1.48
8	A5	3465	U	N3-C4	21.91	1.82	1.38
8	A5	3465	U	C2-N3	19.89	1.77	1.37
8	A5	3465	U	N1-C2	19.74	1.78	1.38
8	A5	3465	U	N1-C6	17.43	1.72	1.38
8	A5	3465	U	C4-C5	13.28	1.70	1.43
8	A5	3465	U	C5-C6	13.15	1.60	1.34
8	A5	3462	C	N1-C2	11.87	1.63	1.40
8	A5	3462	C	N1-C6	10.56	1.58	1.37

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A5	3462	C	C6-N1-C2	-12.62	82.33	120.20
8	A5	3462	C	N1-C1'-C2'	10.27	127.41	112.00
8	A5	600	U	OP1-P-O3'	-9.91	78.28	108.00
8	A5	239	U	OP1-P-O3'	-9.02	80.93	108.00
8	A5	3388	U	OP1-P-O3'	-8.97	81.09	108.00
22	AN	82	PRO	CA-N-CD	-8.94	99.49	112.00
8	A5	239	U	OP2-P-O3'	-8.86	81.41	108.00
8	A5	588	G	OP1-P-O3'	-8.84	81.48	108.00
8	A5	3388	U	OP2-P-O3'	-8.23	83.32	108.00
8	A5	588	G	OP2-P-O3'	-7.92	84.24	108.00
8	A5	600	U	OP2-P-O3'	-7.15	86.56	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A5	3462	C	C5-C6-N1	7.02	142.06	121.00
8	A5	3462	C	N1-C2-N3	6.77	139.51	119.20
8	A5	3462	C	C6-N1-C1'	6.39	139.99	120.80
8	A5	3462	C	C2-N1-C1'	6.27	137.62	118.80
8	A5	3462	C	O4'-C1'-N1	5.77	117.16	108.50
8	A5	3462	C	N3-C2-O2	-5.39	105.73	121.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	AW	28	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AD	1637	1706	1706	30	0
2	AB	1684	1769	1769	15	0
3	AC	1654	1735	1735	23	0
4	AE	2013	2107	2107	31	0
5	A7	2529	1281	1281	12	0
6	A8	3111	1568	1570	19	0
7	B2	31511	15858	15879	321	0
8	A5	64512	32467	32487	554	0
9	AR	976	1009	1009	28	0
10	AK	769	786	786	22	0
11	AW	1028	1082	1082	19	0
12	AS	1205	1248	1248	24	0
13	AT	1111	1149	1148	14	0
14	Aa	803	828	828	14	0
15	Af	397	392	392	8	0
16	AA	1612	1652	1652	35	0
17	AO	1014	1049	1049	11	0
18	AI	1668	1723	1723	30	0
19	AF	1454	1515	1515	22	0
20	AM	904	904	904	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	AV	617	622	622	12	0
22	AN	1217	1297	1297	18	0
23	AZ	564	601	601	9	0
24	Ad	452	443	443	10	0
25	AY	992	1093	1093	34	0
26	AU	796	854	854	18	0
27	AG	1837	1954	1954	23	0
28	Ab	642	663	663	13	0
29	AP	1054	1132	1132	12	0
30	Ac	520	549	549	9	0
31	Ae	364	388	388	12	0
32	AX	1092	1150	1150	18	0
33	AL	1158	1222	1222	11	0
34	AJ	1468	1592	1592	60	0
35	AQ	1124	1181	1181	19	0
36	AH	1544	1643	1643	36	0
37	CF	1743	1791	1790	14	0
38	CS	1470	1506	1506	16	0
39	CV	971	1020	1020	7	0
40	CB	3178	3300	3299	30	0
41	CU	824	868	868	7	0
42	CL	1648	1740	1739	19	0
43	CA	1895	1980	1980	21	0
44	CG	1788	1892	1892	18	0
45	CI	1729	1756	1756	21	0
46	CO	1614	1714	1713	7	0
47	CC	2651	2769	2769	17	0
48	Ch	989	1105	1105	11	0
49	CE	1116	1195	1195	21	0
50	Co	837	902	902	5	0
51	Cf	930	971	971	5	0
52	Ci	836	918	918	9	0
53	Cl	435	487	487	2	0
54	CN	1700	1763	1763	12	0
55	Ca	1136	1163	1163	11	0
56	Cp	678	726	725	8	0
57	CM	1053	1151	1151	8	0
58	Cc	735	762	762	8	0
59	CH	1504	1577	1577	30	0
60	CY	1050	1131	1131	4	0
61	CR	1638	1746	1746	13	0
62	Cb	432	460	460	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	CQ	1473	1550	1550	18	0
64	CT	1283	1338	1338	11	0
65	CD	2328	2373	2372	22	0
66	CZ	1102	1199	1199	13	0
67	CP	1249	1257	1257	5	0
68	Cn	209	252	252	4	0
69	Cg	837	922	922	7	0
70	Ck	559	622	622	9	0
71	Cm	418	456	456	4	0
72	Cd	867	903	903	7	0
73	Ce	1041	1119	1119	8	0
74	CW	702	745	745	4	0
75	Cj	706	727	727	10	0
76	CJ	1507	1555	1555	20	0
77	CX	954	1004	1004	6	0
78	DA	1627	821	821	17	0
78	DB	1627	821	821	16	0
79	DC	200	101	102	3	0
80	A5	10	0	19	1	0
81	A5	20	23	23	1	0
All	All	190332	142393	142449	1798	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 5.

All (1798) 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)
8:A5:3465:U:C6	8:A5:3465:U:N1	1.72	1.56
8:A5:3465:U:N1	8:A5:3465:U:C2	1.78	1.51
8:A5:3465:U:C2	8:A5:3465:U:N3	1.77	1.51
8:A5:3462:C:N1	8:A5:3465:U:C2	1.82	1.48
8:A5:3465:U:N3	8:A5:3465:U:C4	1.82	1.46
8:A5:3462:C:H1'	8:A5:3465:U:C5	1.56	1.41
8:A5:3462:C:C1'	8:A5:3465:U:C2	2.04	1.39
8:A5:3462:C:N1	8:A5:3465:U:N3	1.69	1.39
8:A5:3462:C:H1'	8:A5:3465:U:C6	1.59	1.37
8:A5:3462:C:C1'	8:A5:3465:U:N3	1.89	1.34
8:A5:3462:C:N1	8:A5:3465:U:C4	1.96	1.32
8:A5:3462:C:C1'	8:A5:3465:U:C4	2.19	1.25
8:A5:3462:C:C1'	8:A5:3465:U:N1	2.03	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:3462:C:N1	8:A5:3465:U:N1	1.88	1.20
8:A5:3462:C:N1	8:A5:3462:C:C1'	2.04	1.20
8:A5:3462:C:C1'	8:A5:3465:U:C6	2.23	1.20
8:A5:3462:C:C2	8:A5:3465:U:N3	2.10	1.20
8:A5:3462:C:N1	8:A5:3465:U:C6	2.12	1.17
8:A5:3462:C:N1	8:A5:3465:U:C5	2.14	1.15
7:B2:454:U:O4	7:B2:521:A:N7	1.82	1.12
8:A5:3462:C:C1'	8:A5:3465:U:C5	2.33	1.11
8:A5:3462:C:C6	8:A5:3465:U:C6	2.39	1.10
7:B2:999:C:HO2'	11:AW:2:VAL:N	1.52	1.07
8:A5:3461:U:O3'	8:A5:3463:C:OP1	1.76	1.03
8:A5:3462:C:O4'	8:A5:3465:U:C2	2.11	1.03
8:A5:3462:C:C2'	8:A5:3465:U:C4	2.42	1.03
8:A5:3462:C:C2	8:A5:3465:U:C4	2.47	1.02
8:A5:3462:C:C6	8:A5:3465:U:N1	2.28	1.02
8:A5:3462:C:O2	8:A5:3465:U:N3	1.91	1.02
7:B2:1316:A:O2'	7:B2:1317:U:O5'	1.83	0.96
79:DC:6:U:O3'	79:DC:7:U:OP2	1.84	0.95
8:A5:1907:U:O2'	8:A5:1908:A:OP1	1.85	0.94
8:A5:3320:U:O2'	8:A5:3321:A:OP2	1.86	0.92
8:A5:3462:C:O4'	8:A5:3465:U:N1	2.00	0.92
8:A5:3462:C:C2'	8:A5:3465:U:N3	2.33	0.92
7:B2:836:A:O2'	28:Ab:68:ARG:NH1	2.02	0.91
8:A5:113:A:N1	8:A5:272:G:O2'	2.02	0.90
64:CT:159:ILE:HD12	64:CT:159:ILE:O	1.71	0.90
78:DB:8:U:O2'	78:DB:21:A:N1	2.04	0.90
15:Af:117:GLN:OE1	15:Af:119:SER:OG	1.88	0.90
27:AG:103:ASP:OD1	27:AG:104:ALA:N	2.05	0.89
8:A5:403:A:O2'	8:A5:404:G:O5'	1.91	0.89
8:A5:716:U:OP2	42:CL:36:ARG:NH2	2.06	0.89
8:A5:2655:U:O2'	8:A5:2656:U:O5'	1.90	0.89
7:B2:1039:A:O2'	7:B2:1040:U:OP1	1.90	0.89
7:B2:1006:C:OP1	7:B2:1028:G:N2	2.06	0.88
10:AK:36:GLU:N	10:AK:36:GLU:OE2	2.06	0.88
8:A5:1730:U:OP1	66:CZ:36:ARG:NH2	2.07	0.88
8:A5:139:G:O2'	8:A5:141:U:OP2	1.90	0.88
8:A5:2783:A:O2'	76:CJ:108:ASP:OD1	1.92	0.88
12:AS:61:GLU:N	12:AS:61:GLU:OE2	2.06	0.88
29:AP:30:GLN:OE1	29:AP:30:GLN:N	2.08	0.87
8:A5:288:A:O2'	8:A5:289:A:OP2	1.91	0.87
4:AE:255:MET:HA	4:AE:255:MET:HE3	1.57	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:1750:A:N6	8:A5:1892:A:OP2	2.07	0.86
7:B2:512:C:OP2	34:AJ:174:ARG:NH2	2.09	0.86
7:B2:1511:A:O2'	7:B2:1512:A:OP1	1.94	0.85
8:A5:1733:C:OP2	69:Cg:74:ARG:NH2	2.09	0.85
7:B2:64:U:O2'	7:B2:152:A:N3	2.08	0.85
8:A5:1844:A:O2'	8:A5:1845:A:OP1	1.94	0.85
7:B2:436:U:OP1	25:AY:109:LYS:NZ	2.10	0.85
8:A5:3375:C:O2'	8:A5:3376:A:OP1	1.93	0.85
48:Ch:14:LYS:NZ	48:Ch:18:GLN:OE1	2.08	0.84
8:A5:120:A:N6	8:A5:149:G:O2'	2.10	0.84
8:A5:1125:A:O2'	8:A5:1126:G:OP2	1.95	0.84
32:AX:96:GLU:OE2	32:AX:96:GLU:N	2.10	0.83
22:AN:19:ARG:NH1	36:AH:138:GLU:OE1	2.11	0.83
16:AA:13:GLU:OE1	16:AA:13:GLU:N	2.11	0.83
1:AD:122:TYR:OH	3:AC:142:GLU:OE1	1.96	0.83
8:A5:929:U:OP2	8:A5:2000:C:O2'	1.96	0.83
40:CB:140:GLU:N	40:CB:140:GLU:OE2	2.10	0.83
72:Cd:15:GLU:OE1	72:Cd:88:ARG:NH2	2.12	0.82
40:CB:295:GLU:N	40:CB:295:GLU:OE2	2.12	0.82
7:B2:1111:A:OP1	7:B2:1720:A:N6	2.13	0.82
29:AP:116:GLU:N	29:AP:116:GLU:OE2	2.12	0.82
78:DA:22:G:N7	78:DA:46:G:N2	2.27	0.82
6:A8:111:C:O2'	6:A8:112:A:OP2	1.97	0.82
7:B2:1452:U:O2	7:B2:1467:C:N4	2.13	0.82
78:DA:9:A:O2'	78:DA:10:G:N7	2.13	0.81
8:A5:3281:U:O2'	8:A5:3282:G:OP1	1.97	0.81
8:A5:3283:U:O2'	8:A5:3284:C:OP1	1.99	0.81
42:CL:142:GLU:N	42:CL:142:GLU:OE1	2.14	0.81
39:CV:99:GLU:OE1	74:CW:24:THR:N	2.15	0.80
8:A5:2950:A:N6	8:A5:2962:G:O2'	2.13	0.80
49:CE:98:SER:OG	49:CE:142:ASP:OD1	1.98	0.80
8:A5:553:U:O2'	57:CM:65:ARG:NH2	2.14	0.80
7:B2:1192:G:O2'	7:B2:1193:A:OP1	1.97	0.80
7:B2:4:C:O2	34:AJ:17:ARG:NH2	2.15	0.80
27:AG:23:LYS:NZ	27:AG:41:LEU:O	2.14	0.80
78:DB:18:G:O2'	78:DB:57:G:N2	2.12	0.80
7:B2:66:C:O2'	7:B2:67:A:OP1	2.00	0.80
17:AO:63:VAL:HG11	17:AO:68:ASP:HB2	1.63	0.80
57:CM:47:ARG:NH2	57:CM:68:GLN:O	2.15	0.80
1:AD:5:GLN:OE1	1:AD:5:GLN:N	2.15	0.80
35:AQ:51:GLU:OE1	35:AQ:83:ARG:NH2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Cf:50:GLU:N	51:Cf:50:GLU:OE2	2.14	0.79
8:A5:3462:C:H2'	8:A5:3465:U:C4	2.15	0.79
8:A5:1786:G:HO2'	8:A5:1866:U:HO2'	1.12	0.79
59:CH:46:GLU:OE2	59:CH:54:ARG:NH1	2.15	0.79
8:A5:2630:A:O2'	8:A5:2631:A:OP2	2.01	0.79
12:AS:28:TYR:O	12:AS:31:THR:OG1	2.00	0.79
8:A5:3466:U:O2'	8:A5:3467:U:O4'	2.01	0.79
23:AZ:52:ASP:OD1	23:AZ:53:LYS:N	2.16	0.79
65:CD:231:ASN:ND2	65:CD:233:ASP:OD1	2.16	0.79
8:A5:915:G:OP1	56:Cp:17:ARG:NH1	2.15	0.78
52:Cl:65:ILE:O	52:Cl:66:SER:OG	2.01	0.78
8:A5:2860:A:O2'	65:CD:48:LYS:NZ	2.16	0.78
47:CC:160:PHE:O	47:CC:161:ARG:NH1	2.16	0.78
7:B2:129:A:O2'	7:B2:130:U:O2	1.99	0.78
8:A5:823:G:O2'	8:A5:824:U:O5'	2.01	0.78
7:B2:614:C:O2'	36:AH:116:ARG:NH2	2.17	0.78
8:A5:194:C:O2'	8:A5:195:C:OP1	2.01	0.78
8:A5:816:G:O2'	8:A5:817:U:OP1	2.00	0.78
9:AR:47:ARG:NH1	9:AR:48:ASN:OD1	2.17	0.78
8:A5:1064:G:N2	45:Cl:193:ASP:OD2	2.17	0.77
8:A5:3138:C:OP1	59:CH:96:HIS:ND1	2.17	0.77
7:B2:746:G:N7	25:AY:8:ARG:NH2	2.31	0.77
19:AF:201:GLU:OE1	19:AF:204:ARG:NH1	2.17	0.77
78:DA:10:G:O6	78:DA:45:G:N2	2.16	0.77
3:AC:263:GLN:OE1	16:AA:120:ARG:NH2	2.18	0.77
73:Ce:112:GLU:OE2	73:Ce:116:GLN:NE2	2.17	0.77
8:A5:1148:G:N2	8:A5:1149:U:O4	2.18	0.77
8:A5:2476:A:N3	8:A5:2936:G:O2'	2.16	0.77
16:AA:18:LEU:HD11	16:AA:177:MET:HE1	1.67	0.77
56:Cp:47:MET:HE2	56:Cp:57:CYS:HB2	1.66	0.76
7:B2:228:U:O2'	7:B2:229:U:OP1	2.04	0.76
7:B2:1727:U:OP2	68:Cn:1:MET:N	2.17	0.76
8:A5:1035:G:O2'	8:A5:1036:C:O5'	2.02	0.76
8:A5:2608:G:O2'	8:A5:2609:A:OP1	2.02	0.76
8:A5:3462:C:H6	8:A5:3465:U:C6	2.00	0.76
19:AF:77:ARG:NH2	19:AF:154:ASN:OD1	2.19	0.76
8:A5:62:A:N3	8:A5:77:U:O2'	2.19	0.76
41:CU:76:SER:OG	41:CU:78:VAL:O	2.03	0.76
8:A5:1608:G:HO2'	8:A5:2272:C:HO2'	1.25	0.76
8:A5:3465:U:C6	8:A5:3465:U:C1'	2.68	0.76
50:Co:71:MET:HE3	50:Co:82:LEU:HD12	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:863:A:N6	7:B2:879:G:O2'	2.18	0.76
8:A5:3462:C:C2	8:A5:3465:U:C2	2.73	0.76
34:AJ:62:LEU:O	34:AJ:69:ARG:NH1	2.19	0.76
23:AZ:42:ASN:OD1	23:AZ:76:ARG:N	2.19	0.75
8:A5:2297:G:OP2	43:CA:245:ARG:NH2	2.18	0.75
8:A5:635:C:O2'	8:A5:636:G:OP1	2.04	0.75
38:CS:102:ASP:OD2	38:CS:111:GLN:NE2	2.19	0.75
8:A5:408:A:O2'	8:A5:409:C:OP1	2.05	0.75
8:A5:3376:A:O2'	8:A5:3377:G:OP1	2.05	0.74
8:A5:1841:G:OP1	70:Ck:35:LYS:NZ	2.20	0.74
8:A5:3014:A:OP1	8:A5:3145:A:O2'	2.05	0.74
18:AI:8:TRP:O	18:AI:9:HIS:ND1	2.20	0.74
37:CF:45:GLN:OE1	37:CF:49:ARG:NH1	2.20	0.74
2:AB:222:ASP:OD2	2:AB:225:ARG:NH1	2.21	0.74
8:A5:1650:U:O2'	8:A5:1651:C:OP1	2.05	0.74
7:B2:1105:G:H21	7:B2:1591:A:H8	1.36	0.74
6:A8:111:C:OP1	8:A5:1595:U:O2'	2.06	0.74
8:A5:967:G:OP2	43:CA:9:ARG:NH2	2.21	0.74
27:AG:59:GLN:OE1	27:AG:59:GLN:N	2.21	0.74
40:CB:71:GLU:OE2	40:CB:363:LYS:NZ	2.21	0.73
9:AR:2:SER:OG	9:AR:3:ARG:N	2.20	0.73
8:A5:2214:G:O2'	8:A5:2215:G:OP2	2.05	0.73
27:AG:98:ARG:NH2	27:AG:101:ILE:O	2.20	0.73
7:B2:456:U:OP1	31:Ae:106:ARG:NH1	2.21	0.73
7:B2:1216:U:O2'	7:B2:1217:U:O4'	2.07	0.73
7:B2:908:C:O2'	7:B2:909:A:OP1	2.03	0.73
7:B2:1132:C:OP1	12:AS:130:ARG:NH2	2.21	0.73
9:AR:82:ASP:O	16:AA:85:ARG:NH1	2.20	0.73
1:AD:52:ILE:HD11	1:AD:88:LEU:HD13	1.70	0.73
8:A5:1477:G:OP1	73:Ce:107:ARG:NH2	2.22	0.72
44:CG:96:ALA:HA	44:CG:219:LEU:HD11	1.71	0.72
8:A5:1749:U:O2'	8:A5:1750:A:OP1	2.04	0.72
19:AF:49:GLU:N	19:AF:49:GLU:OE1	2.21	0.72
50:Co:71:MET:CE	50:Co:82:LEU:HD12	2.20	0.72
17:AO:98:LEU:HD11	17:AO:113:ALA:HB1	1.71	0.72
8:A5:642:G:OP1	8:A5:648:G:N2	2.21	0.72
7:B2:822:G:OP1	36:AH:120:ARG:NH2	2.22	0.72
44:CG:100:LEU:HD11	44:CG:157:LEU:HD12	1.72	0.72
66:CZ:121:ARG:O	66:CZ:124:THR:HG22	1.90	0.72
35:AQ:59:GLU:N	35:AQ:59:GLU:OE2	2.23	0.72
55:Ca:96:PRO:HG2	55:Ca:119:LEU:HD23	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AE:140:THR:OG1	4:AE:142:ASP:OD1	2.03	0.71
36:AH:52:GLU:OE1	36:AH:52:GLU:N	2.22	0.71
8:A5:1906:C:O2'	8:A5:1911:A:N3	2.22	0.71
1:AD:195:ASP:OD2	1:AD:198:GLY:N	2.23	0.71
8:A5:2241:U:OP2	8:A5:2246:A:N6	2.24	0.71
8:A5:1347:G:O2'	38:CS:121:ARG:NH1	2.24	0.71
8:A5:1400:A:OP2	63:CQ:37:ARG:NH2	2.23	0.71
27:AG:122:GLU:OE2	27:AG:122:GLU:N	2.24	0.71
7:B2:1633:G:OP2	18:AI:44:ARG:NH2	2.24	0.71
7:B2:1291:C:OP1	9:AR:43:SER:OG	2.05	0.71
24:Ad:40:ARG:NH2	26:Au:67:THR:O	2.24	0.71
36:AH:4:ILE:O	36:AH:4:ILE:HG22	1.90	0.71
7:B2:577:C:OP2	32:AX:108:SER:OG	2.08	0.71
8:A5:22:A:OP2	75:Cj:44:LYS:N	2.24	0.71
18:AI:89:GLU:OE1	18:AI:89:GLU:N	2.24	0.71
27:AG:57:ASP:O	27:AG:107:SER:OG	2.08	0.71
7:B2:1061:G:OP1	11:AW:76:SER:OG	2.08	0.70
7:B2:999:C:OP1	22:AN:3:ARG:NH1	2.22	0.70
8:A5:1470:U:OP2	73:Ce:61:SER:OG	2.09	0.70
7:B2:159:G:O2'	7:B2:160:C:O5'	2.06	0.70
47:CC:161:ARG:NH2	47:CC:214:ALA:O	2.25	0.70
8:A5:201:A:N3	8:A5:226:G:O2'	2.24	0.70
8:A5:2954:U:OP1	8:A5:2956:C:N4	2.24	0.70
16:AA:76:VAL:HG12	16:AA:123:VAL:HB	1.74	0.70
25:AY:41:ARG:HG3	25:AY:55:VAL:HG23	1.72	0.70
5:A7:74:A:O2'	38:CS:56:ARG:NH1	2.25	0.70
7:B2:1280:A:OP2	16:AA:102:ARG:NH1	2.25	0.70
12:AS:35:GLY:O	12:AS:97:GLN:NE2	2.25	0.70
18:AI:53:GLU:OE2	18:AI:55:TYR:OH	2.08	0.70
78:DA:47:U:O2	78:DA:49:A:O2'	2.07	0.69
7:B2:75:A:N3	7:B2:132:A:O2'	2.22	0.69
7:B2:450:A:O2'	7:B2:737:A:N3	2.21	0.69
8:A5:1992:G:O2'	8:A5:2437:U:O4	2.07	0.69
65:CD:88:LEU:HD21	65:CD:239:TYR:HE1	1.58	0.69
7:B2:1670:G:O2'	7:B2:1671:C:O5'	2.09	0.69
57:CM:84:GLU:N	57:CM:84:GLU:OE2	2.22	0.69
8:A5:2658:G:N2	43:CA:87:PHE:O	2.26	0.69
61:CR:104:ASN:OD1	61:CR:107:ARG:NH2	2.26	0.69
8:A5:994:U:OP2	55:Ca:26:ARG:NH1	2.24	0.69
8:A5:1912:A:O2'	8:A5:1913:U:OP1	2.10	0.69
15:Af:135:CYS:SG	15:Af:138:CYS:N	2.64	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:1471:A:O2'	7:B2:1473:A:OP2	2.08	0.69
8:A5:1149:U:OP1	64:CT:116:ARG:NH2	2.26	0.69
39:CV:112:MET:HE1	39:CV:117:ILE:HD11	1.74	0.69
49:CE:138:GLU:N	49:CE:138:GLU:OE2	2.26	0.69
16:AA:33:GLN:HB3	16:AA:154:LEU:HD12	1.75	0.69
7:B2:1437:U:O2'	7:B2:1438:C:OP1	2.10	0.68
7:B2:1309:U:O2'	7:B2:1310:U:OP1	2.11	0.68
75:Cj:21:ARG:NH2	75:Cj:41:ASP:O	2.26	0.68
3:AC:162:ARG:NH1	21:AV:10:GLU:OE2	2.25	0.68
8:A5:3462:C:H2'	8:A5:3465:U:N3	2.07	0.68
16:AA:106:GLY:N	16:AA:136:GLU:OE2	2.26	0.68
15:Af:111:LEU:HD23	15:Af:111:LEU:O	1.93	0.68
43:CA:7:ILE:HD12	43:CA:235:VAL:HG12	1.75	0.68
56:Cp:74:VAL:O	56:Cp:78:THR:HG23	1.92	0.68
35:AQ:114:ASP:OD1	35:AQ:116:SER:N	2.27	0.68
24:Ad:39:CYS:SG	24:Ad:42:CYS:N	2.64	0.68
7:B2:129:A:O2'	7:B2:130:U:OP2	2.11	0.68
8:A5:2215:G:O2'	8:A5:2216:U:OP2	2.12	0.68
4:AE:103:ASP:OD1	4:AE:104:THR:N	2.26	0.68
7:B2:1231:U:O2'	7:B2:1234:A:OP2	2.08	0.68
8:A5:3462:C:C6	8:A5:3465:U:C2	2.82	0.68
6:A8:122:C:N3	8:A5:1695:A:O2'	2.25	0.68
8:A5:1234:U:OP1	38:CS:163:LYS:NZ	2.20	0.68
78:DB:18:G:HO2'	78:DB:57:G:H22	1.42	0.67
3:AC:159:VAL:HG22	3:AC:160:PRO:HD2	1.76	0.67
43:CA:207:VAL:HG13	43:CA:208:GLU:HG3	1.74	0.67
8:A5:3027:U:O2'	8:A5:3047:U:O2	2.11	0.67
3:AC:76:GLU:OE1	3:AC:76:GLU:N	2.26	0.67
76:CJ:117:GLN:OE1	76:CJ:117:GLN:N	2.26	0.67
8:A5:1155:C:O2'	8:A5:1156:G:O5'	2.12	0.67
11:AW:14:ILE:HD11	11:AW:27:ILE:HD11	1.77	0.67
27:AG:41:LEU:O	27:AG:41:LEU:HD13	1.95	0.67
3:AC:77:GLU:O	3:AC:81:ASN:ND2	2.27	0.67
7:B2:130:U:O2'	7:B2:131:A:O5'	2.12	0.66
8:A5:3205:C:O2'	8:A5:3207:A:OP2	2.14	0.66
32:AX:37:LYS:O	32:AX:37:LYS:HD3	1.94	0.66
10:AK:88:VAL:HG22	10:AK:89:PRO:HD2	1.78	0.66
7:B2:927:C:OP2	22:AN:70:LYS:NZ	2.28	0.66
8:A5:1786:G:O2'	8:A5:1866:U:O2'	1.92	0.66
8:A5:2215:G:N2	8:A5:2217:A:O2'	2.29	0.66
24:Ad:2:GLY:N	24:Ad:5:ASN:OD1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:AG:188:LYS:O	27:AG:192:LEU:HD12	1.95	0.66
34:AJ:44:ARG:O	34:AJ:48:THR:HG23	1.96	0.66
49:CE:180:ASP:OD2	49:CE:181:ALA:N	2.29	0.66
20:AM:74:GLU:OE1	20:AM:86:LYS:NZ	2.29	0.66
21:AV:21:ASN:O	21:AV:21:ASN:ND2	2.28	0.66
44:CG:195:VAL:O	44:CG:195:VAL:HG12	1.96	0.66
8:A5:251:C:O2'	8:A5:252:U:O5'	2.13	0.66
6:A8:21:G:O2'	6:A8:22:U:O5'	2.14	0.65
8:A5:823:G:O2'	8:A5:824:U:O4'	2.14	0.65
8:A5:1912:A:HO2'	8:A5:1913:U:P	2.20	0.65
28:Ab:43:ILE:HD12	28:Ab:43:ILE:O	1.96	0.65
49:CE:104:THR:HG23	49:CE:104:THR:O	1.95	0.65
63:CQ:66:LEU:HD22	63:CQ:80:VAL:HG11	1.77	0.65
8:A5:2459:A:H61	8:A5:3095:C:H5	1.45	0.65
8:A5:3386:G:O2'	8:A5:3387:G:OP1	2.14	0.65
76:CJ:127:ASP:OD1	76:CJ:129:SER:OG	2.13	0.65
16:AA:198:GLU:N	16:AA:198:GLU:OE2	2.29	0.65
78:DA:18:G:N2	78:DA:58:A:OP2	2.30	0.65
8:A5:1124:C:O2'	8:A5:1125:A:OP2	2.10	0.65
36:AH:63:VAL:HG22	36:AH:64:PRO:HD2	1.78	0.65
34:AJ:127:ILE:HD12	34:AJ:128:LEU:N	2.12	0.65
36:AH:3:GLU:C	36:AH:4:ILE:HD12	2.21	0.65
20:AM:136:PHE:O	20:AM:140:ASN:ND2	2.30	0.65
4:AE:18:MET:HE3	7:B2:755:A:C5	2.31	0.64
7:B2:1183:A:O2'	7:B2:1184:U:OP1	2.11	0.64
8:A5:1469:G:N2	8:A5:1472:G:OP2	2.27	0.64
7:B2:1550:G:OP2	7:B2:1552:C:N4	2.30	0.64
8:A5:189:G:O2'	8:A5:190:A:OP1	2.12	0.64
8:A5:2410:G:O2'	8:A5:2413:U:OP2	2.14	0.64
19:AF:133:ARG:O	30:Ac:18:SER:OG	2.14	0.64
59:CH:43:MET:HE1	59:CH:71:VAL:HG21	1.78	0.64
12:AS:15:VAL:HG12	12:AS:16:MET:HG3	1.78	0.64
28:Ab:67:THR:OG1	28:Ab:70:LYS:O	2.14	0.64
33:AL:54:ASP:OD1	33:AL:57:CYS:N	2.30	0.64
4:AE:86:MET:HE2	4:AE:122:LEU:HB2	1.79	0.64
1:AD:28:MET:SD	1:AD:175:ARG:NH2	2.71	0.64
8:A5:3462:C:O2	8:A5:3465:U:C4	2.49	0.64
8:A5:580:U:O2'	8:A5:581:G:OP1	2.14	0.64
7:B2:18:U:O2'	7:B2:1096:A:N1	2.28	0.64
7:B2:1711:G:O2'	8:A5:2358:A:O2'	2.14	0.64
7:B2:243:G:O2'	7:B2:244:C:O5'	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:70:GLU:O	1:AD:74:VAL:HG23	1.99	0.63
36:AH:51:VAL:O	36:AH:57:SER:OG	2.08	0.63
8:A5:3285:G:O2'	8:A5:3286:G:OP1	2.16	0.63
8:A5:1875:C:O2'	8:A5:1876:U:OP1	2.16	0.63
8:A5:3333:U:O2'	8:A5:3334:G:O5'	2.15	0.63
34:AJ:85:VAL:HG12	34:AJ:99:LEU:HD22	1.80	0.63
8:A5:3321:A:O2'	8:A5:3322:U:OP2	2.14	0.63
8:A5:2610:C:O2'	8:A5:2611:U:OP1	2.14	0.63
38:CS:89:SER:OG	38:CS:94:HIS:NE2	2.27	0.63
78:DA:18:G:O6	78:DA:55:U:O2	2.17	0.63
7:B2:1193:A:HO2'	15:Af:134:TYR:HH	1.42	0.63
7:B2:1479:G:O2'	7:B2:1480:A:OP1	2.15	0.63
16:AA:151:GLU:OE2	16:AA:151:GLU:N	2.27	0.63
28:Ab:53:VAL:HG23	28:Ab:53:VAL:O	1.99	0.63
49:CE:137:PRO:HD2	49:CE:140:ILE:HD12	1.81	0.63
7:B2:1556:A:O2'	7:B2:1557:G:OP2	2.12	0.63
8:A5:2998:U:O2'	8:A5:2999:A:H2'	1.99	0.63
8:A5:3266:U:OP2	40:CB:132:LYS:NZ	2.32	0.63
8:A5:2495:C:O2'	40:CB:268:ARG:NH2	2.28	0.62
8:A5:3127:C:O2	39:CV:46:ARG:NH2	2.32	0.62
8:A5:3317:G:O6	38:CS:160:ARG:NE	2.30	0.62
36:AH:3:GLU:N	36:AH:3:GLU:OE2	2.32	0.62
7:B2:599:A:N6	7:B2:935:A:OP1	2.29	0.62
7:B2:1747:G:N7	14:Aa:34:LYS:NZ	2.47	0.62
8:A5:2033:G:H21	8:A5:3476:A:H8	1.47	0.62
19:AF:112:GLU:OE1	19:AF:112:GLU:N	2.32	0.62
7:B2:570:A:OP1	34:AJ:38:ASN:ND2	2.32	0.62
7:B2:556:A:O2'	7:B2:558:U:OP1	2.17	0.62
7:B2:1502:G:OP1	12:AS:121:ARG:NH1	2.33	0.62
18:AI:65:PHE:CZ	18:AI:102:ILE:HD11	2.35	0.62
34:AJ:63:GLU:OE1	34:AJ:65:LYS:N	2.32	0.62
44:CG:99:LEU:HD23	44:CG:219:LEU:HD12	1.80	0.62
8:A5:2240:C:O2	8:A5:2247:A:N6	2.31	0.62
34:AJ:118:LEU:HD12	34:AJ:158:PHE:CE1	2.35	0.62
4:AE:99:ARG:NH2	4:AE:120:PHE:O	2.33	0.62
8:A5:321:C:OP1	52:Ci:27:ARG:NH1	2.33	0.62
16:AA:18:LEU:HD11	16:AA:177:MET:CE	2.29	0.62
70:Ck:7:GLU:N	70:Ck:7:GLU:OE1	2.33	0.62
7:B2:1715:U:O2'	7:B2:1716:A:OP2	2.17	0.62
8:A5:3340:G:O2'	8:A5:3341:G:O5'	2.17	0.62
8:A5:2790:A:O2'	8:A5:2791:A:OP1	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AV:3:ASN:N	21:AV:3:ASN:OD1	2.31	0.61
76:CJ:88:GLU:OE1	76:CJ:88:GLU:N	2.33	0.61
8:A5:39:A:OP1	80:A5:3601:SPD:H21	1.99	0.61
22:AN:99:ARG:O	22:AN:103:GLU:OE1	2.18	0.61
8:A5:54:G:O2'	54:CN:108:ARG:NH2	2.32	0.61
8:A5:678:A:OP2	8:A5:2980:U:O2'	2.17	0.61
8:A5:2772:C:OP1	8:A5:2862:C:O2'	2.17	0.61
7:B2:1175:C:O2'	7:B2:1400:A:N6	2.34	0.61
8:A5:635:C:HO2'	8:A5:636:G:P	2.23	0.61
8:A5:870:G:OP2	75:Cj:31:LYS:NZ	2.33	0.61
7:B2:543:A:O2'	32:AX:88:ASP:OD2	2.16	0.61
8:A5:3462:C:H6	8:A5:3465:U:N1	1.97	0.61
7:B2:1490:A:O2'	7:B2:1491:U:O5'	2.16	0.61
8:A5:1729:G:N2	8:A5:1732:A:OP2	2.31	0.61
12:AS:100:SER:OG	12:AS:101:THR:N	2.33	0.61
23:AZ:69:VAL:CG2	23:AZ:80:ALA:HB1	2.30	0.61
45:CI:193:ASP:OD1	45:CI:198:GLN:NE2	2.33	0.61
58:Cc:29:TYR:OH	58:Cc:89:ARG:NH2	2.34	0.61
7:B2:1054:U:O2'	11:AW:19:LYS:NZ	2.34	0.61
10:AK:6:SER:O	10:AK:10:LEU:HD12	2.01	0.61
41:CU:26:GLU:N	41:CU:26:GLU:OE1	2.34	0.61
1:AD:69:LYS:NZ	10:AK:93:LYS:O	2.34	0.60
11:AW:28:ARG:HB3	11:AW:29:PRO:CD	2.32	0.60
31:Ae:112:ARG:NE	31:Ae:112:ARG:O	2.34	0.60
8:A5:544:C:OP2	57:CM:69:ARG:NH2	2.34	0.60
19:AF:34:VAL:O	19:AF:48:LYS:NZ	2.20	0.60
36:AH:19:ILE:O	36:AH:23:VAL:HG23	2.00	0.60
8:A5:1529:U:O2'	8:A5:1531:G:N7	2.32	0.60
19:AF:85:HIS:O	19:AF:87:ARG:N	2.35	0.60
42:CL:167:ARG:NH2	42:CL:173:GLU:OE2	2.34	0.60
73:Ce:89:MET:SD	73:Ce:89:MET:N	2.67	0.60
7:B2:1278:A:O2'	7:B2:1279:U:OP1	2.20	0.60
25:AY:103:PRO:O	25:AY:108:ARG:NH1	2.33	0.60
8:A5:3115:U:O2'	40:CB:182:GLU:OE2	2.18	0.60
59:CH:183:THR:OG1	59:CH:184:THR:N	2.33	0.60
8:A5:2793:C:H5'	76:CJ:75:ILE:HD11	1.84	0.60
8:A5:820:C:O2'	8:A5:821:U:O5'	2.17	0.60
8:A5:3365:U:O2'	8:A5:3366:U:OP1	2.18	0.59
9:AR:31:ASN:OD1	9:AR:55:THR:OG1	2.19	0.59
16:AA:7:HIS:O	16:AA:191:ARG:NH1	2.34	0.59
76:CJ:142:ASP:OD1	76:CJ:143:ARG:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:CJ:175:GLN:C	76:CJ:175:GLN:OE1	2.45	0.59
8:A5:1861:U:O2'	8:A5:1862:G:OP1	2.14	0.59
34:AJ:70:LEU:O	34:AJ:74:ASN:OD1	2.20	0.59
4:AE:18:MET:SD	4:AE:107:ARG:NE	2.75	0.59
4:AE:61:LYS:NZ	7:B2:431:G:O3'	2.31	0.59
58:Cc:105:ASP:N	58:Cc:105:ASP:OD1	2.35	0.59
63:CQ:122:THR:OG1	63:CQ:124:ASP:OD1	2.18	0.59
1:AD:74:VAL:HG21	10:AK:68:TYR:CE1	2.38	0.59
8:A5:290:A:OP2	50:Co:40:ARG:NH1	2.35	0.59
8:A5:1844:A:O2'	8:A5:1845:A:P	2.60	0.59
25:AY:12:VAL:HG22	25:AY:23:MET:HB3	1.82	0.59
7:B2:1444:G:O2'	7:B2:1450:C:O2	2.16	0.59
8:A5:3348:A:O2'	8:A5:3349:G:O5'	2.17	0.59
13:AT:135:ILE:O	13:AT:138:SER:OG	2.17	0.59
42:CL:68:THR:HG21	55:Ca:101:THR:CG2	2.33	0.59
66:CZ:21:ARG:NH2	66:CZ:47:ASP:O	2.35	0.59
6:A8:71:A:N6	6:A8:86:G:O2'	2.35	0.59
75:Cj:25:SER:O	75:Cj:25:SER:OG	2.16	0.59
7:B2:818:U:OP2	61:CR:173:ARG:NH1	2.36	0.59
15:Af:102:ILE:HD11	20:AM:72:LEU:HA	1.83	0.59
34:AJ:112:GLN:HG3	34:AJ:148:VAL:HG21	1.84	0.59
18:AI:65:PHE:HZ	18:AI:102:ILE:HD11	1.68	0.59
58:Cc:42:ASN:OD1	58:Cc:44:LYS:HG3	2.03	0.59
7:B2:172:A:O3'	18:AI:141:ARG:NE	2.35	0.59
8:A5:2860:A:H4'	65:CD:144:VAL:HG11	1.85	0.59
7:B2:999:C:O2'	11:AW:2:VAL:N	2.30	0.58
14:Aa:32:LYS:O	14:Aa:37:LYS:NZ	2.36	0.58
49:CE:130:ASN:OD1	49:CE:132:SER:OG	2.21	0.58
72:Cd:93:ASP:N	72:Cd:93:ASP:OD1	2.36	0.58
8:A5:1956:G:N1	8:A5:1959:C:OP2	2.29	0.58
7:B2:1101:A:OP1	14:Aa:2:THR:N	2.35	0.58
8:A5:194:C:HO2'	8:A5:195:C:P	2.27	0.58
8:A5:3462:C:H4'	8:A5:3466:U:H5'	1.84	0.58
9:AR:91:VAL:HA	9:AR:96:LEU:HD21	1.84	0.58
8:A5:834:G:O2'	8:A5:835:A:OP1	2.15	0.58
36:AH:193:ILE:C	36:AH:193:ILE:HD12	2.27	0.58
78:DA:18:G:OP1	78:DA:60:C:O2'	2.21	0.58
8:A5:1818:C:OP1	56:Cp:36:ARG:NH2	2.35	0.58
8:A5:3338:U:HO2'	8:A5:3339:U:H6	1.50	0.58
8:A5:3462:C:C6	8:A5:3465:U:C5	2.86	0.58
7:B2:1128:G:N1	7:B2:1531:G:OP2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AA:205:ASP:OD1	16:AA:205:ASP:N	2.37	0.58
20:AM:110:LYS:N	20:AM:110:LYS:HE2	2.19	0.58
8:A5:21:G:O2'	8:A5:22:A:OP1	2.22	0.58
45:CI:76:MET:HA	45:CI:76:MET:HE3	1.85	0.58
64:CT:159:ILE:O	64:CT:159:ILE:CD1	2.51	0.58
8:A5:3462:C:N1	8:A5:3462:C:H1'	2.16	0.58
19:AF:79:ALA:O	19:AF:95:THR:HG21	2.03	0.58
32:AX:41:PHE:O	32:AX:76:LYS:NZ	2.36	0.58
7:B2:544:G:OP2	32:AX:68:LYS:NZ	2.36	0.57
40:CB:110:LEU:O	40:CB:115:ARG:NH1	2.37	0.57
44:CG:235:ARG:HD2	44:CG:235:ARG:C	2.29	0.57
5:A7:64:G:OP1	45:CI:204:GLY:N	2.36	0.57
7:B2:568:C:O2'	7:B2:572:U:OP1	2.22	0.57
20:AM:32:ALA:HB2	20:AM:124:ASN:ND2	2.19	0.57
38:CS:9:THR:O	38:CS:9:THR:HG22	2.02	0.57
38:CS:97:TYR:OH	38:CS:99:GLU:OE2	2.15	0.57
7:B2:372:G:OP1	7:B2:1683:U:O2'	2.21	0.57
7:B2:1505:U:OP1	29:AP:48:ARG:NH2	2.24	0.57
8:A5:2006:A:O2'	8:A5:2224:C:O2	2.21	0.57
12:AS:60:THR:OG1	12:AS:63:ASP:OD1	2.07	0.57
35:AQ:30:ILE:HG21	35:AQ:37:LEU:HD11	1.85	0.57
1:AD:74:VAL:HG21	10:AK:68:TYR:HE1	1.69	0.57
8:A5:1154:G:OP2	37:CF:198:LYS:NZ	2.37	0.57
8:A5:3465:U:C2	8:A5:3465:U:C1'	2.86	0.57
63:CQ:124:ASP:OD1	63:CQ:124:ASP:N	2.37	0.57
10:AK:24:LYS:O	10:AK:40:ASN:ND2	2.38	0.57
27:AG:21:GLU:N	27:AG:21:GLU:OE2	2.38	0.57
39:CV:96:ILE:HD12	74:CW:20:ARG:HG3	1.86	0.57
8:A5:1256:A:OP1	45:CI:162:ARG:NH2	2.38	0.57
8:A5:3462:C:H1'	8:A5:3465:U:C4	2.06	0.57
7:B2:1004:C:O2'	7:B2:1005:G:OP2	2.20	0.57
65:CD:85:ARG:NH2	65:CD:86:TYR:OH	2.38	0.57
1:AD:137:GLU:HB2	1:AD:159:MET:HE3	1.87	0.57
8:A5:3283:U:C2'	8:A5:3284:C:OP1	2.53	0.57
34:AJ:88:GLU:N	34:AJ:88:GLU:OE1	2.38	0.57
3:AC:61:THR:OG1	3:AC:87:GLU:OE2	2.21	0.56
34:AJ:60:LEU:HD21	34:AJ:93:LEU:HB2	1.87	0.56
59:CH:169:ASP:O	59:CH:169:ASP:OD2	2.23	0.56
7:B2:226:U:O2'	7:B2:227:G:OP2	2.18	0.56
10:AK:47:LEU:HD12	10:AK:67:TRP:CE3	2.40	0.56
78:DB:25:C:N4	78:DB:45:G:H21	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:1143:U:OP2	62:Cb:52:ARG:NE	2.36	0.56
8:A5:1230:A:N3	8:A5:1380:C:O2'	2.38	0.56
8:A5:1907:U:HO2'	8:A5:1908:A:P	2.25	0.56
8:A5:3453:U:O2'	8:A5:3454:A:OP2	2.19	0.56
22:AN:82:PRO:O	22:AN:82:PRO:HD2	2.04	0.56
23:AZ:60:THR:O	23:AZ:107:ARG:NH2	2.38	0.56
25:AY:78:THR:HG23	25:AY:80:ASP:OD2	2.05	0.56
55:Ca:98:ILE:HD11	55:Ca:119:LEU:HD22	1.87	0.56
76:CJ:127:ASP:OD1	76:CJ:129:SER:N	2.37	0.56
8:A5:1186:G:O2'	8:A5:2754:A:N3	2.36	0.56
20:AM:47:CYS:O	20:AM:50:LEU:HD12	2.05	0.56
65:CD:85:ARG:NH2	65:CD:251:SER:O	2.38	0.56
8:A5:1244:G:O2'	8:A5:1245:A:P	2.63	0.56
47:CC:295:SER:OG	47:CC:297:GLU:OE1	2.24	0.56
60:CY:37:GLU:OE2	60:CY:37:GLU:N	2.28	0.56
8:A5:1271:A:O2'	8:A5:1338:A:N1	2.37	0.56
8:A5:3007:G:O2'	71:Cm:100:TYR:O	2.23	0.56
8:A5:3257:A:H4'	8:A5:3258:G:OP2	2.06	0.56
25:AY:55:VAL:HG12	25:AY:75:VAL:HG22	1.86	0.56
34:AJ:57:ARG:O	34:AJ:61:THR:HG23	2.05	0.56
7:B2:826:A:OP1	22:AN:65:ARG:NH2	2.38	0.56
7:B2:1341:G:OP1	26:AU:86:ARG:NH2	2.39	0.56
8:A5:598:C:O2'	8:A5:599:G:O5'	2.20	0.56
8:A5:3487:C:H2'	8:A5:3488:U:H5'	1.87	0.56
8:A5:1872:G:O2'	8:A5:1874:U:OP2	2.24	0.56
20:AM:79:GLU:O	20:AM:81:GLN:NE2	2.39	0.56
7:B2:1131:G:H21	13:AT:87:VAL:CG2	2.19	0.55
7:B2:1340:A:O2'	7:B2:1341:G:O5'	2.23	0.55
8:A5:1656:C:OP1	8:A5:2627:U:N3	2.36	0.55
15:Af:105:ASN:OD1	15:Af:106:GLY:N	2.39	0.55
41:CU:47:GLU:OE2	41:CU:47:GLU:O	2.23	0.55
18:AI:61:ASP:OD1	18:AI:61:ASP:N	2.38	0.55
18:AI:200:ARG:NH1	18:AI:200:ARG:HB2	2.21	0.55
49:CE:171:GLN:OE1	49:CE:171:GLN:O	2.25	0.55
4:AE:11:LEU:HD11	34:AJ:4:LEU:HD23	1.89	0.55
7:B2:1110:A:O2'	7:B2:1111:A:OP1	2.24	0.55
8:A5:1656:C:HO2'	8:A5:1657:U:H3	1.52	0.55
20:AM:32:ALA:HB3	20:AM:123:GLY:CA	2.36	0.55
35:AQ:98:VAL:HG12	35:AQ:99:ASP:H	1.70	0.55
54:CN:160:GLU:OE1	54:CN:160:GLU:N	2.33	0.55
19:AF:108:LEU:HD11	23:AZ:106:THR:HB	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AM:110:LYS:HE2	20:AM:110:LYS:H	1.71	0.55
44:CG:59:PRO:HG2	44:CG:62:ILE:HD12	1.87	0.55
8:A5:85:G:O2'	8:A5:97:G:O6	2.20	0.55
8:A5:1353:A:H4'	8:A5:1354:A:H5''	1.88	0.55
8:A5:3081:A:N7	43:CA:215:ASN:ND2	2.54	0.55
16:AA:83:ALA:HB2	16:AA:171:ILE:HD11	1.88	0.55
19:AF:190:SER:OG	19:AF:192:ASN:OD1	2.25	0.55
41:CU:20:HIS:C	41:CU:20:HIS:HD1	2.15	0.55
7:B2:1041:C:C2'	7:B2:1042:C:OP1	2.54	0.55
7:B2:1319:U:O2'	7:B2:1322:G:O6	2.18	0.55
8:A5:1209:A:O2'	8:A5:1221:A:N3	2.38	0.55
16:AA:40:LYS:O	16:AA:40:LYS:NZ	2.25	0.55
1:AD:163:GLY:HA3	7:B2:1290:A:H61	1.71	0.55
8:A5:2043:U:OP1	61:CR:108:ARG:NH2	2.40	0.55
8:A5:2445:A:N3	8:A5:3167:U:O2'	2.37	0.55
8:A5:3207:A:OP1	39:CV:15:ARG:NH2	2.41	0.55
36:AH:23:VAL:HG21	36:AH:48:VAL:HG11	1.89	0.55
8:A5:403:A:O2'	8:A5:406:G:OP2	2.25	0.54
8:A5:427:G:O6	8:A5:2486:C:O2'	2.15	0.54
8:A5:1582:G:OP1	53:Cl:41:ARG:NH1	2.40	0.54
8:A5:3277:C:O2'	8:A5:3278:C:O5'	2.24	0.54
8:A5:2347:A:O2'	43:CA:223:SER:OG	2.24	0.54
18:AI:164:GLU:OE1	18:AI:164:GLU:N	2.40	0.54
19:AF:55:LEU:HD12	35:AQ:48:LYS:HG2	1.89	0.54
35:AQ:38:GLU:OE1	35:AQ:38:GLU:N	2.38	0.54
7:B2:568:C:OP1	34:AJ:39:LYS:NZ	2.37	0.54
7:B2:1363:G:O2'	7:B2:1364:C:O5'	2.21	0.54
8:A5:1035:G:O2'	8:A5:1036:C:O4'	2.17	0.54
8:A5:2486:C:OP2	46:CO:86:ARG:NH2	2.40	0.54
20:AM:80:HIS:HB2	20:AM:82:ILE:HD12	1.88	0.54
8:A5:1250:C:OP2	8:A5:1251:C:O2'	2.24	0.54
34:AJ:63:GLU:OE2	34:AJ:66:ASP:N	2.40	0.54
34:AJ:93:LEU:HA	34:AJ:96:VAL:HG12	1.90	0.54
45:CI:51:HIS:ND1	45:CI:137:SER:OG	2.40	0.54
20:AM:128:GLY:HA2	20:AM:131:ILE:HD12	1.89	0.54
31:Ae:84:ARG:HB2	32:AX:88:ASP:OD1	2.07	0.54
36:AH:170:ILE:HD11	36:AH:189:PHE:HE1	1.73	0.54
40:CB:165:HIS:HB3	40:CB:180:LEU:HD23	1.90	0.54
7:B2:507:U:O2'	25:AY:62:SER:O	2.25	0.54
7:B2:1509:G:O2'	7:B2:1510:U:OP1	2.22	0.54
8:A5:408:A:O2'	8:A5:409:C:P	2.65	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:1954:G:OP1	61:CR:60:ARG:NH1	2.41	0.54
54:CN:14:LYS:HA	54:CN:19:LEU:HD23	1.90	0.54
72:CD:90:GLU:HA	72:CD:90:GLU:OE2	2.08	0.54
7:B2:160:C:N4	7:B2:250:A:OP2	2.40	0.54
34:AJ:96:VAL:O	34:AJ:99:LEU:HD12	2.08	0.54
43:CA:242:ARG:NH2	43:CA:243:THR:O	2.41	0.54
34:AJ:161:GLN:OE1	34:AJ:161:GLN:C	2.51	0.53
59:CH:5:GLU:OE1	59:CH:6:SER:N	2.41	0.53
7:B2:1383:A:O2'	7:B2:1384:G:OP1	2.18	0.53
8:A5:3013:G:H2'	8:A5:3014:A:H5''	1.89	0.53
8:A5:2906:G:O2'	8:A5:2907:U:OP2	2.21	0.53
19:AF:110:THR:HG1	19:AF:112:GLU:CD	2.15	0.53
3:AC:157:ALA:O	3:AC:237:TYR:OH	2.27	0.53
10:AK:71:ASP:O	10:AK:74:ILE:HG22	2.08	0.53
48:Ch:2:THR:OG1	48:Ch:3:LYS:N	2.37	0.53
42:CL:88:GLN:OE1	42:CL:92:ARG:NH1	2.41	0.53
64:CT:114:GLU:OE1	64:CT:115:LYS:N	2.41	0.53
8:A5:2609:A:C2'	8:A5:2610:C:OP1	2.57	0.53
8:A5:3487:C:N4	8:A5:3488:U:O4	2.42	0.53
22:AN:56:ASP:OD2	28:Ab:52:THR:OG1	2.25	0.53
23:AZ:43:MET:HE1	23:AZ:50:THR:HG21	1.90	0.53
38:CS:150:ASP:OD1	38:CS:152:LYS:N	2.38	0.53
12:AS:65:ASP:O	12:AS:69:THR:OG1	2.26	0.53
34:AJ:17:ARG:O	34:AJ:23:ARG:NH2	2.40	0.53
7:B2:314:U:O4	18:AI:5:ARG:NH2	2.42	0.53
8:A5:2787:C:OP2	8:A5:2788:G:O2'	2.24	0.53
9:AR:73:LEU:HD22	9:AR:73:LEU:H	1.74	0.53
36:AH:19:ILE:HD13	36:AH:50:GLU:HB2	1.90	0.53
7:B2:45:U:O2'	7:B2:46:A:H2'	2.08	0.53
8:A5:403:A:O2'	8:A5:404:G:P	2.66	0.53
18:AI:45:LEU:HD11	18:AI:53:GLU:OE1	2.09	0.53
20:AM:32:ALA:HB2	20:AM:124:ASN:CG	2.34	0.53
35:AQ:99:ASP:OD1	35:AQ:102:SER:N	2.34	0.53
36:AH:170:ILE:HD11	36:AH:189:PHE:CE1	2.44	0.53
44:CG:109:GLU:OE1	44:CG:109:GLU:N	2.39	0.53
8:A5:1132:U:H4'	65:CD:46:THR:HG21	1.91	0.53
8:A5:2624:G:C2'	8:A5:2625:G:H5'	2.39	0.53
8:A5:3488:U:O2'	8:A5:3489:A:P	2.66	0.53
20:AM:92:ILE:H	20:AM:92:ILE:HD12	1.74	0.53
3:AC:267:GLU:H	3:AC:267:GLU:CD	2.16	0.52
8:A5:3375:C:HO2'	8:A5:3376:A:P	2.31	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AH:97:ARG:NH1	36:AH:132:GLU:OE2	2.42	0.52
4:AE:181:TYR:HD2	4:AE:227:ILE:HD13	1.73	0.52
7:B2:1039:A:C2'	7:B2:1040:U:OP1	2.57	0.52
8:A5:1626:C:O2'	8:A5:1627:G:H5'	2.10	0.52
8:A5:1798:A:H2'	8:A5:1798:A:N3	2.25	0.52
8:A5:1914:U:H3'	8:A5:1915:U:H5''	1.90	0.52
49:CE:77:LEU:HD11	49:CE:91:PHE:HB2	1.90	0.52
1:AD:18:ILE:HD13	24:Ad:50:ILE:CD1	2.38	0.52
7:B2:1512:A:OP2	29:AP:121:TYR:OH	2.27	0.52
8:A5:3460:G:HO2'	8:A5:3461:U:P	2.32	0.52
35:AQ:114:ASP:OD1	35:AQ:114:ASP:C	2.52	0.52
4:AE:18:MET:HE3	7:B2:755:A:C6	2.44	0.52
34:AJ:91:MET:N	34:AJ:91:MET:SD	2.82	0.52
40:CB:185:VAL:O	40:CB:193:LYS:NZ	2.38	0.52
27:AG:159:THR:OG1	27:AG:160:HIS:N	2.41	0.52
40:CB:139:ASP:OD1	40:CB:140:GLU:N	2.42	0.52
61:CR:157:ASP:OD1	61:CR:158:GLN:N	2.43	0.52
63:CQ:66:LEU:CD2	63:CQ:80:VAL:HG11	2.39	0.52
66:CZ:27:LYS:NZ	66:CZ:29:GLN:OE1	2.40	0.52
7:B2:1469:G:O2'	7:B2:1471:A:N3	2.28	0.52
14:Aa:18:VAL:HG11	14:Aa:33:ASP:OD1	2.10	0.52
7:B2:1406:C:O2'	24:Ad:7:TRP:O	2.20	0.52
8:A5:3365:U:HO2'	8:A5:3366:U:P	2.32	0.52
20:AM:90:LYS:HA	20:AM:93:ILE:HD12	1.92	0.52
7:B2:128:G:O2'	7:B2:129:A:OP2	2.25	0.52
8:A5:763:G:C2'	8:A5:764:C:OP1	2.58	0.52
8:A5:892:A:OP1	56:Cp:5:THR:OG1	2.28	0.52
8:A5:971:G:H5'	8:A5:972:A:OP1	2.09	0.52
27:AG:154:THR:HG22	27:AG:176:ILE:HD13	1.92	0.52
40:CB:57:VAL:HG22	40:CB:73:VAL:HG22	1.92	0.52
49:CE:180:ASP:OD2	49:CE:180:ASP:C	2.53	0.52
76:CJ:158:VAL:O	76:CJ:163:ARG:NH1	2.43	0.52
8:A5:154:G:N2	8:A5:155:U:O4	2.42	0.52
34:AJ:118:LEU:HD12	34:AJ:158:PHE:HE1	1.74	0.52
9:AR:116:LEU:HD23	16:AA:16:MET:SD	2.50	0.52
26:AU:94:ALA:O	26:AU:97:LEU:HD12	2.10	0.52
33:AL:49:GLU:O	33:AL:49:GLU:CD	2.53	0.52
34:AJ:26:GLN:C	34:AJ:26:GLN:OE1	2.52	0.52
42:CL:108:GLU:OE1	42:CL:108:GLU:N	2.39	0.52
59:CH:41:LEU:CB	59:CH:43:MET:HE2	2.39	0.52
8:A5:251:C:O2'	8:A5:252:U:P	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:2684:G:O2'	8:A5:2685:C:O5'	2.28	0.51
17:AO:62:LYS:NZ	17:AO:81:ASP:OD2	2.19	0.51
29:AP:141:ALA:O	29:AP:142:THR:OG1	2.18	0.51
35:AQ:105:GLU:O	35:AQ:109:ILE:HG12	2.09	0.51
8:A5:3376:A:C2'	8:A5:3377:G:OP1	2.58	0.51
8:A5:3460:G:O2'	8:A5:3461:U:OP1	2.25	0.51
9:AR:79:GLU:C	9:AR:79:GLU:OE2	2.53	0.51
12:AS:108:ARG:HB3	12:AS:108:ARG:NH1	2.26	0.51
7:B2:1310:U:OP1	35:AQ:9:GLN:NE2	2.43	0.51
8:A5:3309:A:C2'	8:A5:3310:C:OP1	2.58	0.51
12:AS:26:VAL:HG23	12:AS:54:LYS:O	2.10	0.51
20:AM:84:LEU:C	20:AM:84:LEU:HD12	2.35	0.51
78:DB:58:A:H2'	78:DB:60:C:OP2	2.10	0.51
8:A5:2041:G:C4	8:A5:2203:G:N2	2.78	0.51
14:Aa:94:ASP:C	14:Aa:94:ASP:OD2	2.53	0.51
34:AJ:82:LYS:HD3	34:AJ:82:LYS:N	2.26	0.51
7:B2:1630:A:OP1	27:AG:92:ARG:NH2	2.43	0.51
8:A5:856:A:OP1	55:Ca:27:LYS:NZ	2.35	0.51
8:A5:2492:U:H3	8:A5:3102:G:H1	1.58	0.51
8:A5:3488:U:O2'	8:A5:3489:A:OP1	2.28	0.51
7:B2:97:C:OP1	7:B2:363:G:O2'	2.25	0.51
8:A5:67:C:OP2	8:A5:307:G:N2	2.41	0.51
8:A5:1875:C:O2'	8:A5:1876:U:P	2.68	0.51
8:A5:1875:C:C2'	8:A5:1876:U:OP1	2.59	0.51
31:Ae:77:LEU:HD12	32:AX:68:LYS:HD2	1.93	0.51
35:AQ:114:ASP:CG	35:AQ:116:SER:HG	2.18	0.51
65:CD:93:THR:HG22	65:CD:93:THR:O	2.10	0.51
7:B2:17:G:H2'	7:B2:18:U:C6	2.46	0.51
7:B2:150:C:OP1	27:AG:131:ARG:NH2	2.44	0.51
7:B2:615:U:OP2	36:AH:122:LEU:N	2.44	0.51
8:A5:263:U:HO2'	8:A5:264:U:P	2.33	0.51
8:A5:546:G:H2'	8:A5:547:A:C8	2.45	0.51
39:CV:87:GLN:HA	39:CV:97:TYR:HB3	1.91	0.51
45:CI:47:PRO:O	45:CI:178:ARG:NH2	2.42	0.51
67:CP:12:ASN:OD1	67:CP:12:ASN:O	2.29	0.51
8:A5:598:C:O2'	8:A5:599:G:P	2.69	0.51
8:A5:3277:C:O2'	8:A5:3278:C:P	2.69	0.51
36:AH:68:LEU:HD13	36:AH:95:ALA:HB2	1.93	0.51
37:CF:72:GLU:OE2	38:CS:68:LYS:NZ	2.40	0.51
48:Ch:12:GLU:N	48:Ch:12:GLU:OE1	2.44	0.51
59:CH:87:ARG:NE	59:CH:145:GLU:OE2	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:130:GLU:HA	1:AD:130:GLU:OE2	2.11	0.51
8:A5:2215:G:O2'	8:A5:2216:U:P	2.69	0.51
8:A5:3374:C:O2'	8:A5:3375:C:P	2.69	0.51
27:AG:166:ASP:OD1	27:AG:168:VAL:HG22	2.11	0.51
29:AP:50:ARG:HG2	29:AP:90:ILE:HD11	1.92	0.51
3:AC:258:GLU:HA	3:AC:258:GLU:OE2	2.11	0.51
7:B2:745:C:O3'	7:B2:746:G:OP2	2.26	0.51
8:A5:759:A:C2'	8:A5:760:U:OP1	2.59	0.51
8:A5:3348:A:O2'	8:A5:3349:G:P	2.68	0.51
18:AI:160:ALA:O	18:AI:164:GLU:OE1	2.29	0.51
25:AY:17:LEU:H	25:AY:17:LEU:HD23	1.74	0.51
25:AY:88:LYS:O	25:AY:92:VAL:HG23	2.11	0.51
78:DA:18:G:O6	78:DA:55:U:C2	2.63	0.51
2:AB:78:ASP:OD1	17:AO:129:ARG:NH1	2.44	0.50
6:A8:101:G:OP2	6:A8:103:A:O2'	2.27	0.50
7:B2:1129:G:C2	7:B2:1130:A:C8	2.99	0.50
7:B2:1278:A:HO2'	7:B2:1279:U:P	2.34	0.50
8:A5:2261:G:N7	43:CA:152:SER:OG	2.40	0.50
8:A5:3334:G:O2'	8:A5:3335:G:P	2.69	0.50
20:AM:89:ASP:OD2	20:AM:90:LYS:N	2.44	0.50
25:AY:107:GLN:CD	25:AY:107:GLN:H	2.19	0.50
44:CG:139:HIS:CE1	44:CG:195:VAL:HG11	2.46	0.50
45:CI:193:ASP:OD2	45:CI:193:ASP:O	2.29	0.50
49:CE:68:ARG:HB2	49:CE:71:LEU:HD12	1.93	0.50
7:B2:368:G:OP2	7:B2:403:G:O2'	2.29	0.50
7:B2:879:G:HO2'	7:B2:880:A:H8	1.57	0.50
8:A5:833:A:C2'	8:A5:834:G:H5'	2.41	0.50
8:A5:2655:U:O2'	8:A5:2656:U:P	2.70	0.50
8:A5:3226:A:H4'	59:CH:69:ARG:HG2	1.93	0.50
16:AA:2:SER:OG	16:AA:3:GLY:N	2.43	0.50
16:AA:181:GLU:OE1	16:AA:181:GLU:HA	2.10	0.50
8:A5:2467:G:H22	8:A5:2499:G:H1'	1.76	0.50
21:AV:59:ALA:O	21:AV:63:MET:HG3	2.11	0.50
42:CL:57:SER:OG	42:CL:75:GLY:O	2.25	0.50
49:CE:140:ILE:HD11	49:CE:175:ASP:HB3	1.93	0.50
8:A5:3333:U:O2'	8:A5:3334:G:P	2.70	0.50
17:AO:114:GLN:HE21	17:AO:114:GLN:HA	1.76	0.50
43:CA:179:LEU:O	43:CA:181:LYS:N	2.44	0.50
49:CE:174:LYS:HA	49:CE:174:LYS:HE3	1.94	0.50
65:CD:238:THR:O	65:CD:242:VAL:HG23	2.10	0.50
7:B2:1324:G:H21	13:AT:6:SER:HB2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:3247:C:O3'	46:CO:148:GLN:NE2	2.45	0.50
27:AG:152:ASP:OD1	27:AG:154:THR:OG1	2.28	0.50
28:Ab:41:PHE:HD1	28:Ab:41:PHE:O	1.95	0.50
28:Ab:56:CYS:HB3	28:Ab:61:THR:H	1.76	0.50
36:AH:4:ILE:O	36:AH:4:ILE:CG2	2.59	0.50
38:CS:6:LEU:O	38:CS:38:THR:OG1	2.25	0.50
78:DB:67:C:H2'	78:DB:68:G:O4'	2.11	0.50
7:B2:750:G:H2'	7:B2:751:C:C6	2.46	0.50
9:AR:58:MET:HA	9:AR:58:MET:HE3	1.94	0.50
14:Aa:23:CYS:SG	14:Aa:24:THR:N	2.84	0.50
23:AZ:52:ASP:OD1	23:AZ:52:ASP:C	2.53	0.50
34:AJ:65:LYS:HD2	34:AJ:65:LYS:C	2.37	0.50
8:A5:120:A:N6	8:A5:149:G:HO2'	2.07	0.50
8:A5:754:C:O2	8:A5:757:G:N2	2.41	0.50
8:A5:1861:U:HO2'	8:A5:1862:G:P	2.32	0.50
8:A5:2243:A:N6	75:Cj:3:LYS:O	2.45	0.50
8:A5:2927:G:N2	8:A5:2930:U:O2	2.41	0.50
27:AG:147:LEU:HD21	27:AG:156:TYR:CD1	2.46	0.50
36:AH:137:ALA:HB2	36:AH:166:VAL:HG21	1.94	0.50
45:CI:210:ILE:HD13	65:CD:285:LEU:HB3	1.93	0.50
4:AE:138:LEU:C	4:AE:138:LEU:HD12	2.36	0.50
7:B2:735:U:N3	34:AJ:142:ASP:OD1	2.45	0.50
8:A5:1567:G:O2'	8:A5:1568:A:P	2.70	0.50
1:AD:214:GLU:N	1:AD:214:GLU:OE1	2.44	0.50
2:AB:35:ASN:OD1	2:AB:35:ASN:N	2.43	0.50
36:AH:18:GLU:O	36:AH:22:GLN:OE1	2.30	0.50
16:AA:37:TYR:OH	21:AV:67:ASP:OD1	2.30	0.49
26:AU:98:ARG:NE	26:AU:98:ARG:HA	2.27	0.49
36:AH:18:GLU:H	36:AH:18:GLU:CD	2.19	0.49
62:Cb:44:ARG:NH1	62:Cb:44:ARG:HB3	2.27	0.49
7:B2:1540:G:O2'	7:B2:1566:G:O6	2.29	0.49
8:A5:939:A:OP1	75:Cj:5:THR:OG1	2.27	0.49
42:CL:7:GLN:O	55:Ca:49:HIS:NE2	2.44	0.49
45:CI:190:LEU:HD13	45:CI:197:VAL:HG21	1.93	0.49
1:AD:33:GLU:HG3	1:AD:34:ASP:OD1	2.13	0.49
7:B2:242:A:O2'	7:B2:243:G:O4'	2.20	0.49
7:B2:1213:C:C2'	7:B2:1214:G:OP1	2.60	0.49
8:A5:821:U:H5	8:A5:823:G:H21	1.60	0.49
8:A5:3256:A:H4'	8:A5:3257:A:O5'	2.12	0.49
20:AM:58:CYS:SG	20:AM:118:VAL:HG22	2.53	0.49
4:AE:20:ASP:OD1	4:AE:23:GLY:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:128:G:O2'	7:B2:129:A:P	2.70	0.49
7:B2:745:C:HO3'	7:B2:746:G:P	2.35	0.49
8:A5:2630:A:HO2'	8:A5:2631:A:P	2.30	0.49
16:AA:205:ASP:HA	16:AA:208:PHE:CD1	2.47	0.49
25:AY:57:PRO:HD2	25:AY:94:MET:HE1	1.95	0.49
64:CT:158:GLU:HA	64:CT:158:GLU:OE2	2.12	0.49
4:AE:91:ILE:HD13	4:AE:98:PHE:HE1	1.77	0.49
7:B2:850:G:H2'	7:B2:851:U:C6	2.48	0.49
7:B2:1400:A:O2'	7:B2:1402:A:OP2	2.29	0.49
8:A5:3326:C:OP1	57:CM:124:ARG:NH2	2.36	0.49
26:AU:22:THR:HG22	26:AU:87:LEU:CD2	2.42	0.49
7:B2:562:G:OP1	31:Ae:92:LYS:NZ	2.46	0.49
8:A5:275:G:OP2	54:CN:44:ARG:NH1	2.41	0.49
8:A5:584:G:H2'	8:A5:585:G:C8	2.48	0.49
8:A5:600:U:C5'	8:A5:601:G:OP2	2.61	0.49
8:A5:3462:C:H5''	8:A5:3465:U:H5'	1.95	0.49
12:AS:149:SER:O	12:AS:149:SER:OG	2.27	0.49
42:CL:68:THR:HG21	55:Ca:101:THR:HG22	1.93	0.49
6:A8:107:A:C2	6:A8:110:G:C6	3.00	0.49
7:B2:32:U:O2'	7:B2:570:A:N1	2.42	0.49
7:B2:531:A:N3	7:B2:566:U:O2'	2.43	0.49
7:B2:1363:G:O2'	7:B2:1364:C:P	2.70	0.49
8:A5:2216:U:O2	8:A5:2216:U:O4'	2.31	0.49
8:A5:2624:G:H2'	8:A5:2625:G:H5'	1.95	0.49
8:A5:3010:G:OP2	59:CH:171:ARG:NH2	2.44	0.49
43:CA:122:ASP:C	43:CA:122:ASP:OD1	2.56	0.49
65:CD:116:ASP:N	65:CD:116:ASP:OD1	2.44	0.49
1:AD:162:SER:OG	7:B2:1288:A:OP2	2.22	0.49
3:AC:72:ILE:HG23	3:AC:77:GLU:HG3	1.95	0.49
7:B2:373:C:OP2	18:AI:2:GLY:N	2.46	0.49
8:A5:646:A:O2'	8:A5:647:A:P	2.70	0.49
8:A5:1101:A:N3	8:A5:2745:U:O2'	2.45	0.49
8:A5:1705:U:O3'	66:CZ:108:ARG:NH1	2.46	0.49
8:A5:1932:A:H2'	8:A5:1932:A:N3	2.27	0.49
34:AJ:33:THR:OG1	34:AJ:34:PHE:N	2.44	0.49
34:AJ:161:GLN:OE1	34:AJ:161:GLN:O	2.31	0.49
7:B2:172:A:O2'	7:B2:181:C:N4	2.45	0.49
8:A5:1626:C:OP2	77:CX:38:ARG:NH2	2.45	0.49
8:A5:2252:G:H2'	8:A5:2253:A:C5	2.48	0.49
78:DA:8:U:O2'	78:DA:21:A:N1	2.37	0.49
8:A5:2248:A:H1'	8:A5:2384:A:N6	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:2259:C:OP1	43:CA:241:ARG:NH1	2.45	0.48
8:A5:3304:U:O2'	8:A5:3305:G:O5'	2.26	0.48
19:AF:106:ILE:HD12	19:AF:184:ILE:HG13	1.95	0.48
44:CG:166:GLU:OE1	44:CG:166:GLU:N	2.45	0.48
7:B2:448:U:HO2'	7:B2:449:A:P	2.36	0.48
7:B2:1278:A:O2'	7:B2:1279:U:P	2.72	0.48
8:A5:25:A:N3	8:A5:334:U:O2'	2.44	0.48
8:A5:109:G:OP2	42:CL:74:ARG:NH2	2.42	0.48
8:A5:890:G:O2'	8:A5:891:A:OP2	2.29	0.48
13:AT:101:ARG:O	13:AT:105:GLN:HG3	2.12	0.48
25:AY:50:THR:HG22	25:AY:51:THR:N	2.29	0.48
34:AJ:41:GLU:OE2	34:AJ:44:ARG:NH2	2.47	0.48
37:CF:100:LYS:HB3	37:CF:101:PRO:HD3	1.95	0.48
78:DB:25:C:C2	78:DB:26:G:C8	3.01	0.48
5:A7:7:G:O3'	65:CD:33:ARG:NH2	2.46	0.48
6:A8:112:A:O2'	6:A8:113:C:OP2	2.30	0.48
7:B2:1130:A:H2'	7:B2:1131:G:C8	2.48	0.48
7:B2:1436:G:H22	7:B2:1483:U:H3	1.60	0.48
20:AM:60:LEU:HD21	20:AM:73:VAL:HG13	1.94	0.48
32:AX:51:VAL:HG13	32:AX:70:VAL:HG22	1.95	0.48
34:AJ:29:LYS:O	34:AJ:33:THR:HG23	2.13	0.48
66:CZ:35:ASP:C	66:CZ:35:ASP:OD2	2.56	0.48
66:CZ:120:GLU:OE1	66:CZ:120:GLU:O	2.30	0.48
3:AC:229:LEU:O	3:AC:229:LEU:HD13	2.14	0.48
10:AK:13:GLU:C	10:AK:13:GLU:OE2	2.56	0.48
13:AT:98:ASN:OD1	13:AT:101:ARG:NH2	2.46	0.48
20:AM:61:ALA:HA	20:AM:87:VAL:O	2.13	0.48
28:Ab:53:VAL:O	28:Ab:53:VAL:CG2	2.61	0.48
31:Ae:130:SER:OXT	31:Ae:130:SER:OG	2.31	0.48
34:AJ:142:ASP:OD1	34:AJ:142:ASP:N	2.47	0.48
56:Cp:52:THR:HG23	56:Cp:52:THR:O	2.12	0.48
2:AB:87:GLU:OE2	2:AB:221:VAL:HG13	2.14	0.48
8:A5:2451:U:C5	8:A5:2452:U:C5	3.01	0.48
59:CH:14:GLU:N	59:CH:14:GLU:CD	2.71	0.48
76:CJ:6:LYS:HA	76:CJ:9:GLU:HG2	1.96	0.48
4:AE:91:ILE:HD12	4:AE:91:ILE:N	2.29	0.48
7:B2:878:G:O6	8:A5:2310:A:N6	2.47	0.48
8:A5:262:C:C2	8:A5:263:U:C5	3.02	0.48
8:A5:263:U:H2'	8:A5:264:U:H6	1.78	0.48
8:A5:3059:G:C2	40:CB:252:ALA:HB1	2.48	0.48
8:A5:3445:G:O2'	8:A5:3446:U:OP2	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AN:31:GLU:N	22:AN:31:GLU:CD	2.71	0.48
34:AJ:3:ARG:NH1	34:AJ:3:ARG:HB2	2.28	0.48
49:CE:105:GLY:O	49:CE:106:PRO:C	2.56	0.48
7:B2:159:G:H4'	7:B2:160:C:OP1	2.12	0.48
8:A5:428:A:C2	8:A5:2466:A:H4'	2.49	0.48
8:A5:3166:G:C2'	8:A5:3167:U:O5'	2.61	0.48
8:A5:3304:U:O2'	8:A5:3305:G:P	2.72	0.48
17:AO:114:GLN:HA	17:AO:114:GLN:NE2	2.29	0.48
18:AI:29:LEU:C	18:AI:29:LEU:HD12	2.39	0.48
65:CD:88:LEU:HD21	65:CD:239:TYR:CE1	2.44	0.48
65:CD:189:TYR:HH	65:CD:194:HIS:HD1	1.59	0.48
76:CJ:165:GLU:OE1	76:CJ:165:GLU:N	2.47	0.48
7:B2:1006:C:H2'	7:B2:1007:G:C8	2.49	0.48
8:A5:1222:A:OP1	37:CF:218:LYS:O	2.31	0.48
8:A5:3103:U:O2	67:CP:71:ARG:NH2	2.47	0.48
51:Cf:11:SER:O	51:Cf:12:ALA:HB3	2.14	0.48
59:CH:103:LEU:HG	59:CH:134:ILE:HD11	1.96	0.48
75:Cj:69:ASP:C	75:Cj:69:ASP:OD1	2.54	0.48
1:AD:108:ARG:HG2	1:AD:177:VAL:HG22	1.95	0.48
5:A7:24:U:H2'	5:A7:25:G:O4'	2.14	0.48
7:B2:1117:C:O2'	7:B2:1537:C:OP2	2.32	0.48
8:A5:697:U:H2'	8:A5:698:C:C6	2.49	0.48
31:Ae:76:SER:O	31:Ae:77:LEU:HB3	2.14	0.48
32:AX:98:ASP:OD1	32:AX:140:ARG:NH2	2.46	0.48
78:DB:25:C:H41	78:DB:45:G:H21	1.60	0.48
2:AB:80:ARG:HD3	2:AB:101:MET:HE2	1.96	0.48
3:AC:110:LYS:NZ	7:B2:1261:U:OP1	2.37	0.48
8:A5:44:A:OP2	54:CN:85:LYS:HD3	2.14	0.48
8:A5:816:G:O2'	8:A5:817:U:P	2.72	0.48
8:A5:3340:G:O2'	8:A5:3341:G:P	2.71	0.48
31:Ae:112:ARG:NE	31:Ae:112:ARG:C	2.72	0.48
44:CG:75:LEU:HD12	54:CN:25:ILE:HD11	1.95	0.48
61:CR:188:ILE:O	61:CR:192:GLU:HG2	2.14	0.48
7:B2:762:C:O4'	7:B2:762:C:O2	2.32	0.47
7:B2:1544:G:H1	7:B2:1564:U:H3	1.60	0.47
8:A5:2676:A:H2'	8:A5:2677:U:C6	2.49	0.47
11:AW:86:LEU:O	11:AW:90:THR:HG23	2.13	0.47
16:AA:167:GLY:O	16:AA:171:ILE:HG22	2.14	0.47
18:AI:76:THR:OG1	18:AI:77:ARG:N	2.47	0.47
21:AV:21:ASN:C	21:AV:21:ASN:HD22	2.22	0.47
22:AN:30:ALA:O	22:AN:34:GLN:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Ab:19:HIS:HB3	28:Ab:22:LYS:HG3	1.95	0.47
34:AJ:133:HIS:C	34:AJ:134:ILE:HD12	2.39	0.47
49:CE:104:THR:O	49:CE:104:THR:CG2	2.62	0.47
59:CH:111:GLU:OE2	59:CH:113:ARG:NH2	2.47	0.47
77:CX:133:ASP:OD1	77:CX:133:ASP:N	2.45	0.47
8:A5:2495:C:HO2'	40:CB:268:ARG:HH22	1.56	0.47
8:A5:2812:G:O2'	8:A5:2817:A:N1	2.40	0.47
1:AD:24:ASN:OD1	1:AD:24:ASN:C	2.58	0.47
7:B2:591:G:O2'	7:B2:597:A:N1	2.45	0.47
7:B2:1041:C:O2'	7:B2:1042:C:OP1	2.30	0.47
7:B2:1203:A:N3	7:B2:1203:A:O2'	2.38	0.47
8:A5:183:A:H3'	8:A5:184:U:C5'	2.44	0.47
8:A5:2253:A:H4'	43:CA:179:LEU:O	2.14	0.47
9:AR:104:ASP:OD1	9:AR:105:THR:N	2.48	0.47
2:AB:178:ASP:OD1	2:AB:181:GLU:HG3	2.14	0.47
4:AE:63:ILE:HD11	25:AY:18:LEU:HD12	1.96	0.47
7:B2:1280:A:H4'	7:B2:1281:A:O5'	2.14	0.47
18:AI:130:SER:N	18:AI:133:ASP:OD2	2.47	0.47
37:CF:199:GLU:OE1	37:CF:199:GLU:N	2.43	0.47
38:CS:176:ASN:ND2	38:CS:178:HIS:O	2.47	0.47
45:CI:111:LEU:HD11	78:DA:73:A:C2	2.50	0.47
70:Ck:58:GLN:OE1	70:Ck:58:GLN:HA	2.14	0.47
76:CJ:142:ASP:OD2	76:CJ:146:ARG:HD3	2.13	0.47
1:AD:177:VAL:HG21	1:AD:186:ILE:HD11	1.97	0.47
7:B2:881:C:O2	17:AO:56:ARG:NH2	2.47	0.47
8:A5:1657:U:O2	8:A5:1657:U:O4'	2.33	0.47
8:A5:2280:G:C5	43:CA:125:VAL:HG22	2.50	0.47
8:A5:3319:U:O2'	57:CM:98:ARG:NH2	2.47	0.47
40:CB:77:THR:OG1	40:CB:332:GLY:O	2.31	0.47
72:Cd:17:VAL:HG22	72:Cd:18:THR:N	2.30	0.47
76:CJ:127:ASP:OD1	76:CJ:127:ASP:C	2.57	0.47
4:AE:170:ASP:OD1	4:AE:171:SER:N	2.47	0.47
7:B2:115:G:H2'	7:B2:116:G:O4'	2.15	0.47
7:B2:1008:A:H2	7:B2:1034:G:H22	1.62	0.47
7:B2:1121:A:O2'	7:B2:1122:A:OP1	2.28	0.47
7:B2:1276:C:H2'	7:B2:1277:G:O4'	2.14	0.47
8:A5:189:G:O6	8:A5:240:G:N1	2.47	0.47
8:A5:693:C:H2'	8:A5:694:U:C6	2.50	0.47
8:A5:1652:C:H2'	8:A5:1653:C:O4'	2.15	0.47
8:A5:2610:C:O2'	8:A5:2611:U:P	2.72	0.47
8:A5:3453:U:HO2'	8:A5:3454:A:P	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AT:24:LYS:NZ	13:AT:52:ASP:OD2	2.30	0.47
20:AM:99:LEU:C	20:AM:99:LEU:HD12	2.40	0.47
22:AN:28:MET:HE2	22:AN:32:GLU:OE1	2.14	0.47
26:AU:55:MET:HE2	26:AU:55:MET:HA	1.97	0.47
26:AU:97:LEU:O	26:AU:98:ARG:C	2.56	0.47
35:AQ:47:ILE:H	35:AQ:47:ILE:HD12	1.79	0.47
47:CC:285:ALA:N	63:CQ:124:ASP:OD2	2.48	0.47
65:CD:119:TYR:OH	65:CD:138:ARG:O	2.30	0.47
8:A5:2948:C:H5	8:A5:2964:C:H42	1.62	0.47
8:A5:3013:G:H2'	8:A5:3014:A:C5'	2.45	0.47
8:A5:3377:G:O2'	8:A5:3378:A:OP1	2.22	0.47
10:AK:74:ILE:HD11	10:AK:89:PRO:CD	2.45	0.47
11:AW:112:ASP:OD2	11:AW:114:GLU:N	2.47	0.47
34:AJ:138:ARG:NH1	34:AJ:138:ARG:HB2	2.30	0.47
52:CI:38:LYS:O	52:CI:42:VAL:HG23	2.14	0.47
77:CX:95:ASN:OD1	77:CX:95:ASN:N	2.43	0.47
2:AB:74:ASN:C	2:AB:74:ASN:OD1	2.56	0.47
7:B2:301:A:O4'	7:B2:303:A:C8	2.68	0.47
7:B2:889:A:H2'	7:B2:890:G:C8	2.50	0.47
8:A5:133:U:O2'	8:A5:135:G:C5	2.66	0.47
8:A5:928:C:H4'	8:A5:929:U:OP2	2.15	0.47
8:A5:1672:A:H2'	8:A5:1673:G:C8	2.49	0.47
22:AN:13:LYS:NZ	22:AN:14:SER:O	2.48	0.47
25:AY:39:ASP:OD1	25:AY:39:ASP:N	2.48	0.47
52:CI:65:ILE:C	52:CI:66:SER:HG	2.11	0.47
64:CT:102:ARG:HG2	64:CT:102:ARG:HH11	1.80	0.47
71:Cm:83:ARG:O	71:Cm:87:GLN:HG3	2.14	0.47
6:A8:121:G:O2'	6:A8:122:C:O5'	2.30	0.47
7:B2:1266:U:O2	7:B2:1266:U:O4'	2.33	0.47
8:A5:2608:G:HO2'	8:A5:2609:A:P	2.36	0.47
8:A5:3253:G:N7	40:CB:23:ARG:NH2	2.63	0.47
7:B2:379:A:OP1	18:AI:49:ARG:NH2	2.48	0.46
7:B2:1188:G:N2	7:B2:1214:G:O2'	2.48	0.46
7:B2:1201:A:N6	7:B2:1203:A:C6	2.83	0.46
12:AS:5:ILE:HG23	12:AS:5:ILE:O	2.15	0.46
13:AT:112:TRP:NE1	13:AT:131:ASP:OD2	2.43	0.46
70:Ck:23:VAL:HG23	70:Ck:64:ILE:HD13	1.96	0.46
78:DA:3:C:H2'	78:DA:4:U:O4'	2.15	0.46
7:B2:360:U:H1'	34:AJ:3:ARG:O	2.15	0.46
7:B2:1436:G:OP1	13:AT:63:ARG:NE	2.39	0.46
7:B2:1721:G:OP1	7:B2:1724:A:H4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:580:U:C2'	8:A5:581:G:OP1	2.63	0.46
8:A5:1724:G:O2'	8:A5:1725:C:P	2.73	0.46
8:A5:2768:A:H4'	50:Co:97:LYS:HE3	1.97	0.46
8:A5:3160:C:O2'	8:A5:3161:A:H5'	2.14	0.46
6:A8:26:A:O2'	47:CC:52:ALA:O	2.33	0.46
7:B2:269:U:C2'	7:B2:270:C:OP1	2.64	0.46
7:B2:711:U:O2'	7:B2:712:U:OP1	2.22	0.46
8:A5:3389:U:O2'	8:A5:3390:C:P	2.73	0.46
19:AF:132:THR:HG21	30:Ac:22:CYS:SG	2.55	0.46
32:AX:11:ARG:NH2	33:AL:100:GLU:OE1	2.48	0.46
37:CF:234:ASP:O	37:CF:237:ASN:ND2	2.47	0.46
54:CN:46:GLU:OE1	54:CN:50:ARG:NH1	2.48	0.46
58:Cc:13:ALA:O	58:Cc:16:ILE:HG22	2.15	0.46
61:CR:116:ASP:OD1	61:CR:116:ASP:N	2.45	0.46
65:CD:137:ASP:OD1	65:CD:137:ASP:N	2.46	0.46
7:B2:1205:C:O2	7:B2:1205:C:O4'	2.33	0.46
8:A5:646:A:O2'	8:A5:647:A:OP1	2.30	0.46
8:A5:2609:A:O2'	8:A5:2610:C:OP1	2.33	0.46
9:AR:21:TYR:HE1	9:AR:58:MET:HE1	1.81	0.46
25:AY:106:LYS:O	25:AY:110:GLU:HG3	2.15	0.46
5:A7:29:G:O2'	5:A7:50:A:N1	2.45	0.46
8:A5:199:C:O2'	8:A5:201:A:N7	2.47	0.46
8:A5:781:U:O2	8:A5:790:G:O6	2.34	0.46
8:A5:3320:U:O2'	8:A5:3321:A:P	2.73	0.46
9:AR:87:GLU:OE2	9:AR:88:ILE:HG22	2.16	0.46
34:AJ:106:GLU:O	34:AJ:111:THR:OG1	2.29	0.46
49:CE:201:GLY:O	51:Cf:12:ALA:HB2	2.16	0.46
59:CH:45:MET:HG2	59:CH:55:VAL:HG22	1.97	0.46
76:CJ:126:TYR:CD1	76:CJ:126:TYR:C	2.93	0.46
76:CJ:178:ASP:O	76:CJ:178:ASP:OD2	2.33	0.46
78:DB:58:A:H4'	78:DB:59:U:OP1	2.14	0.46
4:AE:64:LEU:HD13	4:AE:79:HIS:HA	1.98	0.46
4:AE:137:VAL:HG12	4:AE:147:ARG:HA	1.98	0.46
7:B2:730:A:OP1	34:AJ:79:ARG:NH2	2.42	0.46
7:B2:1002:C:O2	11:AW:16:ASN:ND2	2.48	0.46
7:B2:1744:C:OP1	14:Aa:10:ARG:NH1	2.45	0.46
8:A5:2683:G:C2'	8:A5:2684:G:H5'	2.46	0.46
10:AK:71:ASP:N	10:AK:71:ASP:OD1	2.49	0.46
25:AY:48:TYR:C	25:AY:49:LYS:HG2	2.40	0.46
27:AG:126:ASP:OD1	27:AG:126:ASP:N	2.47	0.46
49:CE:138:GLU:OE2	49:CE:139:HIS:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Co:71:MET:HE1	50:Co:82:LEU:HD12	1.96	0.46
59:CH:41:LEU:HB2	59:CH:43:MET:HE2	1.97	0.46
66:CZ:84:ARG:NH1	66:CZ:85:TYR:OH	2.48	0.46
66:CZ:113:GLU:OE2	66:CZ:117:LYS:NZ	2.48	0.46
7:B2:894:C:C6	17:AO:138:SER:O	2.68	0.46
7:B2:1305:A:O2'	7:B2:1306:U:O5'	2.24	0.46
8:A5:74:G:H5'	42:CL:59:VAL:HG13	1.98	0.46
8:A5:2436:C:H2'	8:A5:2437:U:O4'	2.16	0.46
8:A5:3072:C:H2'	8:A5:3073:G:C8	2.50	0.46
8:A5:3286:G:N7	51:Cf:65:LYS:NZ	2.64	0.46
8:A5:3320:U:HO2'	8:A5:3321:A:P	2.30	0.46
34:AJ:134:ILE:HD12	34:AJ:134:ILE:N	2.29	0.46
7:B2:159:G:HO2'	7:B2:160:C:P	2.33	0.46
7:B2:1322:G:O2'	7:B2:1323:G:O4'	2.33	0.46
8:A5:833:A:H2'	8:A5:834:G:H5'	1.97	0.46
8:A5:2288:C:O2'	8:A5:2417:U:OP2	2.32	0.46
8:A5:2801:A:H2'	8:A5:2801:A:N3	2.30	0.46
8:A5:3128:C:H2'	8:A5:3129:U:O4'	2.16	0.46
8:A5:3415:C:OP1	40:CB:339:LYS:NZ	2.36	0.46
11:AW:105:THR:O	11:AW:105:THR:HG23	2.15	0.46
40:CB:26:ARG:HG3	40:CB:341:LEU:HD23	1.98	0.46
46:CO:55:TYR:OH	46:CO:74:TYR:O	2.34	0.46
72:Cd:14:ASN:HD22	72:Cd:14:ASN:C	2.22	0.46
8:A5:1244:G:O6	46:CO:57:SER:OG	2.34	0.46
8:A5:3106:A:C5	8:A5:3107:C:C5	3.04	0.46
8:A5:3375:C:O2'	8:A5:3376:A:P	2.73	0.46
9:AR:116:LEU:HB3	9:AR:119:VAL:HG13	1.98	0.46
11:AW:119:LYS:HB2	11:AW:121:LEU:HD12	1.98	0.46
41:CU:30:PRO:CB	41:CU:36:LEU:HD12	2.46	0.46
58:Cc:59:LYS:O	58:Cc:63:GLU:HG3	2.16	0.46
59:CH:169:ASP:OD2	59:CH:169:ASP:C	2.58	0.46
63:CQ:177:ALA:O	63:CQ:184:ARG:HB2	2.16	0.46
4:AE:255:MET:HA	4:AE:255:MET:CE	2.37	0.46
7:B2:1209:U:O2'	7:B2:1210:U:O4'	2.33	0.46
7:B2:1265:C:O2'	7:B2:1266:U:O2	2.33	0.46
8:A5:3288:A:H4'	8:A5:3289:G:OP1	2.15	0.46
34:AJ:82:LYS:N	34:AJ:82:LYS:CD	2.79	0.46
38:CS:88:ASP:OD1	38:CS:93:HIS:CD2	2.69	0.46
42:CL:174:ARG:NH1	55:Ca:139:GLY:O	2.49	0.46
44:CG:195:VAL:O	44:CG:195:VAL:CG1	2.64	0.46
54:CN:103:GLU:OE2	54:CN:118:SER:OG	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:Ca:51:GLY:N	63:CQ:178:ARG:O	2.47	0.46
60:CY:111:ASP:OD2	60:CY:113:ASP:N	2.49	0.46
78:DB:74:C:H2'	78:DB:75:C:C5'	2.46	0.46
1:AD:164:HIS:N	1:AD:165:PRO:HD2	2.30	0.45
7:B2:353:G:O2'	7:B2:354:U:OP1	2.33	0.45
7:B2:1490:A:H4'	7:B2:1491:U:OP1	2.15	0.45
8:A5:1275:A:C2	8:A5:1276:C:C5	3.03	0.45
8:A5:1473:G:OP1	73:Ce:35:ARG:NH2	2.48	0.45
8:A5:3466:U:O4'	18:AI:124:LYS:NZ	2.37	0.45
18:AI:139:LYS:NZ	18:AI:146:MET:HE1	2.31	0.45
24:Ad:46:GLN:O	24:Ad:50:ILE:HG12	2.16	0.45
36:AH:8:LEU:HD22	36:AH:20:GLU:HB3	1.97	0.45
59:CH:87:ARG:NH2	59:CH:145:GLU:OE2	2.47	0.45
8:A5:1063:A:H2'	8:A5:1064:G:O4'	2.16	0.45
8:A5:1246:G:H2'	8:A5:1247:A:C8	2.52	0.45
8:A5:2838:C:O2'	8:A5:2839:A:H2'	2.16	0.45
10:AK:88:VAL:HG22	10:AK:89:PRO:CD	2.45	0.45
61:CR:172:ARG:HE	61:CR:176:ARG:NH2	2.14	0.45
7:B2:1004:C:O2'	7:B2:1005:G:P	2.74	0.45
7:B2:1172:G:O2'	7:B2:1203:A:N6	2.36	0.45
8:A5:1155:C:O2'	8:A5:1156:G:P	2.75	0.45
8:A5:1569:A:N1	8:A5:1580:A:O2'	2.44	0.45
8:A5:3444:U:H2'	8:A5:3445:G:O4'	2.15	0.45
66:CZ:63:GLU:C	66:CZ:63:GLU:OE2	2.59	0.45
67:CP:43:LEU:HD21	67:CP:101:GLU:HG3	1.97	0.45
73:Ce:76:VAL:HB	73:Ce:87:LEU:HD21	1.98	0.45
6:A8:121:G:HO2'	6:A8:122:C:P	2.39	0.45
7:B2:1745:U:OP2	14:Aa:10:ARG:HD2	2.16	0.45
8:A5:134:U:H4'	8:A5:135:G:OP2	2.15	0.45
8:A5:3256:A:H1'	8:A5:3257:A:OP2	2.17	0.45
16:AA:50:ASN:OD1	16:AA:52:LYS:N	2.50	0.45
24:Ad:21:CYS:SG	24:Ad:23:VAL:HG22	2.57	0.45
35:AQ:59:GLU:N	35:AQ:59:GLU:CD	2.75	0.45
62:Cb:35:VAL:HG12	62:Cb:36:ASP:N	2.32	0.45
2:AB:154:THR:CG2	2:AB:159:ILE:HD11	2.46	0.45
7:B2:1491:U:O2	7:B2:1491:U:O4'	2.33	0.45
7:B2:1571:C:H2'	19:AF:66:ARG:HD2	1.99	0.45
8:A5:1277:A:H2'	8:A5:1278:G:C8	2.52	0.45
8:A5:3137:A:C2'	8:A5:3138:C:H5'	2.47	0.45
12:AS:68:VAL:HG13	12:AS:72:GLN:OE1	2.16	0.45
25:AY:17:LEU:H	25:AY:17:LEU:CD2	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AJ:30:LEU:HD22	34:AJ:105:LEU:HD12	1.98	0.45
35:AQ:61:PHE:CZ	35:AQ:90:LEU:HD22	2.51	0.45
42:CL:129:LYS:HE3	48:Ch:117:ARG:HD2	1.99	0.45
47:CC:161:ARG:CZ	47:CC:214:ALA:O	2.64	0.45
1:AD:159:MET:HE2	1:AD:159:MET:HB2	1.91	0.45
8:A5:822:U:O2	8:A5:822:U:O4'	2.35	0.45
10:AK:74:ILE:HD11	10:AK:89:PRO:HD2	1.97	0.45
45:CI:180:ASP:OD2	45:CI:183:ARG:NH1	2.50	0.45
64:CT:114:GLU:CD	64:CT:114:GLU:C	2.84	0.45
3:AC:266:HIS:HB3	16:AA:69:GLU:OE2	2.16	0.45
7:B2:130:U:HO2'	7:B2:131:A:P	2.36	0.45
7:B2:1125:C:OP1	19:AF:85:HIS:N	2.47	0.45
8:A5:194:C:O2'	8:A5:195:C:P	2.72	0.45
10:AK:6:SER:O	10:AK:9:LYS:HB2	2.17	0.45
18:AI:36:THR:OG1	18:AI:57:ALA:O	2.23	0.45
22:AN:32:GLU:OE1	22:AN:32:GLU:C	2.60	0.45
25:AY:36:PRO:O	25:AY:40:ILE:HG13	2.17	0.45
31:Ae:84:ARG:NH2	32:AX:134:PHE:O	2.42	0.45
36:AH:35:ASP:OD1	36:AH:35:ASP:N	2.49	0.45
54:CN:3:ALA:O	54:CN:7:MET:HG3	2.16	0.45
54:CN:85:LYS:HG3	54:CN:86:THR:HG23	1.98	0.45
77:CX:109:VAL:HG11	77:CX:130:LEU:HD13	1.99	0.45
7:B2:110:A:H2'	7:B2:111:U:H5'	1.98	0.45
7:B2:992:A:OP1	7:B2:1743:G:O2'	2.24	0.45
7:B2:1480:A:H2'	7:B2:1481:A:C8	2.51	0.45
8:A5:3331:U:O2	8:A5:3331:U:O4'	2.35	0.45
20:AM:126:GLU:OE1	20:AM:129:ARG:NE	2.49	0.45
42:CL:164:ASP:OD1	42:CL:164:ASP:N	2.49	0.45
7:B2:424:C:N4	7:B2:436:U:H3'	2.32	0.45
7:B2:1121:A:HO2'	7:B2:1122:A:P	2.38	0.45
7:B2:1347:U:H5'	9:AR:48:ASN:HB3	1.99	0.45
7:B2:1348:A:O2'	7:B2:1349:A:OP2	2.32	0.45
8:A5:879:C:O2'	8:A5:1599:A:N3	2.45	0.45
8:A5:955:G:H1'	8:A5:1665:A:N6	2.31	0.45
8:A5:2509:C:H2'	8:A5:2510:C:C6	2.52	0.45
8:A5:3139:G:H21	8:A5:3141:G:H5''	1.81	0.45
30:Ac:35:ASN:OD1	30:Ac:35:ASN:N	2.50	0.45
59:CH:141:GLU:C	59:CH:142:ILE:HD13	2.42	0.45
2:AB:129:ASP:OD2	2:AB:129:ASP:N	2.49	0.45
2:AB:134:ARG:HB2	2:AB:216:ILE:HD11	1.99	0.45
7:B2:385:C:O2'	27:AG:92:ARG:O	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:1712:U:O2'	8:A5:2365:A:N1	2.44	0.45
8:A5:1950:C:N4	8:A5:1951:A:N6	2.65	0.45
8:A5:2625:G:C2'	8:A5:2626:U:O5'	2.65	0.45
8:A5:3283:U:O2'	8:A5:3284:C:P	2.74	0.45
8:A5:3465:U:C6	8:A5:3465:U:C2'	3.00	0.45
9:AR:103:THR:HG22	9:AR:103:THR:O	2.17	0.45
26:AU:61:ARG:C	26:AU:62:ILE:HD12	2.42	0.45
34:AJ:3:ARG:HB2	34:AJ:3:ARG:CZ	2.47	0.45
76:CJ:91:GLU:HG3	76:CJ:92:LYS:N	2.30	0.45
2:AB:104:THR:HG23	17:AO:131:GLU:OE1	2.17	0.44
7:B2:18:U:H2'	7:B2:19:C:C6	2.53	0.44
7:B2:348:U:H2'	7:B2:349:A:O4'	2.17	0.44
7:B2:1295:A:H2'	7:B2:1296:G:O4'	2.16	0.44
7:B2:1715:U:OP2	79:DC:4:U:O2'	2.29	0.44
8:A5:1737:U:O2'	8:A5:1738:U:OP2	2.30	0.44
9:AR:72:LYS:O	9:AR:76:GLU:HG2	2.17	0.44
26:AU:29:LYS:HB2	26:AU:30:PRO:HD3	1.98	0.44
47:CC:36:VAL:HG21	47:CC:245:LEU:HD21	1.99	0.44
66:CZ:99:GLU:H	66:CZ:99:GLU:CD	2.25	0.44
70:Ck:18:LYS:H	70:Ck:18:LYS:HD2	1.82	0.44
8:A5:1150:G:H4'	8:A5:1151:A:O5'	2.17	0.44
8:A5:1385:C:OP1	63:CQ:2:GLY:N	2.50	0.44
8:A5:1926:G:O2'	53:Cl:3:ALA:O	2.35	0.44
8:A5:3186:G:H3'	8:A5:3187:A:H5''	1.98	0.44
8:A5:3474:C:H5''	8:A5:3475:G:OP2	2.17	0.44
11:AW:80:ASN:OD1	11:AW:124:LYS:NZ	2.49	0.44
16:AA:19:LEU:H	16:AA:19:LEU:HD12	1.82	0.44
25:AY:39:ASP:O	25:AY:43:LYS:HG3	2.17	0.44
29:AP:20:LYS:N	29:AP:20:LYS:HD3	2.33	0.44
36:AH:63:VAL:HG22	36:AH:64:PRO:CD	2.47	0.44
7:B2:491:A:H2'	7:B2:492:G:OP1	2.17	0.44
8:A5:303:G:O6	54:CN:12:ARG:NH1	2.43	0.44
8:A5:3347:U:H3	8:A5:3358:G:H1	1.64	0.44
12:AS:110:ASP:O	12:AS:114:MET:HG3	2.17	0.44
19:AF:50:LYS:O	19:AF:53:LYS:NZ	2.50	0.44
26:AU:54:ARG:HD3	26:AU:86:ARG:NE	2.33	0.44
78:DB:44:A:O3'	78:DB:45:G:O4'	2.35	0.44
4:AE:128:VAL:HG13	4:AE:128:VAL:O	2.17	0.44
7:B2:136:C:O3'	27:AG:15:SER:OG	2.35	0.44
7:B2:1670:G:O2'	7:B2:1671:C:P	2.76	0.44
8:A5:1228:C:H3'	8:A5:1229:U:O2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:1650:U:H2'	8:A5:1651:C:C6	2.53	0.44
8:A5:3053:A:OP2	40:CB:258:HIS:ND1	2.51	0.44
8:A5:3156:C:OP1	39:CV:48:ARG:NE	2.48	0.44
19:AF:210:ARG:HD2	30:Ac:59:ARG:NH1	2.33	0.44
34:AJ:118:LEU:HD22	34:AJ:118:LEU:H	1.82	0.44
43:CA:179:LEU:O	43:CA:180:LEU:C	2.61	0.44
65:CD:133:GLU:H	65:CD:133:GLU:CD	2.25	0.44
7:B2:356:C:C2'	7:B2:357:G:O5'	2.66	0.44
7:B2:1040:U:O2	7:B2:1040:U:O4'	2.36	0.44
7:B2:1066:G:O2'	7:B2:1067:G:H5'	2.17	0.44
7:B2:1121:A:O2'	7:B2:1122:A:P	2.76	0.44
8:A5:227:C:O2	8:A5:227:C:O4'	2.31	0.44
8:A5:1838:U:H3'	8:A5:1839:C:C5'	2.48	0.44
8:A5:1905:G:H2'	8:A5:1906:C:C6	2.53	0.44
9:AR:72:LYS:HD3	9:AR:75:GLU:OE2	2.18	0.44
12:AS:124:ARG:NH1	29:AP:129:TYR:OH	2.50	0.44
19:AF:65:ARG:HB2	19:AF:65:ARG:CZ	2.48	0.44
25:AY:41:ARG:CG	25:AY:55:VAL:HG23	2.45	0.44
43:CA:94:ALA:HB3	43:CA:102:VAL:HG12	1.98	0.44
68:Cn:1:MET:N	68:Cn:1:MET:SD	2.91	0.44
2:AB:36:MET:HE3	2:AB:229:LEU:HD21	2.00	0.44
7:B2:1297:C:O2'	7:B2:1298:C:P	2.75	0.44
7:B2:1328:G:H2'	7:B2:1329:U:O4'	2.17	0.44
8:A5:12:C:H5'	8:A5:13:U:OP2	2.18	0.44
8:A5:753:U:H2'	8:A5:754:C:O4'	2.18	0.44
8:A5:1914:U:C2'	8:A5:1915:U:OP1	2.65	0.44
10:AK:83:LEU:HD12	10:AK:83:LEU:N	2.32	0.44
16:AA:121:LEU:HD13	16:AA:122:LEU:N	2.32	0.44
20:AM:104:LYS:HD2	20:AM:104:LYS:C	2.43	0.44
24:Ad:52:PHE:HB3	26:Au:79:PHE:HB3	1.99	0.44
28:Ab:65:GLN:OE1	28:Ab:65:GLN:HA	2.17	0.44
31:Ae:106:ARG:O	31:Ae:110:THR:HG23	2.18	0.44
40:CB:195:ASP:O	40:CB:199:GLU:HG2	2.17	0.44
52:Ci:65:ILE:O	52:Ci:65:ILE:HG22	2.17	0.44
63:CQ:62:SER:OG	63:CQ:89:ASP:OD2	2.36	0.44
65:CD:30:TYR:HA	65:CD:33:ARG:HB3	2.00	0.44
70:Ck:55:LYS:O	70:Ck:59:SER:OG	2.32	0.44
7:B2:360:U:C2	34:AJ:3:ARG:O	2.71	0.44
7:B2:568:C:H2'	7:B2:569:U:O4'	2.17	0.44
7:B2:1429:U:O2	7:B2:1429:U:H2'	2.18	0.44
8:A5:646:A:HO2'	8:A5:647:A:P	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AI:113:TYR:CD1	18:AI:121:LEU:HD22	2.52	0.44
36:AH:80:ARG:HG3	36:AH:81:GLU:N	2.33	0.44
40:CB:220:ILE:HG12	40:CB:278:THR:HG23	1.99	0.44
3:AC:72:ILE:HG23	3:AC:77:GLU:OE1	2.17	0.44
7:B2:491:A:C2'	7:B2:492:G:OP1	2.66	0.44
7:B2:1425:A:H2'	7:B2:1426:C:C6	2.53	0.44
8:A5:306:G:OP2	52:CI:83:ARG:NH2	2.42	0.44
8:A5:3455:G:H21	8:A5:3476:A:H2	1.62	0.44
11:AW:51:GLU:HG3	28:Ab:8:LEU:HD11	2.00	0.44
36:AH:135:TYR:CG	36:AH:136:PRO:HA	2.52	0.44
42:CL:103:THR:HG21	52:CI:27:ARG:HD2	2.00	0.44
48:Ch:37:THR:HG21	77:CX:145:PHE:HA	1.99	0.44
69:Cg:44:CYS:SG	69:Cg:49:VAL:HG22	2.58	0.44
7:B2:3:A:O4'	7:B2:350:A:C8	2.71	0.44
7:B2:30:G:OP1	32:AX:124:LYS:NZ	2.49	0.44
7:B2:346:A:OP1	7:B2:726:U:O2'	2.25	0.44
7:B2:1613:U:H3'	7:B2:1614:G:H5''	2.00	0.44
8:A5:134:U:O2'	48:Ch:85:LEU:HD12	2.17	0.44
8:A5:711:A:H2'	8:A5:712:A:C8	2.52	0.44
8:A5:3184:C:O2	8:A5:3184:C:O4'	2.35	0.44
8:A5:3338:U:H4'	8:A5:3338:U:OP1	2.18	0.44
10:AK:15:LEU:HD12	10:AK:15:LEU:O	2.18	0.44
36:AH:4:ILE:HD12	36:AH:4:ILE:N	2.32	0.44
47:CC:210:TYR:CE1	47:CC:213:ASP:HB2	2.52	0.44
73:Ce:102:VAL:O	73:Ce:107:ARG:NH1	2.51	0.44
78:DB:17:U:C5	78:DB:18:G:H2'	2.52	0.44
79:DC:6:U:O3'	79:DC:7:U:P	2.74	0.44
4:AE:207:ILE:HD11	4:AE:221:ILE:HD12	2.00	0.43
7:B2:746:G:N2	7:B2:750:G:C5	2.85	0.43
7:B2:1280:A:H1'	7:B2:1281:A:OP2	2.18	0.43
7:B2:1552:C:O2	7:B2:1552:C:O5'	2.36	0.43
7:B2:1597:C:O2'	68:Cn:2:ARG:NH1	2.51	0.43
7:B2:1750:C:O2'	14:Aa:95:ARG:NH1	2.51	0.43
8:A5:1226:G:N2	46:CO:88:MET:SD	2.91	0.43
8:A5:1427:A:H2'	8:A5:1428:C:O4'	2.18	0.43
22:AN:63:VAL:HG11	22:AN:71:ILE:HG12	1.99	0.43
30:Ac:24:GLN:NE2	30:Ac:41:ASN:OD1	2.48	0.43
63:CQ:33:ALA:HA	63:CQ:48:LEU:HD22	1.99	0.43
64:CT:25:GLU:OE2	64:CT:29:THR:OG1	2.36	0.43
7:B2:851:U:O2'	17:AO:136:ILE:O	2.34	0.43
7:B2:1511:A:HO2'	7:B2:1512:A:P	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:1573:U:H2'	7:B2:1574:C:C6	2.53	0.43
8:A5:1031:U:H2'	8:A5:1032:C:O4'	2.18	0.43
8:A5:1150:G:H2'	8:A5:1150:G:N3	2.34	0.43
8:A5:1669:A:H4'	69:Cg:60:ILE:HG21	2.00	0.43
8:A5:1865:G:H2'	8:A5:1866:U:O4'	2.17	0.43
8:A5:2992:U:O2	40:CB:252:ALA:HB3	2.17	0.43
8:A5:3305:G:C2'	8:A5:3306:G:OP1	2.65	0.43
8:A5:3465:U:C6	8:A5:3465:U:H2'	2.53	0.43
9:AR:54:ILE:O	9:AR:58:MET:HG2	2.18	0.43
13:AT:133:ASP:OD1	13:AT:133:ASP:N	2.49	0.43
16:AA:11:THR:HG1	16:AA:13:GLU:CD	2.20	0.43
34:AJ:87:ASP:OD2	34:AJ:90:LYS:HB2	2.18	0.43
35:AQ:98:VAL:HG12	35:AQ:99:ASP:N	2.33	0.43
38:CS:24:LYS:HB2	38:CS:24:LYS:NZ	2.33	0.43
4:AE:231:ASN:O	4:AE:231:ASN:CG	2.61	0.43
7:B2:96:G:H1	7:B2:290:C:H5	1.66	0.43
7:B2:1041:C:O2	7:B2:1041:C:O4'	2.35	0.43
7:B2:1316:A:O2'	7:B2:1317:U:H6	2.01	0.43
8:A5:88:A:N7	63:CQ:173:LYS:NZ	2.66	0.43
8:A5:930:G:O2'	8:A5:1984:A:OP1	2.35	0.43
8:A5:1694:G:H2'	8:A5:1695:A:C8	2.54	0.43
8:A5:2472:G:H2'	8:A5:2473:G:C8	2.54	0.43
20:AM:32:ALA:HB3	20:AM:123:GLY:HA2	2.00	0.43
29:AP:36:ARG:NH2	29:AP:94:GLU:OE2	2.51	0.43
36:AH:3:GLU:N	36:AH:3:GLU:CD	2.76	0.43
36:AH:193:ILE:HD12	36:AH:194:PHE:N	2.34	0.43
40:CB:74:GLU:OE2	40:CB:285:TYR:OH	2.31	0.43
57:CM:12:VAL:O	57:CM:58:THR:OG1	2.32	0.43
59:CH:19:THR:HG23	59:CH:19:THR:O	2.18	0.43
1:AD:177:VAL:CG2	1:AD:186:ILE:HD11	2.49	0.43
1:AD:212:ILE:HD12	9:AR:16:LEU:CD2	2.49	0.43
7:B2:1194:C:C2	7:B2:1195:A:C8	3.07	0.43
7:B2:1433:G:OP1	13:AT:45:GLU:N	2.43	0.43
8:A5:93:G:H2'	8:A5:94:A:C8	2.54	0.43
8:A5:263:U:H2'	8:A5:264:U:C6	2.53	0.43
8:A5:1567:G:C4	8:A5:1568:A:C8	3.07	0.43
18:AI:191:GLU:HG3	33:AL:18:ASN:OD1	2.19	0.43
25:AY:64:ILE:C	25:AY:64:ILE:HD12	2.42	0.43
64:CT:90:ASN:C	64:CT:91:ILE:HD13	2.43	0.43
70:Ck:8:ILE:HD13	70:Ck:45:LEU:HD21	2.01	0.43
7:B2:1027:U:H4'	7:B2:1028:G:OP2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:365:U:C2'	8:A5:366:G:O5'	2.66	0.43
8:A5:3059:G:N3	40:CB:252:ALA:HB1	2.33	0.43
8:A5:3309:A:O2'	8:A5:3310:C:OP1	2.34	0.43
11:AW:112:ASP:OD2	11:AW:112:ASP:C	2.61	0.43
27:AG:38:ILE:HG13	27:AG:45:TRP:HB3	2.00	0.43
28:Ab:40:CYS:O	28:Ab:41:PHE:CD1	2.71	0.43
45:CI:177:ASP:OD1	45:CI:180:ASP:HB2	2.18	0.43
48:Ch:82:ASP:OD2	48:Ch:82:ASP:N	2.50	0.43
49:CE:92:LEU:HD11	49:CE:104:THR:HG22	2.00	0.43
51:Cf:123:ASN:C	51:Cf:123:ASN:OD1	2.62	0.43
76:CJ:136:ASP:OD2	76:CJ:136:ASP:N	2.51	0.43
5:A7:28:C:OP2	65:CD:57:ASN:ND2	2.51	0.43
7:B2:242:A:H2'	7:B2:243:G:C8	2.53	0.43
7:B2:318:A:OP2	33:AL:133:LYS:HD2	2.18	0.43
7:B2:1016:G:C2'	7:B2:1017:G:OP1	2.66	0.43
8:A5:3022:A:O2'	8:A5:3243:A:N1	2.49	0.43
8:A5:3052:A:N7	40:CB:2:SER:N	2.67	0.43
8:A5:3321:A:O2'	8:A5:3322:U:P	2.77	0.43
8:A5:3475:G:H2'	8:A5:3476:A:C2	2.53	0.43
8:A5:3487:C:C2'	8:A5:3488:U:H5'	2.49	0.43
9:AR:92:ASP:OD2	9:AR:93:PRO:HD2	2.18	0.43
20:AM:82:ILE:HG22	20:AM:82:ILE:O	2.17	0.43
40:CB:56:ILE:HD13	40:CB:362:LEU:HD22	2.01	0.43
54:CN:121:VAL:HG11	54:CN:131:GLU:HG3	1.99	0.43
59:CH:115:PHE:O	59:CH:118:GLU:HG3	2.19	0.43
74:CW:85:VAL:CG1	74:CW:86:ALA:N	2.81	0.43
76:CJ:53:GLN:NE2	76:CJ:80:THR:O	2.52	0.43
2:AB:73:ASN:O	2:AB:74:ASN:OD1	2.37	0.43
8:A5:1787:U:O2'	8:A5:1788:U:H5'	2.19	0.43
8:A5:2685:C:O2'	8:A5:2686:A:P	2.76	0.43
14:Aa:55:ASP:OD1	14:Aa:55:ASP:N	2.51	0.43
18:AI:8:TRP:O	18:AI:9:HIS:CG	2.72	0.43
22:AN:42:LYS:HG2	22:AN:80:MET:HE1	1.99	0.43
34:AJ:66:ASP:OD2	34:AJ:67:PRO:N	2.52	0.43
52:CI:61:GLU:OE2	52:CI:64:ARG:NH2	2.35	0.43
69:Cg:20:LYS:HB2	69:Cg:32:VAL:HG13	2.01	0.43
70:Ck:31:ASN:OD1	70:Ck:31:ASN:C	2.60	0.43
1:AD:10:LYS:HD2	26:AU:60:LEU:HD22	2.01	0.43
4:AE:131:VAL:HG13	4:AE:137:VAL:HG21	2.01	0.43
6:A8:123:C:O2'	6:A8:125:C:C5	2.71	0.43
7:B2:130:U:H5	7:B2:152:A:N7	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:361:C:OP1	34:AJ:2:ALA:N	2.51	0.43
7:B2:1201:A:O2'	7:B2:1202:A:H5'	2.18	0.43
8:A5:190:A:N3	8:A5:216:C:O2'	2.45	0.43
8:A5:3334:G:O2'	8:A5:3335:G:OP1	2.36	0.43
22:AN:103:GLU:OE1	22:AN:103:GLU:N	2.52	0.43
34:AJ:107:ARG:O	34:AJ:148:VAL:HG22	2.18	0.43
37:CF:108:LEU:O	37:CF:109:ARG:HB2	2.19	0.43
40:CB:286:ARG:NH1	40:CB:299:ASN:O	2.51	0.43
63:CQ:39:THR:OG1	63:CQ:44:ASN:ND2	2.51	0.43
65:CD:50:ARG:NH2	65:CD:72:ASP:OD2	2.44	0.43
7:B2:72:U:H2'	7:B2:73:G:O4'	2.19	0.43
7:B2:513:G:H3'	34:AJ:175:ARG:HH22	1.84	0.43
7:B2:1131:G:H2'	7:B2:1132:C:O4'	2.18	0.43
7:B2:1299:U:C2	7:B2:1301:C:C5	3.06	0.43
8:A5:1048:G:N2	8:A5:1049:U:O4	2.40	0.43
8:A5:1605:C:O4'	8:A5:1605:C:O2	2.35	0.43
8:A5:1781:C:O2	8:A5:1781:C:O4'	2.35	0.43
8:A5:2335:A:H2'	8:A5:2336:A:C8	2.54	0.43
11:AW:66:THR:OG1	11:AW:68:ARG:HG3	2.19	0.43
12:AS:84:LEU:HD12	12:AS:95:THR:HG22	2.00	0.43
14:Aa:51:ARG:CZ	14:Aa:51:ARG:HB3	2.49	0.43
36:AH:41:LYS:HG3	36:AH:42:GLU:OE1	2.19	0.43
44:CG:104:ARG:NH2	44:CG:193:THR:O	2.51	0.43
45:CI:189:ARG:NH2	45:CI:202:GLU:OE2	2.45	0.43
72:Cd:20:GLU:OE1	72:Cd:83:ARG:NE	2.51	0.43
2:AB:161:LYS:O	2:AB:165:GLU:HG3	2.18	0.43
7:B2:127:G:O2'	7:B2:128:G:OP2	2.33	0.43
7:B2:440:A:H2'	7:B2:441:U:H5''	2.01	0.43
7:B2:1027:U:O2'	7:B2:1028:G:P	2.77	0.43
7:B2:1213:C:O2'	7:B2:1214:G:OP1	2.35	0.43
7:B2:1324:G:N3	13:AT:5:THR:OG1	2.52	0.43
8:A5:182:U:H4'	8:A5:183:A:OP2	2.18	0.43
8:A5:443:A:H2'	8:A5:642:G:O2'	2.19	0.43
8:A5:1912:A:O2'	8:A5:1913:U:P	2.70	0.43
8:A5:2838:C:O2	8:A5:2838:C:O5'	2.36	0.43
8:A5:3014:A:OP2	8:A5:3015:A:OP2	2.37	0.43
8:A5:3126:U:H2'	8:A5:3127:C:C6	2.54	0.43
14:Aa:85:ARG:HB3	14:Aa:85:ARG:HH11	1.84	0.43
19:AF:83:MET:HE2	19:AF:90:GLY:H	1.83	0.43
22:AN:25:TRP:NE1	28:Ab:83:GLN:O	2.52	0.43
27:AG:106:MET:HE2	27:AG:106:MET:HB3	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:CF:229:PHE:CD1	37:CF:229:PHE:C	2.95	0.43
40:CB:392:ASP:OD1	40:CB:392:ASP:N	2.49	0.43
44:CG:108:THR:OG1	44:CG:109:GLU:OE1	2.36	0.43
58:Cc:57:LEU:HD13	69:Cg:91:ARG:HG3	2.01	0.43
1:AD:174:VAL:O	1:AD:175:ARG:HD3	2.19	0.42
7:B2:191:U:H2'	7:B2:192:U:C6	2.54	0.42
7:B2:1562:C:H2'	7:B2:1563:G:O4'	2.19	0.42
8:A5:380:A:H4'	8:A5:381:A:OP1	2.18	0.42
8:A5:1844:A:HO2'	8:A5:1845:A:P	2.34	0.42
81:A5:3602:3HE:H20	81:A5:3602:3HE:H6	2.01	0.42
26:AU:39:ILE:HG22	26:AU:43:LYS:HD2	1.99	0.42
30:Ac:59:ARG:HH11	30:Ac:59:ARG:HG3	1.84	0.42
34:AJ:109:LEU:HG	34:AJ:129:ILE:HD11	2.01	0.42
35:AQ:114:ASP:OD1	35:AQ:116:SER:OG	2.37	0.42
37:CF:218:LYS:C	37:CF:220:THR:H	2.27	0.42
47:CC:130:SER:CB	47:CC:249:ILE:HD12	2.49	0.42
61:CR:68:GLU:OE1	61:CR:71:ARG:NH2	2.52	0.42
78:DA:18:G:H4'	78:DA:60:C:C2	2.54	0.42
3:AC:263:GLN:NE2	21:AV:35:ASP:OD1	2.52	0.42
7:B2:510:U:OP1	34:AJ:168:ARG:NH1	2.44	0.42
7:B2:589:G:H4'	7:B2:590:C:OP1	2.19	0.42
7:B2:1216:U:O2'	7:B2:1217:U:O5'	2.37	0.42
7:B2:1414:G:OP1	12:AS:136:THR:N	2.50	0.42
7:B2:1479:G:N7	13:AT:64:HIS:NE2	2.61	0.42
7:B2:1529:A:H4'	7:B2:1530:G:O5'	2.18	0.42
8:A5:3266:U:O2	8:A5:3266:U:O4'	2.36	0.42
12:AS:21:ASP:OD2	12:AS:21:ASP:C	2.63	0.42
34:AJ:78:ARG:O	34:AJ:82:LYS:HG2	2.19	0.42
47:CC:41:ASP:OD2	47:CC:45:ARG:NH1	2.52	0.42
59:CH:18:PHE:O	59:CH:19:THR:HG22	2.19	0.42
60:CY:36:LYS:O	60:CY:40:THR:HG23	2.18	0.42
76:CJ:117:GLN:N	76:CJ:117:GLN:CD	2.77	0.42
7:B2:972:C:H5'	17:AO:152:LEU:HB2	2.00	0.42
7:B2:986:C:O2	7:B2:986:C:H2'	2.18	0.42
7:B2:1307:A:H2'	7:B2:1308:G:O5'	2.19	0.42
8:A5:1759:A:H2'	8:A5:1760:A:C8	2.55	0.42
8:A5:2257:G:H21	43:CA:237:LEU:CD2	2.32	0.42
8:A5:2608:G:O2'	8:A5:2609:A:P	2.76	0.42
11:AW:49:GLU:OE1	36:AH:145:ARG:NE	2.48	0.42
16:AA:15:VAL:O	16:AA:19:LEU:HD12	2.18	0.42
20:AM:129:ARG:O	20:AM:132:LEU:HD12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AV:35:ASP:OD2	21:AV:35:ASP:N	2.51	0.42
36:AH:78:LEU:O	36:AH:82:LEU:HD23	2.18	0.42
41:CU:20:HIS:C	41:CU:20:HIS:ND1	2.75	0.42
42:CL:138:ASP:N	42:CL:138:ASP:OD1	2.51	0.42
48:Ch:19:LYS:O	48:Ch:23:GLU:HG3	2.20	0.42
1:AD:126:ARG:O	1:AD:130:GLU:HG2	2.19	0.42
4:AE:133:LYS:N	7:B2:237:A:OP1	2.51	0.42
4:AE:254:ARG:HH11	4:AE:254:ARG:HG3	1.84	0.42
7:B2:127:G:O2'	7:B2:128:G:P	2.78	0.42
7:B2:904:A:H2'	7:B2:905:A:C8	2.54	0.42
7:B2:945:G:H4'	7:B2:1730:A:H4'	2.02	0.42
7:B2:1119:A:H2'	7:B2:1120:C:C6	2.55	0.42
7:B2:1504:G:OP1	29:AP:24:ARG:NH2	2.52	0.42
7:B2:1550:G:H2'	7:B2:1551:U:O4'	2.20	0.42
8:A5:680:G:O2'	8:A5:1500:A:OP1	2.38	0.42
8:A5:3365:U:O2'	8:A5:3366:U:P	2.77	0.42
8:A5:3392:A:H2'	8:A5:3393:U:O4'	2.19	0.42
9:AR:88:ILE:HA	16:AA:203:MET:HE1	2.00	0.42
11:AW:35:VAL:O	11:AW:39:THR:OG1	2.34	0.42
18:AI:203:ARG:HB3	18:AI:203:ARG:HH11	1.83	0.42
49:CE:131:VAL:O	49:CE:134:VAL:HG12	2.19	0.42
56:Cp:48:LYS:HB3	56:Cp:48:LYS:HE2	1.88	0.42
59:CH:93:VAL:HG22	71:Cm:82:LEU:HB3	2.01	0.42
7:B2:1103:U:HO2'	7:B2:1260:U:HO2'	1.64	0.42
7:B2:1110:A:HO2'	7:B2:1111:A:P	2.42	0.42
7:B2:1512:A:H1'	7:B2:1516:U:OP2	2.20	0.42
8:A5:66:A:N1	8:A5:306:G:O2'	2.44	0.42
8:A5:250:A:H2'	8:A5:251:C:C6	2.54	0.42
8:A5:703:G:OP1	47:CC:32:ARG:NH1	2.42	0.42
8:A5:739:A:OP1	63:CQ:181:ARG:NH2	2.52	0.42
8:A5:816:G:HO2'	8:A5:817:U:P	2.40	0.42
8:A5:1593:G:O2'	8:A5:1664:A:H8	2.03	0.42
8:A5:1627:G:O2'	8:A5:1628:G:OP2	2.31	0.42
8:A5:2204:U:O5'	8:A5:2204:U:O2	2.37	0.42
8:A5:3105:G:H2'	8:A5:3106:A:H8	1.84	0.42
16:AA:115:THR:O	16:AA:115:THR:CG2	2.66	0.42
25:AY:7:ILE:HD12	25:AY:7:ILE:N	2.35	0.42
43:CA:5:ILE:HG22	43:CA:208:GLU:O	2.19	0.42
44:CG:236:LYS:O	44:CG:236:LYS:HG2	2.19	0.42
59:CH:61:VAL:O	59:CH:62:ARG:C	2.62	0.42
6:A8:69:C:H2'	6:A8:70:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B2:1106:A:O2'	7:B2:1592:C:OP2	2.32	0.42
7:B2:1347:U:O2	7:B2:1347:U:O2'	2.30	0.42
7:B2:1427:A:H2	7:B2:1430:G:N3	2.17	0.42
7:B2:1430:G:H2'	7:B2:1431:G:C8	2.55	0.42
7:B2:1465:A:H2'	7:B2:1466:U:O4'	2.20	0.42
8:A5:189:G:H1'	8:A5:190:A:P	2.59	0.42
8:A5:520:A:O2'	8:A5:3382:C:N3	2.50	0.42
8:A5:2324:G:N2	8:A5:2327:A:OP2	2.42	0.42
11:AW:30:ALA:HB2	11:AW:61:ILE:HG13	2.02	0.42
12:AS:3:LEU:O	23:AZ:46:PHE:HB2	2.19	0.42
14:Aa:21:ILE:C	14:Aa:21:ILE:HD12	2.44	0.42
34:AJ:93:LEU:O	34:AJ:96:VAL:HG12	2.19	0.42
78:DA:54:U:O3'	78:DA:55:U:O4'	2.38	0.42
7:B2:67:A:OP2	27:AG:160:HIS:NE2	2.53	0.42
7:B2:933:U:H2'	7:B2:934:C:O4'	2.20	0.42
7:B2:1005:G:O2'	7:B2:1006:C:H5'	2.19	0.42
8:A5:2503:G:C5'	8:A5:2504:A:OP2	2.67	0.42
8:A5:3094:A:O3'	8:A5:3095:C:O2	2.37	0.42
8:A5:3186:G:H2'	8:A5:3187:A:O4'	2.20	0.42
8:A5:3283:U:H2'	8:A5:3284:C:O4'	2.20	0.42
8:A5:3389:U:O2'	8:A5:3390:C:OP1	2.36	0.42
10:AK:69:LEU:HD21	10:AK:77:LEU:HD12	2.01	0.42
10:AK:87:ILE:HD12	10:AK:87:ILE:N	2.34	0.42
20:AM:59:VAL:C	20:AM:60:LEU:HD12	2.45	0.42
24:Ad:6:LEU:HA	24:Ad:9:SER:OG	2.19	0.42
32:AX:95:GLU:OE1	32:AX:140:ARG:NE	2.48	0.42
34:AJ:90:LYS:HD3	34:AJ:95:TYR:HB3	2.02	0.42
4:AE:219:THR:OG1	4:AE:220:ARG:N	2.52	0.42
5:A7:67:U:OP1	65:CD:14:LYS:HG3	2.20	0.42
7:B2:1110:A:O2'	7:B2:1111:A:P	2.78	0.42
7:B2:1417:C:H4'	12:AS:145:THR:HA	2.01	0.42
7:B2:1751:A:O2'	7:B2:1752:U:P	2.77	0.42
8:A5:12:C:H6	8:A5:12:C:H5''	1.85	0.42
8:A5:2681:A:H2'	8:A5:2682:U:C6	2.54	0.42
8:A5:2814:A:OP1	64:CT:23:GLY:HA2	2.19	0.42
10:AK:80:TYR:CD2	10:AK:80:TYR:C	2.98	0.42
13:AT:90:ASN:O	13:AT:91:HIS:ND1	2.53	0.42
16:AA:158:ASP:OD2	21:AV:32:VAL:HG21	2.19	0.42
26:AU:35:CYS:SG	26:AU:52:PRO:HB3	2.59	0.42
32:AX:107:ARG:HG3	32:AX:112:VAL:HG22	2.02	0.42
34:AJ:81:VAL:CG2	34:AJ:91:MET:HE1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:CB:388:LYS:HZ2	40:CB:393:PHE:HE1	1.67	0.42
4:AE:155:VAL:O	4:AE:156:ASN:HB2	2.20	0.42
7:B2:13:U:H2'	7:B2:14:U:C6	2.54	0.42
7:B2:448:U:O2'	7:B2:449:A:P	2.78	0.42
7:B2:453:A:H4'	34:AJ:130:LYS:HD2	2.00	0.42
7:B2:585:U:H4'	7:B2:586:G:O5'	2.20	0.42
8:A5:193:U:O4	60:CY:102:LYS:NZ	2.39	0.42
8:A5:889:U:H2'	8:A5:890:G:O4'	2.20	0.42
8:A5:1386:U:OP1	37:CF:208:LYS:HE3	2.20	0.42
8:A5:1605:C:H5'	8:A5:1606:U:OP2	2.19	0.42
8:A5:3419:C:O2'	67:CP:71:ARG:O	2.32	0.42
12:AS:108:ARG:HB3	12:AS:108:ARG:HH11	1.83	0.42
26:AU:34:VAL:O	26:AU:38:LEU:HD23	2.19	0.42
34:AJ:26:GLN:OE1	34:AJ:27:GLU:N	2.53	0.42
34:AJ:95:TYR:N	34:AJ:95:TYR:CD1	2.87	0.42
59:CH:36:LYS:HG3	59:CH:78:MET:SD	2.60	0.42
59:CH:41:LEU:HB3	59:CH:43:MET:HE2	2.01	0.42
63:CQ:176:ARG:HG2	63:CQ:176:ARG:NH1	2.35	0.42
68:Cn:2:ARG:O	68:Cn:6:ARG:HG3	2.20	0.42
1:AD:212:ILE:HD12	9:AR:16:LEU:HD23	2.02	0.42
7:B2:30:G:H4'	32:AX:129:SER:HB2	2.01	0.42
7:B2:744:G:N7	25:AY:11:LYS:NZ	2.68	0.42
7:B2:825:U:C2'	7:B2:826:A:O5'	2.68	0.42
7:B2:1570:A:O2'	7:B2:1571:C:H5'	2.20	0.42
7:B2:1595:C:H2'	7:B2:1596:C:O4'	2.20	0.42
7:B2:1682:U:H2'	7:B2:1683:U:C6	2.55	0.42
8:A5:382:G:O2'	8:A5:407:A:N1	2.48	0.42
8:A5:642:G:C3'	8:A5:643:U:H5''	2.49	0.42
8:A5:1138:A:H2'	8:A5:1139:A:O4'	2.19	0.42
8:A5:2958:U:O2	8:A5:2958:U:O4'	2.37	0.42
8:A5:3460:G:O2'	8:A5:3461:U:P	2.77	0.42
11:AW:15:ASN:ND2	11:AW:72:ALA:O	2.53	0.42
18:AI:139:LYS:HZ2	18:AI:146:MET:HE1	1.85	0.42
19:AF:106:ILE:HD11	19:AF:180:ALA:HA	2.01	0.42
26:AU:23:LEU:HB2	26:AU:31:LEU:HD11	2.02	0.42
36:AH:25:GLN:O	36:AH:28:ILE:HG12	2.20	0.42
40:CB:285:TYR:HB2	40:CB:329:MET:HG2	2.02	0.42
47:CC:312:PRO:O	47:CC:313:LYS:HB3	2.20	0.42
65:CD:40:ASP:OD1	65:CD:40:ASP:N	2.52	0.42
7:B2:1490:A:H3'	23:AZ:76:ARG:HG3	2.02	0.41
8:A5:428:A:N1	8:A5:2465:C:O2'	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:552:G:N2	38:CS:150:ASP:O	2.50	0.41
8:A5:1737:U:H1'	8:A5:1738:U:OP2	2.20	0.41
8:A5:1750:A:H2'	8:A5:1891:A:OP2	2.20	0.41
8:A5:2204:U:H2'	8:A5:2205:A:C8	2.55	0.41
8:A5:3106:A:C4	8:A5:3107:C:C5	3.07	0.41
9:AR:77:GLU:O	9:AR:81:ARG:HG2	2.20	0.41
10:AK:81:LEU:HB3	10:AK:83:LEU:HD11	2.02	0.41
25:AY:82:ALA:O	25:AY:86:GLU:HB2	2.20	0.41
30:Ac:11:LYS:HE3	30:Ac:11:LYS:HB2	1.91	0.41
41:CU:30:PRO:HB2	41:CU:36:LEU:HD12	2.01	0.41
44:CG:62:ILE:O	44:CG:66:ARG:HG3	2.20	0.41
1:AD:108:ARG:CG	1:AD:177:VAL:HG22	2.50	0.41
7:B2:1122:A:H2'	7:B2:1123:G:O4'	2.20	0.41
8:A5:355:A:H4'	8:A5:356:C:OP2	2.20	0.41
26:AU:99:GLN:O	26:AU:103:ILE:HG12	2.21	0.41
29:AP:20:LYS:N	29:AP:20:LYS:CD	2.83	0.41
49:CE:102:LEU:HD11	49:CE:114:LEU:HD11	2.01	0.41
58:Cc:100:ASP:OD2	58:Cc:100:ASP:C	2.63	0.41
61:CR:151:ARG:HG3	61:CR:151:ARG:NH1	2.35	0.41
66:CZ:47:ASP:C	66:CZ:47:ASP:OD1	2.64	0.41
78:DB:44:A:H3'	78:DB:45:G:C8	2.56	0.41
3:AC:257:LEU:O	21:AV:53:ARG:NH1	2.53	0.41
5:A7:18:G:H2'	5:A7:19:U:C6	2.55	0.41
7:B2:491:A:H62	7:B2:513:G:H21	1.67	0.41
8:A5:440:U:H2'	8:A5:441:U:O4'	2.20	0.41
8:A5:745:A:N1	8:A5:836:G:O2'	2.46	0.41
8:A5:1545:G:O2'	8:A5:1964:U:O4	2.31	0.41
8:A5:1724:G:OP1	66:CZ:115:LYS:NZ	2.52	0.41
8:A5:2217:A:O2'	8:A5:2218:C:H5'	2.20	0.41
8:A5:2241:U:H5	8:A5:2246:A:N7	2.18	0.41
8:A5:3013:G:N2	8:A5:3014:A:C8	2.89	0.41
9:AR:104:ASP:OD1	9:AR:104:ASP:C	2.63	0.41
16:AA:98:ALA:O	16:AA:99:ILE:HD13	2.21	0.41
21:AV:68:ASP:OD1	21:AV:69:ALA:N	2.53	0.41
29:AP:26:VAL:CG2	29:AP:31:LEU:HD13	2.50	0.41
31:Ae:89:LYS:H	31:Ae:89:LYS:HE2	1.85	0.41
34:AJ:135:ARG:HG2	34:AJ:159:SER:HA	2.02	0.41
35:AQ:25:LYS:NZ	35:AQ:25:LYS:HB3	2.35	0.41
45:CI:36:LEU:HD13	45:CI:87:LEU:HD23	2.02	0.41
47:CC:288:ASP:OD1	47:CC:291:ARG:HG3	2.20	0.41
48:Ch:89:ARG:O	48:Ch:93:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:CT:90:ASN:O	64:CT:91:ILE:HD13	2.20	0.41
5:A7:92:G:H2'	5:A7:93:G:C8	2.56	0.41
6:A8:137:U:H2'	6:A8:138:C:C6	2.56	0.41
7:B2:1299:U:O3'	7:B2:1301:C:OP2	2.08	0.41
7:B2:1341:G:H5'	26:AU:28:VAL:HG11	2.02	0.41
8:A5:181:G:H2'	8:A5:182:U:O4'	2.20	0.41
8:A5:248:G:C5	8:A5:249:C:C5	3.08	0.41
8:A5:1426:A:H2'	8:A5:1427:A:C8	2.55	0.41
8:A5:2941:U:C2	8:A5:2942:G:C8	3.09	0.41
8:A5:3417:U:O2	8:A5:3417:U:O5'	2.39	0.41
8:A5:3441:U:H5''	40:CB:314:MET:HE2	2.02	0.41
15:Af:139:HIS:O	15:Af:140:ASP:C	2.64	0.41
18:AI:125:LYS:H	18:AI:125:LYS:HD2	1.85	0.41
25:AY:10:ARG:HD2	25:AY:26:GLU:OE2	2.20	0.41
42:CL:115:ASP:O	42:CL:119:GLU:HG2	2.19	0.41
45:CI:32:ARG:HG3	45:CI:32:ARG:HH11	1.86	0.41
47:CC:195:LEU:HD12	47:CC:195:LEU:N	2.35	0.41
63:CQ:59:GLN:O	63:CQ:84:SER:HB3	2.21	0.41
73:Ce:89:MET:H	73:Ce:89:MET:CE	2.33	0.41
4:AE:53:TYR:O	25:AY:15:ASN:ND2	2.51	0.41
4:AE:142:ASP:OD1	4:AE:142:ASP:N	2.41	0.41
6:A8:87:A:OP1	48:Ch:3:LYS:NZ	2.52	0.41
7:B2:231:A:H4'	33:AL:36:GLU:OE1	2.21	0.41
7:B2:940:C:H4'	22:AN:109:ILE:CG2	2.51	0.41
7:B2:1179:C:OP1	10:AK:49:SER:OG	2.39	0.41
7:B2:1529:A:H1'	7:B2:1530:G:OP2	2.20	0.41
7:B2:1605:U:H2'	7:B2:1606:C:C6	2.55	0.41
8:A5:37:U:H2'	8:A5:38:A:O4'	2.20	0.41
8:A5:998:U:OP1	55:Ca:15:VAL:HA	2.20	0.41
8:A5:1456:G:H1'	8:A5:1483:A:N6	2.35	0.41
9:AR:21:TYR:CE1	9:AR:58:MET:HE1	2.55	0.41
16:AA:18:LEU:HD23	16:AA:51:VAL:HG23	2.02	0.41
25:AY:56:ILE:HG23	25:AY:94:MET:HE2	2.01	0.41
44:CG:107:SER:OG	44:CG:108:THR:N	2.54	0.41
45:CI:49:CYS:HB3	45:CI:168:SER:OG	2.21	0.41
45:CI:63:GLU:OE1	45:CI:63:GLU:N	2.41	0.41
47:CC:129:ALA:HB1	47:CC:135:LEU:HD12	2.03	0.41
67:CP:44:ARG:NH1	67:CP:101:GLU:OE2	2.50	0.41
70:Ck:54:GLU:HA	70:Ck:54:GLU:OE2	2.20	0.41
75:Cj:69:ASP:OD1	75:Cj:73:ARG:HD3	2.21	0.41
1:AD:31:LEU:HD21	1:AD:71:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:250:ASP:OD2	3:AC:250:ASP:C	2.64	0.41
6:A8:86:G:N7	75:Cj:89:GLN:HB3	2.36	0.41
7:B2:1211:C:C2	7:B2:1212:U:C6	3.09	0.41
7:B2:1309:U:O2'	7:B2:1310:U:P	2.78	0.41
8:A5:288:A:HO2'	8:A5:289:A:P	2.31	0.41
8:A5:599:G:OP2	37:CF:241:ARG:NH2	2.52	0.41
8:A5:1616:C:N3	8:A5:1617:U:C5	2.89	0.41
8:A5:2213:C:O2'	8:A5:2214:G:H5'	2.21	0.41
8:A5:2382:A:H2	8:A5:2389:U:H3	1.67	0.41
8:A5:2610:C:OP1	8:A5:2610:C:O4'	2.39	0.41
8:A5:2682:U:C4	8:A5:2683:G:N7	2.89	0.41
8:A5:2948:C:O2'	8:A5:2949:A:O5'	2.36	0.41
8:A5:3076:G:N2	8:A5:3079:A:OP2	2.46	0.41
8:A5:3351:G:H21	8:A5:3354:U:H5''	1.86	0.41
8:A5:3446:U:H4'	8:A5:3447:A:H5'	2.03	0.41
8:A5:3466:U:O2'	8:A5:3467:U:OP2	2.38	0.41
13:AT:139:LEU:O	13:AT:140:ARG:C	2.62	0.41
22:AN:76:LYS:HG2	22:AN:81:ALA:HB2	2.01	0.41
25:AY:23:MET:HB3	25:AY:23:MET:HE2	1.97	0.41
78:DB:25:C:H41	78:DB:45:G:N2	2.18	0.41
7:B2:356:C:HO2'	7:B2:357:G:P	2.44	0.41
7:B2:1415:C:OP2	12:AS:136:THR:OG1	2.36	0.41
7:B2:1511:A:O2'	7:B2:1512:A:P	2.78	0.41
8:A5:598:C:H2'	8:A5:599:G:C8	2.56	0.41
8:A5:790:G:C2'	8:A5:791:U:OP1	2.69	0.41
8:A5:1553:G:C2	8:A5:1554:A:C8	3.09	0.41
8:A5:2777:U:H4'	8:A5:2778:C:OP1	2.21	0.41
33:AL:32:ARG:NH2	33:AL:52:TYR:O	2.42	0.41
34:AJ:22:GLU:OE1	34:AJ:22:GLU:N	2.32	0.41
36:AH:73:LYS:CD	36:AH:73:LYS:C	2.94	0.41
59:CH:37:ASP:C	59:CH:37:ASP:OD1	2.64	0.41
63:CQ:154:PRO:O	63:CQ:163:THR:OG1	2.35	0.41
71:Cm:79:GLU:OE1	71:Cm:81:SER:OG	2.29	0.41
77:CX:82:ASP:OD1	77:CX:82:ASP:N	2.53	0.41
78:DA:75:C:H3'	78:DA:76:A:H5''	2.03	0.41
3:AC:101:GLU:HB2	3:AC:212:MET:HE1	2.03	0.41
7:B2:1516:U:O2	7:B2:1516:U:O4'	2.36	0.41
8:A5:179:U:H2'	8:A5:180:C:C6	2.56	0.41
8:A5:1566:U:O2'	8:A5:1567:G:H8	2.04	0.41
8:A5:1588:C:OP2	8:A5:1680:U:O2'	2.36	0.41
8:A5:1773:G:H1	8:A5:1781:C:H5	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:2529:U:H2'	8:A5:2530:U:C6	2.56	0.41
8:A5:2955:C:H2'	8:A5:2956:C:O5'	2.21	0.41
8:A5:2972:U:H5'	8:A5:3051:G:H5''	2.03	0.41
15:Af:102:ILE:HG12	15:Af:108:ILE:HG22	2.03	0.41
20:AM:84:LEU:C	20:AM:85:ILE:HD12	2.46	0.41
42:CL:141:ALA:O	42:CL:145:LYS:NZ	2.51	0.41
44:CG:44:GLN:O	44:CG:45:ASP:C	2.63	0.41
78:DA:4:U:H3	78:DA:69:G:H22	1.68	0.41
3:AC:67:VAL:HG21	3:AC:90:ILE:HG23	2.03	0.41
5:A7:59:A:H2'	5:A7:60:C:O4'	2.21	0.41
5:A7:63:U:C4	45:CI:202:GLU:O	2.74	0.41
7:B2:273:U:H2'	7:B2:274:C:C6	2.56	0.41
7:B2:943:A:H2'	7:B2:944:A:O4'	2.21	0.41
7:B2:1004:C:H42	7:B2:1039:A:H2	1.69	0.41
7:B2:1073:G:O2'	7:B2:1089:G:O6	2.35	0.41
7:B2:1613:U:H3'	7:B2:1614:G:C5'	2.51	0.41
7:B2:1683:U:H2'	7:B2:1684:U:O4'	2.21	0.41
8:A5:66:A:O2'	8:A5:321:C:O2	2.37	0.41
8:A5:304:U:C6	52:CI:34:VAL:HG22	2.55	0.41
8:A5:763:G:O2'	8:A5:764:C:P	2.79	0.41
8:A5:1563:A:H2'	8:A5:1564:C:C6	2.56	0.41
8:A5:1752:U:H2'	8:A5:1753:C:C6	2.56	0.41
8:A5:2258:A:H2'	8:A5:2259:C:C6	2.56	0.41
8:A5:2376:G:O2'	8:A5:2414:G:O6	2.31	0.41
8:A5:2527:A:H2'	8:A5:2528:G:O4'	2.21	0.41
8:A5:3107:C:H2'	8:A5:3107:C:O2	2.20	0.41
8:A5:3138:C:P	59:CH:96:HIS:HD1	2.39	0.41
8:A5:3162:U:C2'	8:A5:3163:U:O5'	2.69	0.41
8:A5:3169:C:H5''	8:A5:3170:A:OP1	2.21	0.41
8:A5:3267:U:O2	8:A5:3267:U:O4'	2.39	0.41
8:A5:3461:U:C3'	8:A5:3463:C:OP1	2.68	0.41
16:AA:124:ILE:HG22	16:AA:126:ASP:N	2.36	0.41
18:AI:155:THR:HG22	33:AL:24:LEU:HD13	2.03	0.41
20:AM:49:ALA:HB1	20:AM:118:VAL:HG11	2.03	0.41
25:AY:48:TYR:O	25:AY:49:LYS:C	2.64	0.41
25:AY:61:GLU:OE1	25:AY:61:GLU:HA	2.21	0.41
47:CC:207:VAL:O	47:CC:207:VAL:HG13	2.21	0.41
48:Ch:75:ASP:OD2	48:Ch:75:ASP:C	2.64	0.41
56:Cp:28:LYS:NZ	56:Cp:28:LYS:HB3	2.36	0.41
63:CQ:176:ARG:HG2	63:CQ:176:ARG:HH11	1.85	0.41
78:DA:18:G:H4'	78:DA:60:C:N3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:DB:26:G:C5	78:DB:27:U:C5	3.08	0.41
78:DB:52:A:H2'	78:DB:53:G:O4'	2.21	0.41
7:B2:1125:C:H2'	7:B2:1126:G:O4'	2.21	0.41
7:B2:1161:A:N6	7:B2:1413:U:O5'	2.53	0.41
7:B2:1246:A:H4'	7:B2:1247:G:OP1	2.20	0.41
7:B2:1359:A:OP1	9:AR:56:HIS:NE2	2.51	0.41
7:B2:1418:G:N7	12:AS:141:ARG:NH1	2.68	0.41
7:B2:1479:G:HO2'	7:B2:1480:A:P	2.41	0.41
8:A5:1144:C:C2'	8:A5:1145:A:OP1	2.69	0.41
8:A5:2655:U:O2'	43:CA:40:TYR:OH	2.13	0.41
8:A5:3466:U:O2'	8:A5:3467:U:P	2.78	0.41
18:AI:113:TYR:HD1	18:AI:121:LEU:HD22	1.86	0.41
46:CO:6:ARG:HG3	46:CO:6:ARG:HH11	1.86	0.41
47:CC:217:ALA:O	47:CC:221:ARG:HG2	2.21	0.41
61:CR:67:GLU:OE1	61:CR:67:GLU:O	2.39	0.41
61:CR:67:GLU:OE1	61:CR:71:ARG:NH1	2.54	0.41
78:DA:4:U:H3	78:DA:69:G:H1	1.68	0.41
3:AC:159:VAL:HG23	21:AV:27:LYS:HD3	2.03	0.40
3:AC:200:ILE:HD12	3:AC:211:HIS:CE1	2.57	0.40
4:AE:195:GLY:N	4:AE:208:HIS:O	2.51	0.40
7:B2:836:A:H5''	7:B2:837:A:P	2.61	0.40
7:B2:1005:G:H4'	16:AA:32:PHE:CD1	2.55	0.40
7:B2:1203:A:OP2	24:Ad:5:ASN:ND2	2.52	0.40
7:B2:1322:G:N3	7:B2:1322:G:C2'	2.83	0.40
8:A5:414:A:N3	8:A5:684:U:O2'	2.48	0.40
8:A5:1040:U:OP1	37:CF:100:LYS:HE3	2.21	0.40
8:A5:1789:A:H2'	8:A5:1790:A:C8	2.56	0.40
8:A5:2200:A:H2'	8:A5:2201:C:C6	2.56	0.40
18:AI:43:VAL:HG22	18:AI:57:ALA:HA	2.03	0.40
19:AF:82:LEU:HD11	19:AF:179:LEU:HD22	2.03	0.40
30:Ac:56:GLU:OE1	30:Ac:59:ARG:NH1	2.54	0.40
36:AH:75:HIS:N	36:AH:76:PRO:HD2	2.36	0.40
44:CG:68:SER:O	44:CG:72:GLN:HG3	2.21	0.40
57:CM:44:ASP:O	57:CM:44:ASP:CG	2.64	0.40
1:AD:210:VAL:HG13	1:AD:210:VAL:O	2.20	0.40
2:AB:122:ASN:HA	2:AB:135:VAL:O	2.21	0.40
3:AC:183:LYS:HE2	3:AC:185:ALA:O	2.21	0.40
7:B2:832:G:H1	7:B2:925:U:H3	1.69	0.40
7:B2:1203:A:H4'	7:B2:1204:G:OP1	2.20	0.40
7:B2:1216:U:O2'	7:B2:1216:U:O2	2.29	0.40
7:B2:1751:A:N6	14:Aa:84:VAL:HG22	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:765:C:H2'	8:A5:766:G:O4'	2.22	0.40
8:A5:839:U:O2'	8:A5:840:G:OP2	2.29	0.40
8:A5:1104:U:O2	8:A5:1105:U:H5	2.05	0.40
8:A5:1726:G:O4'	8:A5:1738:U:O2'	2.36	0.40
8:A5:3346:G:H2'	8:A5:3347:U:O4'	2.21	0.40
25:AY:21:LYS:N	25:AY:75:VAL:O	2.53	0.40
25:AY:80:ASP:OD2	25:AY:80:ASP:N	2.54	0.40
32:AX:127:ASN:OD1	32:AX:127:ASN:N	2.54	0.40
33:AL:118:HIS:N	33:AL:121:ASP:OD2	2.51	0.40
43:CA:250:LYS:HA	43:CA:250:LYS:HD2	1.86	0.40
45:CI:210:ILE:HD12	45:CI:210:ILE:HA	1.96	0.40
76:CJ:22:LEU:HD23	76:CJ:22:LEU:HA	1.95	0.40
5:A7:11:A:N1	5:A7:66:G:O2'	2.51	0.40
6:A8:56:G:H2'	6:A8:57:C:O4'	2.21	0.40
7:B2:307:U:OP2	33:AL:56:LYS:NZ	2.47	0.40
7:B2:614:C:H3'	7:B2:615:U:C5'	2.51	0.40
7:B2:1670:G:HO2'	7:B2:1671:C:P	2.42	0.40
8:A5:108:A:H4'	8:A5:109:G:OP1	2.22	0.40
8:A5:299:U:H2'	8:A5:300:A:O4'	2.20	0.40
8:A5:1145:A:OP1	8:A5:1145:A:O4'	2.39	0.40
8:A5:1425:U:H2'	8:A5:1426:A:C8	2.56	0.40
8:A5:1632:C:H2'	8:A5:1633:G:O4'	2.21	0.40
8:A5:2826:G:H5'	8:A5:2828:U:C6	2.56	0.40
8:A5:3234:U:H4'	8:A5:3235:A:OP1	2.20	0.40
8:A5:3321:A:OP1	38:CS:173:ALA:HB2	2.21	0.40
9:AR:89:SER:OG	16:AA:203:MET:CG	2.69	0.40
45:CI:66:GLU:O	45:CI:70:ILE:HG13	2.20	0.40
46:CO:185:ALA:O	46:CO:186:ALA:C	2.63	0.40
59:CH:85:GLY:HA3	59:CH:185:ILE:HD12	2.02	0.40
59:CH:105:ASP:OD1	59:CH:105:ASP:N	2.53	0.40
69:Cg:44:CYS:SG	69:Cg:81:SER:HB3	2.61	0.40
6:A8:87:A:H2'	6:A8:88:G:O4'	2.21	0.40
6:A8:112:A:O2'	6:A8:113:C:P	2.79	0.40
8:A5:249:C:H2'	8:A5:250:A:C8	2.57	0.40
8:A5:411:U:H4'	8:A5:1481:G:H4'	2.04	0.40
8:A5:1221:A:H4'	37:CF:219:LYS:HD2	2.01	0.40
8:A5:1945:G:H4'	75:Cj:6:GLN:HG2	2.04	0.40
8:A5:2257:G:H21	43:CA:237:LEU:HD22	1.86	0.40
8:A5:3320:U:H4'	8:A5:3321:A:O5'	2.22	0.40
8:A5:3334:G:HO2'	8:A5:3335:G:P	2.44	0.40
20:AM:130:ALA:O	20:AM:133:THR:OG1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AL:33:TYR:O	33:AL:34:ILE:HD13	2.21	0.40
35:AQ:11:PHE:CD1	35:AQ:11:PHE:C	3.00	0.40
49:CE:174:LYS:N	49:CE:174:LYS:HD2	2.37	0.40
74:CW:85:VAL:O	74:CW:86:ALA:C	2.63	0.40
7:B2:137:G:P	27:AG:15:SER:OG	2.79	0.40
7:B2:545:C:OP1	32:AX:87:ASN:N	2.45	0.40
7:B2:616:A:H2'	7:B2:617:G:O4'	2.21	0.40
8:A5:711:A:O2'	8:A5:712:A:O5'	2.36	0.40
8:A5:2882:A:C6	8:A5:2883:A:N6	2.90	0.40
8:A5:2988:C:H2'	8:A5:2989:G:O4'	2.22	0.40
8:A5:3014:A:N7	8:A5:3015:A:H1'	2.35	0.40
20:AM:132:LEU:HA	20:AM:135:TYR:HB3	2.03	0.40
25:AY:56:ILE:HA	25:AY:94:MET:CE	2.52	0.40
30:Ac:4:LEU:HD22	30:Ac:53:THR:OG1	2.21	0.40
31:Ae:112:ARG:C	31:Ae:112:ARG:HE	2.30	0.40
42:CL:178:ILE:N	55:Ca:131:GLU:OE2	2.54	0.40
49:CE:211:TYR:O	49:CE:215:MET:HG3	2.22	0.40
58:Cc:40:LEU:HD13	58:Cc:65:TYR:HB3	2.03	0.40
59:CH:128:GLU:HA	59:CH:128:GLU:OE1	2.21	0.40
61:CR:151:ARG:HG3	61:CR:151:ARG:HH11	1.85	0.40
69:Cg:87:GLU:OE1	69:Cg:91:ARG:NH2	2.54	0.40
72:Cd:38:ALA:HB3	72:Cd:39:PRO:HD3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AD	209/247 (85%)	206 (99%)	3 (1%)	0	100	100
2	AB	208/257 (81%)	200 (96%)	8 (4%)	0	100	100
3	AC	213/272 (78%)	207 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AE	253/259 (98%)	244 (96%)	9 (4%)	0	100	100
9	AR	119/130 (92%)	111 (93%)	8 (7%)	0	100	100
10	AK	91/149 (61%)	88 (97%)	3 (3%)	0	100	100
11	AW	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	24
12	AS	146/154 (95%)	143 (98%)	3 (2%)	0	100	100
13	AT	138/146 (94%)	132 (96%)	6 (4%)	0	100	100
14	Aa	97/117 (83%)	94 (97%)	3 (3%)	0	100	100
15	Af	48/163 (29%)	44 (92%)	4 (8%)	0	100	100
16	AA	203/276 (74%)	194 (96%)	9 (4%)	0	100	100
17	AO	133/152 (88%)	129 (97%)	4 (3%)	0	100	100
18	AI	205/208 (99%)	198 (97%)	7 (3%)	0	100	100
19	AF	181/210 (86%)	170 (94%)	10 (6%)	1 (1%)	21	31
20	AM	113/140 (81%)	101 (89%)	12 (11%)	0	100	100
21	AV	79/88 (90%)	77 (98%)	2 (2%)	0	100	100
22	AN	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
23	AZ	69/117 (59%)	68 (99%)	1 (1%)	0	100	100
24	Ad	53/56 (95%)	53 (100%)	0	0	100	100
25	AY	121/131 (92%)	114 (94%)	7 (6%)	0	100	100
26	AU	98/117 (84%)	90 (92%)	8 (8%)	0	100	100
27	AG	226/246 (92%)	221 (98%)	5 (2%)	0	100	100
28	Ab	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
29	AP	130/151 (86%)	124 (95%)	6 (5%)	0	100	100
30	Ac	63/65 (97%)	63 (100%)	0	0	100	100
31	Ae	41/130 (32%)	37 (90%)	4 (10%)	0	100	100
32	AX	138/143 (96%)	135 (98%)	3 (2%)	0	100	100
33	AL	141/155 (91%)	137 (97%)	4 (3%)	0	100	100
34	AJ	175/189 (93%)	168 (96%)	7 (4%)	0	100	100
35	AQ	138/144 (96%)	133 (96%)	5 (4%)	0	100	100
36	AH	190/194 (98%)	177 (93%)	13 (7%)	0	100	100
37	CF	211/244 (86%)	203 (96%)	8 (4%)	0	100	100
38	CS	177/180 (98%)	171 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	CV	126/140 (90%)	126 (100%)	0	0	100	100
40	CB	393/401 (98%)	387 (98%)	6 (2%)	0	100	100
41	CU	98/130 (75%)	95 (97%)	3 (3%)	0	100	100
42	CL	202/207 (98%)	200 (99%)	2 (1%)	0	100	100
43	CA	247/260 (95%)	238 (96%)	9 (4%)	0	100	100
44	CG	217/265 (82%)	214 (99%)	3 (1%)	0	100	100
45	CI	211/214 (99%)	207 (98%)	4 (2%)	0	100	100
46	CO	199/202 (98%)	196 (98%)	3 (2%)	0	100	100
47	CC	333/345 (96%)	320 (96%)	13 (4%)	0	100	100
48	Ch	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
49	CE	135/217 (62%)	127 (94%)	8 (6%)	0	100	100
50	Co	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
51	Cf	115/124 (93%)	112 (97%)	3 (3%)	0	100	100
52	Ci	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
53	Cl	48/51 (94%)	48 (100%)	0	0	100	100
54	CN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
55	Ca	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
56	Cp	86/91 (94%)	84 (98%)	2 (2%)	0	100	100
57	CM	130/135 (96%)	127 (98%)	3 (2%)	0	100	100
58	Cc	94/115 (82%)	93 (99%)	1 (1%)	0	100	100
59	CH	186/189 (98%)	174 (94%)	12 (6%)	0	100	100
60	CY	130/142 (92%)	126 (97%)	4 (3%)	0	100	100
61	CR	192/198 (97%)	191 (100%)	1 (0%)	0	100	100
62	Cb	50/62 (81%)	47 (94%)	3 (6%)	0	100	100
63	CQ	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
64	CT	158/161 (98%)	154 (98%)	4 (2%)	0	100	100
65	CD	287/293 (98%)	279 (97%)	8 (3%)	0	100	100
66	CZ	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
67	CP	152/187 (81%)	147 (97%)	5 (3%)	0	100	100
68	Cn	20/22 (91%)	19 (95%)	1 (5%)	0	100	100
69	Cg	102/110 (93%)	101 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	Ck	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
71	Cm	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
72	Cd	103/122 (84%)	100 (97%)	3 (3%)	0	100	100
73	Ce	126/134 (94%)	123 (98%)	3 (2%)	0	100	100
74	CW	84/159 (53%)	82 (98%)	2 (2%)	0	100	100
75	Cj	86/92 (94%)	84 (98%)	2 (2%)	0	100	100
76	CJ	184/196 (94%)	179 (97%)	5 (3%)	0	100	100
77	CX	117/146 (80%)	115 (98%)	2 (2%)	0	100	100
All	All	10473/11907 (88%)	10136 (97%)	335 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	AW	29	PRO
19	AF	86	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AD	173/204 (85%)	169 (98%)	4 (2%)	44	65
2	AB	191/228 (84%)	184 (96%)	7 (4%)	30	49
3	AC	175/202 (87%)	169 (97%)	6 (3%)	32	52
4	AE	218/221 (99%)	213 (98%)	5 (2%)	44	65
9	AR	111/118 (94%)	108 (97%)	3 (3%)	39	60
10	AK	82/122 (67%)	80 (98%)	2 (2%)	43	64
11	AW	110/111 (99%)	107 (97%)	3 (3%)	39	60
12	AS	130/134 (97%)	124 (95%)	6 (5%)	24	39
13	AT	116/120 (97%)	113 (97%)	3 (3%)	40	61
14	Aa	84/94 (89%)	82 (98%)	2 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	Af	42/134 (31%)	40 (95%)	2 (5%)	23	37
16	AA	172/228 (75%)	161 (94%)	11 (6%)	16	26
17	AO	103/115 (90%)	96 (93%)	7 (7%)	14	23
18	AI	172/173 (99%)	166 (96%)	6 (4%)	32	51
19	AF	156/172 (91%)	153 (98%)	3 (2%)	50	70
20	AM	94/108 (87%)	90 (96%)	4 (4%)	26	42
21	AV	68/75 (91%)	64 (94%)	4 (6%)	18	29
22	AN	130/130 (100%)	128 (98%)	2 (2%)	57	74
23	AZ	62/98 (63%)	60 (97%)	2 (3%)	34	54
24	Ad	46/47 (98%)	43 (94%)	3 (6%)	15	26
25	AY	107/112 (96%)	103 (96%)	4 (4%)	30	49
26	AU	90/104 (86%)	85 (94%)	5 (6%)	19	31
27	AG	195/212 (92%)	189 (97%)	6 (3%)	35	55
28	Ab	75/76 (99%)	73 (97%)	2 (3%)	39	60
29	AP	112/128 (88%)	112 (100%)	0	100	100
30	Ac	58/58 (100%)	55 (95%)	3 (5%)	21	34
31	Ae	37/107 (35%)	35 (95%)	2 (5%)	20	33
32	AX	115/118 (98%)	113 (98%)	2 (2%)	53	72
33	AL	126/136 (93%)	123 (98%)	3 (2%)	43	64
34	AJ	160/167 (96%)	155 (97%)	5 (3%)	35	55
35	AQ	115/119 (97%)	110 (96%)	5 (4%)	26	42
36	AH	170/172 (99%)	166 (98%)	4 (2%)	43	64
37	CF	184/210 (88%)	182 (99%)	2 (1%)	65	79
38	CS	156/157 (99%)	151 (97%)	5 (3%)	34	54
39	CV	101/107 (94%)	99 (98%)	2 (2%)	48	68
40	CB	335/338 (99%)	332 (99%)	3 (1%)	70	82
41	CU	92/116 (79%)	87 (95%)	5 (5%)	20	33
42	CL	167/170 (98%)	164 (98%)	3 (2%)	51	71
43	CA	191/202 (95%)	183 (96%)	8 (4%)	26	44
44	CG	192/228 (84%)	188 (98%)	4 (2%)	47	67
45	CI	179/180 (99%)	174 (97%)	5 (3%)	38	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	CO	165/166 (99%)	163 (99%)	2 (1%)	63	78
47	CC	279/286 (98%)	274 (98%)	5 (2%)	51	71
48	Ch	106/107 (99%)	102 (96%)	4 (4%)	29	48
49	CE	122/188 (65%)	121 (99%)	1 (1%)	73	84
50	Co	90/93 (97%)	89 (99%)	1 (1%)	65	79
51	Cf	95/99 (96%)	93 (98%)	2 (2%)	47	67
52	Ci	86/86 (100%)	85 (99%)	1 (1%)	63	78
53	Cl	46/47 (98%)	46 (100%)	0	100	100
54	CN	172/173 (99%)	170 (99%)	2 (1%)	63	78
55	Ca	116/117 (99%)	113 (97%)	3 (3%)	40	61
56	Cp	68/71 (96%)	68 (100%)	0	100	100
57	CM	111/114 (97%)	110 (99%)	1 (1%)	70	82
58	Cc	80/95 (84%)	79 (99%)	1 (1%)	61	76
59	CH	167/168 (99%)	162 (97%)	5 (3%)	36	56
60	CY	114/123 (93%)	111 (97%)	3 (3%)	40	61
61	CR	172/174 (99%)	167 (97%)	5 (3%)	37	57
62	Cb	47/56 (84%)	47 (100%)	0	100	100
63	CQ	152/153 (99%)	149 (98%)	3 (2%)	48	68
64	CT	135/136 (99%)	135 (100%)	0	100	100
65	CD	239/242 (99%)	236 (99%)	3 (1%)	61	76
66	CZ	119/120 (99%)	119 (100%)	0	100	100
67	CP	130/159 (82%)	124 (95%)	6 (5%)	24	39
68	Cn	20/20 (100%)	20 (100%)	0	100	100
69	Cg	92/98 (94%)	90 (98%)	2 (2%)	45	66
70	Ck	63/64 (98%)	61 (97%)	2 (3%)	34	54
71	Cm	47/115 (41%)	47 (100%)	0	100	100
72	Cd	96/112 (86%)	94 (98%)	2 (2%)	47	67
73	Ce	111/117 (95%)	110 (99%)	1 (1%)	70	82
74	CW	73/128 (57%)	72 (99%)	1 (1%)	59	75
75	Cj	73/77 (95%)	70 (96%)	3 (4%)	27	44
76	CJ	160/170 (94%)	155 (97%)	5 (3%)	35	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	CX	103/124 (83%)	102 (99%)	1 (1%)	68	80
All	All	9041/10049 (90%)	8813 (98%)	228 (2%)	42	63

All (228) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AD	8	THR
1	AD	104	CYS
1	AD	158	LEU
1	AD	176	HIS
2	AB	75	SER
2	AB	93	ASN
2	AB	102	SER
2	AB	104	THR
2	AB	123	THR
2	AB	144	SER
2	AB	172	LYS
3	AC	75	LEU
3	AC	118	THR
3	AC	159	VAL
3	AC	181	THR
3	AC	212	MET
3	AC	225	SER
4	AE	135	VAL
4	AE	145	THR
4	AE	164	SER
4	AE	166	GLN
4	AE	246	SER
9	AR	92	ASP
9	AR	94	SER
9	AR	101	VAL
10	AK	75	LEU
10	AK	88	VAL
11	AW	71	LYS
11	AW	102	LEU
11	AW	126	LEU
12	AS	2	SER
12	AS	43	VAL
12	AS	69	THR
12	AS	72	GLN
12	AS	126	TYR
12	AS	145	THR

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Mol	Chain	Res	Type
13	AT	35	SER
13	AT	87	VAL
13	AT	100	LEU
14	Aa	26	CYS
14	Aa	43	ASN
15	Af	99	TYR
15	Af	101	LYS
16	AA	2	SER
16	AA	8	SER
16	AA	34	MET
16	AA	37	TYR
16	AA	49	ILE
16	AA	122	LEU
16	AA	136	GLU
16	AA	146	SER
16	AA	170	SER
16	AA	198	GLU
16	AA	210	ARG
17	AO	37	SER
17	AO	91	ILE
17	AO	98	LEU
17	AO	115	SER
17	AO	139	ASP
17	AO	147	ARG
17	AO	152	LEU
18	AI	4	SER
18	AI	7	SER
18	AI	105	ASP
18	AI	142	SER
18	AI	153	GLN
18	AI	164	GLU
19	AF	22	GLU
19	AF	37	SER
19	AF	49	GLU
20	AM	27	ARG
20	AM	116	SER
20	AM	125	GLU
20	AM	127	GLN
21	AV	3	ASN
21	AV	42	GLU
21	AV	65	GLU
21	AV	66	SER

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Mol	Chain	Res	Type
22	AN	21	SER
22	AN	143	SER
23	AZ	76	ARG
23	AZ	103	VAL
24	Ad	8	PHE
24	Ad	9	SER
24	Ad	20	SER
25	AY	51	THR
25	AY	75	VAL
25	AY	78	THR
25	AY	126	VAL
26	AU	17	HIS
26	AU	23	LEU
26	AU	25	SER
26	AU	97	LEU
26	AU	110	ASP
27	AG	49	VAL
27	AG	96	SER
27	AG	114	VAL
27	AG	126	ASP
27	AG	149	LYS
27	AG	163	THR
28	Ab	37	CYS
28	Ab	43	ILE
30	Ac	24	GLN
30	Ac	37	SER
30	Ac	60	GLU
31	Ae	95	LYS
31	Ae	130	SER
32	AX	45	SER
32	AX	55	ILE
33	AL	27	SER
33	AL	117	ILE
33	AL	143	ASN
34	AJ	4	LEU
34	AJ	70	LEU
34	AJ	114	PHE
34	AJ	122	ILE
34	AJ	156	ILE
35	AQ	7	SER
35	AQ	18	THR
35	AQ	44	ILE

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Mol	Chain	Res	Type
35	AQ	56	VAL
35	AQ	144	ARG
36	AH	24	SER
36	AH	119	SER
36	AH	143	ARG
36	AH	161	SER
37	CF	97	LEU
37	CF	107	ILE
38	CS	3	THR
38	CS	51	VAL
38	CS	89	SER
38	CS	133	GLN
38	CS	157	LEU
39	CV	54	SER
39	CV	138	SER
40	CB	260	SER
40	CB	306	LEU
40	CB	392	ASP
41	CU	20	HIS
41	CU	24	ASN
41	CU	27	CYS
41	CU	77	GLU
41	CU	97	SER
42	CL	59	VAL
42	CL	132	SER
42	CL	204	GLU
43	CA	27	SER
43	CA	74	THR
43	CA	77	VAL
43	CA	112	THR
43	CA	125	VAL
43	CA	168	LEU
43	CA	208	GLU
43	CA	250	LYS
44	CG	80	THR
44	CG	88	LEU
44	CG	141	VAL
44	CG	244	SER
45	CI	83	ASP
45	CI	104	SER
45	CI	112	GLN
45	CI	140	ILE

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Mol	Chain	Res	Type
45	CI	177	ASP
46	CO	125	SER
46	CO	183	LYS
47	CC	70	ARG
47	CC	142	VAL
47	CC	173	SER
47	CC	302	ILE
47	CC	310	VAL
48	Ch	8	SER
48	Ch	12	GLU
48	Ch	22	ASP
48	Ch	117	ARG
49	CE	122	VAL
50	Co	2	VAL
51	Cf	14	THR
51	Cf	109	SER
52	Ci	34	VAL
54	CN	109	ARG
54	CN	155	VAL
55	Ca	15	VAL
55	Ca	16	SER
55	Ca	127	SER
57	CM	43	SER
58	Cc	60	SER
59	CH	28	THR
59	CH	33	THR
59	CH	52	THR
59	CH	144	VAL
59	CH	183	THR
60	CY	92	SER
60	CY	93	THR
60	CY	114	ARG
61	CR	2	SER
61	CR	12	SER
61	CR	72	LYS
61	CR	131	ASN
61	CR	192	GLU
63	CQ	82	THR
63	CQ	158	VAL
63	CQ	183	SER
65	CD	40	ASP
65	CD	132	VAL

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Mol	Chain	Res	Type
65	CD	233	ASP
67	CP	3	LYS
67	CP	7	SER
67	CP	14	THR
67	CP	16	SER
67	CP	26	VAL
67	CP	144	SER
69	Cg	47	THR
69	Cg	67	ARG
70	Ck	50	LYS
70	Ck	52	LYS
72	Cd	14	ASN
72	Cd	93	ASP
73	Ce	61	SER
74	CW	19	LYS
75	Cj	25	SER
75	Cj	36	SER
75	Cj	82	THR
76	CJ	9	GLU
76	CJ	54	THR
76	CJ	88	GLU
76	CJ	91	GLU
76	CJ	161	SER
77	CX	30	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
1	AD	5	GLN
1	AD	25	ASN
1	AD	209	HIS
2	AB	51	GLN
11	AW	12	ASN
11	AW	70	ASN
11	AW	120	HIS
12	AS	73	ASN
12	AS	81	ASN
14	Aa	8	HIS
14	Aa	69	HIS
16	AA	33	GLN
17	AO	88	GLN
17	AO	114	GLN

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Mol	Chain	Res	Type
18	AI	52	ASN
18	AI	165	GLN
19	AF	143	GLN
19	AF	155	GLN
20	AM	44	HIS
20	AM	127	GLN
21	AV	21	ASN
21	AV	33	GLN
22	AN	36	GLN
22	AN	62	GLN
23	AZ	100	HIS
25	AY	113	ASN
26	AU	37	GLN
26	AU	46	HIS
26	AU	84	HIS
27	AG	56	ASN
31	Ae	108	GLN
33	AL	18	ASN
33	AL	109	HIS
33	AL	138	ASN
34	AJ	74	ASN
34	AJ	155	HIS
36	AH	72	HIS
36	AH	104	GLN
37	CF	95	ASN
37	CF	98	HIS
37	CF	238	ASN
38	CS	175	GLN
40	CB	121	ASN
40	CB	282	ASN
40	CB	373	HIS
43	CA	8	GLN
43	CA	118	ASN
44	CG	142	ASN
44	CG	160	HIS
45	CI	42	ASN
45	CI	73	ASN
46	CO	30	GLN
46	CO	64	ASN
46	CO	170	GLN
46	CO	180	GLN
47	CC	115	ASN

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Mol	Chain	Res	Type
47	CC	118	GLN
48	Ch	24	GLN
48	Ch	65	GLN
48	Ch	98	HIS
50	Co	26	GLN
50	Co	95	GLN
50	Co	101	GLN
51	Cf	104	HIS
52	Ci	26	GLN
54	CN	156	HIS
54	CN	201	HIS
55	Ca	19	HIS
55	Ca	64	ASN
55	Ca	68	HIS
59	CH	100	ASN
61	CR	36	ASN
62	Cb	6	ASN
62	Cb	10	HIS
62	Cb	12	GLN
63	CQ	59	GLN
64	CT	22	HIS
65	CD	287	GLN
67	CP	12	ASN
67	CP	118	HIS
69	Cg	40	GLN
71	Cm	94	GLN
72	Cd	56	ASN
74	CW	82	ASN
75	Cj	30	GLN
76	CJ	30	ASN
76	CJ	49	GLN
77	CX	29	ASN
77	CX	83	HIS
77	CX	108	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	A7	118/119 (99%)	8 (6%)	0
6	A8	144/153 (94%)	29 (20%)	0
7	B2	1458/1754 (83%)	341 (23%)	28 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	DA	75/76 (98%)	18 (24%)	0
78	DB	75/76 (98%)	22 (29%)	1 (1%)
79	DC	9/10 (90%)	2 (22%)	0
8	A5	3006/3510 (85%)	636 (21%)	74 (2%)
All	All	4885/5698 (85%)	1056 (21%)	103 (2%)

All (1056) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A7	7	G
5	A7	53	U
5	A7	54	A
5	A7	64	G
5	A7	97	G
5	A7	98	G
5	A7	100	A
5	A7	110	G
6	A8	20	G
6	A8	21	G
6	A8	22	U
6	A8	23	U
6	A8	32	U
6	A8	34	U
6	A8	35	C
6	A8	51	U
6	A8	52	U
6	A8	59	U
6	A8	62	C
6	A8	63	U
6	A8	68	A
6	A8	77	A
6	A8	89	U
6	A8	93	G
6	A8	95	A
6	A8	100	C
6	A8	102	A
6	A8	104	C
6	A8	105	G
6	A8	110	G
6	A8	112	A
6	A8	113	C
6	A8	115	A

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Mol	Chain	Res	Type
6	A8	116	A
6	A8	121	G
6	A8	122	C
6	A8	147	G
7	B2	5	C
7	B2	18	U
7	B2	34	A
7	B2	36	G
7	B2	42	G
7	B2	43	A
7	B2	45	U
7	B2	47	A
7	B2	54	C
7	B2	57	G
7	B2	58	C
7	B2	65	U
7	B2	66	C
7	B2	67	A
7	B2	73	G
7	B2	94	G
7	B2	104	C
7	B2	105	A
7	B2	109	U
7	B2	111	U
7	B2	112	C
7	B2	116	G
7	B2	126	U
7	B2	128	G
7	B2	129	A
7	B2	130	U
7	B2	137	G
7	B2	140	A
7	B2	142	U
7	B2	143	A
7	B2	152	A
7	B2	154	U
7	B2	160	C
7	B2	168	C
7	B2	169	C
7	B2	181	C
7	B2	184	G
7	B2	187	G

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Mol	Chain	Res	Type
7	B2	191	U
7	B2	197	G
7	B2	227	G
7	B2	229	U
7	B2	233	U
7	B2	234	C
7	B2	238	A
7	B2	241	A
7	B2	243	G
7	B2	245	A
7	B2	249	U
7	B2	250	A
7	B2	251	C
7	B2	254	U
7	B2	270	C
7	B2	274	C
7	B2	296	C
7	B2	298	A
7	B2	302	G
7	B2	309	G
7	B2	317	G
7	B2	318	A
7	B2	332	U
7	B2	339	A
7	B2	340	A
7	B2	341	C
7	B2	350	A
7	B2	354	U
7	B2	357	G
7	B2	370	G
7	B2	373	C
7	B2	380	A
7	B2	381	A
7	B2	382	C
7	B2	384	G
7	B2	387	A
7	B2	396	A
7	B2	397	A
7	B2	404	C
7	B2	406	G
7	B2	409	G
7	B2	412	G

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Mol	Chain	Res	Type
7	B2	414	G
7	B2	419	U
7	B2	420	U
7	B2	423	C
7	B2	424	C
7	B2	425	A
7	B2	427	U
7	B2	430	U
7	B2	436	U
7	B2	441	U
7	B2	446	A
7	B2	449	A
7	B2	453	A
7	B2	455	A
7	B2	492	G
7	B2	496	A
7	B2	502	A
7	B2	503	A
7	B2	509	C
7	B2	523	G
7	B2	524	A
7	B2	533	G
7	B2	534	U
7	B2	538	G
7	B2	540	G
7	B2	541	C
7	B2	555	A
7	B2	558	U
7	B2	565	C
7	B2	570	A
7	B2	571	G
7	B2	585	U
7	B2	587	C
7	B2	595	A
7	B2	596	A
7	B2	599	A
7	B2	600	G
7	B2	614	C
7	B2	615	U
7	B2	617	G
7	B2	712	U
7	B2	713	U

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Mol	Chain	Res	Type
7	B2	723	A
7	B2	724	A
7	B2	733	G
7	B2	734	C
7	B2	742	A
7	B2	743	A
7	B2	747	C
7	B2	749	U
7	B2	750	G
7	B2	753	U
7	B2	754	G
7	B2	756	A
7	B2	758	A
7	B2	759	G
7	B2	773	A
7	B2	778	A
7	B2	779	A
7	B2	820	A
7	B2	826	A
7	B2	827	A
7	B2	835	A
7	B2	837	A
7	B2	838	C
7	B2	841	G
7	B2	851	U
7	B2	871	A
7	B2	879	G
7	B2	880	A
7	B2	882	C
7	B2	883	G
7	B2	898	A
7	B2	900	A
7	B2	909	A
7	B2	925	U
7	B2	931	A
7	B2	935	A
7	B2	936	A
7	B2	952	G
7	B2	957	A
7	B2	969	U
7	B2	970	A
7	B2	976	C

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Mol	Chain	Res	Type
7	B2	978	A
7	B2	991	A
7	B2	993	C
7	B2	996	U
7	B2	997	G
7	B2	1004	C
7	B2	1005	G
7	B2	1017	G
7	B2	1018	U
7	B2	1028	G
7	B2	1029	C
7	B2	1033	G
7	B2	1040	U
7	B2	1042	C
7	B2	1050	A
7	B2	1051	A
7	B2	1057	U
7	B2	1097	A
7	B2	1109	G
7	B2	1110	A
7	B2	1111	A
7	B2	1115	C
7	B2	1116	A
7	B2	1117	C
7	B2	1119	A
7	B2	1122	A
7	B2	1123	G
7	B2	1126	G
7	B2	1144	U
7	B2	1153	A
7	B2	1154	C
7	B2	1155	A
7	B2	1158	G
7	B2	1159	G
7	B2	1160	A
7	B2	1161	A
7	B2	1165	U
7	B2	1175	C
7	B2	1176	G
7	B2	1177	G
7	B2	1184	U
7	B2	1191	U

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Mol	Chain	Res	Type
7	B2	1193	A
7	B2	1194	C
7	B2	1196	G
7	B2	1202	A
7	B2	1203	A
7	B2	1204	G
7	B2	1205	C
7	B2	1206	U
7	B2	1209	U
7	B2	1214	G
7	B2	1215	A
7	B2	1216	U
7	B2	1217	U
7	B2	1222	G
7	B2	1224	U
7	B2	1244	U
7	B2	1248	U
7	B2	1250	G
7	B2	1254	G
7	B2	1256	G
7	B2	1265	C
7	B2	1272	A
7	B2	1273	U
7	B2	1274	U
7	B2	1279	U
7	B2	1280	A
7	B2	1281	A
7	B2	1296	G
7	B2	1298	C
7	B2	1299	U
7	B2	1301	C
7	B2	1302	U
7	B2	1303	A
7	B2	1304	A
7	B2	1305	A
7	B2	1306	U
7	B2	1307	A
7	B2	1308	G
7	B2	1310	U
7	B2	1311	G
7	B2	1316	A
7	B2	1317	U

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Mol	Chain	Res	Type
7	B2	1320	U
7	B2	1322	G
7	B2	1323	G
7	B2	1324	G
7	B2	1325	U
7	B2	1327	C
7	B2	1333	A
7	B2	1335	U
7	B2	1336	U
7	B2	1341	G
7	B2	1347	U
7	B2	1348	A
7	B2	1350	G
7	B2	1358	U
7	B2	1360	G
7	B2	1364	C
7	B2	1368	A
7	B2	1371	U
7	B2	1372	U
7	B2	1373	G
7	B2	1381	A
7	B2	1383	A
7	B2	1384	G
7	B2	1387	C
7	B2	1391	G
7	B2	1392	A
7	B2	1400	A
7	B2	1402	A
7	B2	1403	U
7	B2	1414	G
7	B2	1415	C
7	B2	1416	A
7	B2	1427	A
7	B2	1433	G
7	B2	1434	G
7	B2	1438	C
7	B2	1442	G
7	B2	1443	G
7	B2	1452	U
7	B2	1460	A
7	B2	1462	G
7	B2	1470	U

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Mol	Chain	Res	Type
7	B2	1472	A
7	B2	1473	A
7	B2	1477	U
7	B2	1479	G
7	B2	1480	A
7	B2	1481	A
7	B2	1491	U
7	B2	1493	U
7	B2	1494	C
7	B2	1495	C
7	B2	1499	A
7	B2	1510	U
7	B2	1512	A
7	B2	1513	U
7	B2	1515	A
7	B2	1524	A
7	B2	1528	G
7	B2	1529	A
7	B2	1530	G
7	B2	1546	G
7	B2	1553	A
7	B2	1557	G
7	B2	1563	G
7	B2	1572	G
7	B2	1576	C
7	B2	1587	A
7	B2	1588	C
7	B2	1613	U
7	B2	1614	G
7	B2	1640	G
7	B2	1671	C
7	B2	1681	U
7	B2	1689	C
7	B2	1695	U
7	B2	1703	G
7	B2	1709	A
7	B2	1711	G
7	B2	1714	G
7	B2	1716	A
7	B2	1720	A
7	B2	1721	G
7	B2	1723	U

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Mol	Chain	Res	Type
7	B2	1734	G
7	B2	1736	A
7	B2	1746	G
7	B2	1747	G
7	B2	1748	A
7	B2	1749	U
7	B2	1750	C
7	B2	1752	U
7	B2	1754	G
8	A5	12	C
8	A5	13	U
8	A5	22	A
8	A5	39	A
8	A5	42	A
8	A5	44	A
8	A5	48	U
8	A5	58	G
8	A5	59	A
8	A5	64	A
8	A5	65	A
8	A5	69	A
8	A5	73	A
8	A5	91	G
8	A5	108	A
8	A5	109	G
8	A5	110	C
8	A5	119	G
8	A5	125	A
8	A5	133	U
8	A5	134	U
8	A5	135	G
8	A5	139	G
8	A5	140	C
8	A5	141	U
8	A5	149	G
8	A5	156	A
8	A5	157	U
8	A5	158	A
8	A5	159	G
8	A5	166	G
8	A5	169	U
8	A5	178	G

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Mol	Chain	Res	Type
8	A5	179	U
8	A5	181	G
8	A5	183	A
8	A5	184	U
8	A5	185	G
8	A5	189	G
8	A5	190	A
8	A5	193	U
8	A5	194	C
8	A5	195	C
8	A5	203	U
8	A5	204	G
8	A5	208	C
8	A5	209	C
8	A5	211	U
8	A5	212	A
8	A5	226	G
8	A5	227	C
8	A5	238	C
8	A5	239	U
8	A5	240	G
8	A5	241	G
8	A5	247	G
8	A5	248	G
8	A5	249	C
8	A5	250	A
8	A5	252	U
8	A5	260	C
8	A5	261	G
8	A5	262	C
8	A5	263	U
8	A5	264	U
8	A5	272	G
8	A5	273	G
8	A5	275	G
8	A5	289	A
8	A5	290	A
8	A5	291	G
8	A5	301	A
8	A5	304	U
8	A5	305	G
8	A5	311	U

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Mol	Chain	Res	Type
8	A5	317	U
8	A5	318	C
8	A5	329	A
8	A5	335	C
8	A5	336	G
8	A5	345	G
8	A5	357	A
8	A5	358	A
8	A5	366	G
8	A5	368	G
8	A5	382	G
8	A5	404	G
8	A5	405	A
8	A5	408	A
8	A5	409	C
8	A5	424	G
8	A5	427	G
8	A5	428	A
8	A5	435	G
8	A5	516	G
8	A5	518	C
8	A5	522	G
8	A5	535	C
8	A5	536	G
8	A5	542	G
8	A5	546	G
8	A5	577	U
8	A5	578	C
8	A5	581	G
8	A5	585	G
8	A5	588	G
8	A5	590	A
8	A5	594	G
8	A5	598	C
8	A5	599	G
8	A5	600	U
8	A5	601	G
8	A5	602	G
8	A5	634	A
8	A5	635	C
8	A5	636	G
8	A5	638	C

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Mol	Chain	Res	Type
8	A5	639	G
8	A5	640	G
8	A5	641	U
8	A5	643	U
8	A5	644	G
8	A5	645	A
8	A5	646	A
8	A5	647	A
8	A5	655	A
8	A5	656	C
8	A5	666	C
8	A5	678	A
8	A5	689	A
8	A5	706	A
8	A5	711	A
8	A5	712	A
8	A5	716	U
8	A5	717	G
8	A5	720	A
8	A5	728	G
8	A5	729	C
8	A5	738	G
8	A5	742	G
8	A5	745	A
8	A5	746	A
8	A5	747	G
8	A5	751	A
8	A5	755	U
8	A5	756	C
8	A5	758	A
8	A5	759	A
8	A5	760	U
8	A5	763	G
8	A5	764	C
8	A5	767	A
8	A5	768	C
8	A5	791	U
8	A5	797	G
8	A5	804	G
8	A5	816	G
8	A5	817	U
8	A5	821	U

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Mol	Chain	Res	Type
8	A5	822	U
8	A5	823	G
8	A5	834	G
8	A5	835	A
8	A5	836	G
8	A5	840	G
8	A5	854	C
8	A5	861	A
8	A5	868	G
8	A5	872	A
8	A5	904	C
8	A5	916	U
8	A5	919	G
8	A5	929	U
8	A5	934	U
8	A5	935	G
8	A5	951	A
8	A5	961	A
8	A5	962	G
8	A5	963	G
8	A5	969	A
8	A5	971	G
8	A5	972	A
8	A5	976	A
8	A5	978	C
8	A5	992	G
8	A5	999	C
8	A5	1001	U
8	A5	1014	C
8	A5	1015	U
8	A5	1016	C
8	A5	1017	A
8	A5	1029	U
8	A5	1032	C
8	A5	1034	G
8	A5	1036	C
8	A5	1039	U
8	A5	1048	G
8	A5	1049	U
8	A5	1056	A
8	A5	1064	G
8	A5	1090	A

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Mol	Chain	Res	Type
8	A5	1101	A
8	A5	1103	C
8	A5	1104	U
8	A5	1110	U
8	A5	1118	A
8	A5	1119	A
8	A5	1123	G
8	A5	1125	A
8	A5	1126	G
8	A5	1134	A
8	A5	1135	G
8	A5	1137	G
8	A5	1145	A
8	A5	1150	G
8	A5	1151	A
8	A5	1156	G
8	A5	1168	G
8	A5	1169	G
8	A5	1183	G
8	A5	1196	U
8	A5	1205	A
8	A5	1207	C
8	A5	1211	A
8	A5	1220	U
8	A5	1224	G
8	A5	1226	G
8	A5	1232	C
8	A5	1233	U
8	A5	1234	U
8	A5	1244	G
8	A5	1245	A
8	A5	1250	C
8	A5	1253	U
8	A5	1261	G
8	A5	1264	G
8	A5	1272	U
8	A5	1273	U
8	A5	1274	G
8	A5	1275	A
8	A5	1279	C
8	A5	1339	A
8	A5	1354	A

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Mol	Chain	Res	Type
8	A5	1359	G
8	A5	1360	A
8	A5	1361	U
8	A5	1368	U
8	A5	1375	G
8	A5	1377	G
8	A5	1383	U
8	A5	1430	A
8	A5	1440	U
8	A5	1441	C
8	A5	1448	G
8	A5	1449	U
8	A5	1453	G
8	A5	1467	G
8	A5	1496	G
8	A5	1499	G
8	A5	1502	C
8	A5	1511	A
8	A5	1512	G
8	A5	1515	G
8	A5	1534	C
8	A5	1546	A
8	A5	1548	G
8	A5	1567	G
8	A5	1568	A
8	A5	1573	U
8	A5	1604	A
8	A5	1606	U
8	A5	1607	G
8	A5	1608	G
8	A5	1612	A
8	A5	1614	G
8	A5	1619	G
8	A5	1620	U
8	A5	1621	A
8	A5	1626	C
8	A5	1627	G
8	A5	1628	G
8	A5	1650	U
8	A5	1651	C
8	A5	1655	G
8	A5	1658	U

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Mol	Chain	Res	Type
8	A5	1659	G
8	A5	1663	A
8	A5	1664	A
8	A5	1665	A
8	A5	1670	A
8	A5	1671	U
8	A5	1681	A
8	A5	1704	U
8	A5	1725	C
8	A5	1727	C
8	A5	1728	G
8	A5	1736	A
8	A5	1738	U
8	A5	1739	C
8	A5	1749	U
8	A5	1750	A
8	A5	1756	U
8	A5	1768	C
8	A5	1769	U
8	A5	1772	A
8	A5	1775	U
8	A5	1776	U
8	A5	1777	U
8	A5	1780	U
8	A5	1781	C
8	A5	1787	U
8	A5	1796	G
8	A5	1798	A
8	A5	1801	C
8	A5	1810	U
8	A5	1811	G
8	A5	1817	G
8	A5	1833	U
8	A5	1837	U
8	A5	1838	U
8	A5	1839	C
8	A5	1840	C
8	A5	1842	A
8	A5	1843	A
8	A5	1845	A
8	A5	1851	G
8	A5	1853	G

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Mol	Chain	Res	Type
8	A5	1862	G
8	A5	1868	U
8	A5	1870	G
8	A5	1873	C
8	A5	1874	U
8	A5	1875	C
8	A5	1876	U
8	A5	1882	C
8	A5	1883	G
8	A5	1887	C
8	A5	1891	A
8	A5	1893	A
8	A5	1904	G
8	A5	1908	A
8	A5	1910	U
8	A5	1913	U
8	A5	1914	U
8	A5	1915	U
8	A5	1917	C
8	A5	1919	C
8	A5	1932	A
8	A5	1935	U
8	A5	1938	G
8	A5	1939	C
8	A5	1948	U
8	A5	1967	A
8	A5	1971	G
8	A5	1972	A
8	A5	1973	U
8	A5	1979	A
8	A5	1982	G
8	A5	1999	G
8	A5	2205	A
8	A5	2211	A
8	A5	2215	G
8	A5	2216	U
8	A5	2218	C
8	A5	2225	A
8	A5	2226	G
8	A5	2235	A
8	A5	2244	U
8	A5	2246	A

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Mol	Chain	Res	Type
8	A5	2248	A
8	A5	2253	A
8	A5	2262	A
8	A5	2273	G
8	A5	2281	A
8	A5	2295	C
8	A5	2308	U
8	A5	2309	G
8	A5	2310	A
8	A5	2311	A
8	A5	2312	U
8	A5	2313	G
8	A5	2326	A
8	A5	2333	G
8	A5	2341	G
8	A5	2347	A
8	A5	2352	G
8	A5	2358	A
8	A5	2359	A
8	A5	2361	U
8	A5	2375	G
8	A5	2376	G
8	A5	2382	A
8	A5	2384	A
8	A5	2410	G
8	A5	2413	U
8	A5	2416	A
8	A5	2418	G
8	A5	2437	U
8	A5	2439	U
8	A5	2474	G
8	A5	2475	A
8	A5	2476	A
8	A5	2477	C
8	A5	2478	G
8	A5	2488	A
8	A5	2496	G
8	A5	2500	A
8	A5	2503	G
8	A5	2505	A
8	A5	2506	G
8	A5	2507	A

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Mol	Chain	Res	Type
8	A5	2514	U
8	A5	2538	G
8	A5	2546	U
8	A5	2547	C
8	A5	2609	A
8	A5	2610	C
8	A5	2611	U
8	A5	2612	C
8	A5	2619	U
8	A5	2620	A
8	A5	2625	G
8	A5	2626	U
8	A5	2627	U
8	A5	2631	A
8	A5	2633	A
8	A5	2636	A
8	A5	2656	U
8	A5	2658	G
8	A5	2659	A
8	A5	2660	A
8	A5	2666	A
8	A5	2671	G
8	A5	2672	A
8	A5	2684	G
8	A5	2685	C
8	A5	2686	A
8	A5	2694	U
8	A5	2698	C
8	A5	2705	A
8	A5	2706	C
8	A5	2718	G
8	A5	2719	G
8	A5	2726	G
8	A5	2731	G
8	A5	2738	A
8	A5	2763	G
8	A5	2764	U
8	A5	2768	A
8	A5	2786	A
8	A5	2789	G
8	A5	2791	A
8	A5	2792	A

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Mol	Chain	Res	Type
8	A5	2797	U
8	A5	2801	A
8	A5	2803	A
8	A5	2806	A
8	A5	2808	A
8	A5	2814	A
8	A5	2815	A
8	A5	2816	A
8	A5	2839	A
8	A5	2840	G
8	A5	2841	U
8	A5	2843	C
8	A5	2859	A
8	A5	2865	G
8	A5	2874	A
8	A5	2882	A
8	A5	2883	A
8	A5	2889	A
8	A5	2890	U
8	A5	2908	G
8	A5	2911	A
8	A5	2912	G
8	A5	2913	A
8	A5	2922	C
8	A5	2929	A
8	A5	2930	U
8	A5	2950	A
8	A5	2954	U
8	A5	2956	C
8	A5	2957	A
8	A5	2959	A
8	A5	2972	U
8	A5	2979	C
8	A5	2983	G
8	A5	2984	A
8	A5	2998	U
8	A5	2999	A
8	A5	3010	G
8	A5	3011	C
8	A5	3012	A
8	A5	3013	G
8	A5	3014	A

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Mol	Chain	Res	Type
8	A5	3023	A
8	A5	3028	U
8	A5	3035	U
8	A5	3047	U
8	A5	3048	A
8	A5	3053	A
8	A5	3054	C
8	A5	3059	G
8	A5	3063	G
8	A5	3066	U
8	A5	3080	G
8	A5	3083	A
8	A5	3092	U
8	A5	3095	C
8	A5	3102	G
8	A5	3106	A
8	A5	3109	U
8	A5	3112	U
8	A5	3113	A
8	A5	3119	A
8	A5	3124	A
8	A5	3125	A
8	A5	3129	U
8	A5	3130	G
8	A5	3132	U
8	A5	3134	A
8	A5	3138	C
8	A5	3140	A
8	A5	3141	G
8	A5	3142	A
8	A5	3146	A
8	A5	3162	U
8	A5	3163	U
8	A5	3167	U
8	A5	3170	A
8	A5	3171	U
8	A5	3180	U
8	A5	3185	A
8	A5	3187	A
8	A5	3188	U
8	A5	3191	A
8	A5	3199	A

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Mol	Chain	Res	Type
8	A5	3205	C
8	A5	3206	C
8	A5	3207	A
8	A5	3212	A
8	A5	3231	C
8	A5	3235	A
8	A5	3238	U
8	A5	3243	A
8	A5	3244	U
8	A5	3254	U
8	A5	3255	C
8	A5	3257	A
8	A5	3258	G
8	A5	3259	G
8	A5	3268	U
8	A5	3278	C
8	A5	3279	G
8	A5	3280	G
8	A5	3282	G
8	A5	3284	C
8	A5	3285	G
8	A5	3286	G
8	A5	3288	A
8	A5	3289	G
8	A5	3292	A
8	A5	3293	U
8	A5	3294	C
8	A5	3298	A
8	A5	3299	U
8	A5	3305	G
8	A5	3306	G
8	A5	3310	C
8	A5	3315	G
8	A5	3317	G
8	A5	3318	C
8	A5	3320	U
8	A5	3321	A
8	A5	3322	U
8	A5	3331	U
8	A5	3332	A
8	A5	3333	U
8	A5	3334	G

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Mol	Chain	Res	Type
8	A5	3335	G
8	A5	3337	C
8	A5	3338	U
8	A5	3339	U
8	A5	3341	G
8	A5	3347	U
8	A5	3349	G
8	A5	3351	G
8	A5	3352	A
8	A5	3354	U
8	A5	3364	C
8	A5	3366	U
8	A5	3371	A
8	A5	3373	G
8	A5	3375	C
8	A5	3376	A
8	A5	3377	G
8	A5	3378	A
8	A5	3380	C
8	A5	3381	A
8	A5	3385	U
8	A5	3386	G
8	A5	3387	G
8	A5	3388	U
8	A5	3389	U
8	A5	3390	C
8	A5	3393	U
8	A5	3397	G
8	A5	3399	G
8	A5	3401	C
8	A5	3405	A
8	A5	3406	A
8	A5	3415	C
8	A5	3426	G
8	A5	3436	C
8	A5	3454	A
8	A5	3457	G
8	A5	3461	U
8	A5	3463	C
8	A5	3464	U
8	A5	3465	U
8	A5	3466	U

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Mol	Chain	Res	Type
8	A5	3467	U
8	A5	3468	A
8	A5	3469	U
8	A5	3470	A
8	A5	3472	U
8	A5	3474	C
8	A5	3482	U
8	A5	3483	G
8	A5	3488	U
8	A5	3489	A
8	A5	3494	U
8	A5	3495	U
8	A5	3496	G
8	A5	3497	A
8	A5	3509	G
78	DA	4	U
78	DA	9	A
78	DA	16	U
78	DA	17	U
78	DA	19	G
78	DA	21	A
78	DA	22	G
78	DA	38	A
78	DA	46	G
78	DA	47	U
78	DA	51	C
78	DA	55	U
78	DA	57	G
78	DA	58	A
78	DA	59	U
78	DA	61	C
78	DA	75	C
78	DA	76	A
78	DB	4	U
78	DB	9	A
78	DB	16	U
78	DB	17	U
78	DB	18	G
78	DB	19	G
78	DB	20	G
78	DB	21	A
78	DB	22	G

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Mol	Chain	Res	Type
78	DB	40	C
78	DB	44	A
78	DB	45	G
78	DB	46	G
78	DB	47	U
78	DB	48	C
78	DB	55	U
78	DB	56	C
78	DB	59	U
78	DB	60	C
78	DB	68	G
78	DB	74	C
78	DB	75	C
79	DC	4	U
79	DC	7	U

All (103) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	B2	159	G
7	B2	228	U
7	B2	353	G
7	B2	356	C
7	B2	448	U
7	B2	711	U
7	B2	908	C
7	B2	1027	U
7	B2	1039	A
7	B2	1041	C
7	B2	1110	A
7	B2	1121	A
7	B2	1183	A
7	B2	1192	G
7	B2	1213	C
7	B2	1278	A
7	B2	1280	A
7	B2	1305	A
7	B2	1309	U
7	B2	1363	G
7	B2	1371	U
7	B2	1437	U
7	B2	1490	A

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Mol	Chain	Res	Type
7	B2	1509	G
7	B2	1511	A
7	B2	1529	A
7	B2	1715	U
7	B2	1751	A
8	A5	12	C
8	A5	21	G
8	A5	133	U
8	A5	134	U
8	A5	189	G
8	A5	194	C
8	A5	238	C
8	A5	251	C
8	A5	263	U
8	A5	288	A
8	A5	403	A
8	A5	408	A
8	A5	576	G
8	A5	580	U
8	A5	589	U
8	A5	598	C
8	A5	635	C
8	A5	646	A
8	A5	711	A
8	A5	754	C
8	A5	759	A
8	A5	763	G
8	A5	816	G
8	A5	834	G
8	A5	928	C
8	A5	971	G
8	A5	1035	G
8	A5	1118	A
8	A5	1150	G
8	A5	1155	C
8	A5	1650	U
8	A5	1658	U
8	A5	1737	U
8	A5	1749	U
8	A5	1844	A
8	A5	1861	U
8	A5	1875	C

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Mol	Chain	Res	Type
8	A5	1907	U
8	A5	1909	U
8	A5	1912	A
8	A5	2475	A
8	A5	2608	G
8	A5	2609	A
8	A5	2610	C
8	A5	2630	A
8	A5	2658	G
8	A5	2790	A
8	A5	3047	U
8	A5	3139	G
8	A5	3234	U
8	A5	3256	A
8	A5	3257	A
8	A5	3258	G
8	A5	3277	C
8	A5	3281	U
8	A5	3283	U
8	A5	3285	G
8	A5	3297	U
8	A5	3304	U
8	A5	3309	A
8	A5	3320	U
8	A5	3321	A
8	A5	3333	U
8	A5	3334	G
8	A5	3338	U
8	A5	3340	G
8	A5	3348	A
8	A5	3365	U
8	A5	3374	C
8	A5	3375	C
8	A5	3376	A
8	A5	3377	G
8	A5	3389	U
8	A5	3460	G
78	DB	58	A

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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	$\# Z > 2$
80	SPD	A5	3601	-	9,9,9	0.34	0	8,8,8	0.80	0
81	3HE	A5	3602	-	21,21,21	0.51	0	23,30,30	0.96	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
80	SPD	A5	3601	-	-	2/7/7/7	-
81	3HE	A5	3602	-	-	1/8/36/36	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

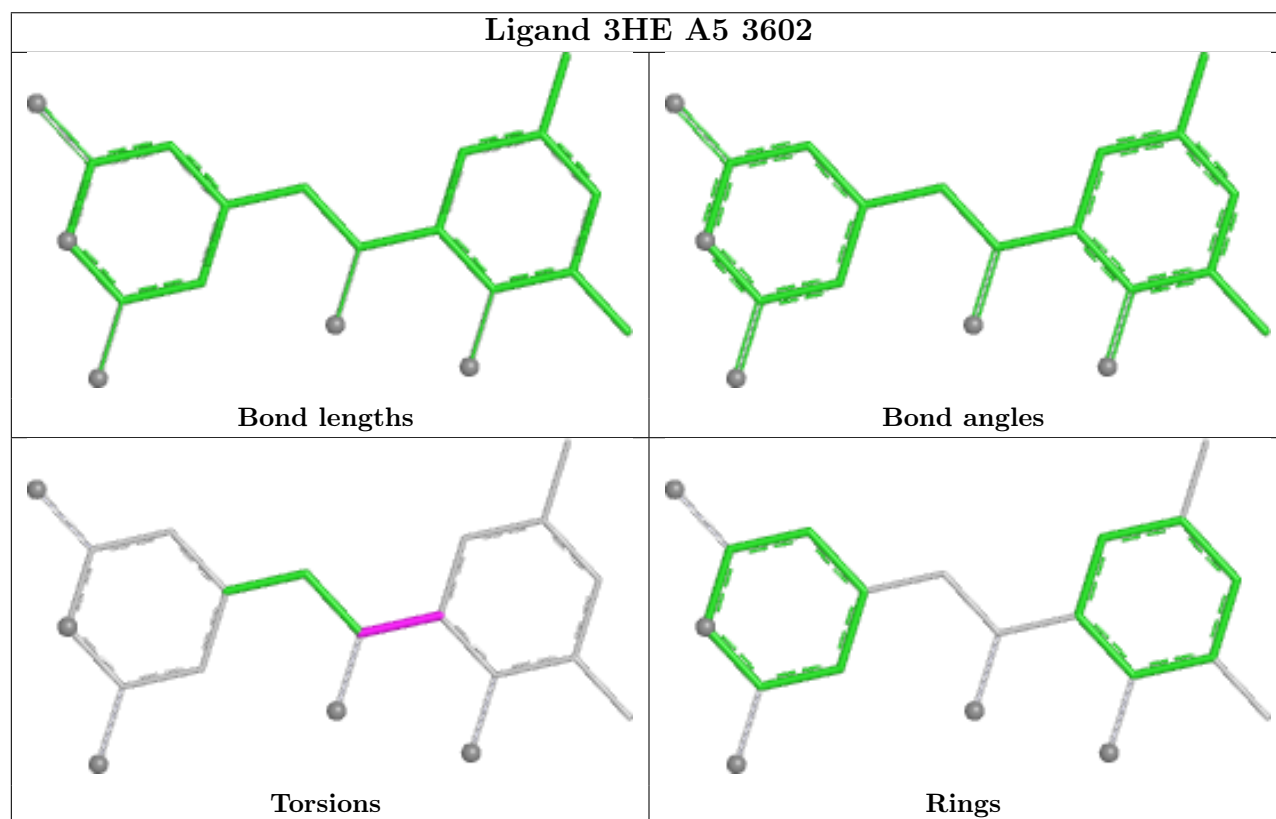
Mol	Chain	Res	Type	Atoms
81	A5	3602	3HE	C6-C5-C7-O3
80	A5	3601	SPD	C4-C5-N6-C7
80	A5	3601	SPD	C8-C7-N6-C5

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
80	A5	3601	SPD	1	0
81	A5	3602	3HE	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	A5	1
7	B2	1
79	DC	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	3461:U	O3'	3462:C	P	7.49
1	B2	745:C	O3'	746:G	P	2.82
1	DC	6:U	O3'	7:U	P	2.74

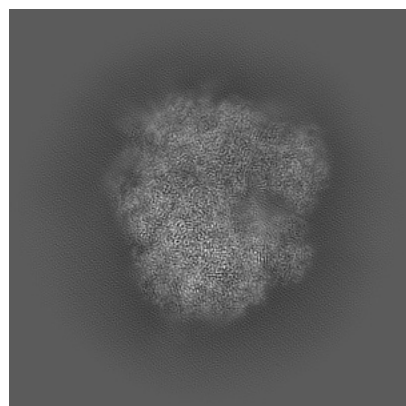
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44533. These allow visual inspection of the internal detail of the map and identification of artifacts.

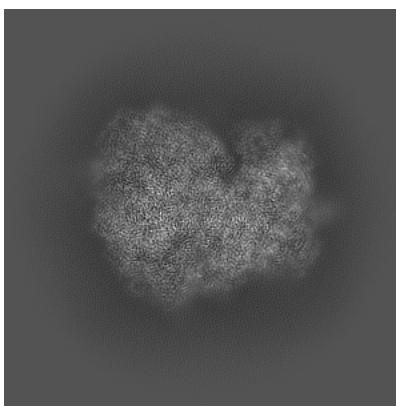
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

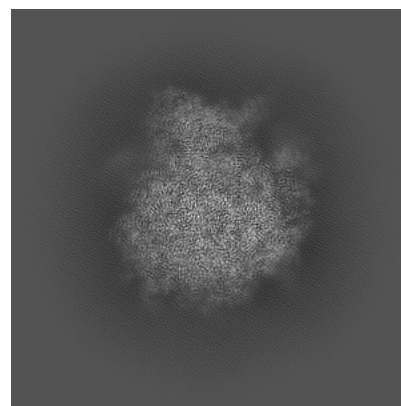
6.1.1 Primary map



X

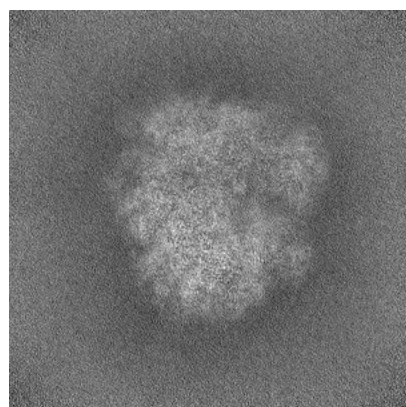


Y

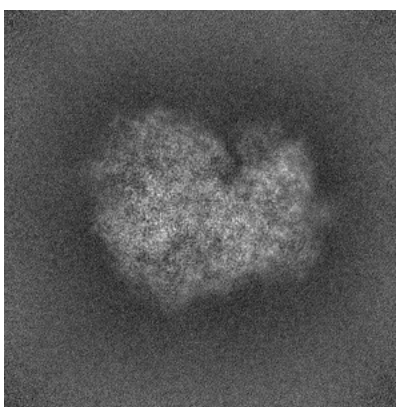


Z

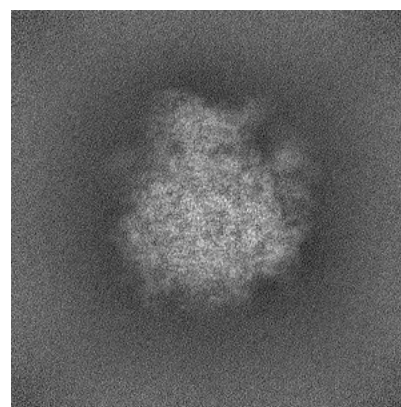
6.1.2 Raw map



X



Y

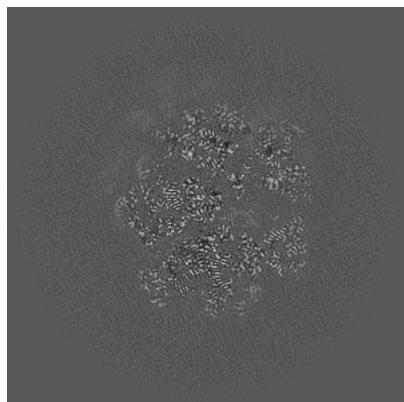


Z

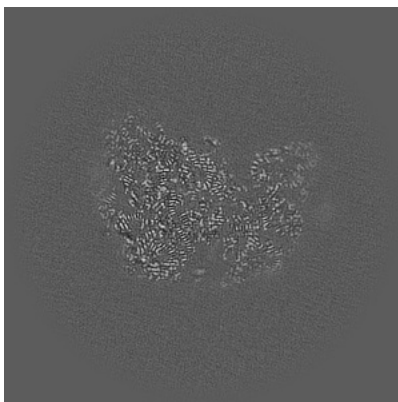
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

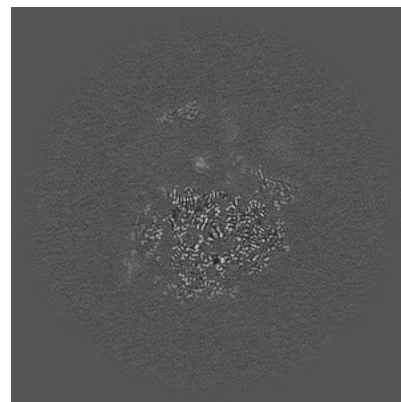
6.2.1 Primary map



X Index: 340

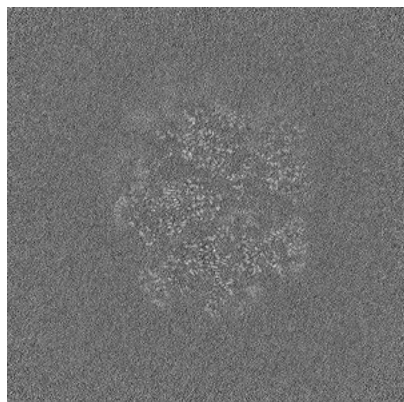


Y Index: 340

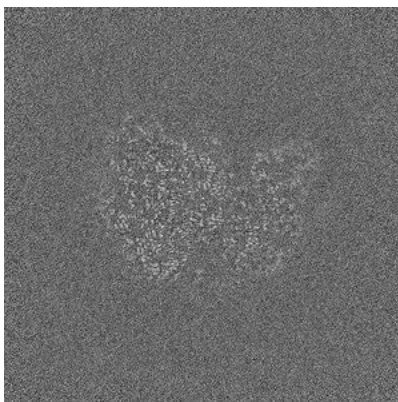


Z Index: 340

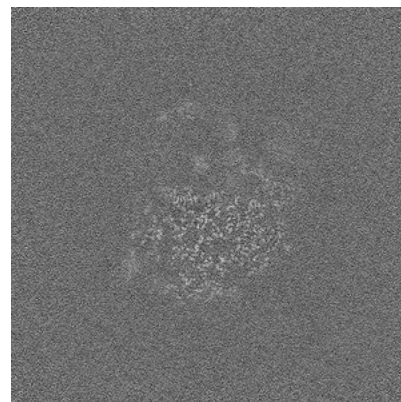
6.2.2 Raw map



X Index: 340



Y Index: 340

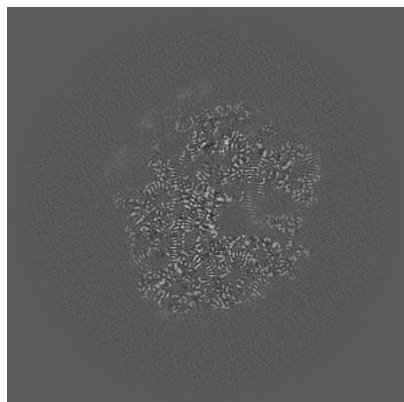


Z Index: 340

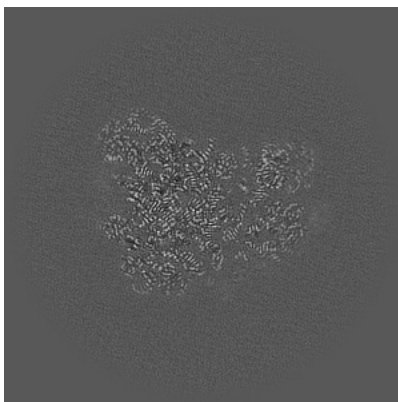
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

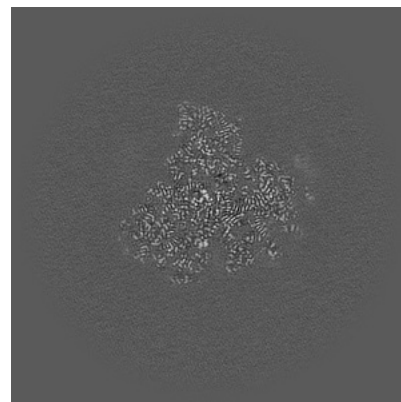
6.3.1 Primary map



X Index: 318

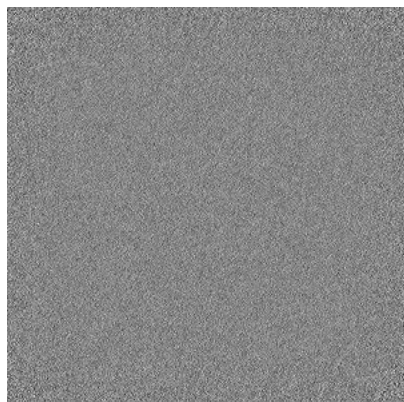


Y Index: 326

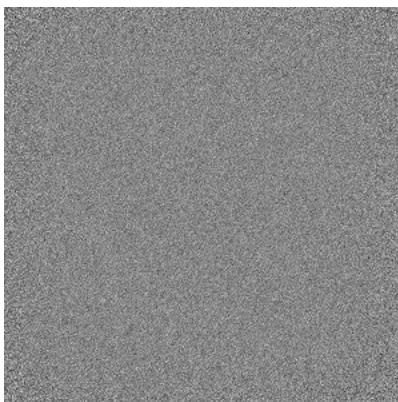


Z Index: 266

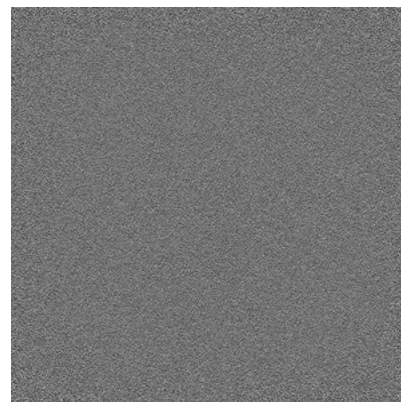
6.3.2 Raw map



X Index: 0



Y Index: 0

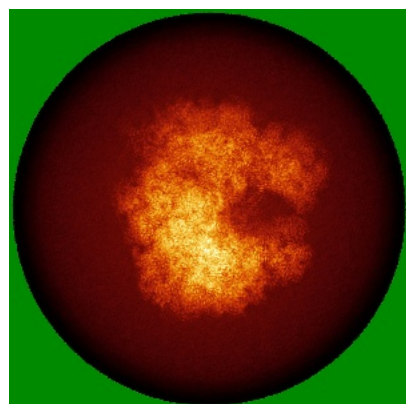


Z Index: 679

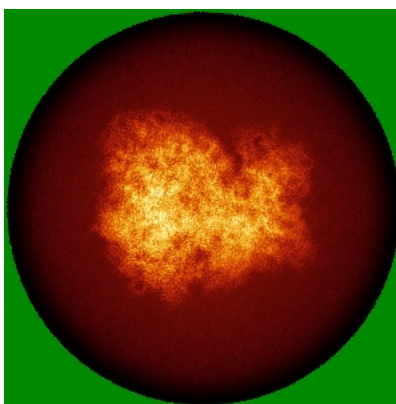
The images above show the largest variance slices of the map in three orthogonal directions.

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

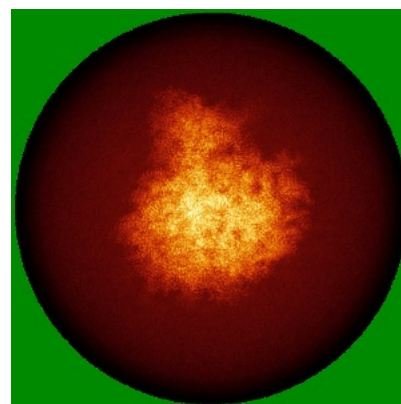
6.4.1 Primary map



X

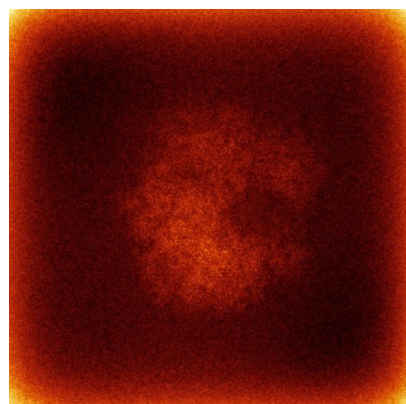


Y

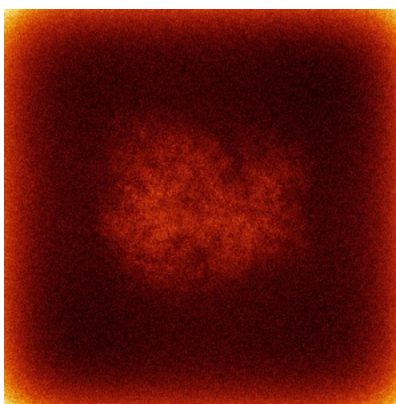


Z

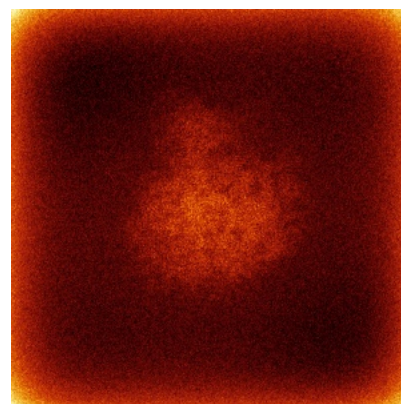
6.4.2 Raw map



X



Y

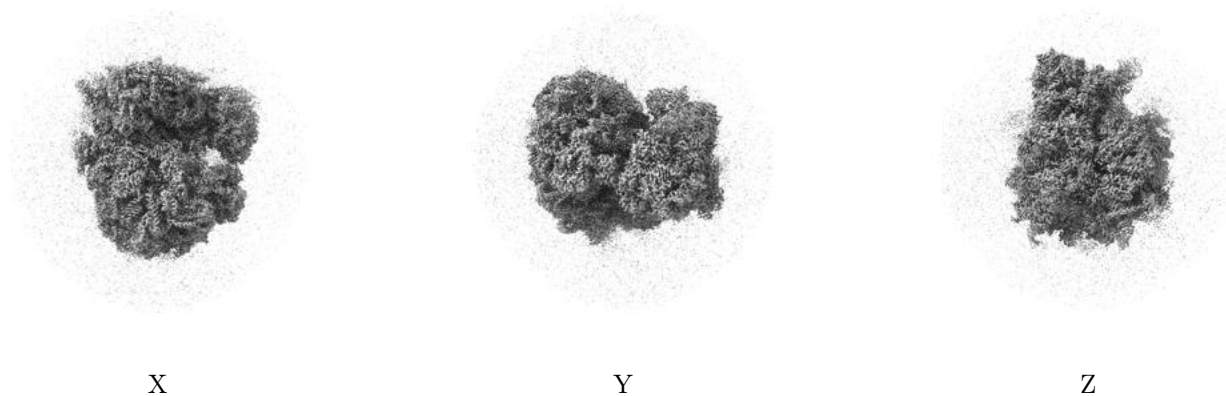


Z

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

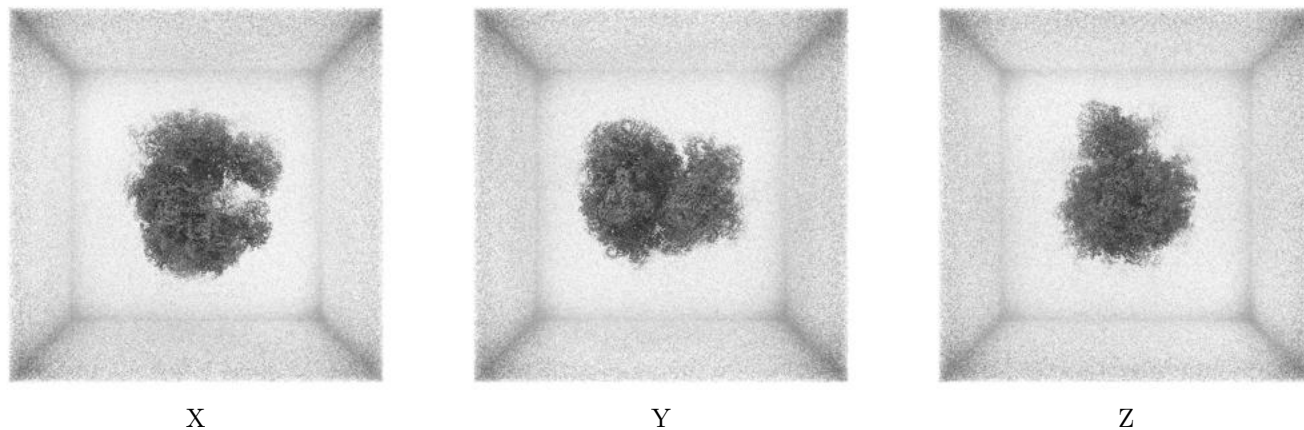
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.182. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

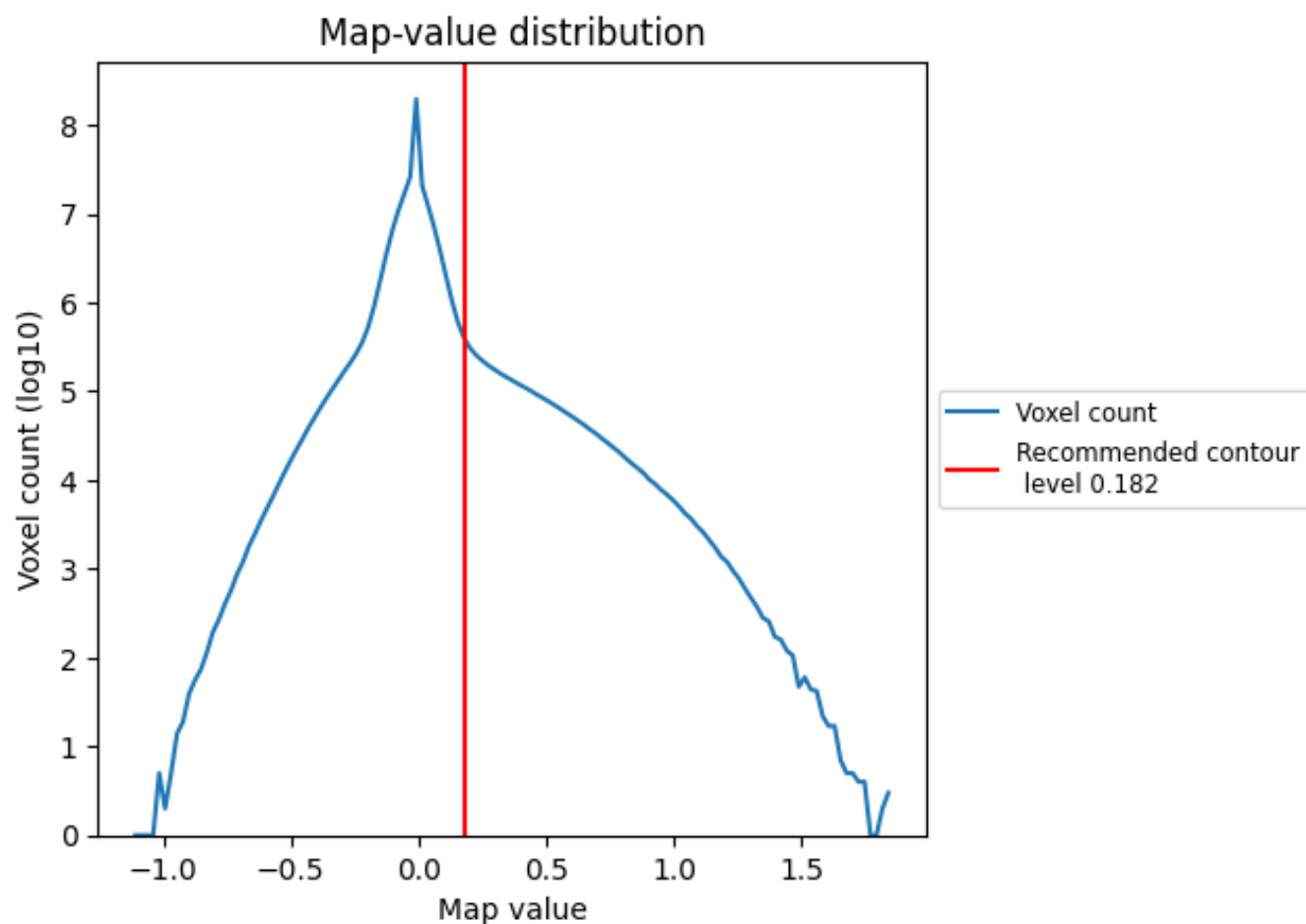
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

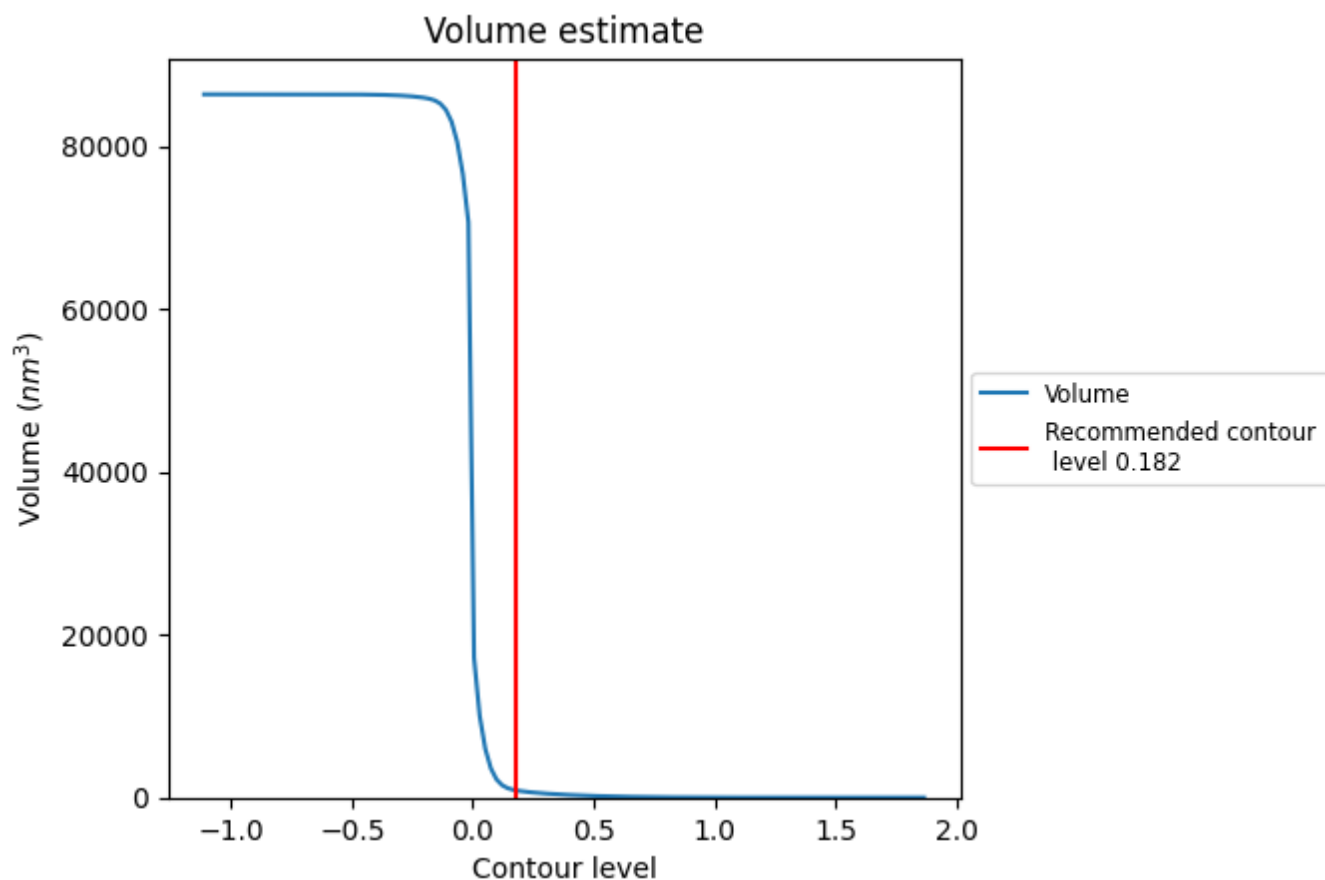
This section contains the results of statistical analysis of the map.

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.

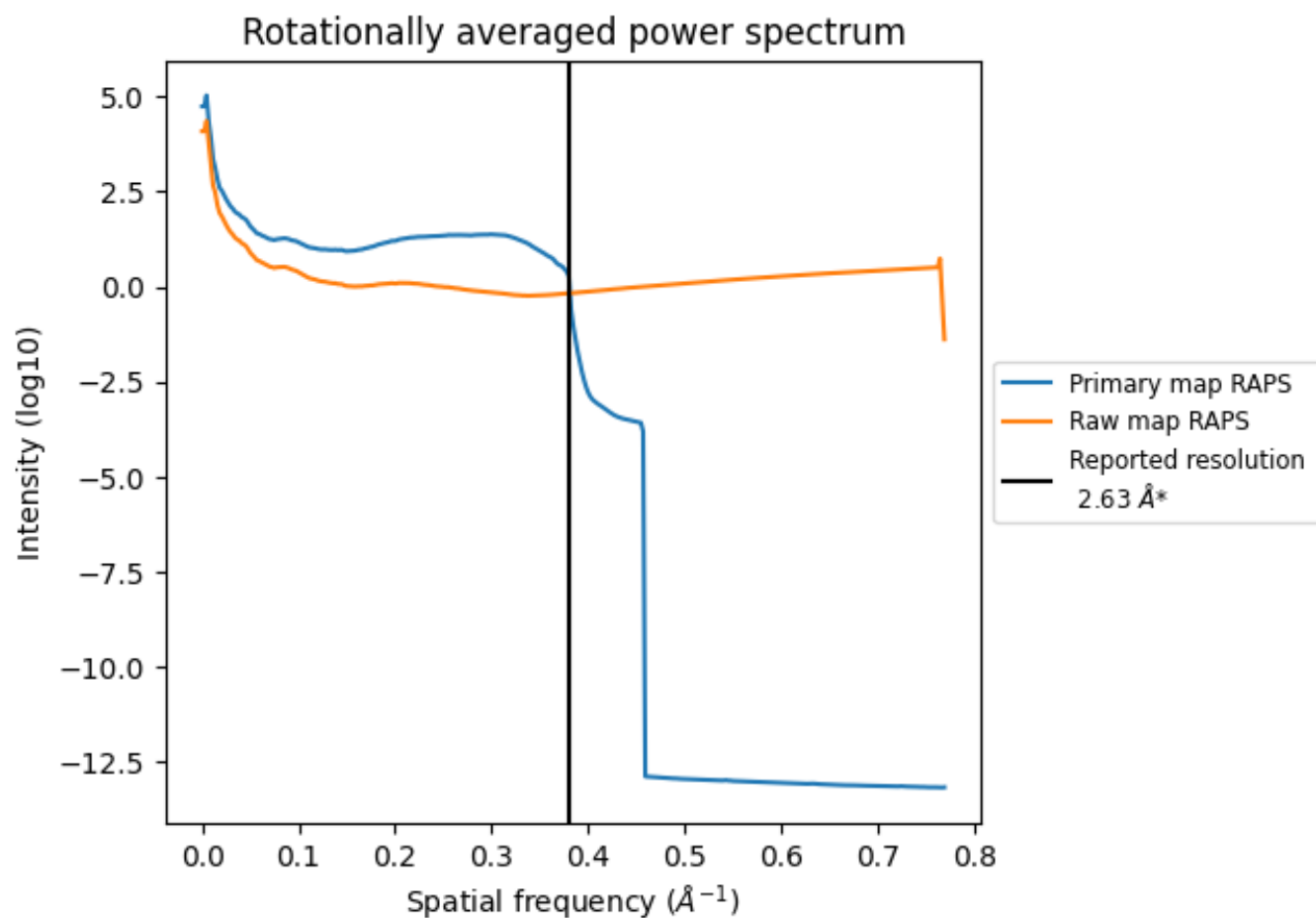
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 874 nm³; this corresponds to an approximate mass of 789 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 ⓘ

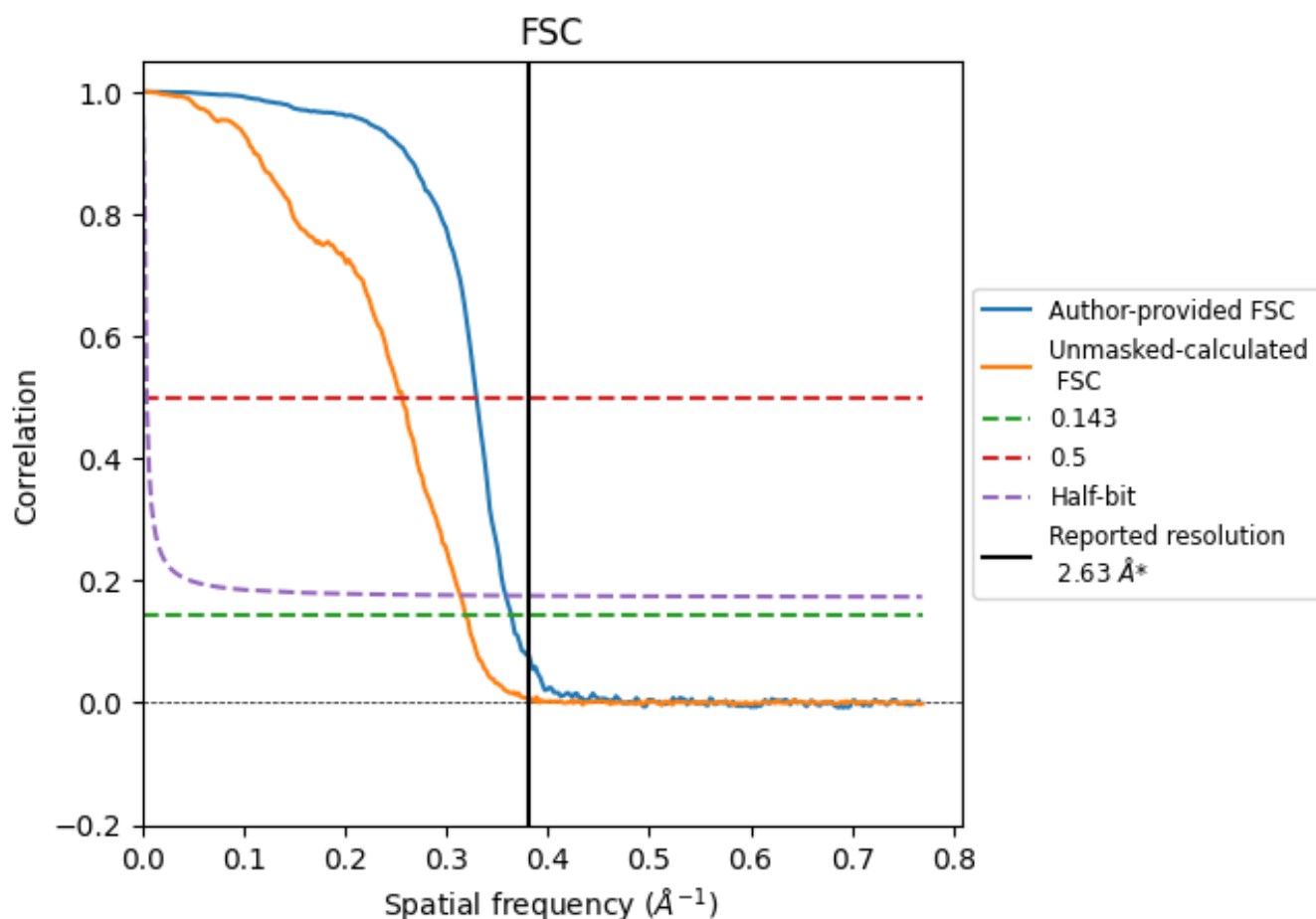


*Reported resolution corresponds to spatial frequency of 0.380 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.380 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

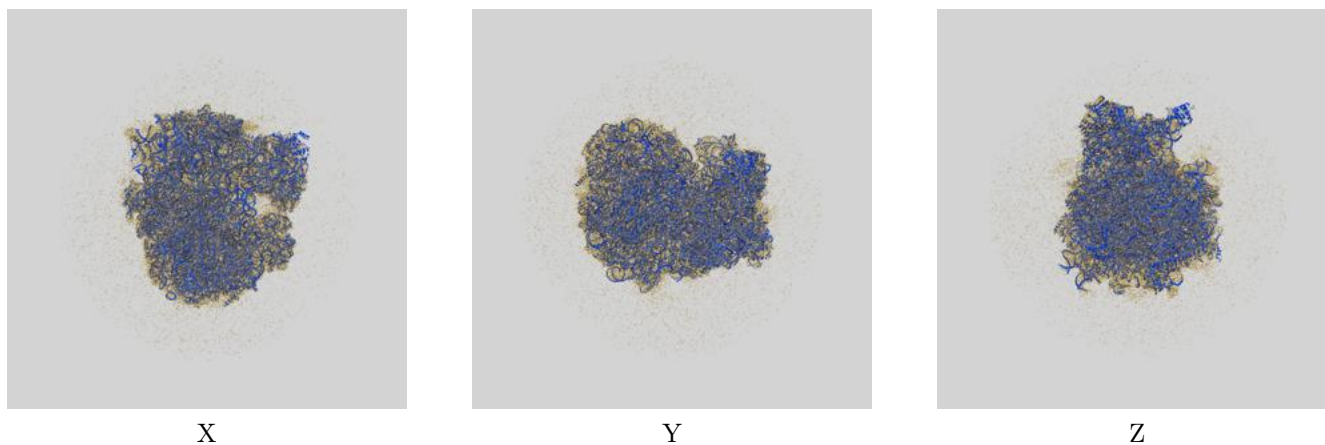
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.63	-	-
Author-provided FSC curve	2.75	3.03	2.79
Unmasked-calculated*	3.14	3.90	3.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.14 differs from the reported value 2.63 by more than 10 %

9 Map-model fit [i](#)

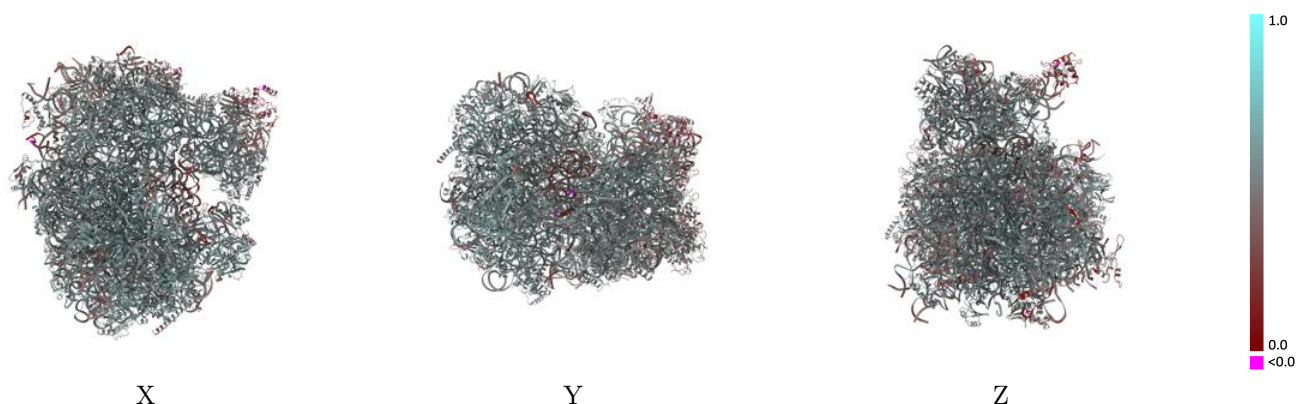
This section contains information regarding the fit between EMDB map EMD-44533 and PDB model 9BH5. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



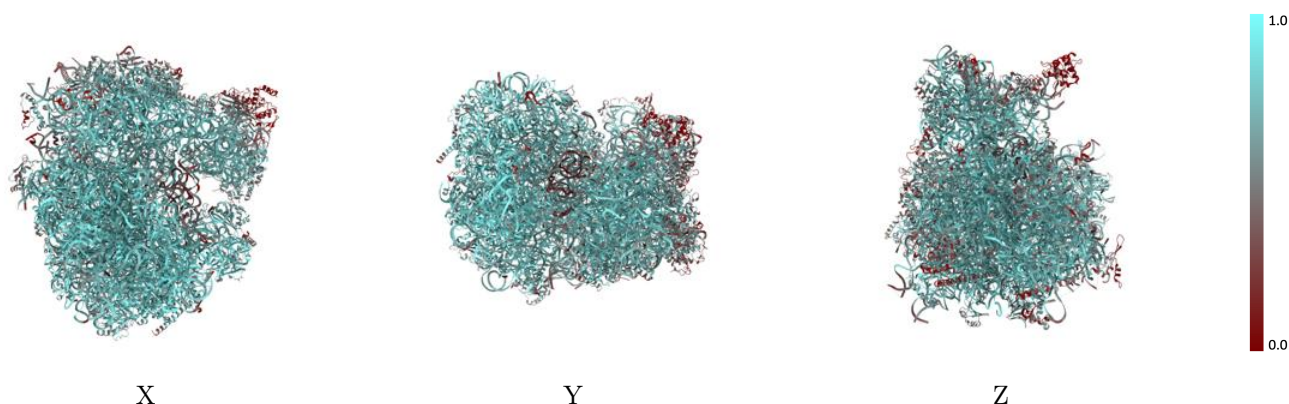
The images above show the 3D surface view of the map at the recommended contour level 0.182 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



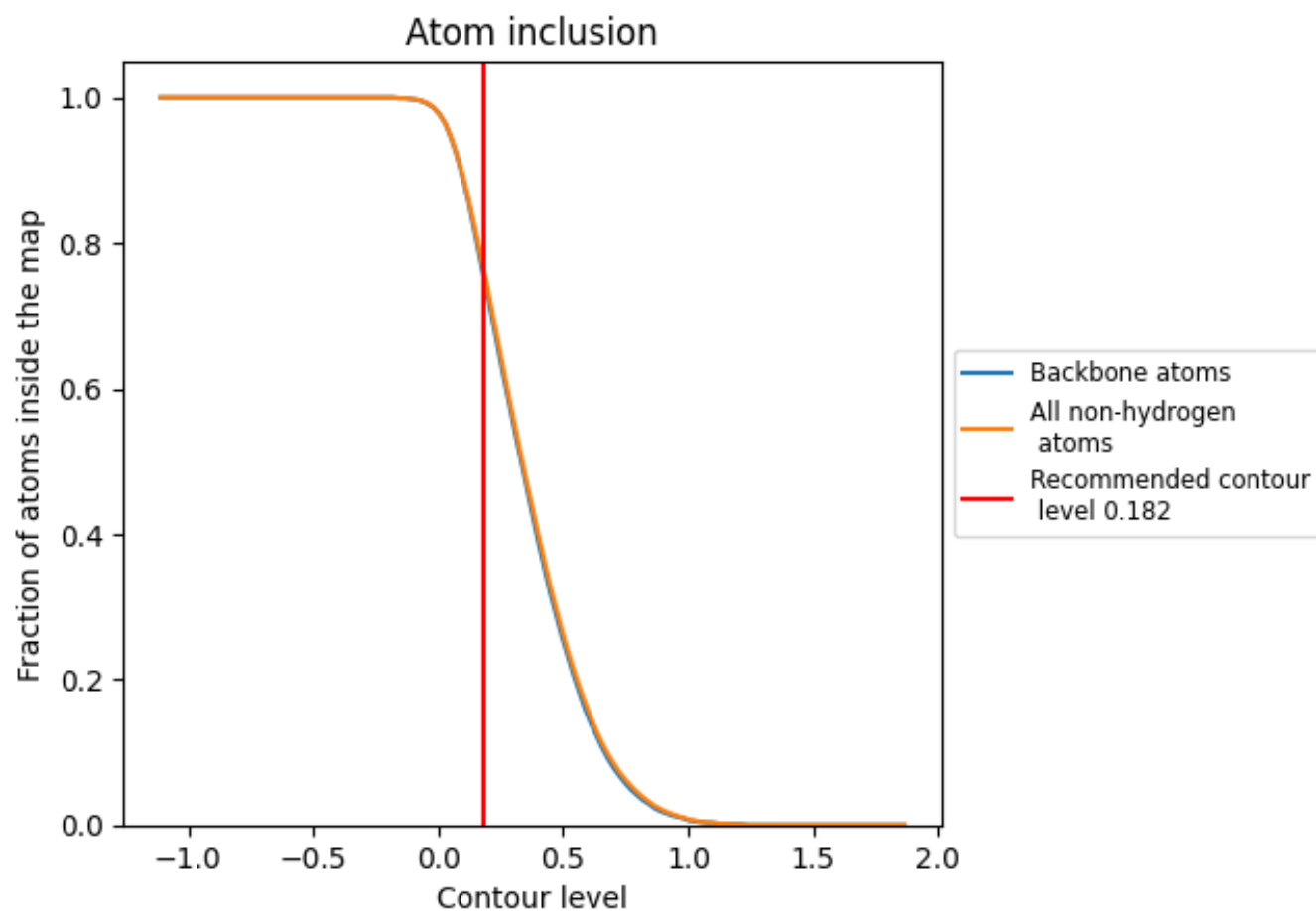
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.182).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 76% 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 (0.182) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7650	 0.5170
A5	 0.8320	 0.5250
A7	 0.8770	 0.5550
A8	 0.8550	 0.5490
AA	 0.5930	 0.4810
AB	 0.6720	 0.5130
AC	 0.7080	 0.5050
AD	 0.5530	 0.4690
AE	 0.6650	 0.4930
AF	 0.6990	 0.5180
AG	 0.5320	 0.4610
AH	 0.4250	 0.4300
AI	 0.6760	 0.4980
AJ	 0.4940	 0.4110
AK	 0.4840	 0.4600
AL	 0.7490	 0.5260
AM	 0.0600	 0.2510
AN	 0.5850	 0.4850
AO	 0.7520	 0.5280
AP	 0.6540	 0.5120
AQ	 0.6700	 0.5090
AR	 0.4630	 0.4320
AS	 0.6950	 0.5170
AT	 0.6980	 0.5070
AU	 0.5100	 0.4430
AV	 0.5910	 0.4640
AW	 0.7490	 0.5180
AX	 0.7870	 0.5530
AY	 0.5300	 0.4550
AZ	 0.5670	 0.4950
Aa	 0.7350	 0.5120
Ab	 0.4640	 0.4510
Ac	 0.5900	 0.4940
Ad	 0.7240	 0.5110
Ae	 0.6020	 0.4780



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Chain	Atom inclusion	Q-score
Af	 0.0980	 0.2960
B2	 0.8070	 0.5200
CA	 0.8600	 0.5500
CB	 0.8460	 0.5530
CC	 0.8070	 0.5450
CD	 0.7580	 0.5450
CE	 0.7230	 0.5240
CF	 0.8240	 0.5480
CG	 0.6770	 0.5070
CH	 0.7460	 0.5270
CI	 0.6500	 0.5170
CJ	 0.6730	 0.5040
CL	 0.7600	 0.5410
CM	 0.8020	 0.5460
CN	 0.8830	 0.5650
CO	 0.8310	 0.5520
CP	 0.8460	 0.5530
CQ	 0.8650	 0.5590
CR	 0.6670	 0.4970
CS	 0.8240	 0.5500
CT	 0.8020	 0.5450
CU	 0.6020	 0.4950
CV	 0.8170	 0.5430
CW	 0.6000	 0.4730
CX	 0.7570	 0.5310
CY	 0.7940	 0.5450
CZ	 0.7420	 0.5200
Ca	 0.8680	 0.5600
Cb	 0.7310	 0.5150
Cc	 0.7310	 0.5160
Cd	 0.7890	 0.5430
Ce	 0.7940	 0.5460
Cf	 0.8500	 0.5560
Cg	 0.7830	 0.5390
Ch	 0.7520	 0.5270
Ci	 0.7440	 0.5360
Cj	 0.8670	 0.5470
Ck	 0.5970	 0.5070
Cl	 0.8230	 0.5540
Cm	 0.6060	 0.5010
Cn	 0.6720	 0.4830
Co	 0.7980	 0.5500

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Chain	Atom inclusion	Q-score
Cp	 0.7870	 0.5230
DA	 0.5200	 0.3710
DB	 0.3900	 0.3550
DC	 0.7850	 0.4680