



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 01:50 AM UTC

PDB ID : 7P7U / pdb_00007p7u
EMDB ID : EMD-13245
Title : E. faecalis 70S ribosome with P-tRNA, state IV
Authors : Crowe-McAuliffe, C.; Wilson, D.N.
Deposited on : 2021-07-20
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

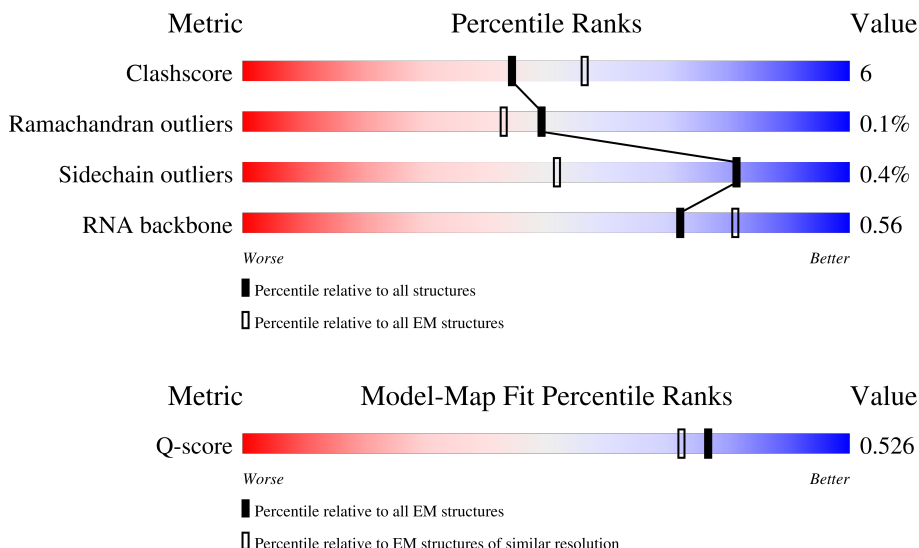
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	1	62	
2	2	59	
3	3	89	

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Mol	Chain	Length	Quality of chain
4	4	59	
5	5	49	
6	6	44	
7	7	66	
8	8	38	
9	A	2912	
10	B	116	
11	D	77	
12	G	276	
13	H	209	
14	I	207	
15	J	179	
16	K	178	
17	M	147	
18	N	122	
19	O	146	
20	P	144	
21	Q	127	
22	R	118	
23	S	115	
24	T	119	
25	U	102	
26	V	115	
27	W	96	
28	X	103	

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Mol	Chain	Length	Quality of chain
29	Y	95	
30	Z	62	
31	a	1558	
32	b	19	
33	c	261	
34	d	218	
35	e	203	
36	f	166	
37	g	100	
38	h	156	
39	i	132	
40	j	130	
41	k	102	
42	l	129	
43	m	137	
44	n	121	
45	o	61	
46	p	89	
47	q	91	
48	r	88	
49	s	79	
50	t	92	
51	u	83	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 139826 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	59	Total	C	N	O	S	0	0
			491	307	91	92	1		

- Molecule 2 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	57	Total	C	N	O	S	0	0
			428	266	80	81	1		

- Molecule 3 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	80	Total	C	N	O	S	0	0
			647	409	110	126	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	53	Total	C	N	O	S	0	0
			406	248	84	69	5		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	48	Total	C	N	O	S	0	0
			410	247	84	75	4		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	44	Total	C	N	O	S	0	0
			374	227	91	54	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			522	320	122	78	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			305	188	66	45	6		

- Molecule 9 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2824	Total	C	N	O	P	0	0
			60606	27054	11141	19587	2824		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	114	Total	C	N	O	P	0	0
			2439	1088	439	798	114		

- Molecule 11 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	77	Total	C	N	O	P	0	0
			1644	733	298	536	77		

- Molecule 12 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	274	Total	C	N	O	S	0	0
			2106	1305	414	380	7		

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	206	Total	C	N	O	S	0	0
			1572	990	291	287	4		

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	205	Total	C	N	O	S	0	0
			1572	984	289	297	2		

- Molecule 15 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	177	Total	C	N	O	S	0	0
			1392	887	239	260	6		

- Molecule 16 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	174	Total	C	N	O	S	0	0
			1335	838	242	251	4		

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	147	Total	C	N	O	S	0	0
			1146	726	207	209	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	122	Total	C	N	O	S	0	0
			923	574	176	171	2		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	146	Total	C	N	O	S	0	0
			1096	677	212	206	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	134	Total	C	N	O	S	0	0
			1070	683	209	173	5		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	125	Total	C	N	O	S	0	0
			997	615	192	187	3		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	118	Total	C	N	O	S	0	0
			908	561	176	169	2		

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	114	Total	C	N	O	S	0	0
			925	582	185	158			

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	118	Total	C	N	O	S	0	0
			950	602	184	160	4		

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	101	Total	C	N	O	S	0	0
			779	497	138	142	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	111	Total	C	N	O	S	0	0
			841	527	154	158	2		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	91	Total	C	N	O	S	0	0
			736	469	129	134	4		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	101	Total	C	N	O	S	0	0
			763	486	135	140	2		

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	74	Total	C	N	O		0	0
			559	344	107	108			

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	61	Total	C	N	O	S	0	0
			480	299	97	82	2		

- Molecule 31 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1521	Total	C	N	O	P	0	0
			32595	14542	5954	10578	1521		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	13	Total	C	N	O	P	0	0
			285	127	57	88	13		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	222	Total	C	N	O	S	0	0
			1773	1126	312	326	9		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	205	Total	C	N	O	S	0	0
			1618	1018	304	293	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	200	Total	C	N	O	S	0	0
			1611	1010	301	296	4		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	163	Total	C	N	O	S	0	0
			1204	759	222	221	2		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	96	Total	C	N	O	S	0	0
			786	496	135	152	3		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	153	Total	C	N	O	S	0	0
			1218	759	232	221	6		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	131	Total	C	N	O	S	0	0
			1041	662	184	193	2		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	127	Total	C	N	O	S	0	0
			980	610	195	174	1		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	96	Total	C	N	O	S	0	0
			773	487	142	142	2		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	116	Total	C	N	O	S	0	0
			854	527	163	160	4		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	134	Total	C	N	O	S	0	0
			1051	652	211	186	2		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	114	Total	C	N	O	S	0	0
			902	552	183	166	1		

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	60	Total	C	N	O	S	0	0
			492	310	100	77	5		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	85	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	87	Total	C	N	O	S	0	0
			692	437	128	125	2		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	80	Total	C	N	O	S	0	0
			660	414	124	119	3		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	63	Total	C	N	O	S	0	0
			511	328	95	87	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	82	Total	C	N	O	S	0	0
			663	426	122	113	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	81	Total	C	N	O	S	0	0
			608	371	118	117	2		

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	4	1	Total	Zn	0
			1	1	
52	5	1	Total	Zn	0
			1	1	
52	8	1	Total	Zn	0
			1	1	
52	o	1	Total	Zn	0
			1	1	

- Molecule 53 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
53	7	2	Total	K	0
			2	2	
53	A	103	Total	K	0
			103	103	
53	B	3	Total	K	0
			3	3	
53	G	3	Total	K	0
			3	3	
53	P	1	Total	K	0
			1	1	
53	a	38	Total	K	0
			38	38	

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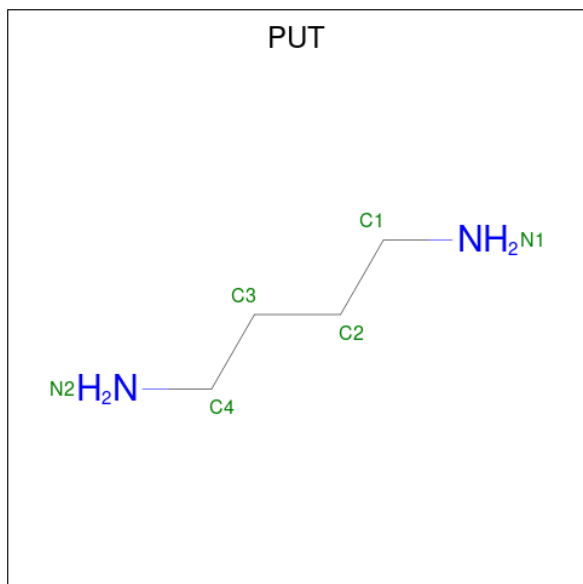
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Mol	Chain	Residues	Atoms		AltConf
53	g	1	Total	K	0
			1	1	
53	o	1	Total	K	0
			1	1	

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

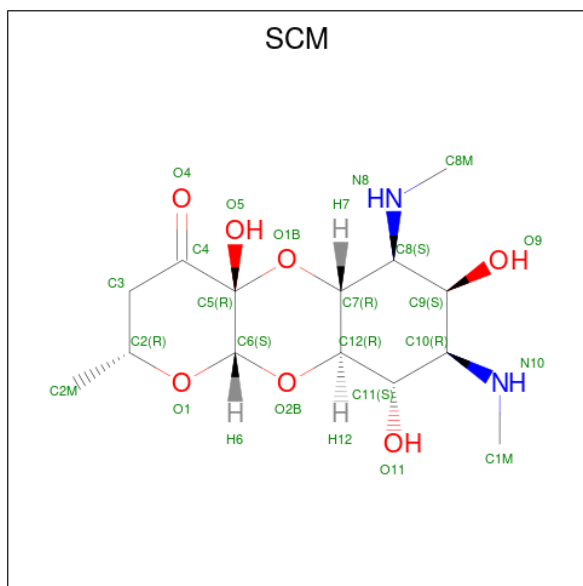
Mol	Chain	Residues	Atoms		AltConf
54	A	138	Total	Mg	0
			138	138	
54	B	1	Total	Mg	0
			1	1	
54	G	1	Total	Mg	0
			1	1	
54	Q	1	Total	Mg	0
			1	1	
54	a	44	Total	Mg	0
			44	44	
54	n	1	Total	Mg	0
			1	1	

- Molecule 55 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).



Mol	Chain	Residues	Atoms			AltConf
55	a	1	Total	C	N	0
			6	4	2	

- Molecule 56 is SPECTINOMYCIN (CCD ID: SCM) (formula: $C_{14}H_{24}N_2O_7$).



Mol	Chain	Residues	Atoms				AltConf
56	a	1	Total	C	N	O	0
			23	14	2	7	

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L29

Chain 1:  94% • 5%



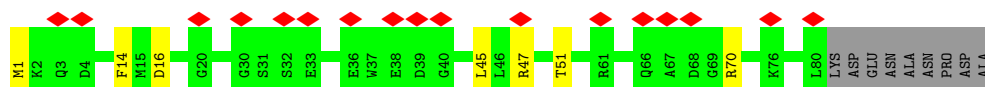
- Molecule 2: 50S ribosomal protein L30

Chain 2:  85% 12% •



- Molecule 3: 50S ribosomal protein L31 type B

Chain 3:  19% 82% 8% 10%



- Molecule 4: 50S ribosomal protein L32

Chain 4:  78% 12% 10%



- Molecule 5: 50S ribosomal protein L33

Chain 5:  84% 14% •



- Molecule 6: 50S ribosomal protein L34

Chain 6:  82% 18%



- Molecule 7: 50S ribosomal protein L35

Chain 7:  80% 17%



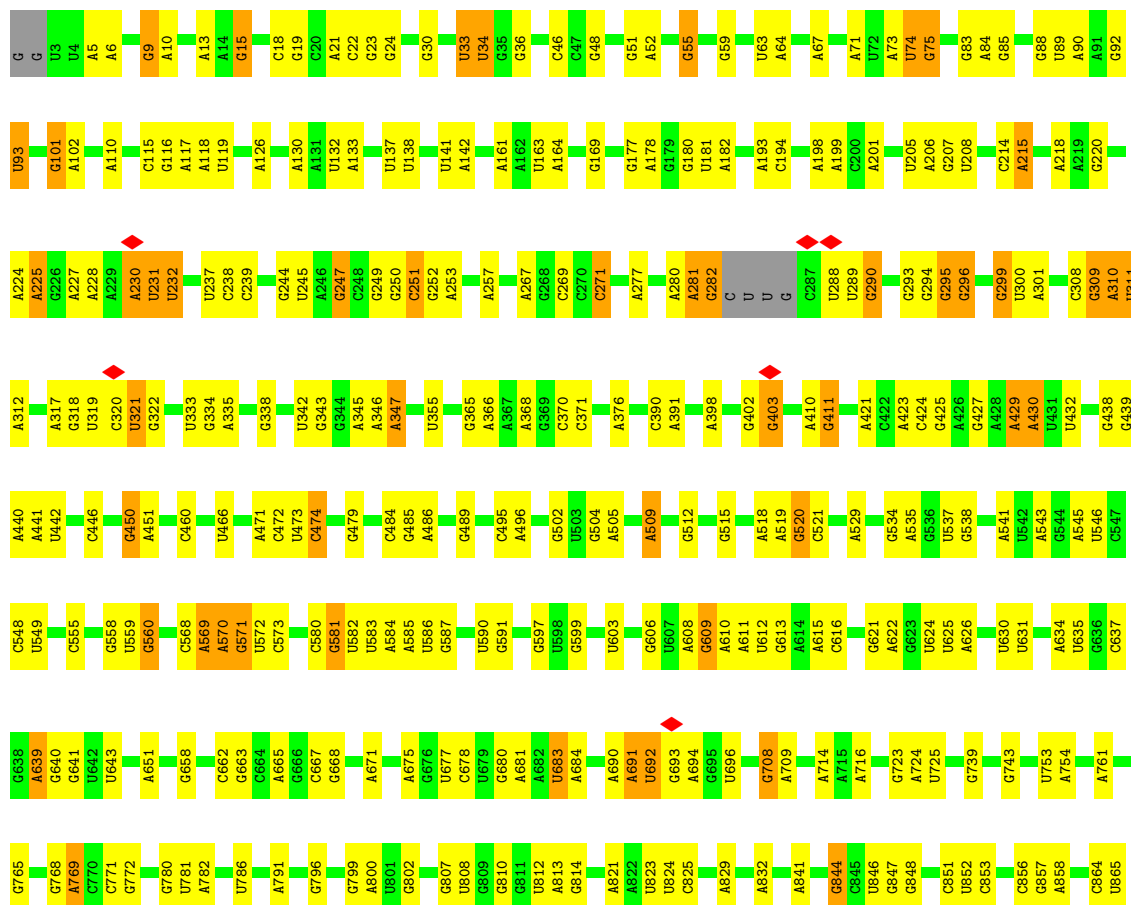
- Molecule 8: 50S ribosomal protein L36

Chain 8:  87% 13%

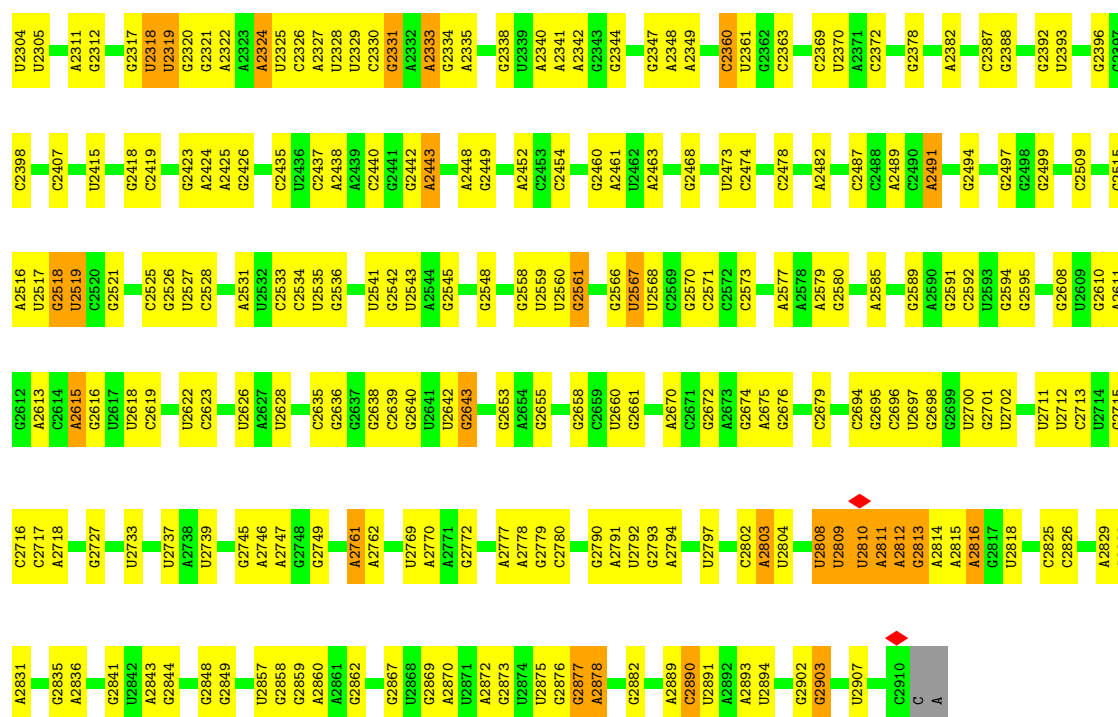


- Molecule 9: 23S rRNA

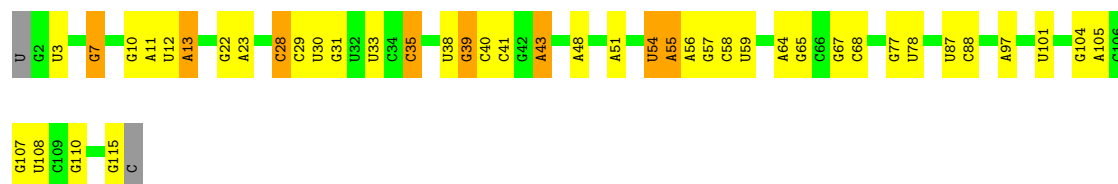
Chain A:  61% 31% 6%







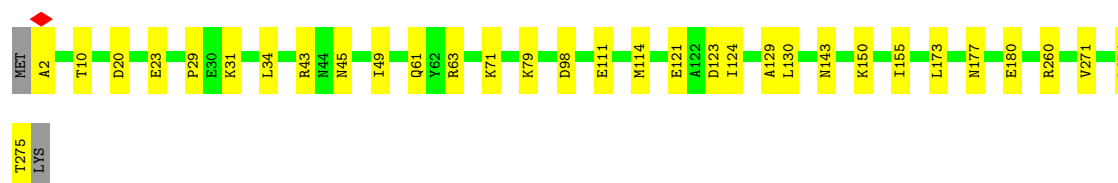
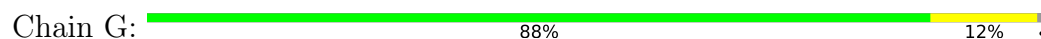
• Molecule 10: 5S rRNA



• Molecule 11: tRNA-fMet

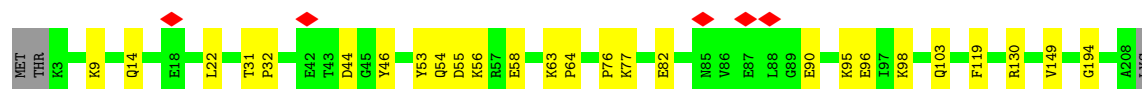


• Molecule 12: 50S ribosomal protein L2



• Molecule 13: 50S ribosomal protein L3

Chain H:  86% 12%



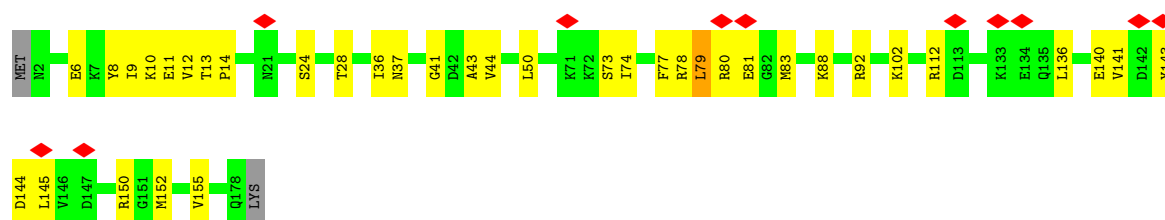
- Molecule 14: 50S ribosomal protein L4

Chain I:  86% 13%



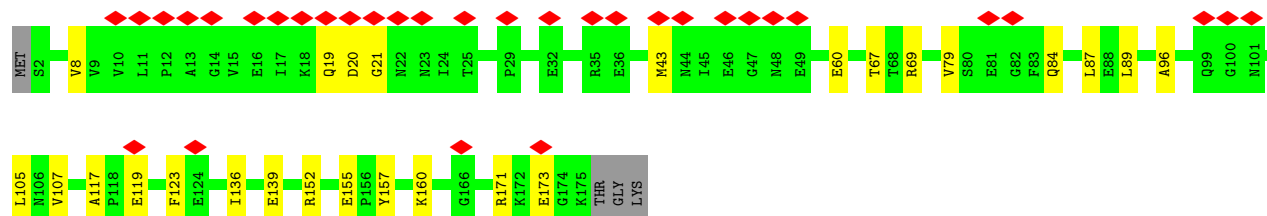
- Molecule 15: 50S ribosomal protein L5

Chain J:  6% 78% 20%



- Molecule 16: 50S ribosomal protein L6

Chain K:  19% 83% 15%



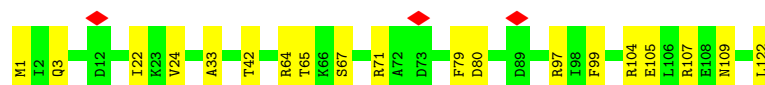
- Molecule 17: 50S ribosomal protein L13

Chain M:  88% 12%

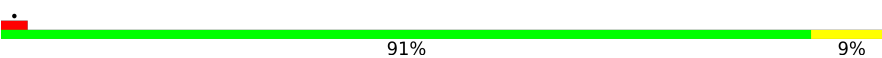


- Molecule 18: 50S ribosomal protein L14

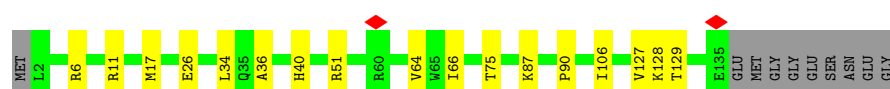
Chain N:  84% 16%



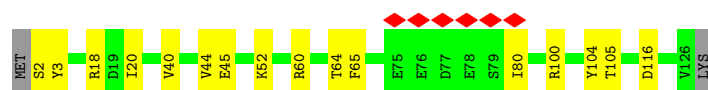
• Molecule 19: 50S ribosomal protein L15

Chain O:  91% 9%

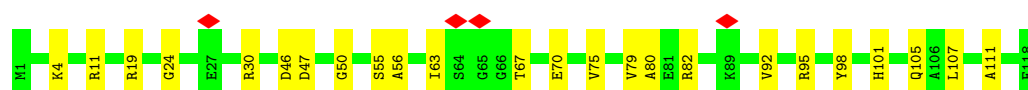
• Molecule 20: 50S ribosomal protein L16

Chain P:  81% 12% 7%

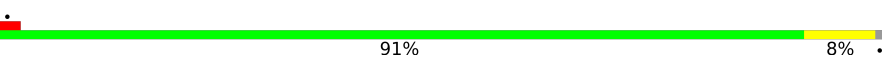
• Molecule 21: 50S ribosomal protein L17

Chain Q:  5% 86% 13%

• Molecule 22: 50S ribosomal protein L18

Chain R:  80% 20%

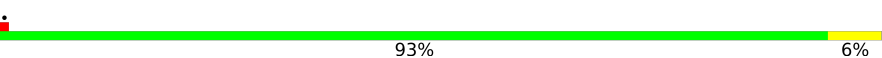
• Molecule 23: 50S ribosomal protein L19

Chain S:  91% 8%

• Molecule 24: 50S ribosomal protein L20

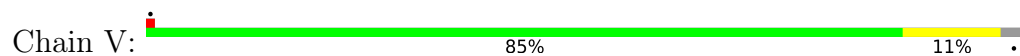
Chain T:  82% 18%

• Molecule 25: 50S ribosomal protein L21

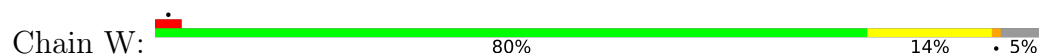
Chain U:  93% 6%



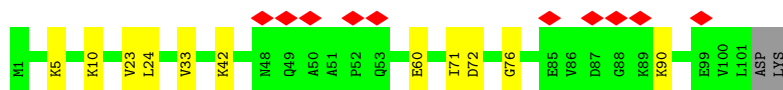
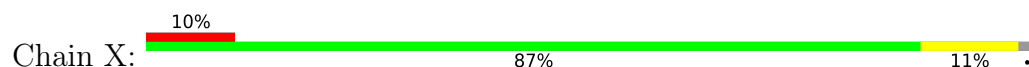
- Molecule 26: 50S ribosomal protein L22



- Molecule 27: 50S ribosomal protein L23



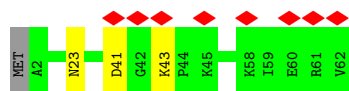
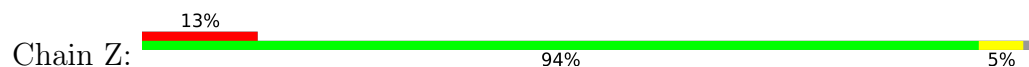
- Molecule 28: 50S ribosomal protein L24



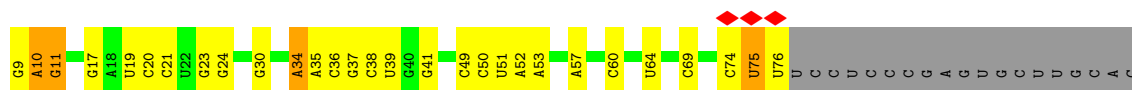
- Molecule 29: 50S ribosomal protein L27



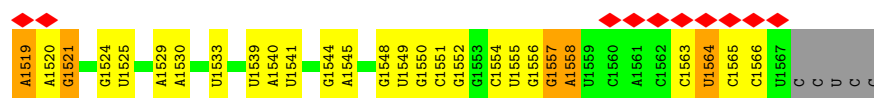
- Molecule 30: 50S ribosomal protein L28



- Molecule 31: 16S rRNA



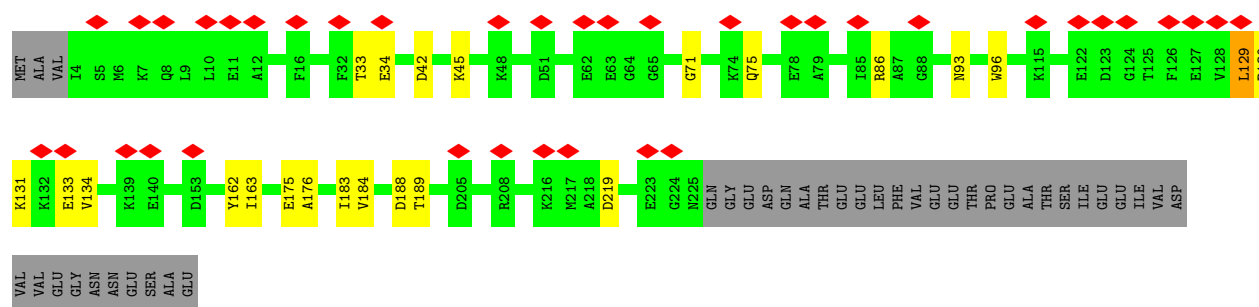
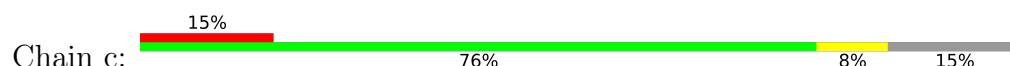
C1393	G1302	A1205	A1107	U1036	U948	C837	A713	A585	G493	A399	G302	A196	U
G1396	A1306	A1206	U1113	A1039	G949	G838	G714	U590	A483	A400	C303	U197	C
U1398	U1307	G1207	G1040	A1040	A950	A841	C715	U591	U495	U401	C304	A199	A
A1401	A1313	U1209	G1121	A1043	G952	C843	U727	A598	A498	C405	A308	A201	U
U1402	A1314	G1210	U1122	U1044	G953	G844	G729	A599	C499	G406	A314	G202	G
G1413	C1317	G1216	G1126	A1045	G961	U846	A730	U501	G500	A409	G315	U203	U
A1420	U1318	A1128	A1128	A1047	A962	G847	G736	C602	C502	G414	U322	G204	G
	C1322	A1222	G1130	G1048	A964	G849	G739	G603	G510	C417	U323	A213	A
C1423	G1326	C1226	C1134	U1050	A965	A855	G740	G604	G511	G418	A326	G215	
A1424	U1327	A1227	G1135	U1051	G966	G856	A741	G605	A517		A332		
C1425	U1328	U1052	U1062	U1062	C967	U857	A742	G607	A518	A423	A332	G222	
G1431	C1329	C1229	C1053	C1053	G968	G858	U749	G607	A523	G424	G336	G224	
	G1330	A1230	U1145	U1054	G971	G862	G750	G627	A524	C425	G335	G131	
C1438	G1331	A1239	U1147	U1055	G972	A754		G630	C527	C426	C337	A132	
A1439	U1332	G1241	U1149	U1056	A973	G757		A633	G528	C427	C338	A135	
	U1333	A1242	U1151	U1057	G974	G758		A636	A529	G430	A339	A136	
G1445	U1341	C1243	U1152	G1058	U987	U868	U762	G637	C533	U431	G348	A137	
U1448	G1342	A1244	U1153	G1059	G993	U869	G763	C638	U534	A438	U349	A138	
G1449	C1343	C1245	U1154	G1060	C994	C870	U764	C639	A535	G439	G350	A146	
	A1344	U1245	G1155	G1061	A995	C871	G765	C644	A536	A440	C355	G	
C1455	A1345	G1248	C1156	A1063	A996	G872	U766	C644	C537	G441	A356	G240	
A1456	U1346	C1249	U1159	C1064	G997	G873	G767	A647	C540	G442	G357	G241	
C1457	U1347	U1250	U1160	A1065	G998	C874	G768		G541		C358	U242	
G1458	G1348	A1251	A1066	A1066	A1001		A775		U542	U446	C359	G246	
A1459	U1349	C1252	U1067	A1067	A1002	G882		A688	C543	U447	C360	C247	
	U1352	A1253	G1068	U1069	G1003	G883	U783		C544	C448	C361	G163	
U1460	G1353	C1254	U1161	A1072	A1005	A899	G784		C545	G449	A362	G164	
G1461	C1354	A1255	U1163	A1006	A1006	A900	A785		A546	G450	G363	G165	
U1466	A1355	G1262	G1165	C1007	C1007	G901	G786		G547	A451	A364	G267	
G1467	U1357	C1263	U1166	U1008	U1008	G902	G787		G550	U455	C365	U271	
A1468	A1264	A1265	G1074	A1010	A1010	A903		A688	C552	A458	A370	A272	
	U1266	G1267	C1081	A1082	A1013	C904	A792		G553	A459	G372	A276	
A1472	G1364	G1268	U1083	U1083	G1014	U905	A793		G556	U465	G373	G277	
U1476		G1269	U1087	U1087	U1019	G908	G795		U557		C378	U278	
U1477	A1372	C1275	G1088	G1088	A803	C909	A803		A561	A470	A379	G281	
U1478	U1376	C1283	U1089	U1089	G804	G917	G804		G690	G471	G380	G281	
U1479	U1377	U1185	G1186	C1090	C805	G692	C805		A691	A472	C381	G285	
U1480	C1378	U1286	G1187	G1091	A806	G693	A806		G563	G473	A382	G288	
G1481	G1379	G1292	G1192	U1092	U1027	A928	U815		C571	A477	G386	A288	
		C1293	C1093	C1093	U1028		A816		A572	A478	G387	A289	
G1486		G1294	U1097	U1097	U1029		G817		A573	C479	A478	C290	
G1500	G1382	A1383	C1098	C1098	U1030		A818		U580	C485	U391	G291	
G1501	U1383	A1295	G1099	G1099	A1031		U819		C581	G486	U393	G292	
G1513	A1386	G1296	U1100	U1100	G1032		A820		G582	U487	U393	C293	
G1514	U1197	C1197	G1032	G1032	U1033		G821		G583	U488	G397	C297	
G1515	C1390	C1299	A1300	A1300	C1033		C822		G584	A489	C398	G301	
U1517	U1517	U1301	G1104	U1105	A1034								
G1518	C1392		G1106		C1035								



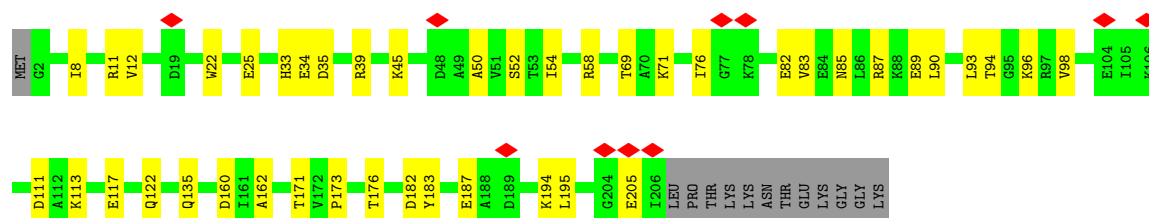
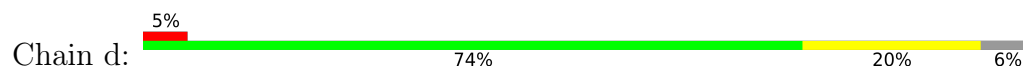
• Molecule 32: mRNA



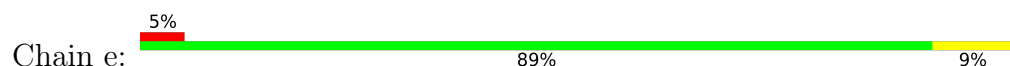
• Molecule 33: 30S ribosomal protein S2



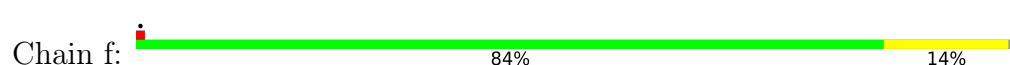
• Molecule 34: 30S ribosomal protein S3



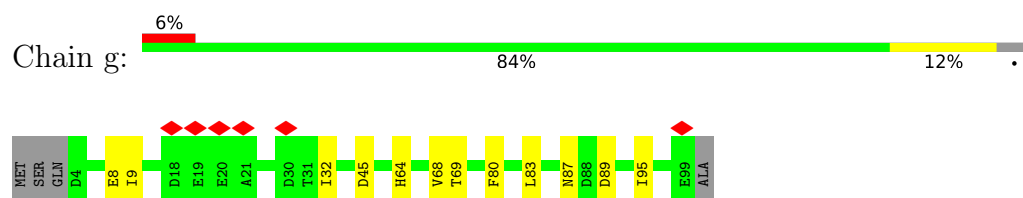
• Molecule 35: 30S ribosomal protein S4



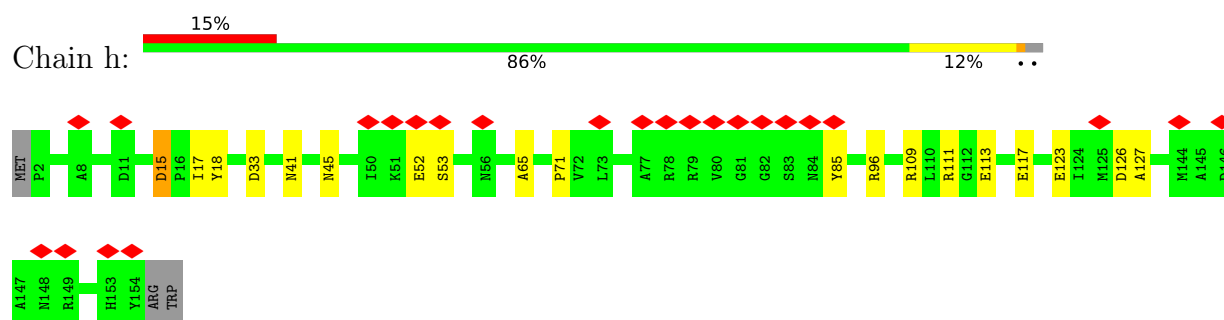
• Molecule 36: 30S ribosomal protein S5



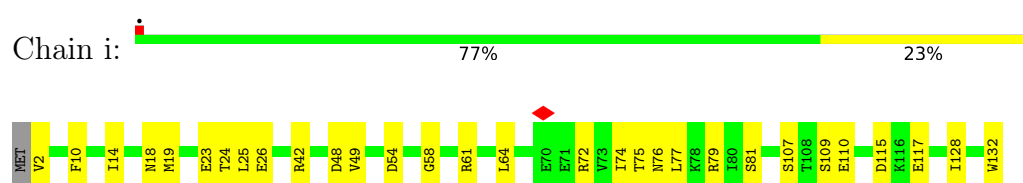
- Molecule 37: 30S ribosomal protein S6



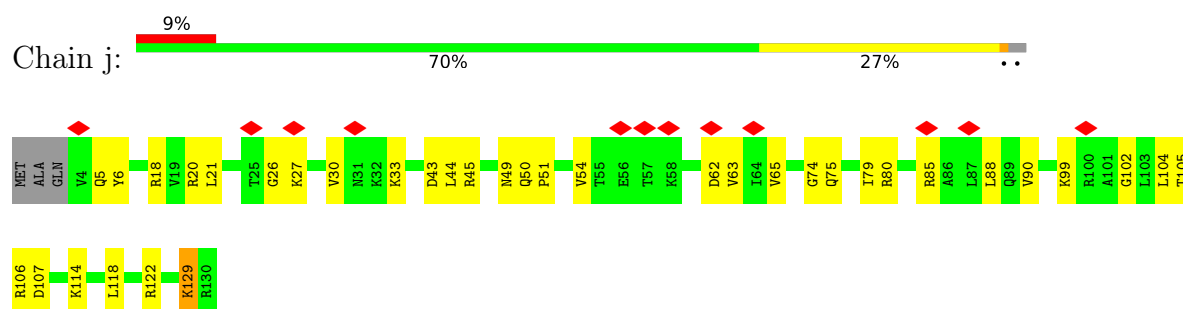
- Molecule 38: 30S ribosomal protein S7



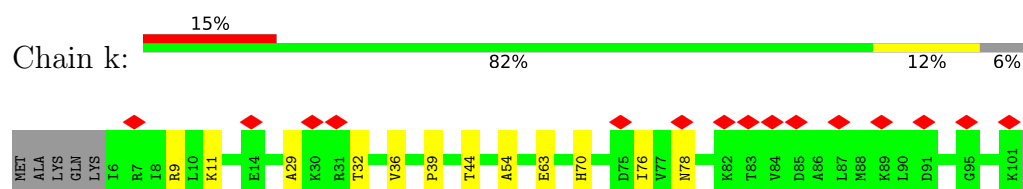
- Molecule 39: 30S ribosomal protein S8



- Molecule 40: 30S ribosomal protein S9

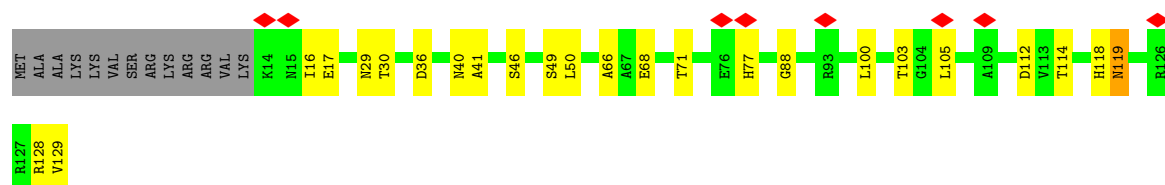


- Molecule 41: 30S ribosomal protein S10

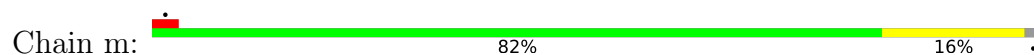


- Molecule 42: 30S ribosomal protein S11

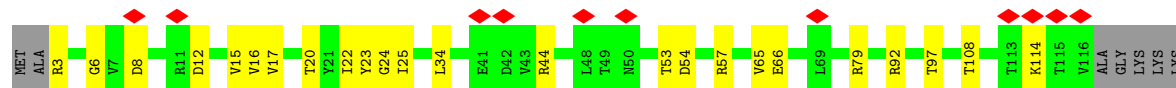
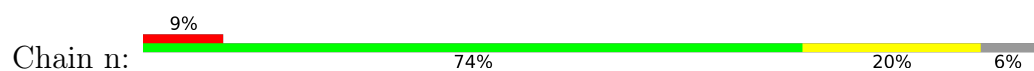




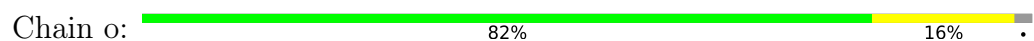
- Molecule 43: 30S ribosomal protein S12



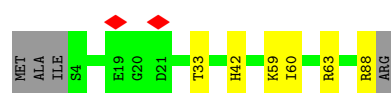
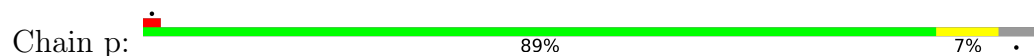
- Molecule 44: 30S ribosomal protein S13



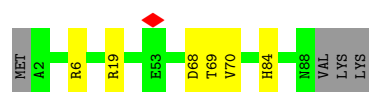
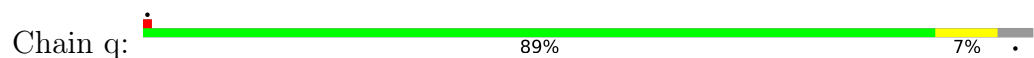
- Molecule 45: 30S ribosomal protein S14 type Z



- Molecule 46: 30S ribosomal protein S15



- Molecule 47: 30S ribosomal protein S16

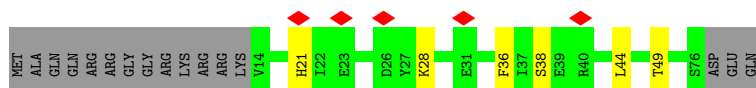


- Molecule 48: 30S ribosomal protein S17

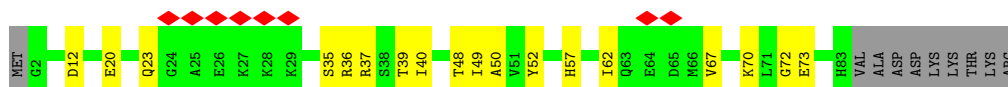




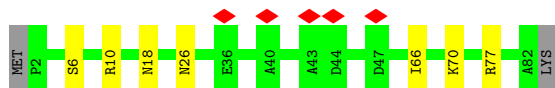
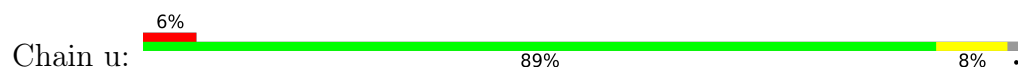
- Molecule 49: 30S ribosomal protein S18



- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18512	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30.255	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	344.4, 344.4, 344.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1	0.15	0/492	0.24	0/654
2	2	0.17	0/430	0.29	0/579
3	3	0.18	0/664	0.34	0/896
4	4	0.18	0/413	0.30	0/549
5	5	0.20	0/414	0.29	0/552
6	6	0.20	0/377	0.27	0/491
7	7	0.19	0/528	0.29	0/689
8	8	0.20	0/310	0.32	0/409
9	A	0.21	0/67888	0.28	0/105890
10	B	0.17	0/2728	0.24	0/4252
11	D	0.16	0/1837	0.28	0/2862
12	G	0.20	0/2141	0.31	0/2881
13	H	0.19	0/1594	0.31	0/2140
14	I	0.19	0/1595	0.28	0/2157
15	J	0.18	0/1411	0.37	0/1897
16	K	0.15	0/1355	0.30	0/1825
17	M	0.20	0/1167	0.28	0/1576
18	N	0.20	0/930	0.30	0/1247
19	O	0.19	0/1106	0.27	0/1474
20	P	0.20	0/1093	0.28	0/1457
21	Q	0.19	0/1006	0.33	0/1349
22	R	0.19	0/917	0.34	0/1226
23	S	0.18	0/939	0.31	0/1262
24	T	0.20	0/963	0.28	0/1280
25	U	0.24	0/791	0.30	0/1061
26	V	0.20	0/850	0.32	0/1145
27	W	0.19	0/743	0.30	0/993
28	X	0.18	0/772	0.32	0/1035
29	Y	0.20	0/565	0.30	0/755
30	Z	0.16	0/486	0.28	0/648
31	a	0.19	0/36487	0.27	1/56905 (0.0%)
32	b	0.12	0/319	0.33	0/494

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.32	0/1803	0.48	0/2430
34	d	0.18	0/1643	0.31	0/2208
35	e	0.17	0/1641	0.32	0/2206
36	f	0.18	0/1217	0.30	0/1641
37	g	0.18	0/798	0.31	0/1075
38	h	0.15	0/1238	0.30	0/1668
39	i	0.18	0/1054	0.33	0/1417
40	j	0.16	0/993	0.30	0/1331
41	k	0.18	0/785	0.29	0/1059
42	l	0.16	0/869	0.29	0/1174
43	m	0.18	0/1068	0.35	0/1435
44	n	0.15	0/908	0.31	0/1219
45	o	0.17	0/504	0.26	0/669
46	p	0.17	0/726	0.27	0/969
47	q	0.17	0/704	0.34	0/945
48	r	0.17	0/668	0.30	0/891
49	s	0.16	0/518	0.29	0/694
50	t	0.16	0/680	0.28	0/911
51	u	0.17	0/611	0.33	0/818
All	All	0.20	0/151739	0.29	1/227390 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	1390	C	N1-C1'-C2'	5.16	119.74	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	491	0	527	0	0
2	2	428	0	463	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	647	0	616	5	0
4	4	406	0	417	7	0
5	5	410	0	422	5	0
6	6	374	0	424	16	0
7	7	522	0	575	9	0
8	8	305	0	337	5	0
9	A	60606	0	30437	620	0
10	B	2439	0	1228	21	0
11	D	1644	0	835	29	0
12	G	2106	0	2189	21	0
13	H	1572	0	1654	18	0
14	I	1572	0	1614	17	0
15	J	1392	0	1454	43	0
16	K	1335	0	1369	18	0
17	M	1146	0	1191	14	0
18	N	923	0	985	16	0
19	O	1096	0	1149	10	0
20	P	1070	0	1136	13	0
21	Q	997	0	1033	13	0
22	R	908	0	944	16	0
23	S	925	0	979	8	0
24	T	950	0	1009	16	0
25	U	779	0	821	4	0
26	V	841	0	898	11	0
27	W	736	0	795	10	0
28	X	763	0	823	8	0
29	Y	559	0	568	9	0
30	Z	480	0	522	2	0
31	a	32595	0	16412	378	0
32	b	285	0	143	3	0
33	c	1773	0	1810	16	0
34	d	1618	0	1664	29	0
35	e	1611	0	1628	20	0
36	f	1204	0	1280	21	0
37	g	786	0	781	10	0
38	h	1218	0	1246	12	0
39	i	1041	0	1092	21	0
40	j	980	0	1027	24	0
41	k	773	0	814	16	0
42	l	854	0	869	19	0
43	m	1051	0	1115	18	0
44	n	902	0	956	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	o	492	0	508	9	0
46	p	716	0	727	5	0
47	q	692	0	724	7	0
48	r	660	0	699	15	0
49	s	511	0	549	6	0
50	t	663	0	675	12	0
51	u	608	0	635	7	0
52	4	1	0	0	0	0
52	5	1	0	0	0	0
52	8	1	0	0	0	0
52	o	1	0	0	0	0
53	7	2	0	0	0	0
53	A	103	0	0	0	0
53	B	3	0	0	0	0
53	G	3	0	0	0	0
53	P	1	0	0	0	0
53	a	38	0	0	0	0
53	g	1	0	0	0	0
53	o	1	0	0	0	0
54	A	138	0	0	0	0
54	B	1	0	0	0	0
54	G	1	0	0	0	0
54	Q	1	0	0	0	0
54	a	44	0	0	0	0
54	n	1	0	0	0	0
55	a	6	0	12	0	0
56	a	23	0	24	2	0
All	All	139826	0	92804	1441	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 6.

All (1441) 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)
6:6:1:MET:HE2	6:6:3:ARG:NH2	1.46	1.28
6:6:1:MET:CE	6:6:3:ARG:NH2	2.10	1.13
41:k:36:VAL:HG12	41:k:76:ILE:CD1	1.85	1.07
36:f:86:ILE:HG12	36:f:95:LEU:HD13	1.36	1.06
9:A:295:G:O2'	9:A:296:G:O5'	1.72	1.05
6:6:1:MET:CE	6:6:3:ARG:HH22	1.67	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:102:LEU:HD23	35:e:166:VAL:HG21	1.38	1.01
36:f:86:ILE:CG1	36:f:95:LEU:HD13	1.91	0.99
9:A:1413:A:O2'	9:A:1414:U:O5'	1.80	0.98
5:5:30:LEU:HD11	5:5:32:LYS:HE2	1.48	0.96
51:u:66:ILE:HB	51:u:70:LYS:HD3	1.49	0.94
41:k:36:VAL:HG12	41:k:76:ILE:HD13	1.48	0.94
35:e:102:LEU:HD23	35:e:166:VAL:CG2	2.00	0.92
9:A:2026:A:HO2'	26:V:99:SER:HG	0.99	0.90
41:k:36:VAL:HG12	41:k:76:ILE:HD12	1.54	0.90
31:a:857:U:O2'	31:a:1566:C:OP1	1.89	0.90
3:3:47:ARG:NH2	44:n:54:ASP:OD1	2.04	0.90
9:A:1591:G:OP2	9:A:1591:G:N2	2.04	0.90
31:a:227:A:O2'	31:a:228:A:O5'	1.90	0.89
9:A:1828:A:O2'	9:A:1829:A:O5'	1.90	0.88
9:A:1355:G:OP2	9:A:1355:G:N2	2.06	0.87
31:a:9:G:O2'	31:a:10:A:OP1	1.92	0.87
31:a:1390:C:O2'	31:a:1391:G:OP1	1.91	0.87
36:f:86:ILE:HG12	36:f:95:LEU:CD1	2.04	0.86
9:A:450:G:OP2	9:A:2419:C:O2'	1.93	0.86
9:A:1564:G:OP2	9:A:1565:A:O2'	1.95	0.85
9:A:2210:U:O2'	9:A:2211:A:O5'	1.94	0.85
9:A:1792:U:OP2	9:A:1797:A:N6	2.10	0.84
9:A:2797:U:H4'	13:H:44:ASP:OD1	1.78	0.84
11:D:17:C:OP2	11:D:18:A:O2'	1.93	0.84
9:A:228:A:O2'	9:A:231:U:O4	1.94	0.84
31:a:1003:G:OP2	31:a:1384:U:O2'	1.96	0.84
9:A:319:U:O2'	9:A:321:U:OP2	1.96	0.83
31:a:1104:G:N2	31:a:1107:A:OP2	2.12	0.83
31:a:527:C:OP1	43:m:127:ARG:NH2	2.11	0.83
9:A:1125:A:O2'	9:A:1126:G:N7	2.11	0.83
9:A:2907:U:O2'	17:M:137:GLN:OE1	1.97	0.82
9:A:1067:A:N3	9:A:2499:G:O2'	2.12	0.82
9:A:2318:U:O2'	9:A:2319:U:O5'	1.97	0.82
31:a:1209:U:O2'	31:a:1210:G:OP1	1.98	0.82
9:A:1575:A:OP2	9:A:1583:G:N2	2.12	0.81
31:a:1150:A:O2'	41:k:39:PRO:O	1.98	0.81
6:6:1:MET:HE1	6:6:3:ARG:HH22	1.44	0.81
9:A:1086:G:N2	9:A:1149:G:O2'	2.14	0.80
35:e:102:LEU:CD2	35:e:166:VAL:CG2	2.59	0.80
31:a:214:U:O2	48:r:68:ARG:NH1	2.13	0.80
34:d:187:GLU:OE1	34:d:194:LYS:NZ	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:355:A:O2'	31:a:358:G:N7	2.14	0.80
15:J:143:TYR:CD1	44:n:8:ASP:OD2	2.35	0.80
31:a:1275:C:O2'	40:j:75:GLN:OE1	2.00	0.80
15:J:143:TYR:CE1	44:n:8:ASP:OD2	2.34	0.80
9:A:1451:G:O2'	9:A:1452:U:O4'	1.99	0.79
38:h:111:ARG:NH2	38:h:126:ASP:OD2	2.16	0.79
31:a:75:U:O2'	31:a:76:U:O5'	1.99	0.79
9:A:1065:A:OP2	9:A:1173:C:O2'	2.00	0.78
43:m:112:ARG:NH1	43:m:118:ALA:O	2.17	0.78
27:W:19:ALA:HB1	27:W:24:LYS:HG3	1.66	0.78
9:A:509:A:OP1	14:I:79:ARG:NH2	2.17	0.78
10:B:3:U:OP1	10:B:59:U:O2'	2.01	0.78
31:a:1178:G:OP1	41:k:70:HIS:ND1	2.16	0.77
9:A:1061:G:O2'	9:A:1062:U:OP2	2.01	0.77
12:G:23:GLU:N	12:G:23:GLU:OE1	2.16	0.77
9:A:295:G:HO2'	9:A:296:G:C5'	1.98	0.77
41:k:36:VAL:CG1	41:k:76:ILE:CD1	2.61	0.77
9:A:899:G:O2'	9:A:956:G:O6	2.02	0.77
9:A:2890:C:O3'	21:Q:100:ARG:NH2	2.18	0.77
16:K:119:GLU:OE1	16:K:119:GLU:N	2.18	0.77
39:i:26:GLU:OE2	39:i:61:ARG:NH1	2.17	0.77
41:k:36:VAL:CG1	41:k:76:ILE:HD12	2.15	0.77
9:A:281:A:O2'	9:A:282:G:O5'	2.03	0.76
9:A:2867:G:N2	9:A:2870:A:OP2	2.14	0.76
31:a:1294:G:N2	31:a:1352:U:O2	2.17	0.76
6:6:1:MET:HE2	6:6:3:ARG:CZ	2.15	0.76
9:A:83:G:H1	9:A:101:G:HO2'	1.31	0.76
31:a:1376:A:O2'	38:h:33:ASP:OD1	2.02	0.76
9:A:2902:G:OP2	9:A:2902:G:N2	2.16	0.76
9:A:231:U:O2'	9:A:232:U:OP2	2.04	0.76
12:G:121:GLU:N	12:G:121:GLU:OE1	2.18	0.76
9:A:1413:A:HO2'	9:A:1414:U:P	2.08	0.75
31:a:950:A:O2'	31:a:1425:C:OP2	2.03	0.75
9:A:205:U:OP2	9:A:206:A:O2'	2.02	0.75
9:A:2076:C:HO2'	11:D:77:A:HO2'	1.14	0.75
2:2:11:SER:OG	9:A:1028:G:OP2	2.02	0.75
17:M:42:LYS:NZ	17:M:51:THR:O	2.15	0.75
39:i:110:GLU:N	39:i:110:GLU:OE1	2.20	0.75
9:A:137:U:O2	9:A:142:A:N6	2.19	0.75
31:a:837:C:O2'	31:a:928:A:N1	2.19	0.75
31:a:1107:A:OP1	36:f:52:LYS:NZ	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:90:LEU:O	34:d:94:THR:HG22	1.87	0.75
27:W:88:GLU:N	27:W:88:GLU:OE1	2.20	0.74
31:a:1248:G:OP2	31:a:1348:C:N4	2.20	0.74
9:A:1124:A:O2'	9:A:1125:A:O4'	2.05	0.74
9:A:2044:A:N3	9:A:2468:G:O2'	2.18	0.74
9:A:2349:A:H61	29:Y:52:THR:HG21	1.52	0.74
31:a:1563:C:O2'	31:a:1564:U:OP1	2.04	0.74
9:A:1189:U:O2'	9:A:1190:A:O5'	2.03	0.74
15:J:78:ARG:O	15:J:79:LEU:HD13	1.86	0.74
48:r:52:GLU:N	48:r:52:GLU:OE1	2.21	0.74
9:A:1104:U:O2	9:A:1112:A:N6	2.21	0.74
14:I:21:GLU:N	14:I:21:GLU:OE1	2.19	0.74
27:W:57:ASN:OD1	27:W:76:ARG:NH1	2.21	0.74
31:a:1519:A:O2'	31:a:1520:A:O4'	2.06	0.74
9:A:199:A:N6	9:A:2443:A:O2'	2.22	0.73
16:K:173:GLU:N	16:K:173:GLU:OE1	2.21	0.73
31:a:845:A:O2'	31:a:846:U:OP1	2.06	0.73
9:A:753:U:O4	46:p:88:ARG:NH2	2.21	0.73
9:A:1755:U:O2'	9:A:1758:G:O6	2.05	0.73
18:N:22:ILE:HD11	18:N:42:THR:OG1	1.87	0.73
31:a:849:G:HO2'	39:i:2:VAL:N	1.87	0.73
24:T:115:ASP:OD1	24:T:119:LYS:NZ	2.22	0.73
31:a:1386:A:OP2	45:o:35:ARG:NH2	2.21	0.73
16:K:19:GLN:NE2	16:K:43:MET:SD	2.61	0.73
31:a:1020:G:O2'	31:a:1021:A:N7	2.21	0.73
35:e:183:ARG:NH2	35:e:187:TYR:O	2.22	0.73
30:Z:41:ASP:OD1	30:Z:43:LYS:NZ	2.21	0.73
48:r:30:THR:HG22	48:r:31:LYS:N	2.03	0.73
31:a:868:U:O2'	31:a:871:C:N4	2.22	0.73
13:H:58:GLU:N	13:H:58:GLU:OE1	2.22	0.72
14:I:141:GLN:NE2	14:I:145:ASN:OD1	2.21	0.72
9:A:832:A:OP2	9:A:2084:A:O2'	2.06	0.72
34:d:35:ASP:OD1	34:d:58:ARG:NH2	2.22	0.72
9:A:1828:A:HO2'	9:A:1829:A:P	2.13	0.72
18:N:105:GLU:OE1	18:N:105:GLU:N	2.22	0.72
9:A:116:G:OP2	9:A:118:A:O2'	2.05	0.72
9:A:1245:G:O2'	9:A:1273:A:N1	2.18	0.72
10:B:11:A:O2'	10:B:13:A:OP2	2.07	0.72
4:4:16:ARG:NH2	9:A:1300:G:OP1	2.22	0.72
9:A:1376:U:OP2	9:A:1429:U:O2'	2.07	0.72
9:A:1105:U:N3	9:A:1108:A:OP2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:57:C:OP1	15:J:73:SER:OG	2.06	0.71
31:a:871:C:H5'	49:s:21:HIS:CE1	2.25	0.71
37:g:8:GLU:OE2	49:s:28:LYS:CE	2.38	0.71
36:f:54:GLN:N	36:f:54:GLN:OE1	2.23	0.71
43:m:84:GLY:O	43:m:112:ARG:NH2	2.23	0.71
34:d:85:ASN:ND2	34:d:89:GLU:OE2	2.24	0.71
9:A:846:U:OP2	19:O:41:ARG:NH2	2.24	0.70
9:A:2092:U:O2'	30:Z:23:ASN:OD1	2.09	0.70
9:A:1814:A:OP2	12:G:150:LYS:NZ	2.23	0.70
31:a:1486:C:OP1	51:u:26:ASN:ND2	2.22	0.70
9:A:1311:G:OP2	9:A:1687:G:O2'	2.03	0.70
9:A:309:G:O2'	9:A:310:A:OP2	2.10	0.70
9:A:2535:U:O2'	9:A:2660:U:OP1	2.10	0.70
31:a:584:G:OP2	31:a:585:A:O2'	2.09	0.70
31:a:1248:G:OP1	31:a:1347:U:O2'	2.06	0.70
11:D:58:A:N7	15:J:80:ARG:NH2	2.40	0.69
9:A:1106:A:N1	9:A:1134:A:O2'	2.22	0.69
43:m:75:GLU:N	43:m:75:GLU:OE1	2.25	0.69
6:6:1:MET:HE1	9:A:791:A:P	2.32	0.69
40:j:5:GLN:OE1	40:j:20:ARG:NH1	2.25	0.69
9:A:1926:A:N6	31:a:1520:A:O5'	2.23	0.69
9:A:1936:U:OP1	11:D:25:U:O2'	2.10	0.69
7:7:38:LYS:NZ	9:A:2361:U:OP1	2.23	0.69
31:a:1390:C:HO2'	31:a:1391:G:P	2.15	0.69
9:A:2258:U:O2'	9:A:2449:G:OP2	2.06	0.69
13:H:56:LYS:N	13:H:76:PRO:O	2.25	0.69
31:a:1525:U:O2'	32:b:14:U:OP1	2.08	0.69
42:l:36:ASP:OD1	42:l:40:ASN:N	2.25	0.69
9:A:559:U:O2'	9:A:560:G:N7	2.25	0.69
9:A:637:C:O2'	9:A:641:G:OP1	2.10	0.69
16:K:8:VAL:O	16:K:69:ARG:NH2	2.25	0.69
18:N:104:ARG:N	18:N:122:LEU:OXT	2.25	0.69
26:V:72:GLU:N	26:V:72:GLU:OE1	2.24	0.69
5:5:17:TYR:OH	9:A:2360:C:O2'	2.11	0.69
6:6:1:MET:HE1	9:A:791:A:OP1	1.93	0.69
9:A:538:G:N1	9:A:541:A:OP2	2.25	0.69
31:a:533:C:OP2	31:a:534:U:O2'	2.04	0.69
9:A:1029:A:N1	25:U:77:LYS:NZ	2.41	0.68
9:A:2808:U:O2'	9:A:2809:U:OP1	2.11	0.68
31:a:1004:A:O2'	31:a:1006:C:OP2	2.11	0.68
9:A:1164:G:OP2	9:A:1165:A:O2'	2.05	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1451:G:O2'	9:A:1452:U:O5'	2.10	0.68
31:a:302:G:OP1	48:r:17:SER:OG	2.09	0.68
44:n:23:TYR:N	44:n:66:GLU:OE2	2.25	0.68
9:A:2349:A:H61	29:Y:52:THR:CG2	2.06	0.68
9:A:1096:A:OP2	9:A:1128:G:N2	2.21	0.68
36:f:86:ILE:CG1	36:f:95:LEU:CD1	2.67	0.68
40:j:45:ARG:O	40:j:49:ASN:ND2	2.27	0.68
9:A:2452:A:O2'	9:A:2613:A:OP1	2.12	0.68
23:S:20:PHE:O	23:S:50:ARG:NH1	2.27	0.68
31:a:1341:U:O2'	31:a:1386:A:N3	2.26	0.68
10:B:41:C:O2	15:J:92:ARG:NH1	2.25	0.68
31:a:399:A:O2'	31:a:477:A:N7	2.26	0.68
9:A:299:G:O2'	9:A:460:C:OP2	2.07	0.67
35:e:92:GLU:OE1	35:e:97:ASN:ND2	2.27	0.67
47:q:68:ASP:OD1	47:q:69:THR:N	2.28	0.67
9:A:1029:A:O2'	9:A:1031:C:OP2	2.12	0.67
34:d:22:TRP:NE1	34:d:35:ASP:OD2	2.27	0.67
39:i:79:ARG:NH1	39:i:81:SER:O	2.28	0.67
17:M:118:LYS:O	17:M:121:THR:OG1	2.13	0.67
9:A:1003:C:O2'	9:A:2286:A:N3	2.25	0.67
40:j:88:LEU:HD11	40:j:104:LEU:HD22	1.77	0.67
48:r:84:GLU:N	48:r:84:GLU:OE1	2.27	0.67
9:A:1696:A:O2'	13:H:119:PHE:O	2.13	0.67
9:A:2815:A:O2'	9:A:2816:A:O5'	2.13	0.67
15:J:140:GLU:OE1	15:J:140:GLU:N	2.28	0.67
46:p:33:THR:OG1	46:p:63:ARG:NH1	2.27	0.67
9:A:739:G:O2'	9:A:1674:A:N3	2.27	0.67
9:A:2670:A:O3'	16:K:160:LYS:NZ	2.27	0.67
9:A:2875:U:OP2	9:A:2876:G:O2'	2.10	0.67
38:h:113:GLU:N	38:h:113:GLU:OE1	2.28	0.67
40:j:26:GLY:N	40:j:62:ASP:OD1	2.28	0.67
16:K:60:GLU:N	16:K:60:GLU:OE1	2.28	0.66
9:A:1691:G:O2'	21:Q:116:ASP:OD2	2.11	0.66
9:A:1107:G:O2'	9:A:1135:A:O4'	2.12	0.66
34:d:25:GLU:OE2	41:k:11:LYS:NZ	2.20	0.66
9:A:2594:G:OP2	9:A:2594:G:N2	2.26	0.66
10:B:39:G:OP1	10:B:41:C:N4	2.26	0.66
31:a:872:G:O2'	31:a:873:C:OP1	2.12	0.66
39:i:48:ASP:OD1	39:i:49:VAL:N	2.29	0.66
22:R:95:ARG:NH1	22:R:98:TYR:O	2.28	0.66
31:a:727:U:OP1	31:a:728:A:O2'	2.04	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:45:LYS:NZ	34:d:82:GLU:OE2	2.28	0.66
9:A:1189:U:HO2'	9:A:1190:A:C5'	2.08	0.65
33:c:176:ALA:HB3	33:c:183:ILE:HD11	1.77	0.65
9:A:2263:G:O2'	9:A:2509:C:OP1	2.15	0.65
9:A:2808:U:N3	9:A:2809:U:O2	2.30	0.65
10:B:12:U:OP2	10:B:68:C:O2'	2.15	0.65
23:S:39:ARG:NH1	31:a:372:G:OP1	2.30	0.65
50:t:12:ASP:OD2	50:t:35:SER:OG	2.07	0.65
9:A:30:G:O2'	9:A:1250:A:N3	2.29	0.65
9:A:1170:G:N2	9:A:1171:U:O4	2.26	0.65
9:A:1885:G:OP2	9:A:1885:G:N2	2.28	0.65
19:O:116:GLU:N	19:O:116:GLU:OE1	2.29	0.65
31:a:750:G:OP2	31:a:858:G:N2	2.30	0.65
5:5:17:TYR:HH	9:A:2360:C:HO2'	1.38	0.65
9:A:2826:C:O2	9:A:2893:A:O2'	2.14	0.65
31:a:1013:A:N3	50:t:52:TYR:OH	2.28	0.65
31:a:406:G:N2	31:a:409:A:OP2	2.26	0.64
9:A:343:G:N1	9:A:346:A:OP2	2.28	0.64
31:a:350:G:N1	31:a:353:A:OP2	2.30	0.64
22:R:46:ASP:O	22:R:50:GLY:N	2.29	0.64
31:a:699:G:H2'	31:a:700:G:C8	2.31	0.64
9:A:1967:G:O2'	9:A:1969:U:O4	2.12	0.64
34:d:34:GLU:OE2	34:d:94:THR:OG1	2.14	0.64
35:e:102:LEU:CD2	35:e:166:VAL:HG21	2.18	0.64
9:A:1709:G:O2'	9:A:2004:U:O4	2.10	0.64
31:a:690:G:H22	31:a:767:G:H1	1.43	0.64
9:A:33:U:O2'	9:A:34:U:O5'	2.16	0.64
9:A:295:G:HO2'	9:A:296:G:P	2.17	0.64
9:A:1710:A:O2'	9:A:1716:G:N7	2.20	0.64
27:W:52:ASN:OD1	27:W:53:VAL:N	2.31	0.64
16:K:20:ASP:OD1	16:K:21:GLY:N	2.29	0.63
15:J:136:LEU:HD23	15:J:141:VAL:HG11	1.80	0.63
31:a:1294:G:N3	31:a:1352:U:O2'	2.27	0.63
48:r:30:THR:HG22	48:r:31:LYS:H	1.62	0.63
12:G:274:ARG:O	12:G:275:THR:OG1	2.09	0.63
31:a:139:C:OP1	31:a:337:C:O2'	2.16	0.63
14:I:150:THR:OG1	14:I:190:ASN:OD1	2.04	0.63
6:6:1:MET:CE	9:A:791:A:P	2.86	0.63
9:A:1917:G:O2'	9:A:1941:A:N1	2.31	0.63
50:t:50:ALA:HB1	50:t:57:HIS:HB3	1.80	0.63
9:A:502:G:N2	9:A:505:A:OP2	2.26	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1034:C:O2	17:M:4:THR:OG1	2.10	0.63
9:A:1758:G:O2'	9:A:1759:G:OP2	2.15	0.63
9:A:1954:C:N4	9:A:1978:C:O4'	2.32	0.63
9:A:2318:U:HO2'	9:A:2319:U:C5'	2.11	0.63
31:a:1292:G:N2	31:a:1295:A:OP2	2.15	0.63
9:A:2635:C:O2'	9:A:2835:G:N7	2.31	0.63
31:a:793:A:O2'	31:a:1551:C:O2	2.16	0.63
31:a:871:C:H5'	49:s:21:HIS:HE1	1.62	0.62
31:a:431:U:OP1	31:a:432:G:O2'	2.12	0.62
31:a:1043:A:HO2'	31:a:1243:C:HO2'	1.46	0.62
31:a:1173:C:O2	40:j:18:ARG:NH1	2.31	0.62
9:A:2304:U:OP1	9:A:2393:U:O2'	2.16	0.62
37:g:87:ASN:OD1	37:g:89:ASP:N	2.32	0.62
9:A:1420:A:O2'	9:A:1431:U:O2	2.17	0.62
23:S:34:GLU:OE1	23:S:34:GLU:N	2.32	0.62
8:8:12:GLU:OE1	8:8:12:GLU:N	2.31	0.62
9:A:586:U:OP1	25:U:92:TYR:OH	2.14	0.62
10:B:55:A:O4'	15:J:24:SER:OG	2.17	0.62
16:K:107:VAL:O	16:K:152:ARG:NH1	2.33	0.62
9:A:249:G:OP2	9:A:251:C:N4	2.24	0.62
9:A:668:G:N2	9:A:671:A:OP2	2.29	0.62
9:A:2518:G:O2'	9:A:2519:U:O5'	2.10	0.62
9:A:2536:G:HO2'	9:A:2777:A:HO2'	1.38	0.62
12:G:123:ASP:OD1	12:G:124:ILE:N	2.33	0.62
44:n:12:ASP:O	44:n:44:ARG:NH1	2.33	0.62
9:A:2718:A:O2'	9:A:2862:G:OP1	2.14	0.61
31:a:11:G:OP2	36:f:126:LYS:NZ	2.21	0.61
38:h:111:ARG:NE	38:h:123:GLU:OE1	2.33	0.61
9:A:613:G:O2'	9:A:1290:A:OP1	2.18	0.61
9:A:2577:A:OP1	9:A:2661:G:O2'	2.11	0.61
37:g:45:ASP:OD1	37:g:64:HIS:ND1	2.32	0.61
9:A:2701:G:N1	9:A:2733:U:OP2	2.29	0.61
9:A:2797:U:C4'	13:H:44:ASP:OD1	2.48	0.61
18:N:71:ARG:NE	18:N:105:GLU:OE2	2.32	0.61
31:a:703:U:H3	31:a:739:G:H22	1.49	0.61
31:a:1006:C:O2	45:o:19:GLN:NE2	2.34	0.61
9:A:2857:U:OP1	23:S:96:LYS:NZ	2.27	0.61
20:P:26:GLU:N	20:P:26:GLU:OE1	2.34	0.61
9:A:2320:G:O6	15:J:41:GLY:N	2.33	0.61
31:a:290:C:O2'	48:r:69:PRO:O	2.19	0.61
31:a:768:G:OP1	46:p:59:LYS:NZ	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2482:A:N6	9:A:2494:G:O2'	2.33	0.61
34:d:11:ARG:NH2	34:d:176:THR:O	2.33	0.61
29:Y:65:ASP:OD1	29:Y:67:THR:HG23	2.01	0.61
31:a:227:A:O2'	31:a:228:A:O4'	2.16	0.60
21:Q:60:ARG:O	21:Q:64:THR:HG23	2.01	0.60
40:j:65:VAL:HG11	40:j:79:ILE:HG12	1.82	0.60
9:A:2344:G:O2'	9:A:2349:A:N1	2.34	0.60
34:d:76:ILE:HA	34:d:83:VAL:HG13	1.81	0.60
31:a:783:U:OP1	31:a:848:A:O2'	2.18	0.60
9:A:2210:U:HO2'	9:A:2211:A:P	2.23	0.60
31:a:401:U:OP1	47:q:69:THR:OG1	2.09	0.60
9:A:220:G:H22	9:A:237:U:H4'	1.67	0.60
9:A:965:U:O2'	9:A:966:C:OP1	2.19	0.60
31:a:1557:G:O2'	31:a:1558:A:OP2	2.13	0.60
9:A:2859:G:O2'	9:A:2876:G:N2	2.34	0.60
21:Q:20:ILE:HG21	21:Q:40:VAL:HG21	1.84	0.60
28:X:10:LYS:HB2	28:X:71:ILE:HD11	1.83	0.60
14:I:146:LEU:O	14:I:147:SER:OG	2.18	0.60
15:J:11:GLU:N	15:J:11:GLU:OE1	2.35	0.60
51:u:66:ILE:CB	51:u:70:LYS:HD3	2.29	0.60
9:A:691:A:OP2	9:A:692:U:O2'	2.19	0.59
31:a:132:A:H61	31:a:339:A:H1'	1.66	0.59
9:A:267:A:N1	9:A:466:U:O2'	2.35	0.59
18:N:97:ARG:NH2	31:a:364:A:OP1	2.36	0.59
9:A:995:G:OP2	20:P:87:LYS:NZ	2.35	0.59
16:K:155:GLU:OE2	16:K:160:LYS:N	2.34	0.59
37:g:9:ILE:HG23	37:g:95:ILE:HG12	1.84	0.59
9:A:1792:U:O2	9:A:1796:A:N6	2.36	0.59
13:H:103:GLN:N	13:H:103:GLN:OE1	2.36	0.59
29:Y:48:ARG:HH11	29:Y:67:THR:HG21	1.67	0.59
38:h:117:GLU:OE1	38:h:117:GLU:N	2.32	0.59
40:j:30:VAL:N	40:j:33:LYS:O	2.34	0.59
9:A:910:U:OP1	20:P:6:ARG:NE	2.27	0.58
31:a:1001:A:OP2	45:o:32:SER:OG	2.19	0.58
11:D:55:U:H2'	11:D:56:U:N1	2.18	0.58
9:A:2076:C:O2'	11:D:77:A:O2'	1.95	0.58
12:G:143:ASN:ND2	12:G:143:ASN:O	2.36	0.58
31:a:739:G:H2'	31:a:740:G:C8	2.38	0.58
42:l:46:SER:N	42:l:49:SER:OG	2.34	0.58
9:A:901:A:N3	10:B:77:G:O2'	2.36	0.58
9:A:918:A:N6	9:A:939:G:O2'	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:89:LEU:O	16:K:89:LEU:HD12	2.02	0.58
31:a:1423:C:OP2	36:f:29:ARG:NH2	2.36	0.58
31:a:938:U:OP2	43:m:107:ARG:NH2	2.37	0.58
31:a:446:U:O2'	31:a:449:G:O6	2.12	0.58
39:i:76:ASN:OD1	39:i:77:LEU:N	2.35	0.58
42:l:29:ASN:OD1	42:l:30:THR:N	2.37	0.58
3:3:16:ASP:OD2	3:3:51:THR:N	2.37	0.58
31:a:703:U:O2	31:a:803:A:O2'	2.21	0.58
38:h:15:ASP:OD1	38:h:18:TYR:N	2.34	0.58
16:K:96:ALA:HB2	16:K:105:LEU:HD23	1.86	0.58
40:j:50:GLN:OE1	40:j:80:ARG:NE	2.37	0.58
9:A:743:G:O2'	9:A:765:G:N2	2.34	0.58
9:A:1133:U:N3	9:A:1136:U:OP2	2.36	0.58
18:N:65:THR:OG1	18:N:67:SER:O	2.18	0.58
9:A:569:A:OP1	9:A:597:G:N1	2.37	0.58
9:A:2772:G:N2	16:K:139:GLU:OE2	2.37	0.58
11:D:57:C:C6	15:J:80:ARG:HD3	2.39	0.58
31:a:965:A:N3	31:a:1402:U:O2'	2.29	0.58
31:a:1091:G:O2'	31:a:1216:G:N2	2.37	0.58
9:A:1926:A:N6	31:a:1521:G:OP2	2.37	0.57
20:P:75:THR:HG22	20:P:90:PRO:HA	1.86	0.57
31:a:1043:A:O2'	31:a:1243:C:O2'	2.21	0.57
39:i:18:ASN:ND2	39:i:74:ILE:O	2.36	0.57
3:3:70:ARG:NH1	50:t:67:VAL:O	2.36	0.57
9:A:1061:G:O2'	9:A:1062:U:P	2.62	0.57
39:i:107:SER:HB2	39:i:128:ILE:HD11	1.86	0.57
42:l:71:THR:OG1	42:l:100:LEU:HD23	2.03	0.57
6:6:9:LYS:NZ	9:A:1345:G:OP2	2.27	0.57
9:A:680:G:N2	9:A:683:U:OP2	2.26	0.57
9:A:769:A:OP1	9:A:1788:U:O2'	2.18	0.57
9:A:1227:G:OP1	19:O:30:THR:OG1	2.22	0.57
31:a:1342:G:N1	31:a:1345:A:OP2	2.38	0.57
40:j:43:ASP:OD1	40:j:44:LEU:N	2.37	0.57
43:m:27:GLY:N	43:m:36:THR:O	2.37	0.57
15:J:44:VAL:HG22	15:J:79:LEU:HD11	1.86	0.57
18:N:107:ARG:NH2	23:S:34:GLU:HB2	2.19	0.57
14:I:177:THR:OG1	14:I:179:ASP:OD1	2.22	0.57
31:a:1331:G:O2'	31:a:1332:A:OP2	2.20	0.57
9:A:1469:C:O2'	9:A:1614:A:OP2	2.16	0.57
31:a:712:U:O2'	31:a:713:A:OP2	2.18	0.57
34:d:69:THR:HG22	34:d:71:LYS:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:192:GLU:OE1	35:e:192:GLU:N	2.35	0.57
9:A:429:A:HO2'	9:A:430:A:H8	1.53	0.56
9:A:1263:G:N7	24:T:16:LYS:NZ	2.47	0.56
31:a:165:G:O2'	31:a:1472:A:N3	2.31	0.56
9:A:662:C:O2'	9:A:696:U:OP1	2.23	0.56
20:P:51:ARG:HG3	20:P:66:ILE:HD11	1.88	0.56
9:A:2317:G:H22	9:A:2325:U:H3	1.53	0.56
18:N:64:ARG:NH2	18:N:99:PHE:O	2.35	0.56
27:W:13:THR:H	27:W:16:SER:HG	1.52	0.56
31:a:399:A:N1	31:a:417:C:O2'	2.36	0.56
31:a:571:C:OP1	35:e:54:LYS:NZ	2.38	0.56
31:a:713:A:N6	31:a:727:U:O4'	2.38	0.56
34:d:52:SER:OG	34:d:111:ASP:OD2	2.16	0.56
44:n:17:VAL:O	44:n:20:THR:OG1	2.21	0.56
9:A:48:G:N1	9:A:178:A:OP2	2.35	0.56
9:A:83:G:O2'	9:A:101:G:N2	2.35	0.56
9:A:24:G:O2'	26:V:83:GLU:O	2.21	0.56
22:R:101:HIS:O	22:R:105:GLN:NE2	2.36	0.56
41:k:29:ALA:O	41:k:32:THR:OG1	2.21	0.56
48:r:30:THR:CG2	48:r:31:LYS:N	2.69	0.56
9:A:515:G:N1	9:A:518:A:OP2	2.32	0.56
31:a:1082:A:O2'	34:d:160:ASP:O	2.15	0.56
9:A:521:C:O2'	9:A:535:A:N1	2.37	0.56
31:a:822:C:OP1	42:l:128:ARG:N	2.39	0.56
31:a:1413:G:H5''	56:a:1660:SCM:H8M3	1.87	0.56
10:B:35:C:O2	22:R:101:HIS:NE2	2.39	0.56
31:a:792:A:OP2	31:a:838:G:N2	2.39	0.56
31:a:1563:C:HO2'	31:a:1564:U:P	2.27	0.56
36:f:66:ASP:OD1	36:f:70:ASN:ND2	2.38	0.56
9:A:1211:A:H2'	9:A:1214:A:H61	1.70	0.56
31:a:715:C:OP1	42:l:29:ASN:ND2	2.39	0.56
31:a:171:A:N6	31:a:185:G:O6	2.39	0.55
9:A:295:G:C2'	9:A:296:G:O5'	2.54	0.55
9:A:1833:U:OP1	12:G:177:ASN:ND2	2.39	0.55
43:m:92:VAL:N	43:m:116:ASP:OD2	2.38	0.55
12:G:111:GLU:HB2	12:G:114:MET:HE3	1.87	0.55
31:a:1023:A:N1	31:a:1072:C:O2'	2.32	0.55
44:n:22:ILE:CG2	44:n:25:ILE:HD13	2.37	0.55
9:A:411:G:O2'	9:A:439:G:O6	2.23	0.55
9:A:429:A:O2'	9:A:430:A:H8	1.88	0.55
31:a:323:G:N2	31:a:326:A:OP2	2.30	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:128:ASP:N	35:e:128:ASP:OD1	2.35	0.55
6:6:1:MET:HE1	6:6:3:ARG:NH2	2.04	0.55
7:7:39:LYS:NZ	9:A:2378:G:N7	2.53	0.55
5:5:31:GLU:OE2	5:5:46:ARG:NE	2.37	0.55
9:A:1310:A:N1	9:A:1330:C:O2'	2.32	0.55
45:o:24:CYS:O	45:o:28:GLY:N	2.34	0.55
9:A:857:G:N1	9:A:1225:U:OP2	2.31	0.55
9:A:1102:G:C2	9:A:1103:C:C5	2.95	0.55
9:A:2341:A:H2'	9:A:2342:A:C8	2.42	0.55
37:g:8:GLU:OE2	49:s:28:LYS:HE2	2.06	0.55
42:l:71:THR:HG21	42:l:103:THR:OG1	2.06	0.55
42:l:88:GLY:H	42:l:114:THR:HG22	1.71	0.55
31:a:1354:C:C2	31:a:1355:A:C8	2.95	0.55
39:i:23:GLU:HG3	39:i:24:THR:HG23	1.89	0.55
9:A:1656:A:N6	26:V:97:SER:O	2.31	0.54
9:A:1926:A:H61	31:a:1520:A:P	2.30	0.54
43:m:103:LEU:HD13	43:m:106:VAL:HG21	1.89	0.54
9:A:580:C:O2'	9:A:581:G:O5'	2.24	0.54
9:A:2216:G:O2'	9:A:2217:C:OP2	2.23	0.54
9:A:2829:A:O2'	9:A:2831:A:N7	2.31	0.54
31:a:1333:U:O4'	44:n:108:THR:HG21	2.07	0.54
33:c:75:GLN:OE1	33:c:75:GLN:N	2.38	0.54
9:A:2518:G:HO2'	9:A:2519:U:P	2.30	0.54
31:a:601:G:O2'	31:a:847:G:OP2	2.18	0.54
33:c:188:ASP:OD1	33:c:189:THR:N	2.37	0.54
9:A:1455:G:H2'	9:A:1627:G:H22	1.72	0.54
9:A:2534:C:C2	9:A:2558:G:N2	2.75	0.54
31:a:1425:C:O2	31:a:1529:A:N6	2.39	0.54
41:k:78:ASN:O	41:k:78:ASN:ND2	2.40	0.54
42:l:71:THR:HG23	42:l:105:LEU:HD12	1.88	0.54
7:7:57:ARG:NH2	19:O:51:GLU:OE2	2.41	0.54
9:A:2114:G:C6	9:A:2202:G:C6	2.96	0.54
9:A:2222:C:OP2	9:A:2223:U:O2'	2.24	0.54
31:a:1177:A:OP1	41:k:44:THR:HG22	2.08	0.54
38:h:15:ASP:OD1	38:h:17:ILE:N	2.38	0.54
9:A:1061:G:O2'	9:A:1063:G:N7	2.41	0.54
9:A:2521:G:HO2'	9:A:2567:U:HO2'	1.51	0.54
31:a:972:G:C2	31:a:973:A:C8	2.96	0.54
48:r:30:THR:CG2	48:r:31:LYS:H	2.20	0.54
9:A:714:A:OP1	14:l:63:LYS:NZ	2.40	0.54
10:B:7:G:OP1	22:R:19:ARG:NE	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1347:U:OP2	31:a:1348:C:O2'	2.25	0.54
9:A:1032:A:OP1	24:T:50:ARG:NE	2.34	0.54
12:G:43:ARG:NH2	12:G:49:ILE:HD11	2.23	0.54
31:a:64:U:O2'	31:a:405:C:O2	2.26	0.54
31:a:427:C:O2'	31:a:647:A:N3	2.32	0.54
36:f:84:GLU:OE2	36:f:95:LEU:HD11	2.08	0.54
9:A:928:C:OP1	44:n:92:ARG:NE	2.41	0.53
9:A:2212:A:N1	9:A:2239:C:N4	2.56	0.53
31:a:123:G:N7	51:u:10:ARG:NH1	2.56	0.53
31:a:872:G:O2'	31:a:873:C:P	2.66	0.53
44:n:25:ILE:HD11	44:n:65:VAL:HG11	1.89	0.53
50:t:70:LYS:N	50:t:73:GLU:OE2	2.40	0.53
9:A:2545:G:N2	9:A:2676:G:O2'	2.41	0.53
31:a:765:C:O2'	46:p:42:HIS:ND1	2.39	0.53
31:a:1478:U:O2'	31:a:1479:U:O5'	2.25	0.53
31:a:1563:C:O2'	31:a:1564:U:P	2.66	0.53
41:k:36:VAL:CG1	41:k:76:ILE:HD13	2.31	0.53
9:A:64:A:C5	27:W:65:MET:HE2	2.43	0.53
31:a:795:G:H4'	31:a:1540:A:H4'	1.89	0.53
31:a:1079:U:O4	31:a:1226:C:O2'	2.25	0.53
31:a:1313:A:N3	31:a:1379:G:O2'	2.34	0.53
7:7:54:ASP:OD2	9:A:2372:C:O2'	2.26	0.53
9:A:928:C:N4	9:A:930:C:O2'	2.35	0.53
9:A:1812:G:O2'	12:G:180:GLU:OE2	2.16	0.53
9:A:2608:G:N2	9:A:2611:A:OP2	2.33	0.53
28:X:5:LYS:NZ	28:X:24:LEU:O	2.40	0.53
15:J:112:ARG:NH1	44:n:6:GLY:O	2.42	0.53
21:Q:2:SER:OG	21:Q:3:TYR:N	2.41	0.53
31:a:23:G:H2'	31:a:24:G:C8	2.43	0.53
31:a:1090:C:OP2	31:a:1091:G:O2'	2.23	0.53
9:A:681:A:N1	9:A:2382:A:O2'	2.39	0.53
31:a:1384:U:OP2	31:a:1385:C:N4	2.35	0.53
9:A:2640:G:O2'	9:A:2794:A:N1	2.34	0.53
17:M:5:TYR:O	24:T:64:ARG:NH2	2.40	0.52
21:Q:20:ILE:CG2	21:Q:40:VAL:HG21	2.38	0.52
9:A:2589:G:O2'	9:A:2592:C:OP2	2.27	0.52
31:a:52:A:O2'	31:a:386:G:N2	2.42	0.52
31:a:1162:U:O2'	31:a:1164:A:N7	2.39	0.52
9:A:247:G:O2'	9:A:423:A:N1	2.39	0.52
9:A:281:A:HO2'	9:A:282:G:P	2.32	0.52
31:a:148:C:O2'	31:a:288:A:N3	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:21:C:OP2	36:f:132:THR:OG1	2.25	0.52
4:4:39:SER:HG	9:A:2825:C:HO2'	1.55	0.52
9:A:2075:A:N7	9:A:2516:A:N6	2.58	0.52
9:A:2655:G:OP2	17:M:86:LYS:NZ	2.41	0.52
11:D:7:G:H3'	11:D:8:U:C5'	2.39	0.52
31:a:762:U:H2'	31:a:763:C:C6	2.45	0.52
33:c:34:GLU:OE1	33:c:34:GLU:N	2.38	0.52
7:7:7:HIS:NE2	9:A:253:A:OP1	2.39	0.52
9:A:1413:A:O2'	9:A:1414:U:C6	2.62	0.52
49:s:38:SER:HB3	49:s:44:LEU:HD21	1.90	0.52
9:A:570:A:H4'	9:A:571:G:C8	2.45	0.52
9:A:1118:C:H2'	9:A:1118:C:O2	2.09	0.52
13:H:90:GLU:O	13:H:95:LYS:NZ	2.39	0.52
14:I:26:ILE:HG12	14:I:115:SER:OG	2.09	0.52
22:R:24:GLY:N	22:R:47:ASP:OD2	2.43	0.52
38:h:41:ASN:OD1	38:h:45:ASN:ND2	2.43	0.52
39:i:14:ILE:HG12	39:i:25:LEU:HD21	1.91	0.52
49:s:36:PHE:HD1	49:s:49:THR:HG21	1.74	0.52
9:A:1069:G:OP2	20:P:128:LYS:NZ	2.42	0.52
31:a:949:G:O2'	31:a:1424:A:N1	2.41	0.52
31:a:1372:A:OP1	40:j:122:ARG:NH1	2.41	0.52
7:7:12:LYS:NZ	9:A:251:C:O2	2.42	0.52
31:a:1513:G:H2'	31:a:1514:G:C8	2.45	0.52
12:G:61:GLN:O	12:G:63:ARG:NH1	2.43	0.51
31:a:1035:C:O2'	31:a:1036:U:P	2.68	0.51
11:D:57:C:H2'	11:D:57:C:O2	2.09	0.51
15:J:36:ILE:HD11	15:J:152:MET:SD	2.50	0.51
23:S:2:ASN:ND2	23:S:6:GLN:OE1	2.40	0.51
31:a:700:G:H2'	31:a:701:A:H8	1.74	0.51
34:d:171:THR:HG22	34:d:173:PRO:HD3	1.92	0.51
9:A:1467:G:N7	12:G:31:LYS:NZ	2.59	0.51
12:G:71:LYS:NZ	12:G:98:ASP:OD2	2.39	0.51
39:i:42:ARG:NH2	39:i:117:GLU:OE2	2.44	0.51
9:A:2111:U:O2'	9:A:2112:U:P	2.69	0.51
31:a:222:G:H2'	31:a:223:A:C8	2.46	0.51
31:a:1005:A:C2	31:a:1345:A:C4	2.98	0.51
39:i:54:ASP:OD1	39:i:58:GLY:N	2.38	0.51
2:2:26:LEU:HD12	2:2:50:ILE:HD11	1.91	0.51
19:O:51:GLU:OE1	19:O:54:GLN:NE2	2.43	0.51
31:a:272:A:C2	31:a:308:A:C5	2.99	0.51
31:a:888:G:HO2'	31:a:901:G:HO2'	1.56	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1398:U:OP1	40:j:74:GLY:N	2.40	0.51
42:l:68:GLU:HA	42:l:103:THR:HG21	1.91	0.51
9:A:2271:C:O2'	9:A:2440:C:OP2	2.25	0.51
12:G:2:ALA:N	12:G:20:ASP:OD2	2.43	0.51
36:f:86:ILE:CD1	36:f:95:LEU:HD13	2.39	0.51
9:A:2585:A:N7	13:H:149:VAL:HG11	2.26	0.51
9:A:2810:U:O2'	9:A:2811:A:OP2	2.23	0.51
11:D:57:C:H3'	15:J:80:ARG:NH1	2.25	0.51
38:h:71:PRO:O	38:h:96:ARG:NE	2.44	0.51
4:4:13:LYS:NZ	9:A:1299:U:OP1	2.39	0.51
9:A:2640:G:N2	9:A:2790:G:OP2	2.43	0.51
31:a:188:A:O2'	31:a:189:A:O4'	2.21	0.51
35:e:102:LEU:HD21	35:e:166:VAL:CG2	2.41	0.51
9:A:2324:A:HO2'	9:A:2325:U:H6	1.59	0.51
26:V:7:SER:HB3	26:V:113:THR:HG22	1.93	0.51
43:m:120:VAL:O	43:m:132:THR:HG21	2.09	0.51
9:A:441:A:H2'	9:A:442:U:O4'	2.11	0.51
9:A:1536:A:O2'	9:A:1537:A:P	2.69	0.51
44:n:16:VAL:HG12	44:n:34:LEU:HD12	1.93	0.51
9:A:2327:A:H2'	9:A:2328:U:C6	2.46	0.50
11:D:56:U:H2'	15:J:80:ARG:CZ	2.40	0.50
22:R:55:SER:O	22:R:82:ARG:NH1	2.42	0.50
36:f:102:GLY:N	36:f:122:ASP:OD2	2.38	0.50
9:A:1965:A:OP1	18:N:42:THR:HG21	2.12	0.50
9:A:2672:G:N2	9:A:2675:A:OP2	2.43	0.50
24:T:48:ARG:NH1	24:T:49:ASP:OD1	2.41	0.50
31:a:1092:U:O2'	31:a:1093:C:OP2	2.26	0.50
31:a:1343:C:O2	50:t:37:ARG:NH1	2.43	0.50
13:H:55:ASP:OD1	13:H:77:LYS:NZ	2.41	0.50
31:a:1500:G:H2'	31:a:1501:G:C8	2.46	0.50
8:8:19:ARG:NE	9:A:2769:U:OP2	2.40	0.50
11:D:31:G:OP1	31:a:1255:A:O2'	2.29	0.50
31:a:199:A:H1'	31:a:201:A:N7	2.27	0.50
31:a:740:G:H2'	31:a:741:A:C8	2.46	0.50
39:i:75:THR:N	39:i:132:TRP:OXT	2.45	0.50
9:A:622:A:N1	9:A:848:G:O2'	2.44	0.50
9:A:824:U:H2'	9:A:825:C:C6	2.46	0.50
9:A:1005:G:O4'	9:A:2280:A:N6	2.44	0.50
9:A:1583:G:O2'	9:A:1584:U:P	2.70	0.50
13:H:96:GLU:OE1	13:H:98:LYS:NZ	2.45	0.50
31:a:164:G:H2'	31:a:165:G:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1192:G:N1	31:a:1195:A:OP2	2.44	0.50
9:A:293:G:C2	9:A:294:G:C8	3.00	0.50
9:A:1752:G:H1'	9:A:2869:G:H21	1.76	0.50
9:A:1877:U:OP1	9:A:2423:G:O2'	2.30	0.50
9:A:2443:A:N3	9:A:2443:A:H2'	2.27	0.50
31:a:30:G:O2'	31:a:322:U:OP1	2.28	0.50
31:a:1113:U:H3	31:a:1126:G:H22	1.57	0.50
31:a:1393:C:P	40:j:114:LYS:HZ1	2.34	0.50
34:d:94:THR:HG23	34:d:96:LYS:H	1.75	0.50
39:i:25:LEU:C	39:i:25:LEU:HD12	2.36	0.50
40:j:106:ARG:NH1	40:j:107:ASP:O	2.40	0.50
4:4:24:ILE:HG23	4:4:24:ILE:O	2.12	0.50
9:A:342:U:H2'	9:A:343:G:O4'	2.12	0.50
9:A:958:A:N3	10:B:78:U:O2'	2.44	0.50
13:H:46:TYR:OH	13:H:82:GLU:OE1	2.19	0.50
18:N:80:ASP:OD2	23:S:62:ARG:NH2	2.42	0.50
31:a:1516:G:O2'	31:a:1517:U:O5'	2.26	0.50
34:d:182:ASP:OD1	34:d:183:TYR:N	2.44	0.50
9:A:2697:U:OP2	23:S:51:ARG:NH1	2.45	0.50
31:a:868:U:N3	31:a:870:C:OP1	2.45	0.50
31:a:1062:G:O2'	31:a:1063:A:O5'	2.30	0.50
36:f:25:VAL:HG22	36:f:26:LYS:N	2.27	0.50
36:f:73:GLU:OE2	36:f:149:ARG:NH2	2.43	0.50
9:A:21:A:N6	9:A:558:G:O6	2.44	0.49
9:A:1691:G:HO2'	21:Q:116:ASP:CG	2.16	0.49
11:D:39:A:O2'	31:a:816:A:OP1	2.27	0.49
28:X:72:ASP:O	28:X:76:GLY:N	2.37	0.49
13:H:9:LYS:NZ	13:H:194:GLY:O	2.37	0.49
31:a:428:G:OP1	35:e:67:GLN:NE2	2.42	0.49
35:e:184:ASP:N	35:e:184:ASP:OD1	2.45	0.49
36:f:74:VAL:HG23	36:f:74:VAL:O	2.12	0.49
9:A:2063:C:H2'	9:A:2064:A:O4'	2.12	0.49
14:I:178:SER:OG	14:I:201:GLN:OE1	2.28	0.49
31:a:222:G:H2'	31:a:223:A:H8	1.77	0.49
33:c:86:ARG:NH2	33:c:219:ASP:OD1	2.38	0.49
38:h:65:ALA:HB1	38:h:127:ALA:HB3	1.94	0.49
41:k:44:THR:HG23	41:k:44:THR:O	2.12	0.49
9:A:1318:G:N2	9:A:1321:A:OP2	2.43	0.49
9:A:2318:U:O2'	9:A:2319:U:P	2.70	0.49
9:A:2536:G:O2'	9:A:2777:A:O2'	2.15	0.49
9:A:916:C:H2'	9:A:917:U:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:934:U:N3	9:A:935:U:O4	2.45	0.49
9:A:2318:U:HO2'	9:A:2319:U:P	2.32	0.49
10:B:28:C:H2'	10:B:28:C:O2	2.12	0.49
31:a:304:C:OP2	48:r:46:LYS:NZ	2.42	0.49
31:a:845:A:H4'	31:a:846:U:OP2	2.12	0.49
34:d:87:ARG:NH2	34:d:98:VAL:O	2.46	0.49
15:J:50:LEU:HD13	15:J:50:LEU:C	2.37	0.49
9:A:782:A:O2'	9:A:1701:U:OP1	2.30	0.49
11:D:56:U:H2'	15:J:80:ARG:NH2	2.27	0.49
31:a:1382:G:H2'	31:a:1383:A:C8	2.48	0.49
44:n:25:ILE:N	44:n:25:ILE:HD12	2.27	0.49
4:4:6:ARG:NH2	9:A:2032:U:OP2	2.45	0.49
9:A:13:A:O2'	9:A:15:G:N7	2.46	0.49
9:A:52:A:OP2	9:A:116:G:N1	2.40	0.49
9:A:180:G:H2'	9:A:181:U:O4'	2.13	0.49
22:R:11:ARG:HD2	22:R:98:TYR:CZ	2.48	0.49
31:a:1516:G:O2'	31:a:1517:U:P	2.71	0.49
37:g:9:ILE:HG12	37:g:95:ILE:HG23	1.94	0.49
45:o:23:ARG:NH1	45:o:28:GLY:O	2.43	0.49
9:A:294:G:C6	9:A:295:G:C6	3.01	0.49
9:A:1124:A:HO2'	9:A:1125:A:C1'	2.25	0.49
31:a:767:G:H2'	31:a:768:G:O4'	2.12	0.49
9:A:1108:A:H4'	9:A:1109:A:H2'	1.94	0.48
31:a:794:A:N3	31:a:1539:U:O2'	2.46	0.48
31:a:865:G:O2'	31:a:866:G:P	2.70	0.48
9:A:781:U:H2'	9:A:782:A:C8	2.48	0.48
9:A:1784:C:O2'	9:A:1799:A:O4'	2.26	0.48
25:U:27:VAL:O	25:U:65:HIS:NE2	2.42	0.48
31:a:397:G:H2'	31:a:398:C:O4'	2.13	0.48
31:a:573:A:OP2	35:e:2:SER:N	2.47	0.48
9:A:345:A:N3	9:A:365:G:O2'	2.43	0.48
9:A:368:A:O2'	9:A:370:C:OP2	2.26	0.48
9:A:896:G:H2'	9:A:897:A:C8	2.49	0.48
9:A:2087:U:O2'	9:A:2610:G:H1'	2.12	0.48
10:B:48:A:H5''	22:R:67:THR:HG23	1.94	0.48
11:D:58:A:OP2	15:J:80:ARG:NH1	2.43	0.48
31:a:1171:C:H4'	31:a:1172:A:O5'	2.13	0.48
3:3:45:LEU:HD13	3:3:45:LEU:C	2.38	0.48
7:7:10:LEU:O	7:7:14:VAL:HG22	2.13	0.48
9:A:67:A:H1'	9:A:88:G:N2	2.29	0.48
9:A:1302:G:O5'	26:V:20:ARG:NH2	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:498:A:O2'	47:q:84:HIS:ND1	2.32	0.48
31:a:1206:A:OP1	40:j:105:THR:OG1	2.26	0.48
9:A:2712:U:H2'	9:A:2713:C:C6	2.48	0.48
9:A:2802:C:O2'	9:A:2803:A:OP2	2.25	0.48
31:a:542:U:O2'	31:a:545:C:N3	2.43	0.48
31:a:1457:C:H2'	31:a:1458:G:O4'	2.13	0.48
9:A:1189:U:HO2'	9:A:1190:A:P	2.31	0.48
9:A:1356:A:C4	9:A:1357:A:C8	3.01	0.48
9:A:1678:U:H2'	9:A:1679:C:C6	2.49	0.48
9:A:2279:A:H4'	9:A:2280:A:N3	2.29	0.48
10:B:104:G:H2'	10:B:105:A:O4'	2.14	0.48
18:N:1:MET:N	18:N:67:SER:OG	2.47	0.48
19:O:71:ARG:NE	19:O:73:ASP:OD1	2.46	0.48
31:a:818:A:H1'	31:a:820:A:N7	2.29	0.48
4:4:40:HIS:N	9:A:2894:U:O4	2.40	0.48
9:A:520:G:O2'	9:A:545:A:N6	2.46	0.48
9:A:537:U:H2'	9:A:538:G:O4'	2.14	0.48
31:a:173:U:H1'	31:a:183:G:N2	2.29	0.48
44:n:53:THR:HG22	44:n:57:ARG:NH1	2.28	0.48
50:t:49:ILE:HD13	50:t:62:ILE:HD12	1.95	0.48
9:A:277:A:N6	9:A:293:G:O6	2.47	0.48
9:A:624:U:H2'	9:A:625:U:C6	2.48	0.48
9:A:1120:U:H2'	9:A:1121:U:C6	2.48	0.48
31:a:637:C:C4	31:a:638:C:C5	3.02	0.48
56:a:1660:SCM:H32	36:f:26:LYS:HD3	1.95	0.48
9:A:451:A:N6	9:A:2425:A:O4'	2.47	0.48
9:A:927:U:O2	9:A:929:U:N3	2.47	0.48
9:A:1456:A:N6	9:A:1627:G:O2'	2.41	0.48
9:A:2618:U:H2'	9:A:2619:C:C6	2.48	0.48
31:a:783:U:H2'	31:a:784:G:O4'	2.14	0.48
31:a:815:U:O2'	31:a:817:G:N7	2.36	0.48
9:A:59:G:O2'	9:A:74:U:OP2	2.21	0.48
9:A:2541:U:O2'	9:A:2543:U:OP1	2.25	0.48
9:A:2715:G:C2	9:A:2716:C:C6	3.02	0.48
31:a:604:A:O2'	31:a:754:A:N3	2.38	0.48
31:a:1317:C:C2	31:a:1318:U:C5	3.01	0.48
31:a:1540:A:H2'	31:a:1541:U:C6	2.49	0.48
22:R:30:ARG:NH2	22:R:47:ASP:OD1	2.40	0.47
31:a:1186:G:C2	31:a:1187:C:C6	3.02	0.47
31:a:1480:U:O2'	31:a:1481:G:P	2.71	0.47
9:A:2340:A:H2'	9:A:2341:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2695:G:C2	9:A:2696:C:C6	3.02	0.47
9:A:2877:G:O2'	9:A:2878:A:P	2.72	0.47
31:a:1098:C:H2'	31:a:1099:G:H8	1.79	0.47
31:a:1156:C:O4'	31:a:1172:A:N6	2.44	0.47
40:j:21:LEU:CD2	40:j:63:VAL:HG22	2.44	0.47
9:A:1180:U:H4'	9:A:1181:A:O4'	2.14	0.47
9:A:1277:C:C2	9:A:1278:U:C5	3.02	0.47
9:A:1509:C:O2'	9:A:1510:C:OP2	2.21	0.47
31:a:563:G:OP1	43:m:123:ARG:NH1	2.44	0.47
40:j:88:LEU:HD11	40:j:104:LEU:CD2	2.44	0.47
9:A:1421:C:H2'	9:A:1422:A:H8	1.79	0.47
15:J:13:THR:HB	15:J:14:PRO:HD3	1.96	0.47
16:K:87:LEU:N	16:K:87:LEU:HD12	2.30	0.47
31:a:1152:U:C2	31:a:1154:G:C8	3.03	0.47
44:n:22:ILE:HG22	44:n:25:ILE:HD13	1.96	0.47
9:A:2487:C:O2	9:A:2487:C:O4'	2.32	0.47
31:a:710:U:O2'	42:l:41:ALA:O	2.30	0.47
31:a:1480:U:O2'	31:a:1481:G:O5'	2.32	0.47
39:i:115:ASP:OD1	39:i:115:ASP:N	2.48	0.47
42:l:128:ARG:O	42:l:129:VAL:HG13	2.14	0.47
9:A:19:G:N1	9:A:560:G:C6	2.82	0.47
9:A:277:A:C6	9:A:293:G:C6	3.02	0.47
9:A:874:A:C4	9:A:875:G:C8	3.03	0.47
9:A:1362:C:H2'	9:A:1363:G:O4'	2.14	0.47
14:I:26:ILE:HD11	14:I:111:LYS:C	2.39	0.47
31:a:1153:U:O4	41:k:9:ARG:NH1	2.46	0.47
9:A:294:G:C2'	9:A:295:G:O5'	2.63	0.47
9:A:2010:A:OP2	13:H:130:ARG:NH1	2.48	0.47
14:I:132:ASP:OD1	14:I:132:ASP:N	2.45	0.47
15:J:9:ILE:HG23	15:J:10:LYS:HG2	1.97	0.47
31:a:135:A:OP2	31:a:314:A:N6	2.44	0.47
31:a:363:G:H2'	31:a:364:A:C8	2.50	0.47
31:a:1006:C:O2	31:a:1006:C:H2'	2.14	0.47
31:a:1461:G:H2'	31:a:1462:U:C6	2.50	0.47
33:c:129:LEU:HG	33:c:133:GLU:HB3	1.97	0.47
5:5:10:THR:O	5:5:13:LYS:NZ	2.42	0.47
9:A:1345:G:N2	9:A:1348:U:C4	2.83	0.47
9:A:1433:C:C2	9:A:1434:C:C5	3.02	0.47
48:r:22:LYS:NZ	48:r:52:GLU:O	2.25	0.47
9:A:667:C:O2	9:A:677:U:O2'	2.32	0.47
9:A:997:U:O2'	9:A:998:A:OP1	2.25	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1420:A:O2'	9:A:1421:C:OP2	2.26	0.47
9:A:1808:C:H2'	9:A:1809:U:O4'	2.15	0.47
10:B:22:G:O6	10:B:54:U:O2'	2.26	0.47
31:a:1331:G:HO2'	31:a:1332:A:P	2.36	0.47
9:A:138:U:N3	9:A:141:U:OP2	2.47	0.47
9:A:1375:U:OP1	27:W:15:LYS:NZ	2.46	0.47
9:A:2848:G:C4	9:A:2849:G:C8	3.03	0.47
9:A:2849:G:O2'	21:Q:45:GLU:OE1	2.24	0.47
20:P:127:VAL:O	20:P:129:THR:HG23	2.15	0.47
31:a:1047:A:C2	31:a:1048:G:C5	3.02	0.47
31:a:1204:G:N1	31:a:1207:G:OP2	2.48	0.47
8:8:37:GLN:NE2	9:A:1070:G:N3	2.56	0.46
9:A:1107:G:N3	9:A:1134:A:O2'	2.48	0.46
9:A:1434:C:C2	9:A:1435:U:C5	3.03	0.46
9:A:1854:U:C2	9:A:1855:G:C8	3.03	0.46
31:a:19:U:H2'	31:a:20:C:C6	2.50	0.46
31:a:973:A:H2'	31:a:974:G:C8	2.50	0.46
31:a:1101:G:O2'	31:a:1128:A:N1	2.46	0.46
2:2:56:ILE:HG12	2:2:56:VAL:HG12	1.96	0.46
9:A:1570:G:N1	9:A:1589:A:OP2	2.41	0.46
9:A:1812:G:OP1	12:G:260:ARG:NH1	2.35	0.46
9:A:2679:C:O2	9:A:2679:C:O4'	2.33	0.46
15:J:144:ASP:OD1	15:J:145:LEU:N	2.48	0.46
16:K:79:VAL:HG22	16:K:136:ILE:HD11	1.96	0.46
31:a:1210:G:C2	31:a:1211:G:C8	3.04	0.46
9:A:904:G:H2'	9:A:905:C:C6	2.50	0.46
9:A:1590:A:H2'	9:A:1591:G:O4'	2.16	0.46
9:A:2256:U:H2'	9:A:2257:U:C6	2.50	0.46
31:a:19:U:O2'	31:a:1106:G:H1'	2.15	0.46
31:a:711:G:N1	31:a:730:A:OP2	2.40	0.46
31:a:1230:A:O2'	34:d:194:LYS:NZ	2.46	0.46
31:a:1242:A:C2	31:a:1243:C:C5	3.03	0.46
9:A:1421:C:H2'	9:A:1422:A:C8	2.51	0.46
9:A:2279:A:H4'	9:A:2280:A:O5'	2.15	0.46
31:a:359:C:C2	31:a:360:C:C5	3.04	0.46
31:a:553:G:O2'	31:a:561:A:N1	2.47	0.46
31:a:713:A:N7	31:a:727:U:N3	2.63	0.46
31:a:1045:A:C2	31:a:1046:G:C5	3.04	0.46
35:e:163:PRO:O	35:e:166:VAL:HG12	2.16	0.46
9:A:1445:G:H2'	9:A:1446:U:C6	2.51	0.46
9:A:2328:U:H2'	9:A:2329:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:55:U:H2'	11:D:56:U:C1'	2.46	0.46
15:J:79:LEU:HD12	15:J:83:MET:HB2	1.97	0.46
28:X:23:VAL:HG13	28:X:33:VAL:CG2	2.45	0.46
9:A:1135:A:H2'	9:A:1136:U:O4'	2.15	0.46
9:A:1247:U:H3'	9:A:1248:G:H5'	1.98	0.46
9:A:2761:A:H2'	9:A:2762:A:O4'	2.16	0.46
20:P:34:LEU:HD11	20:P:129:THR:OG1	2.15	0.46
31:a:131:G:H5''	31:a:132:A:OP1	2.16	0.46
31:a:606:C:H2'	31:a:607:G:O4'	2.15	0.46
31:a:844:G:O2'	31:a:846:U:OP2	2.33	0.46
31:a:846:U:H4'	31:a:847:G:OP2	2.15	0.46
31:a:1480:U:C2'	31:a:1481:G:O5'	2.63	0.46
9:A:1494:A:H62	9:A:1501:G:H22	1.64	0.46
9:A:2653:G:OP1	17:M:100:ARG:NH1	2.49	0.46
9:A:2877:G:C2'	9:A:2878:A:OP2	2.64	0.46
22:R:67:THR:O	22:R:70:GLU:HG2	2.16	0.46
31:a:399:A:C2	31:a:400:A:C8	3.04	0.46
31:a:1299:C:H2'	31:a:1300:A:O4'	2.16	0.46
9:A:484:C:H2'	9:A:485:G:O4'	2.16	0.46
9:A:519:A:O2'	28:X:42:LYS:O	2.33	0.46
9:A:1033:C:O2'	9:A:1035:A:OP1	2.19	0.46
9:A:1574:G:H21	9:A:1585:A:H2	1.62	0.46
31:a:353:A:O2'	31:a:354:C:O4'	2.28	0.46
31:a:668:A:N3	39:i:107:SER:OG	2.46	0.46
31:a:1183:A:C2	31:a:1207:G:C4	3.04	0.46
40:j:114:LYS:NZ	40:j:118:LEU:O	2.47	0.46
47:q:6:ARG:HA	47:q:70:VAL:HG21	1.97	0.46
50:t:49:ILE:N	50:t:49:ILE:HD12	2.30	0.46
9:A:995:G:N2	9:A:999:A:OP2	2.45	0.46
9:A:2046:A:O2'	9:A:2048:G:OP2	2.25	0.46
9:A:2330:C:H2'	9:A:2331:G:O4'	2.15	0.46
31:a:458:A:C4	31:a:459:A:C8	3.04	0.46
44:n:15:VAL:HG13	44:n:34:LEU:HD11	1.98	0.46
9:A:1495:U:HO2'	9:A:1496:U:H3'	1.81	0.46
9:A:2076:C:O2	9:A:2463:A:N1	2.49	0.46
9:A:2089:U:O2	9:A:2089:U:O4'	2.34	0.46
27:W:56:LEU:HD12	27:W:56:LEU:N	2.31	0.46
29:Y:81:LYS:N	29:Y:85:LYS:O	2.41	0.46
34:d:194:LYS:C	34:d:195:LEU:HD12	2.41	0.46
4:4:3:VAL:HG12	9:A:2028:A:C2	2.51	0.45
31:a:391:U:H5'	31:a:392:C:OP1	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:780:G:H2'	9:A:781:U:O4'	2.16	0.45
9:A:2809:U:H2'	9:A:2810:U:N1	2.31	0.45
31:a:35:A:N3	43:m:42:GLN:NE2	2.58	0.45
31:a:741:A:H2'	31:a:742:A:C8	2.52	0.45
31:a:1241:G:C2	31:a:1242:A:C8	3.05	0.45
45:o:14:ALA:HB1	45:o:19:GLN:HB2	1.98	0.45
9:A:244:G:O2'	9:A:245:U:OP2	2.31	0.45
9:A:1376:U:OP1	9:A:1432:U:N3	2.42	0.45
9:A:1536:A:H2'	9:A:1537:A:C8	2.52	0.45
9:A:2860:A:P	9:A:2876:G:H22	2.39	0.45
31:a:37:G:O2'	43:m:128:SER:O	2.20	0.45
31:a:131:G:H1'	31:a:132:A:N7	2.31	0.45
31:a:865:G:O2'	31:a:866:G:OP1	2.34	0.45
34:d:8:ILE:O	34:d:12:VAL:HG23	2.15	0.45
34:d:39:ARG:NH1	34:d:54:ILE:O	2.47	0.45
36:f:11:LEU:HB3	36:f:39:VAL:HG22	1.99	0.45
9:A:231:U:O2'	9:A:232:U:P	2.74	0.45
9:A:1279:U:O2'	19:O:6:LEU:O	2.32	0.45
15:J:78:ARG:C	15:J:79:LEU:HD13	2.41	0.45
31:a:171:A:C6	31:a:185:G:C6	3.05	0.45
31:a:873:C:C2	31:a:874:C:C5	3.04	0.45
31:a:1322:C:H4'	31:a:1328:U:O4	2.16	0.45
34:d:50:ALA:C	34:d:69:THR:HG23	2.41	0.45
42:l:46:SER:O	42:l:49:SER:OG	2.31	0.45
50:t:39:THR:HG22	50:t:40:ILE:N	2.31	0.45
6:6:14:LYS:NZ	9:A:810:G:OP1	2.47	0.45
9:A:871:G:H2'	9:A:872:C:C6	2.52	0.45
24:T:24:TYR:O	24:T:29:HIS:ND1	2.45	0.45
31:a:952:G:C2	31:a:954:G:C8	3.05	0.45
43:m:95:LEU:HD22	43:m:95:LEU:N	2.32	0.45
48:r:61:ILE:O	48:r:82:VAL:N	2.49	0.45
9:A:1123:A:C2	9:A:1145:A:H1'	2.51	0.45
9:A:2304:U:H2'	9:A:2305:U:C6	2.52	0.45
17:M:70:ALA:O	17:M:91:GLY:N	2.48	0.45
20:P:17:MET:HE1	20:P:40:HIS:HA	1.99	0.45
31:a:1313:A:H2'	31:a:1314:A:C8	2.51	0.45
31:a:1341:U:H2'	31:a:1342:G:O4'	2.16	0.45
31:a:1376:A:H2'	31:a:1377:U:O4'	2.17	0.45
31:a:1477:U:N3	31:a:1478:U:O3'	2.50	0.45
37:g:68:VAL:HG22	37:g:69:THR:N	2.32	0.45
9:A:1233:C:C2	9:A:1234:G:C8	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1395:G:N7	9:A:1396:G:C8	2.85	0.45
9:A:1395:G:C8	9:A:1396:G:C8	3.05	0.45
9:A:1758:G:O2'	9:A:1759:G:P	2.75	0.45
9:A:1803:C:H2'	9:A:1804:A:C8	2.52	0.45
9:A:2327:A:OP1	15:J:88:LYS:NZ	2.47	0.45
9:A:2811:A:C5	9:A:2813:G:C8	3.05	0.45
31:a:75:U:C2'	31:a:76:U:O5'	2.64	0.45
31:a:202:G:C5	31:a:203:U:C5	3.05	0.45
31:a:791:G:N1	31:a:838:G:O2'	2.41	0.45
31:a:1010:A:O2'	31:a:1227:A:N6	2.49	0.45
33:c:163:ILE:HD12	33:c:183:ILE:CG2	2.47	0.45
42:l:112:ASP:OD1	42:l:114:THR:HG23	2.16	0.45
9:A:1098:G:C8	9:A:1099:U:H2'	2.52	0.45
9:A:2333:A:N3	9:A:2333:A:H2'	2.32	0.45
16:K:157:TYR:O	16:K:171:ARG:NH2	2.50	0.45
31:a:335:G:O2'	31:a:633:A:N1	2.47	0.45
31:a:904:C:C2	31:a:905:U:C5	3.05	0.45
31:a:1149:U:H2'	31:a:1150:A:O4'	2.17	0.45
31:a:1355:A:C5	31:a:1356:U:C5	3.05	0.45
43:m:27:GLY:O	43:m:36:THR:N	2.49	0.45
44:n:24:GLY:C	44:n:25:ILE:HD12	2.42	0.45
9:A:2418:G:O2'	9:A:2424:A:N6	2.50	0.45
26:V:7:SER:CB	26:V:113:THR:HG22	2.46	0.45
26:V:77:SER:OG	26:V:113:THR:HG23	2.17	0.45
31:a:550:G:H2'	31:a:551:C:C6	2.52	0.45
31:a:865:G:HO2'	31:a:866:G:P	2.40	0.45
39:i:10:PHE:CZ	39:i:14:ILE:HD11	2.52	0.45
41:k:63:GLU:OE1	45:o:49:TYR:OH	2.27	0.45
9:A:590:U:H2'	9:A:591:G:O4'	2.17	0.45
9:A:846:U:O2'	9:A:2073:A:N1	2.48	0.45
9:A:1123:A:O2'	9:A:1124:A:N7	2.50	0.45
9:A:1803:C:C3'	9:A:1804:A:C8	3.00	0.45
9:A:2891:U:O2'	21:Q:105:THR:O	2.34	0.45
15:J:102:LYS:NZ	15:J:140:GLU:OE2	2.47	0.45
31:a:763:C:C2	31:a:764:U:C5	3.05	0.45
32:b:18:A:H2'	32:b:19:A:O4'	2.16	0.45
39:i:10:PHE:CE1	39:i:14:ILE:HD11	2.51	0.45
9:A:634:A:H2'	9:A:635:U:C6	2.51	0.44
9:A:708:G:N3	9:A:708:G:H2'	2.32	0.44
9:A:768:G:O2'	9:A:802:G:H4'	2.18	0.44
9:A:1136:U:C5	9:A:1137:A:C8	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1541:U:H2'	9:A:1542:U:O4'	2.17	0.44
11:D:57:C:C5	15:J:80:ARG:HD3	2.52	0.44
17:M:8:LYS:N	17:M:11:GLU:OE2	2.46	0.44
31:a:425:G:H2'	31:a:426:C:C6	2.52	0.44
31:a:627:G:C6	31:a:664:G:C6	3.05	0.44
31:a:1028:U:H3	31:a:1065:A:H61	1.64	0.44
31:a:1068:G:H2'	31:a:1069:U:C6	2.52	0.44
9:A:1061:G:O6	17:M:69:LYS:CE	2.66	0.44
9:A:1088:C:C2	9:A:1089:A:C8	3.04	0.44
9:A:2567:U:C2	9:A:2568:U:C5	3.04	0.44
9:A:2615:A:H4'	9:A:2616:G:H5'	1.99	0.44
9:A:2716:C:C2	9:A:2717:C:C5	3.05	0.44
9:A:2793:G:N2	17:M:103:GLU:OE2	2.48	0.44
31:a:60:C:H2'	31:a:60:C:O2	2.17	0.44
31:a:1122:U:OP1	31:a:1135:G:N2	2.47	0.44
31:a:1393:C:OP2	40:j:114:LYS:NZ	2.37	0.44
31:a:1438:C:H2'	31:a:1439:A:C8	2.52	0.44
33:c:163:ILE:HD12	33:c:183:ILE:HG21	1.99	0.44
42:l:16:ILE:HG22	42:l:17:GLU:N	2.32	0.44
6:6:1:MET:HE3	9:A:791:A:P	2.56	0.44
9:A:294:G:H2'	9:A:295:G:O5'	2.17	0.44
9:A:630:U:H2'	9:A:631:U:C6	2.53	0.44
9:A:754:A:C4	46:p:60:ILE:HD13	2.51	0.44
9:A:1083:A:O2'	9:A:1150:A:N1	2.51	0.44
9:A:1629:G:C6	9:A:1630:A:C5	3.05	0.44
28:X:60:GLU:OE1	28:X:60:GLU:N	2.46	0.44
31:a:652:G:OP1	47:q:19:ARG:NH1	2.48	0.44
31:a:1145:U:H2'	31:a:1146:U:O4'	2.16	0.44
31:a:1345:A:C8	31:a:1349:G:C6	3.05	0.44
9:A:309:G:O2'	9:A:310:A:P	2.75	0.44
9:A:403:G:N2	9:A:403:G:OP2	2.51	0.44
9:A:677:U:H2'	9:A:678:C:C6	2.53	0.44
9:A:1327:G:H2'	9:A:1328:U:C6	2.52	0.44
9:A:2008:U:O2	18:N:3:GLN:NE2	2.46	0.44
9:A:2272:G:C8	9:A:2440:C:C4	3.05	0.44
9:A:2275:U:OP2	29:Y:25:SER:OG	2.28	0.44
9:A:2369:C:H2'	9:A:2370:U:O4'	2.17	0.44
31:a:1352:U:H2'	31:a:1353:G:H8	1.82	0.44
33:c:33:THR:HG22	33:c:34:GLU:N	2.33	0.44
40:j:27:LYS:N	40:j:62:ASP:OD1	2.43	0.44
40:j:51:PRO:HA	40:j:54:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:33:U:HO2'	9:A:34:U:P	2.40	0.44
9:A:251:C:OP2	9:A:2407:C:O2'	2.29	0.44
9:A:311:U:O2	9:A:311:U:O4'	2.36	0.44
9:A:625:U:H2'	9:A:626:A:H8	1.81	0.44
9:A:867:U:H2'	9:A:868:A:C8	2.52	0.44
24:T:88:ILE:HG22	24:T:90:ILE:HG22	1.99	0.44
31:a:638:C:C2	31:a:639:C:C5	3.06	0.44
34:d:33:HIS:CE1	45:o:25:GLU:HB2	2.52	0.44
9:A:84:A:C2	9:A:102:A:C5	3.06	0.44
9:A:1466:G:H2'	9:A:1467:G:C8	2.52	0.44
9:A:1647:C:H2'	9:A:1648:G:O4'	2.18	0.44
9:A:2700:U:H2'	9:A:2701:G:O4'	2.17	0.44
11:D:54:G:H2'	11:D:55:U:C6	2.53	0.44
37:g:32:ILE:HD13	37:g:83:LEU:HD13	2.00	0.44
51:u:6:SER:O	51:u:10:ARG:HG2	2.17	0.44
9:A:280:A:H2'	9:A:281:A:O4'	2.18	0.44
9:A:902:G:H2'	9:A:903:A:O4'	2.17	0.44
9:A:927:U:H5'	9:A:928:C:OP1	2.17	0.44
9:A:1101:G:N1	9:A:1116:A:C2	2.86	0.44
9:A:1355:G:C2	9:A:1364:U:H5'	2.53	0.44
16:K:117:ALA:HB2	16:K:123:PHE:CZ	2.52	0.44
29:Y:65:ASP:CG	29:Y:67:THR:HG23	2.42	0.44
31:a:177:A:H2'	31:a:178:A:O4'	2.17	0.44
31:a:1003:G:P	31:a:1384:U:O2'	2.75	0.44
9:A:1180:U:OP2	17:M:66:THR:OG1	2.31	0.44
9:A:1713:U:O2'	9:A:1715:G:N7	2.45	0.44
9:A:1761:C:C2	9:A:1762:A:C8	3.05	0.44
9:A:1902:A:H2'	9:A:1903:A:O4'	2.18	0.44
9:A:2525:C:H2'	9:A:2526:G:O4'	2.18	0.44
10:B:43:A:O4'	15:J:92:ARG:NE	2.51	0.44
11:D:57:C:H5'	15:J:79:LEU:C	2.43	0.44
31:a:402:G:H5''	47:q:6:ARG:HB2	1.98	0.44
31:a:607:G:N1	31:a:785:A:OP2	2.48	0.44
31:a:967:C:H2'	31:a:968:G:O4'	2.17	0.44
31:a:1254:C:H4'	44:n:114:LYS:O	2.16	0.44
31:a:1476:U:H2'	31:a:1477:U:C6	2.53	0.44
9:A:1720:A:C4	9:A:1721:A:C8	3.06	0.44
17:M:5:TYR:O	24:T:64:ARG:NH1	2.50	0.44
31:a:607:G:N2	31:a:785:A:OP2	2.50	0.44
9:A:115:C:H2'	9:A:116:G:O4'	2.18	0.43
9:A:640:G:O6	9:A:663:G:C6	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1516:A:H2'	9:A:1517:U:O4'	2.18	0.43
9:A:1564:G:OP2	9:A:1565:A:C2'	2.66	0.43
2:2:8:LEU:O	2:2:32:ASN:N	2.45	0.43
9:A:280:A:N1	9:A:290:G:C6	2.86	0.43
9:A:852:U:O2'	9:A:1261:G:H1'	2.18	0.43
9:A:1712:C:H2'	9:A:1713:U:O4'	2.17	0.43
9:A:1804:A:C2	9:A:1842:A:H4'	2.53	0.43
9:A:1820:G:N2	9:A:1823:A:OP2	2.44	0.43
9:A:2387:C:N4	9:A:2388:G:O6	2.51	0.43
14:I:153:LEU:HB2	14:I:189:ALA:HB2	2.00	0.43
15:J:13:THR:HG23	15:J:28:THR:HG21	1.99	0.43
15:J:44:VAL:CG2	15:J:79:LEU:HD11	2.47	0.43
31:a:290:C:H2'	31:a:291:G:O4'	2.18	0.43
31:a:583:G:H2'	31:a:584:G:O4'	2.17	0.43
31:a:966:G:H21	31:a:1401:A:H2	1.65	0.43
31:a:1083:U:OP1	34:d:162:ALA:N	2.44	0.43
31:a:1554:C:H2'	31:a:1555:U:C6	2.53	0.43
44:n:97:THR:O	44:n:97:THR:HG22	2.17	0.43
9:A:1119:A:C2	9:A:1120:U:C5	3.05	0.43
14:I:123:LEU:C	14:I:123:LEU:HD13	2.44	0.43
15:J:136:LEU:HD22	15:J:143:TYR:HA	2.00	0.43
21:Q:80:ILE:HD12	21:Q:80:ILE:N	2.32	0.43
31:a:276:A:N6	31:a:301:G:O6	2.50	0.43
31:a:386:G:C6	31:a:387:G:C6	3.06	0.43
31:a:1005:A:C2	31:a:1345:A:N3	2.86	0.43
43:m:42:GLN:HB2	43:m:94:LEU:HD11	1.99	0.43
9:A:609:G:N1	9:A:2044:A:OP1	2.45	0.43
9:A:844:G:N2	9:A:868:A:OP1	2.51	0.43
9:A:852:U:H2'	9:A:853:C:C6	2.52	0.43
9:A:2116:A:C2	9:A:2200:A:C2	3.07	0.43
11:D:57:C:O2'	15:J:78:ARG:HA	2.17	0.43
17:M:18:VAL:HG23	17:M:138:PRO:HB2	2.01	0.43
29:Y:57:GLY:N	29:Y:88:VAL:O	2.49	0.43
31:a:227:A:HO2'	31:a:228:A:C4'	2.28	0.43
31:a:636:G:C2	31:a:637:C:C6	3.07	0.43
31:a:987:U:O2'	31:a:1249:C:H4'	2.18	0.43
31:a:1356:U:H2'	31:a:1357:G:O4'	2.18	0.43
31:a:1397:G:C6	31:a:1398:U:C4	3.07	0.43
39:i:19:MET:O	39:i:72:ARG:NH2	2.50	0.43
9:A:639:A:N1	9:A:663:G:O2'	2.46	0.43
9:A:807:G:N2	9:A:1414:U:O2'	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1422:A:C6	9:A:1436:G:N1	2.86	0.43
9:A:2841:G:O2'	9:A:2894:U:OP1	2.30	0.43
11:D:63:C:H2'	11:D:64:U:C6	2.54	0.43
31:a:971:G:N1	31:a:1364:G:OP2	2.48	0.43
33:c:71:GLY:O	33:c:93:ASN:HA	2.19	0.43
33:c:130:PRO:HD2	33:c:133:GLU:HB2	1.99	0.43
35:e:143:ARG:NH2	35:e:146:SER:OG	2.47	0.43
9:A:230:A:H3'	9:A:231:U:O4'	2.19	0.43
9:A:643:U:C5	9:A:658:G:C5	3.07	0.43
9:A:1879:A:C6	9:A:1889:A:N7	2.87	0.43
9:A:2304:U:C2	9:A:2305:U:C5	3.07	0.43
9:A:2527:U:H2'	9:A:2528:C:C6	2.54	0.43
9:A:2638:G:H2'	9:A:2639:C:C6	2.53	0.43
18:N:105:GLU:O	18:N:109:ASN:ND2	2.43	0.43
31:a:501:U:C2	31:a:502:C:C5	3.07	0.43
31:a:993:G:O2'	40:j:129:LYS:O	2.36	0.43
31:a:1087:U:H2'	31:a:1088:G:H8	1.83	0.43
31:a:1345:A:C8	31:a:1349:G:C5	3.07	0.43
31:a:1353:G:H2'	31:a:1354:C:H6	1.83	0.43
31:a:1548:G:H2'	31:a:1549:U:O4'	2.19	0.43
6:6:13:GLN:NE2	6:6:44:ALA:O	2.51	0.43
9:A:421:A:C2	9:A:432:U:C2	3.06	0.43
9:A:724:A:C8	9:A:812:U:C4	3.06	0.43
9:A:1017:G:O4'	9:A:1040:A:H2	2.02	0.43
9:A:1086:G:O2'	9:A:1087:A:OP2	2.35	0.43
9:A:1165:A:H4'	9:A:1166:A:C5'	2.49	0.43
9:A:1583:G:HO2'	9:A:1584:U:P	2.41	0.43
18:N:64:ARG:HB2	18:N:79:PHE:CG	2.54	0.43
21:Q:52:LYS:NZ	21:Q:104:TYR:OH	2.40	0.43
27:W:84:GLU:O	27:W:85:ASP:HB2	2.18	0.43
28:X:23:VAL:HG13	28:X:33:VAL:HG23	2.01	0.43
31:a:1165:G:H1'	31:a:1166:U:OP2	2.19	0.43
31:a:1204:G:N2	31:a:1206:A:H3'	2.32	0.43
9:A:625:U:OP1	19:O:16:ARG:NH2	2.47	0.43
9:A:1116:A:H2'	9:A:1117:C:O4'	2.18	0.43
9:A:1799:A:H1'	9:A:1951:A:N6	2.34	0.43
9:A:2526:G:H2'	9:A:2527:U:C6	2.53	0.43
21:Q:40:VAL:O	21:Q:44:VAL:HG12	2.18	0.43
31:a:547:G:N7	43:m:63:ARG:NH1	2.62	0.43
31:a:1228:U:C2	45:o:42:ILE:HG21	2.53	0.43
32:b:5:G:H2'	32:b:6:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:8:7:VAL:HG23	8:8:7:VAL:O	2.18	0.43
9:A:1287:A:OP1	24:T:10:THR:OG1	2.31	0.43
9:A:2392:G:H2'	9:A:2393:U:C6	2.54	0.43
9:A:2770:A:N1	16:K:67:THR:OG1	2.50	0.43
31:a:195:C:C2	31:a:196:A:C8	3.07	0.43
31:a:636:G:C6	31:a:637:C:C5	3.07	0.43
31:a:949:G:H2'	31:a:950:A:C8	2.54	0.43
33:c:129:LEU:HD12	33:c:129:LEU:HA	1.82	0.43
6:6:30:VAL:O	6:6:34:ARG:HG2	2.19	0.43
9:A:83:G:OP1	28:X:90:LYS:NZ	2.50	0.43
9:A:572:U:O2'	24:T:49:ASP:OD2	2.07	0.43
9:A:723:G:C6	9:A:813:A:C4	3.06	0.43
9:A:799:G:H2'	9:A:800:A:O4'	2.19	0.43
9:A:1241:G:H2'	9:A:1242:G:O4'	2.19	0.43
9:A:1876:G:H4'	9:A:2424:A:H4'	2.00	0.43
20:P:127:VAL:HG12	20:P:128:LYS:O	2.19	0.43
31:a:400:A:C6	31:a:401:U:C4	3.07	0.43
31:a:637:C:O2	31:a:637:C:H2'	2.17	0.43
31:a:1330:G:N1	31:a:1358:A:OP2	2.50	0.43
34:d:93:LEU:C	34:d:93:LEU:HD13	2.44	0.43
9:A:852:U:O5'	19:O:24:SER:OG	2.37	0.42
9:A:950:A:N3	9:A:2277:C:O2'	2.46	0.42
9:A:951:A:N6	20:P:11:ARG:O	2.49	0.42
9:A:1005:G:C1'	9:A:2280:A:H62	2.31	0.42
9:A:2636:G:OP1	9:A:2836:A:O2'	2.19	0.42
12:G:29:PRO:HB2	12:G:34:LEU:HD21	1.99	0.42
20:P:64:VAL:HG22	20:P:106:ILE:HG22	2.00	0.42
31:a:381:C:O2'	31:a:414:G:N3	2.40	0.42
31:a:486:G:C6	31:a:500:G:C6	3.07	0.42
31:a:498:A:HO2'	47:q:84:HIS:CE1	2.27	0.42
31:a:1046:G:N1	31:a:1047:A:C5	2.87	0.42
9:A:18:C:O2'	9:A:590:U:OP1	2.32	0.42
9:A:238:C:C2	9:A:239:C:C5	3.07	0.42
9:A:271:C:O2	9:A:271:C:H2'	2.19	0.42
9:A:1122:U:H2'	9:A:1123:A:O2'	2.18	0.42
9:A:1445:G:H2'	9:A:1446:U:H6	1.85	0.42
9:A:2814:A:O2'	9:A:2815:A:H5'	2.19	0.42
13:H:54:GLN:O	13:H:55:ASP:C	2.62	0.42
31:a:1549:U:H2'	31:a:1550:G:H8	1.84	0.42
33:c:42:ASP:OD2	33:c:45:LYS:NZ	2.49	0.42
33:c:129:LEU:HB3	33:c:134:VAL:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:113:LYS:NZ	34:d:117:GLU:OE2	2.45	0.42
42:l:118:HIS:O	42:l:119:ASN:HB2	2.19	0.42
44:n:3:ARG:O	44:n:57:ARG:NH2	2.52	0.42
9:A:346:A:O2'	9:A:347:A:OP2	2.29	0.42
9:A:368:A:C2	9:A:371:C:C5	3.07	0.42
9:A:504:G:H2'	9:A:505:A:C8	2.53	0.42
9:A:1451:G:N2	9:A:1629:G:C4	2.87	0.42
9:A:1507:G:H2'	9:A:1508:U:O4'	2.19	0.42
9:A:1724:A:H2'	9:A:1725:C:C6	2.54	0.42
9:A:1814:A:H3'	9:A:1815:A:H5'	2.01	0.42
9:A:1884:C:O2	9:A:1884:C:H3'	2.19	0.42
9:A:2005:G:C1'	9:A:2007:C:H41	2.32	0.42
9:A:2517:U:O2	9:A:2517:U:O4'	2.36	0.42
9:A:2534:C:H2'	9:A:2535:U:O4'	2.18	0.42
12:G:129:ALA:C	12:G:130:LEU:HD12	2.44	0.42
31:a:361:C:C2	31:a:362:A:C8	3.07	0.42
31:a:1097:U:H2'	31:a:1098:C:C6	2.55	0.42
6:6:1:MET:HE3	9:A:791:A:OP2	2.19	0.42
9:A:74:U:H5''	9:A:75:G:O4'	2.19	0.42
9:A:333:U:H2'	9:A:334:G:O4'	2.19	0.42
9:A:690:A:H2'	9:A:691:A:O4'	2.19	0.42
9:A:1752:G:C6	9:A:1762:A:C6	3.07	0.42
9:A:1825:A:HO2'	12:G:45:ASN:H	1.65	0.42
9:A:2077:C:H2'	9:A:2078:C:H6	1.84	0.42
13:H:14:GLN:HB2	13:H:22:LEU:HD11	2.01	0.42
14:I:113:VAL:HG11	14:I:183:VAL:HG13	2.01	0.42
31:a:36:C:H2'	31:a:37:G:H8	1.84	0.42
31:a:349:U:H2'	31:a:350:G:O4'	2.19	0.42
31:a:713:A:N7	31:a:727:U:C4	2.88	0.42
35:e:92:GLU:OE2	35:e:186:LEU:HD22	2.19	0.42
36:f:20:ARG:HD3	36:f:31:LEU:HD23	2.01	0.42
42:l:71:THR:HG23	42:l:105:LEU:CD1	2.49	0.42
9:A:950:A:H2'	9:A:951:A:C8	2.54	0.42
9:A:1560:U:C2	9:A:1561:U:C5	3.07	0.42
9:A:1583:G:C2'	9:A:1584:U:OP2	2.67	0.42
9:A:2077:C:H2'	9:A:2078:C:C6	2.54	0.42
9:A:2877:G:O2'	9:A:2878:A:H8	2.03	0.42
11:D:52:A:C6	11:D:65:G:C6	3.08	0.42
11:D:57:C:O4'	15:J:80:ARG:N	2.52	0.42
24:T:66:ASN:O	24:T:70:ARG:HG2	2.19	0.42
31:a:9:G:HO2'	31:a:10:A:P	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:122:C:H2'	31:a:123:G:O4'	2.19	0.42
31:a:902:C:C4	31:a:903:A:N7	2.87	0.42
31:a:1300:A:H2'	31:a:1301:U:C6	2.54	0.42
31:a:1431:G:O2'	31:a:1545:A:O2'	2.34	0.42
50:t:20:GLU:HA	50:t:23:GLN:HG2	2.01	0.42
50:t:48:THR:C	50:t:49:ILE:HD12	2.44	0.42
9:A:9:G:O2'	9:A:2812:A:N6	2.52	0.42
9:A:177:G:O2'	9:A:178:A:H5'	2.20	0.42
9:A:293:G:N3	9:A:294:G:C8	2.87	0.42
9:A:1137:A:C4	9:A:1138:G:C8	3.07	0.42
9:A:1619:C:C2	9:A:1620:U:C5	3.06	0.42
9:A:2087:U:H2'	9:A:2088:U:C6	2.53	0.42
9:A:2110:G:C2	9:A:2206:C:C2	3.08	0.42
9:A:2872:A:C2	9:A:2873:G:C5	3.07	0.42
10:B:29:C:C2	10:B:30:U:C5	3.07	0.42
10:B:58:C:H2'	10:B:59:U:C6	2.55	0.42
11:D:27:G:C2	11:D:28:U:C6	3.07	0.42
31:a:493:A:H2'	31:a:494:C:O4'	2.20	0.42
6:6:1:MET:CE	9:A:791:A:OP2	2.67	0.42
9:A:606:G:H2'	9:A:2043:A:N7	2.35	0.42
9:A:808:U:HO2'	9:A:1414:U:H6	1.64	0.42
9:A:898:G:OP2	29:Y:86:LYS:NZ	2.52	0.42
9:A:2088:U:OP2	9:A:2251:G:O2'	2.24	0.42
31:a:1053:C:C2	31:a:1063:A:C2	3.08	0.42
31:a:1268:G:C4	31:a:1269:G:C8	3.08	0.42
31:a:1353:G:C4	31:a:1354:C:C5	3.07	0.42
9:A:1086:G:HO2'	9:A:1087:A:P	2.43	0.42
9:A:1319:A:H2'	9:A:1320:G:O4'	2.20	0.42
9:A:1710:A:N3	9:A:1712:C:C4	2.87	0.42
9:A:2008:U:H3'	9:A:2009:C:H2'	2.02	0.42
11:D:17:C:H3'	11:D:18:A:H2'	2.01	0.42
22:R:56:ALA:HB3	22:R:79:VAL:HB	2.02	0.42
31:a:571:C:H2'	31:a:572:A:O4'	2.20	0.42
31:a:908:G:H2'	31:a:909:C:O4'	2.20	0.42
31:a:1039:A:N6	31:a:1045:A:N6	2.67	0.42
31:a:1092:U:HO2'	31:a:1093:C:P	2.41	0.42
31:a:1266:U:O4	38:h:109:ARG:NE	2.53	0.42
31:a:1477:U:C2	31:a:1478:U:O3'	2.72	0.42
35:e:163:PRO:HD2	35:e:166:VAL:HG11	2.02	0.42
9:A:334:G:O2'	9:A:376:A:N6	2.53	0.42
9:A:986:A:H2'	9:A:987:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1536:A:HO2'	9:A:1537:A:P	2.43	0.42
9:A:2106:G:O2'	9:A:2211:A:N1	2.35	0.42
10:B:56:A:C4	10:B:57:G:C8	3.08	0.42
22:R:80:ALA:HB2	22:R:111:ALA:HA	2.02	0.42
31:a:203:U:C2	31:a:204:U:C5	3.08	0.42
33:c:162:TYR:HA	33:c:184:VAL:O	2.20	0.42
38:h:52:GLU:OE1	38:h:53:SER:N	2.52	0.42
43:m:110:ILE:CG2	43:m:117:THR:HG21	2.50	0.42
9:A:193:A:H2'	9:A:194:C:C6	2.55	0.42
9:A:693:G:N3	9:A:693:G:H2'	2.35	0.42
9:A:2860:A:N7	9:A:2878:A:O2'	2.53	0.42
31:a:925:G:N2	31:a:928:A:OP2	2.43	0.42
36:f:13:ASP:OD2	36:f:64:ILE:HD11	2.20	0.42
48:r:65:MET:HE3	48:r:79:LEU:HD21	2.01	0.42
9:A:390:C:H2'	9:A:391:A:C8	2.55	0.41
9:A:1075:G:C6	9:A:1159:G:C6	3.08	0.41
9:A:2327:A:H1'	15:J:155:VAL:HG11	2.02	0.41
10:B:11:A:N1	10:B:67:G:O2'	2.35	0.41
22:R:107:LEU:HD23	22:R:107:LEU:C	2.45	0.41
31:a:197:U:O2'	31:a:198:A:H5'	2.20	0.41
31:a:580:U:H2'	31:a:581:C:C6	2.55	0.41
34:d:205:GLU:OE1	34:d:205:GLU:N	2.41	0.41
9:A:33:U:O4	9:A:485:G:O2'	2.27	0.41
9:A:75:G:H22	9:A:110:A:H2	1.65	0.41
9:A:429:A:O2'	9:A:430:A:C8	2.70	0.41
9:A:768:G:OP1	12:G:10:THR:OG1	2.31	0.41
9:A:1420:A:C4	9:A:1438:A:C2	3.08	0.41
13:H:31:THR:O	13:H:32:PRO:C	2.62	0.41
14:I:157:GLU:OE1	14:I:157:GLU:N	2.43	0.41
31:a:281:G:OP1	48:r:74:LYS:NZ	2.51	0.41
31:a:488:U:H2'	31:a:489:A:C8	2.55	0.41
31:a:805:C:H2'	31:a:806:A:O4'	2.19	0.41
31:a:1035:C:O2'	31:a:1036:U:OP1	2.35	0.41
31:a:1564:U:H2'	31:a:1565:C:C6	2.55	0.41
39:i:64:LEU:N	39:i:64:LEU:HD22	2.35	0.41
44:n:16:VAL:CG1	44:n:34:LEU:HD12	2.49	0.41
9:A:921:G:C6	9:A:922:G:O6	2.73	0.41
9:A:1189:U:O2'	9:A:1190:A:P	2.77	0.41
9:A:1615:A:H2'	9:A:1616:A:C8	2.55	0.41
9:A:2073:A:O2'	9:A:2074:G:OP2	2.34	0.41
9:A:2558:G:H2'	9:A:2559:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2658:G:H4'	9:A:2745:G:O2'	2.20	0.41
22:R:63:ILE:CD1	22:R:75:VAL:HG22	2.51	0.41
31:a:34:A:H2'	31:a:35:A:C8	2.55	0.41
31:a:963:C:C4	31:a:964:A:N7	2.88	0.41
31:a:1146:U:H2'	31:a:1147:G:C8	2.56	0.41
31:a:1301:U:H2'	31:a:1302:G:C8	2.55	0.41
42:l:50:LEU:HD11	42:l:66:ALA:HA	2.02	0.41
9:A:214:C:H2'	9:A:215:A:O4'	2.20	0.41
9:A:424:C:O2'	9:A:427:G:N2	2.52	0.41
9:A:572:U:H2'	9:A:573:C:C6	2.56	0.41
9:A:856:C:O2'	9:A:878:U:H5''	2.20	0.41
9:A:1235:U:H2'	9:A:1236:U:C6	2.56	0.41
9:A:1566:C:O2'	9:A:1567:G:OP1	2.37	0.41
9:A:1884:C:O2	9:A:1885:G:O4'	2.39	0.41
9:A:1936:U:H2'	9:A:1937:C:C6	2.54	0.41
15:J:73:SER:OG	15:J:81:GLU:N	2.53	0.41
31:a:17:G:O2'	36:f:22:THR:HG21	2.20	0.41
31:a:161:G:H2'	31:a:162:G:O4'	2.21	0.41
31:a:938:U:H2'	31:a:939:C:C6	2.55	0.41
31:a:1007:C:H2'	31:a:1008:U:O4'	2.19	0.41
9:A:36:G:N3	9:A:489:G:O2'	2.53	0.41
9:A:940:A:C4	9:A:941:A:C8	3.07	0.41
9:A:2111:U:HO2'	9:A:2112:U:P	2.43	0.41
11:D:44:A:H2'	11:D:45:A:C8	2.55	0.41
13:H:53:TYR:CG	13:H:54:GLN:N	2.88	0.41
15:J:6:GLU:HA	15:J:9:ILE:HG22	2.02	0.41
31:a:430:G:OP2	35:e:112:ARG:NH2	2.50	0.41
31:a:699:G:H2'	31:a:700:G:H8	1.84	0.41
31:a:917:G:O2'	31:a:933:G:O6	2.30	0.41
31:a:1087:U:O2'	41:k:54:ALA:HB2	2.20	0.41
31:a:1460:A:H2'	31:a:1461:G:O4'	2.20	0.41
37:g:32:ILE:HD13	37:g:83:LEU:CD1	2.50	0.41
44:n:16:VAL:HG23	44:n:17:VAL:N	2.35	0.41
9:A:295:G:H2'	9:A:296:G:C8	2.55	0.41
9:A:1024:C:C2	9:A:1025:C:C5	3.08	0.41
9:A:1104:U:O2	9:A:1113:G:O6	2.39	0.41
9:A:1254:C:OP2	24:T:15:LYS:NZ	2.42	0.41
9:A:1792:U:H5	9:A:1797:A:N7	2.18	0.41
9:A:2221:A:H2'	9:A:2222:C:C6	2.55	0.41
9:A:2299:A:H4'	9:A:2300:A:O4'	2.19	0.41
9:A:2857:U:H2'	9:A:2858:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:V:88:LYS:O	26:V:89:ARG:NH1	2.47	0.41
31:a:1134:C:OP1	34:d:171:THR:HG23	2.19	0.41
31:a:1183:A:C5	31:a:1206:A:C6	3.08	0.41
31:a:1346:C:H2'	31:a:1347:U:C6	2.55	0.41
31:a:1456:C:H2'	31:a:1457:C:O4'	2.21	0.41
37:g:9:ILE:HG21	37:g:80:PHE:CE1	2.56	0.41
9:A:1008:G:H2'	9:A:1009:U:C6	2.56	0.41
9:A:1069:G:C6	9:A:1164:G:N2	2.89	0.41
9:A:1288:G:N2	24:T:37:GLU:OE2	2.43	0.41
9:A:1536:A:O2'	9:A:1537:A:O5'	2.39	0.41
9:A:1548:U:H2'	9:A:1549:U:O4'	2.21	0.41
9:A:2473:U:C2	9:A:2474:C:C6	3.09	0.41
18:N:24:VAL:HG13	18:N:33:ALA:HB2	2.02	0.41
31:a:69:C:O2'	31:a:188:A:H1'	2.21	0.41
31:a:591:U:OP2	31:a:592:G:O2'	2.33	0.41
31:a:1074:G:O2'	31:a:1241:G:O2'	2.34	0.41
9:A:55:G:O2'	9:A:126:A:N1	2.44	0.41
9:A:603:U:OP1	19:O:35:GLN:NE2	2.39	0.41
9:A:1103:C:C5	9:A:1104:U:C4	3.08	0.41
9:A:1809:U:H2'	9:A:1810:C:C6	2.55	0.41
9:A:1965:A:N3	9:A:2573:C:O2'	2.46	0.41
9:A:2311:A:H2'	9:A:2312:G:O4'	2.21	0.41
9:A:2325:U:N3	9:A:2326:C:C5	2.88	0.41
9:A:2570:G:H2'	9:A:2571:C:C6	2.55	0.41
11:D:62:C:O2	11:D:62:C:H2'	2.21	0.41
14:I:26:ILE:HD13	14:I:111:LYS:HB3	2.02	0.41
15:J:43:ALA:HB2	15:J:50:LEU:HB2	2.02	0.41
18:N:97:ARG:NE	31:a:365:C:OP2	2.53	0.41
31:a:348:C:O2'	51:u:18:ASN:HB2	2.21	0.41
31:a:517:A:H2'	31:a:518:A:H8	1.85	0.41
31:a:693:G:OP1	31:a:758:C:O2'	2.35	0.41
42:l:88:GLY:N	42:l:114:THR:HG22	2.35	0.41
43:m:42:GLN:CB	43:m:94:LEU:HD11	2.50	0.41
7:7:23:LYS:NZ	9:A:668:G:OP1	2.36	0.41
9:A:89:U:OP2	9:A:90:A:O2'	2.30	0.41
9:A:132:U:N3	9:A:133:A:N7	2.69	0.41
9:A:182:A:H5'	9:A:474:C:O2'	2.20	0.41
9:A:486:A:C4	9:A:512:G:N7	2.89	0.41
9:A:608:A:H5''	9:A:609:G:OP2	2.21	0.41
9:A:612:U:H2'	9:A:613:G:C8	2.56	0.41
9:A:615:A:H2'	9:A:616:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:846:U:C2	9:A:847:G:C8	3.09	0.41
9:A:864:C:H2'	9:A:865:U:O4'	2.21	0.41
9:A:1030:C:C5	9:A:1222:U:C4	3.09	0.41
9:A:1117:C:H4'	9:A:1118:C:O5'	2.21	0.41
9:A:1122:U:H2'	9:A:1123:A:C2'	2.51	0.41
9:A:1145:A:C4	9:A:1146:G:C8	3.09	0.41
9:A:1350:C:O2'	9:A:1427:G:H1'	2.20	0.41
9:A:1429:U:H2'	9:A:1430:A:O4'	2.21	0.41
9:A:1576:A:H2'	9:A:1577:A:C8	2.56	0.41
9:A:1583:G:O2'	9:A:1584:U:O5'	2.36	0.41
9:A:1718:A:H2'	9:A:1719:A:O4'	2.21	0.41
9:A:1853:G:C6	9:A:1854:U:C4	3.09	0.41
9:A:2105:U:H4'	9:A:2106:G:H5'	2.03	0.41
9:A:2810:U:H1'	9:A:2811:A:OP2	2.21	0.41
15:J:80:ARG:O	15:J:81:GLU:C	2.63	0.41
31:a:24:G:O2'	31:a:940:A:N1	2.49	0.41
31:a:159:G:H2'	31:a:160:A:O4'	2.21	0.41
31:a:223:A:C2	31:a:224:G:C5	3.09	0.41
31:a:241:G:H2'	31:a:242:U:O4'	2.20	0.41
31:a:529:A:O2'	31:a:536:A:N1	2.50	0.41
31:a:630:G:C6	31:a:661:A:C6	3.09	0.41
31:a:668:A:N7	39:i:109:SER:HA	2.36	0.41
31:a:963:C:C2	31:a:964:A:C8	3.09	0.41
31:a:1040:G:N2	31:a:1043:A:OP2	2.40	0.41
31:a:1359:A:H2'	31:a:1360:G:O4'	2.20	0.41
31:a:1551:C:C2	31:a:1552:G:C8	3.09	0.41
33:c:96:TRP:NE1	33:c:175:GLU:OE2	2.48	0.41
35:e:108:ARG:NH1	35:e:187:TYR:OH	2.48	0.41
3:3:1:MET:N	10:B:38:U:O4	2.43	0.41
8:8:2:LYS:NZ	9:A:2491:A:OP2	2.44	0.41
9:A:22:C:C2	9:A:23:G:C8	3.09	0.41
9:A:335:A:N3	9:A:355:U:O2'	2.49	0.41
9:A:548:C:C2	9:A:549:U:C6	3.09	0.41
9:A:856:C:O2'	9:A:878:U:OP1	2.39	0.41
9:A:1105:U:C4	9:A:1108:A:OP2	2.74	0.41
9:A:1328:U:H2'	9:A:1329:C:C6	2.56	0.41
14:I:32:VAL:HG12	14:I:109:ALA:HB2	2.03	0.41
31:a:290:C:O2	48:r:69:PRO:HG2	2.21	0.41
31:a:430:G:O2'	31:a:524:A:N1	2.45	0.41
31:a:1244:C:H2'	31:a:1245:U:C6	2.56	0.41
31:a:1516:G:H2'	31:a:1517:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:122:GLN:NE2	34:d:135:GLN:OE1	2.48	0.41
40:j:6:TYR:CD2	40:j:90:VAL:HG22	2.56	0.41
9:A:92:G:H2'	9:A:93:U:C6	2.56	0.40
9:A:194:C:O2'	9:A:841:A:N3	2.48	0.40
9:A:231:U:H4'	9:A:231:U:OP1	2.21	0.40
9:A:472:C:O2'	9:A:473:U:H5'	2.21	0.40
9:A:1543:U:OP1	12:G:79:LYS:CE	2.70	0.40
9:A:1680:C:O2	9:A:2711:U:O2'	2.37	0.40
9:A:1698:C:C2	9:A:1699:U:C5	3.09	0.40
9:A:2560:U:C2	9:A:2561:G:N7	2.89	0.40
9:A:2694:C:C2	9:A:2737:U:O4	2.74	0.40
11:D:58:A:N7	15:J:80:ARG:CZ	2.83	0.40
24:T:35:ALA:O	24:T:39:VAL:HG23	2.20	0.40
31:a:276:A:O4'	31:a:278:U:C6	2.74	0.40
31:a:947:U:H2'	31:a:948:U:C6	2.56	0.40
31:a:1126:G:H2'	31:a:1127:C:O4'	2.21	0.40
31:a:1127:C:N4	31:a:1130:C:OP1	2.54	0.40
31:a:1146:U:H2'	31:a:1147:G:H8	1.86	0.40
9:A:59:G:H1'	9:A:73:A:H2'	2.02	0.40
9:A:84:A:O3'	9:A:85:G:O4'	2.38	0.40
9:A:471:A:C6	9:A:472:C:C4	3.09	0.40
9:A:1153:G:O2'	9:A:1154:A:H5'	2.20	0.40
9:A:1310:A:H4'	9:A:1311:G:OP1	2.21	0.40
9:A:1804:A:C2	9:A:1842:A:C4'	3.04	0.40
9:A:2638:G:H2'	9:A:2639:C:O4'	2.22	0.40
15:J:74:ILE:HG21	15:J:77:PHE:CD2	2.56	0.40
25:U:80:LYS:O	25:U:81:HIS:C	2.63	0.40
31:a:713:A:C2	31:a:730:A:C5	3.09	0.40
31:a:1035:C:HO2'	31:a:1036:U:P	2.44	0.40
35:e:119:HIS:C	35:e:120:ILE:HD12	2.46	0.40
40:j:99:LYS:O	40:j:102:GLY:N	2.51	0.40
50:t:36:ARG:NH2	50:t:72:GLY:O	2.54	0.40
7:7:48:SER:OG	7:7:49:MET:N	2.49	0.40
9:A:207:G:O2'	9:A:208:U:OP2	2.39	0.40
9:A:616:C:H4'	24:T:31:LEU:HD13	2.03	0.40
9:A:621:G:N1	9:A:1289:A:OP2	2.42	0.40
9:A:743:G:C2	9:A:765:G:C4	3.09	0.40
9:A:871:G:C6	9:A:872:C:N4	2.89	0.40
9:A:1350:C:O2'	9:A:1427:G:N3	2.49	0.40
9:A:1758:G:H2'	9:A:1758:G:N3	2.36	0.40
9:A:2318:U:H2'	9:A:2319:U:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2425:A:H2'	9:A:2426:G:O4'	2.21	0.40
31:a:202:G:C6	31:a:203:U:C4	3.09	0.40
31:a:285:G:OP1	51:u:77:ARG:HD2	2.22	0.40
31:a:870:C:H2'	31:a:871:C:O4'	2.22	0.40
31:a:1013:A:H2'	31:a:1014:G:O4'	2.21	0.40
9:A:18:C:OP1	24:T:26:GLY:N	2.50	0.40
9:A:1058:U:O2'	9:A:1060:A:N7	2.52	0.40
9:A:1101:G:C6	9:A:1102:G:C5	3.10	0.40
9:A:1913:A:O2'	9:A:1914:A:OP1	2.33	0.40
9:A:2051:G:H2'	9:A:2052:G:O4'	2.21	0.40
9:A:2566:G:O4'	9:A:2595:G:O2'	2.33	0.40
15:J:8:TYR:HA	15:J:12:VAL:HB	2.03	0.40
20:P:36:ALA:HB1	20:P:127:VAL:HG11	2.02	0.40
22:R:92:VAL:HG13	22:R:92:VAL:O	2.22	0.40
31:a:38:C:H2'	31:a:39:U:O4'	2.21	0.40
31:a:246:G:C2	31:a:247:C:C6	3.10	0.40
31:a:858:G:C6	31:a:882:G:C5	3.10	0.40
31:a:1065:A:C8	31:a:1066:A:C8	3.10	0.40
31:a:1197:A:H2'	31:a:1198:C:C6	2.57	0.40
9:A:5:A:H2'	9:A:6:A:C8	2.56	0.40
9:A:21:A:O2'	9:A:22:C:H5'	2.20	0.40
9:A:36:G:C6	9:A:484:C:N4	2.90	0.40
9:A:225:A:N1	9:A:446:C:O2'	2.40	0.40
9:A:438:G:H2'	9:A:439:G:O4'	2.21	0.40
9:A:555:C:O2'	26:V:23:ARG:NH2	2.54	0.40
9:A:771:C:H2'	9:A:772:G:O4'	2.21	0.40
9:A:780:G:H2'	9:A:781:U:C6	2.56	0.40
9:A:1642:C:OP1	27:W:76:ARG:NH1	2.55	0.40
9:A:2084:A:C2	9:A:2085:G:C5	3.10	0.40
9:A:2643:G:O4'	9:A:2903:G:H1'	2.22	0.40
9:A:2772:G:H21	16:K:139:GLU:CD	2.30	0.40
9:A:2779:G:C2	9:A:2780:C:C6	3.10	0.40
10:B:30:U:C4	10:B:31:G:N7	2.90	0.40
12:G:173:LEU:HD11	12:G:271:VAL:HG21	2.03	0.40
13:H:63:LYS:N	13:H:64:PRO:HD2	2.37	0.40
21:Q:18:ARG:NE	21:Q:65:PHE:O	2.45	0.40
26:V:29:ILE:HG21	26:V:41:LEU:HD21	2.03	0.40
31:a:196:A:C4	31:a:197:U:C5	3.09	0.40
31:a:358:G:C2	31:a:359:C:C6	3.10	0.40
31:a:430:G:H2'	31:a:431:U:O4'	2.21	0.40
31:a:1396:G:C2	31:a:1397:G:C8	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	57/62 (92%)	56 (98%)	1 (2%)	0	100	100
2	2	55/59 (93%)	54 (98%)	1 (2%)	0	100	100
3	3	78/89 (88%)	73 (94%)	5 (6%)	0	100	100
4	4	51/59 (86%)	49 (96%)	2 (4%)	0	100	100
5	5	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
6	6	42/44 (96%)	42 (100%)	0	0	100	100
7	7	62/66 (94%)	62 (100%)	0	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
12	G	272/276 (99%)	265 (97%)	6 (2%)	1 (0%)	30	61
13	H	204/209 (98%)	195 (96%)	9 (4%)	0	100	100
14	I	203/207 (98%)	201 (99%)	2 (1%)	0	100	100
15	J	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
16	K	172/178 (97%)	165 (96%)	7 (4%)	0	100	100
17	M	145/147 (99%)	144 (99%)	1 (1%)	0	100	100
18	N	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
19	O	144/146 (99%)	140 (97%)	3 (2%)	1 (1%)	18	49
20	P	132/144 (92%)	131 (99%)	1 (1%)	0	100	100
21	Q	123/127 (97%)	120 (98%)	3 (2%)	0	100	100
22	R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
23	S	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
24	T	116/119 (98%)	114 (98%)	2 (2%)	0	100	100
25	U	99/102 (97%)	97 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	V	109/115 (95%)	107 (98%)	2 (2%)	0	100	100
27	W	89/96 (93%)	88 (99%)	1 (1%)	0	100	100
28	X	99/103 (96%)	96 (97%)	3 (3%)	0	100	100
29	Y	72/95 (76%)	68 (94%)	4 (6%)	0	100	100
30	Z	59/62 (95%)	59 (100%)	0	0	100	100
33	c	220/261 (84%)	209 (95%)	10 (4%)	1 (0%)	24	57
34	d	203/218 (93%)	197 (97%)	6 (3%)	0	100	100
35	e	198/203 (98%)	193 (98%)	5 (2%)	0	100	100
36	f	161/166 (97%)	159 (99%)	2 (1%)	0	100	100
37	g	94/100 (94%)	92 (98%)	2 (2%)	0	100	100
38	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
39	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
40	j	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
41	k	94/102 (92%)	93 (99%)	1 (1%)	0	100	100
42	l	114/129 (88%)	110 (96%)	3 (3%)	1 (1%)	14	44
43	m	132/137 (96%)	125 (95%)	7 (5%)	0	100	100
44	n	112/121 (93%)	110 (98%)	2 (2%)	0	100	100
45	o	58/61 (95%)	58 (100%)	0	0	100	100
46	p	83/89 (93%)	82 (99%)	1 (1%)	0	100	100
47	q	85/91 (93%)	83 (98%)	2 (2%)	0	100	100
48	r	78/88 (89%)	75 (96%)	3 (4%)	0	100	100
49	s	61/79 (77%)	59 (97%)	2 (3%)	0	100	100
50	t	80/92 (87%)	80 (100%)	0	0	100	100
51	u	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
All	All	5245/5564 (94%)	5107 (97%)	134 (3%)	4 (0%)	49	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	c	131	LYS
42	l	119	ASN
19	O	29	LYS
12	G	155	ILE

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	1	54/56 (96%)	53 (98%)	1 (2%)	50	73
2	2	48/50 (96%)	48 (100%)	0	100	100
3	3	72/79 (91%)	71 (99%)	1 (1%)	59	76
4	4	43/48 (90%)	43 (100%)	0	100	100
5	5	48/49 (98%)	48 (100%)	0	100	100
6	6	39/39 (100%)	39 (100%)	0	100	100
7	7	51/53 (96%)	51 (100%)	0	100	100
8	8	35/35 (100%)	35 (100%)	0	100	100
12	G	224/226 (99%)	224 (100%)	0	100	100
13	H	169/172 (98%)	169 (100%)	0	100	100
14	I	172/173 (99%)	171 (99%)	1 (1%)	78	83
15	J	154/156 (99%)	151 (98%)	3 (2%)	50	73
16	K	145/148 (98%)	144 (99%)	1 (1%)	76	82
17	M	124/124 (100%)	124 (100%)	0	100	100
18	N	98/98 (100%)	98 (100%)	0	100	100
19	O	112/112 (100%)	111 (99%)	1 (1%)	70	80
20	P	107/114 (94%)	107 (100%)	0	100	100
21	Q	107/109 (98%)	107 (100%)	0	100	100
22	R	92/92 (100%)	91 (99%)	1 (1%)	65	78
23	S	97/98 (99%)	97 (100%)	0	100	100
24	T	94/95 (99%)	93 (99%)	1 (1%)	65	78
25	U	83/83 (100%)	83 (100%)	0	100	100
26	V	94/98 (96%)	94 (100%)	0	100	100
27	W	82/85 (96%)	81 (99%)	1 (1%)	63	78
28	X	85/87 (98%)	85 (100%)	0	100	100
29	Y	59/75 (79%)	59 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Z	54/55 (98%)	54 (100%)	0	100	100
33	c	187/220 (85%)	186 (100%)	1 (0%)	81	85
34	d	163/174 (94%)	163 (100%)	0	100	100
35	e	174/177 (98%)	173 (99%)	1 (1%)	78	83
36	f	126/128 (98%)	126 (100%)	0	100	100
37	g	85/88 (97%)	85 (100%)	0	100	100
38	h	130/133 (98%)	128 (98%)	2 (2%)	57	75
39	i	112/113 (99%)	112 (100%)	0	100	100
40	j	100/102 (98%)	98 (98%)	2 (2%)	48	72
41	k	87/92 (95%)	87 (100%)	0	100	100
42	l	90/101 (89%)	89 (99%)	1 (1%)	65	78
43	m	117/119 (98%)	117 (100%)	0	100	100
44	n	98/102 (96%)	97 (99%)	1 (1%)	68	79
45	o	51/52 (98%)	51 (100%)	0	100	100
46	p	76/79 (96%)	76 (100%)	0	100	100
47	q	77/81 (95%)	77 (100%)	0	100	100
48	r	74/81 (91%)	74 (100%)	0	100	100
49	s	54/67 (81%)	54 (100%)	0	100	100
50	t	70/79 (89%)	70 (100%)	0	100	100
51	u	62/64 (97%)	62 (100%)	0	100	100
All	All	4475/4661 (96%)	4456 (100%)	19 (0%)	81	86

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	58	ARG
3	3	14	PHE
14	I	49	HIS
15	J	37	ASN
15	J	79	LEU
15	J	150	ARG
16	K	84	GLN
19	O	1	MET
22	R	4	LYS
24	T	51	ARG

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Mol	Chain	Res	Type
27	W	56	LEU
33	c	129	LEU
35	e	128	ASP
38	h	15	ASP
38	h	85	TYR
40	j	85	ARG
40	j	129	LYS
42	l	77	HIS
44	n	79	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	31	GLN
2	2	32	ASN
4	4	48	HIS
7	7	61	GLN
14	I	141	GLN
14	I	145	ASN
15	J	37	ASN
15	J	63	GLN
20	P	9	HIS
24	T	101	ASN
25	U	86	GLN
26	V	65	ASN
28	X	18	ASN
33	c	44	GLN
34	d	122	GLN
34	d	133	GLN
35	e	59	HIS
35	e	86	ASN
35	e	93	GLN
35	e	138	GLN
36	f	45	HIS
39	i	99	ASN
41	k	56	HIS
46	p	9	ASN
46	p	76	GLN
49	s	21	HIS
51	u	21	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	113/116 (97%)	23 (20%)	0
11	D	76/77 (98%)	20 (26%)	0
31	a	1518/1558 (97%)	219 (14%)	0
32	b	11/19 (57%)	2 (18%)	0
9	A	2820/2912 (96%)	405 (14%)	30 (1%)
All	All	4538/4682 (96%)	669 (14%)	30 (0%)

All (669) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	10	A
9	A	15	G
9	A	34	U
9	A	46	C
9	A	51	G
9	A	55	G
9	A	63	U
9	A	71	A
9	A	74	U
9	A	75	G
9	A	93	U
9	A	101	G
9	A	117	A
9	A	119	U
9	A	130	A
9	A	161	A
9	A	163	U
9	A	164	A
9	A	169	G
9	A	198	A
9	A	201	A
9	A	215	A
9	A	218	A
9	A	224	A
9	A	225	A
9	A	230	A
9	A	231	U
9	A	232	U
9	A	247	G
9	A	250	G
9	A	251	C

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Mol	Chain	Res	Type
9	A	252	G
9	A	257	A
9	A	269	C
9	A	271	C
9	A	281	A
9	A	282	G
9	A	289	U
9	A	290	G
9	A	295	G
9	A	296	G
9	A	299	G
9	A	300	U
9	A	301	A
9	A	308	C
9	A	309	G
9	A	310	A
9	A	311	U
9	A	312	A
9	A	317	A
9	A	318	G
9	A	320	C
9	A	321	U
9	A	322	G
9	A	338	G
9	A	347	A
9	A	366	A
9	A	398	A
9	A	402	G
9	A	403	G
9	A	410	A
9	A	411	G
9	A	425	G
9	A	430	A
9	A	440	A
9	A	450	G
9	A	474	C
9	A	479	G
9	A	495	C
9	A	496	A
9	A	509	A
9	A	520	G
9	A	529	A

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Mol	Chain	Res	Type
9	A	534	G
9	A	543	A
9	A	546	U
9	A	560	G
9	A	568	C
9	A	569	A
9	A	570	A
9	A	571	G
9	A	581	G
9	A	582	U
9	A	583	U
9	A	584	A
9	A	585	A
9	A	587	G
9	A	599	G
9	A	609	G
9	A	610	A
9	A	611	A
9	A	639	A
9	A	651	A
9	A	665	A
9	A	675	A
9	A	683	U
9	A	684	A
9	A	691	A
9	A	692	U
9	A	694	A
9	A	708	G
9	A	709	A
9	A	716	A
9	A	725	U
9	A	761	A
9	A	769	A
9	A	786	U
9	A	796	G
9	A	814	G
9	A	821	A
9	A	823	U
9	A	829	A
9	A	844	G
9	A	851	C
9	A	858	A

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Mol	Chain	Res	Type
9	A	866	U
9	A	867	U
9	A	885	U
9	A	886	G
9	A	899	G
9	A	922	G
9	A	923	C
9	A	926	A
9	A	928	C
9	A	929	U
9	A	931	G
9	A	933	G
9	A	935	U
9	A	936	A
9	A	947	A
9	A	950	A
9	A	952	C
9	A	954	C
9	A	957	A
9	A	965	U
9	A	966	C
9	A	972	U
9	A	974	U
9	A	984	A
9	A	985	G
9	A	998	A
9	A	1000	G
9	A	1013	A
9	A	1022	A
9	A	1035	A
9	A	1044	C
9	A	1051	U
9	A	1052	A
9	A	1061	G
9	A	1062	U
9	A	1064	G
9	A	1066	A
9	A	1072	U
9	A	1086	G
9	A	1101	G
9	A	1109	A
9	A	1110	G

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Mol	Chain	Res	Type
9	A	1111	C
9	A	1115	C
9	A	1118	C
9	A	1122	U
9	A	1123	A
9	A	1126	G
9	A	1127	A
9	A	1151	G
9	A	1155	C
9	A	1167	A
9	A	1171	U
9	A	1172	A
9	A	1174	C
9	A	1175	G
9	A	1181	A
9	A	1182	A
9	A	1190	A
9	A	1196	G
9	A	1212	U
9	A	1213	U
9	A	1225	U
9	A	1243	G
9	A	1248	G
9	A	1265	A
9	A	1267	G
9	A	1272	G
9	A	1274	G
9	A	1286	G
9	A	1289	A
9	A	1292	G
9	A	1307	G
9	A	1308	A
9	A	1310	A
9	A	1311	G
9	A	1335	U
9	A	1336	A
9	A	1364	U
9	A	1380	C
9	A	1385	C
9	A	1387	U
9	A	1394	A
9	A	1395	G

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Mol	Chain	Res	Type
9	A	1400	A
9	A	1414	U
9	A	1421	C
9	A	1430	A
9	A	1431	U
9	A	1451	G
9	A	1452	U
9	A	1454	U
9	A	1455	G
9	A	1460	A
9	A	1461	U
9	A	1468	A
9	A	1469	C
9	A	1474	U
9	A	1495	U
9	A	1496	U
9	A	1497	G
9	A	1503	G
9	A	1509	C
9	A	1511	A
9	A	1520	G
9	A	1524	U
9	A	1526	A
9	A	1530	G
9	A	1534	U
9	A	1535	A
9	A	1536	A
9	A	1537	A
9	A	1538	U
9	A	1550	U
9	A	1551	A
9	A	1564	G
9	A	1565	A
9	A	1567	G
9	A	1569	G
9	A	1575	A
9	A	1576	A
9	A	1583	G
9	A	1584	U
9	A	1611	A
9	A	1614	A
9	A	1623	U

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Mol	Chain	Res	Type
9	A	1625	G
9	A	1627	G
9	A	1629	G
9	A	1649	U
9	A	1650	A
9	A	1652	A
9	A	1688	A
9	A	1689	G
9	A	1690	C
9	A	1707	A
9	A	1716	G
9	A	1717	C
9	A	1742	A
9	A	1756	U
9	A	1758	G
9	A	1759	G
9	A	1769	G
9	A	1775	A
9	A	1776	G
9	A	1777	G
9	A	1786	A
9	A	1795	C
9	A	1804	A
9	A	1813	C
9	A	1814	A
9	A	1828	A
9	A	1829	A
9	A	1830	G
9	A	1842	A
9	A	1860	A
9	A	1872	A
9	A	1873	U
9	A	1883	U
9	A	1884	C
9	A	1885	G
9	A	1907	C
9	A	1919	G
9	A	1926	A
9	A	1927	C
9	A	1942	G
9	A	1943	G
9	A	1949	A

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Mol	Chain	Res	Type
9	A	1951	A
9	A	1953	U
9	A	1968	U
9	A	1980	C
9	A	1983	A
9	A	1984	A
9	A	1985	G
9	A	2004	U
9	A	2006	U
9	A	2009	C
9	A	2010	A
9	A	2034	G
9	A	2035	U
9	A	2036	A
9	A	2044	A
9	A	2045	G
9	A	2046	A
9	A	2056	C
9	A	2068	C
9	A	2069	G
9	A	2073	A
9	A	2074	G
9	A	2075	A
9	A	2082	G
9	A	2096	G
9	A	2108	G
9	A	2112	U
9	A	2201	U
9	A	2207	C
9	A	2211	A
9	A	2212	A
9	A	2216	G
9	A	2217	C
9	A	2224	A
9	A	2225	A
9	A	2238	A
9	A	2251	G
9	A	2252	G
9	A	2259	G
9	A	2281	A
9	A	2292	G
9	A	2296	C

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Mol	Chain	Res	Type
9	A	2300	A
9	A	2318	U
9	A	2319	U
9	A	2321	G
9	A	2322	A
9	A	2324	A
9	A	2331	G
9	A	2333	A
9	A	2334	G
9	A	2335	A
9	A	2338	G
9	A	2347	G
9	A	2348	A
9	A	2360	C
9	A	2363	C
9	A	2396	G
9	A	2398	C
9	A	2415	U
9	A	2435	C
9	A	2437	C
9	A	2438	A
9	A	2442	G
9	A	2443	A
9	A	2448	A
9	A	2454	C
9	A	2460	G
9	A	2461	A
9	A	2478	C
9	A	2489	A
9	A	2491	A
9	A	2497	G
9	A	2515	G
9	A	2518	G
9	A	2519	U
9	A	2531	A
9	A	2533	C
9	A	2542	G
9	A	2548	G
9	A	2561	G
9	A	2567	U
9	A	2579	A
9	A	2580	G

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Mol	Chain	Res	Type
9	A	2591	G
9	A	2615	A
9	A	2622	U
9	A	2623	C
9	A	2626	U
9	A	2628	U
9	A	2642	U
9	A	2643	G
9	A	2674	G
9	A	2698	G
9	A	2702	U
9	A	2727	G
9	A	2739	U
9	A	2746	A
9	A	2747	A
9	A	2749	G
9	A	2761	A
9	A	2778	A
9	A	2791	A
9	A	2792	U
9	A	2803	A
9	A	2804	U
9	A	2809	U
9	A	2810	U
9	A	2811	A
9	A	2812	A
9	A	2813	G
9	A	2816	A
9	A	2818	U
9	A	2830	G
9	A	2843	A
9	A	2844	G
9	A	2877	G
9	A	2878	A
9	A	2882	G
9	A	2889	A
9	A	2890	C
9	A	2903	G
10	B	7	G
10	B	10	G
10	B	13	A
10	B	23	A

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Mol	Chain	Res	Type
10	B	28	C
10	B	33	U
10	B	35	C
10	B	39	G
10	B	40	C
10	B	43	A
10	B	51	A
10	B	54	U
10	B	55	A
10	B	64	A
10	B	65	G
10	B	87	U
10	B	88	C
10	B	97	A
10	B	101	U
10	B	107	G
10	B	108	U
10	B	110	G
10	B	115	G
11	D	3	C
11	D	6	G
11	D	7	G
11	D	8	U
11	D	9	G
11	D	13	C
11	D	19	G
11	D	20	G
11	D	22	A
11	D	23	G
11	D	47	G
11	D	49	C
11	D	54	G
11	D	56	U
11	D	57	C
11	D	62	C
11	D	63	C
11	D	68	C
11	D	76	C
11	D	77	A
31	a	10	A
31	a	11	G
31	a	34	A

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Mol	Chain	Res	Type
31	a	41	G
31	a	49	C
31	a	50	C
31	a	51	U
31	a	53	A
31	a	57	A
31	a	74	C
31	a	75	U
31	a	117	A
31	a	132	A
31	a	135	A
31	a	137	C
31	a	146	A
31	a	161	G
31	a	163	G
31	a	166	A
31	a	168	A
31	a	172	C
31	a	177	A
31	a	179	A
31	a	180	C
31	a	182	G
31	a	191	A
31	a	200	C
31	a	213	A
31	a	215	G
31	a	227	A
31	a	228	A
31	a	229	A
31	a	230	G
31	a	266	U
31	a	267	G
31	a	271	U
31	a	272	A
31	a	273	G
31	a	277	G
31	a	292	G
31	a	293	C
31	a	297	C
31	a	315	G
31	a	332	A
31	a	354	C

Continued on next page...

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Mol	Chain	Res	Type
31	a	355	A
31	a	356	C
31	a	358	G
31	a	370	A
31	a	373	G
31	a	378	C
31	a	380	G
31	a	382	A
31	a	391	U
31	a	393	U
31	a	398	C
31	a	418	G
31	a	423	A
31	a	432	G
31	a	438	A
31	a	439	G
31	a	440	A
31	a	442	G
31	a	446	U
31	a	447	U
31	a	448	C
31	a	451	A
31	a	455	U
31	a	465	U
31	a	470	A
31	a	471	G
31	a	473	G
31	a	478	A
31	a	479	C
31	a	485	C
31	a	488	U
31	a	494	C
31	a	495	U
31	a	510	G
31	a	511	G
31	a	523	A
31	a	524	A
31	a	537	C
31	a	540	C
31	a	544	C
31	a	553	G
31	a	556	G

Continued on next page...

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Mol	Chain	Res	Type
31	a	557	U
31	a	573	A
31	a	585	A
31	a	590	U
31	a	598	A
31	a	599	A
31	a	602	C
31	a	603	G
31	a	607	G
31	a	644	C
31	a	659	U
31	a	675	G
31	a	679	U
31	a	691	A
31	a	713	A
31	a	714	G
31	a	736	G
31	a	749	U
31	a	750	G
31	a	757	G
31	a	775	A
31	a	787	G
31	a	803	A
31	a	819	U
31	a	820	A
31	a	841	A
31	a	843	C
31	a	846	U
31	a	855	A
31	a	862	G
31	a	866	G
31	a	870	C
31	a	873	C
31	a	882	G
31	a	899	A
31	a	941	A
31	a	953	G
31	a	954	G
31	a	961	C
31	a	962	A
31	a	972	G
31	a	987	U

Continued on next page...

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Mol	Chain	Res	Type
31	a	995	A
31	a	996	A
31	a	998	G
31	a	1002	A
31	a	1003	G
31	a	1004	A
31	a	1019	U
31	a	1020	G
31	a	1028	U
31	a	1030	G
31	a	1031	A
31	a	1033	C
31	a	1036	U
31	a	1045	A
31	a	1050	U
31	a	1051	U
31	a	1052	U
31	a	1055	C
31	a	1058	C
31	a	1059	G
31	a	1060	G
31	a	1063	A
31	a	1064	C
31	a	1065	A
31	a	1067	A
31	a	1073	A
31	a	1081	C
31	a	1082	A
31	a	1092	U
31	a	1121	G
31	a	1122	U
31	a	1128	A
31	a	1159	C
31	a	1161	U
31	a	1163	U
31	a	1165	G
31	a	1166	U
31	a	1172	A
31	a	1183	A
31	a	1185	U
31	a	1194	C
31	a	1210	G

Continued on next page...

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Mol	Chain	Res	Type
31	a	1222	A
31	a	1223	A
31	a	1226	C
31	a	1239	A
31	a	1251	A
31	a	1253	A
31	a	1262	A
31	a	1264	A
31	a	1283	C
31	a	1286	U
31	a	1296	G
31	a	1306	A
31	a	1307	U
31	a	1326	G
31	a	1328	U
31	a	1331	G
31	a	1341	U
31	a	1344	A
31	a	1348	C
31	a	1372	A
31	a	1379	G
31	a	1390	C
31	a	1391	G
31	a	1420	A
31	a	1423	C
31	a	1424	A
31	a	1445	G
31	a	1448	U
31	a	1449	G
31	a	1455	C
31	a	1466	U
31	a	1468	A
31	a	1472	A
31	a	1478	U
31	a	1479	U
31	a	1480	U
31	a	1481	G
31	a	1517	U
31	a	1519	A
31	a	1521	G
31	a	1524	G
31	a	1530	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
31	a	1533	U
31	a	1544	G
31	a	1556	G
31	a	1557	G
31	a	1558	A
31	a	1564	U
32	b	6	U
32	b	16	A

All (30) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	9	G
9	A	33	U
9	A	227	A
9	A	251	C
9	A	288	U
9	A	295	G
9	A	429	A
9	A	1057	U
9	A	1061	G
9	A	1117	C
9	A	1189	U
9	A	1224	G
9	A	1393	G
9	A	1413	A
9	A	1451	G
9	A	1525	G
9	A	1536	A
9	A	1583	G
9	A	1828	A
9	A	1829	A
9	A	1926	A
9	A	2005	G
9	A	2111	U
9	A	2210	U
9	A	2216	G
9	A	2318	U
9	A	2518	G
9	A	2808	U
9	A	2810	U
9	A	2877	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 344 ligands modelled in this entry, 342 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
56	SCM	a	1660	-	23,25,25	1.34	3 (13%)	27,39,39	1.57	4 (14%)
55	PUT	a	1610	-	5,5,5	0.11	0	4,4,4	0.15	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
56	SCM	a	1660	-	-	0/4/57/57	0/3/3/3
55	PUT	a	1610	-	-	0/3/3/3	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	a	1660	SCM	C10-N10	-2.35	1.43	1.47
56	a	1660	SCM	C3-C4	-2.17	1.47	1.50
56	a	1660	SCM	C8-N8	-2.10	1.44	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	a	1660	SCM	C8M-N8-C8	-4.24	108.75	114.23
56	a	1660	SCM	C1M-N10-C10	-4.17	108.84	114.23
56	a	1660	SCM	C2M-C2-C3	-2.75	108.33	113.27
56	a	1660	SCM	O1-C2-C3	2.52	112.14	108.62

There are no chirality outliers.

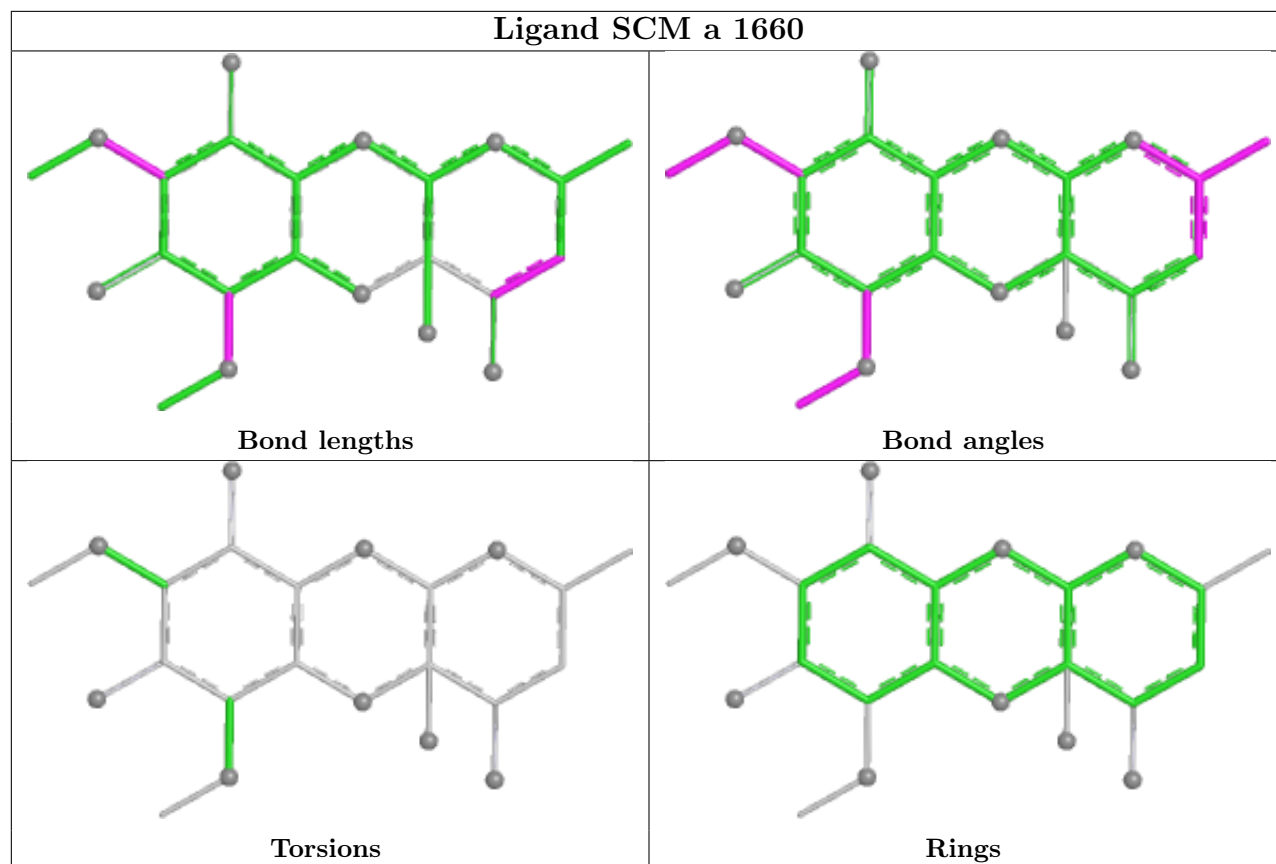
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	a	1660	SCM	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

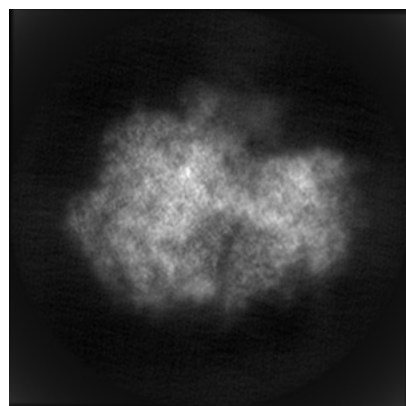
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13245. These allow visual inspection of the internal detail of the map and identification of artifacts.

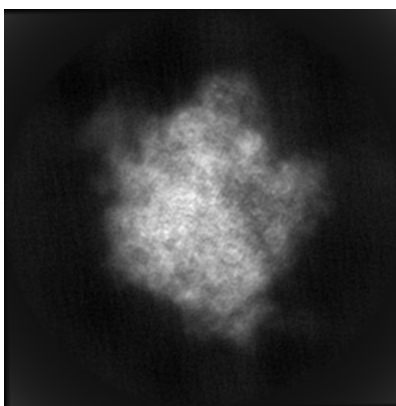
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

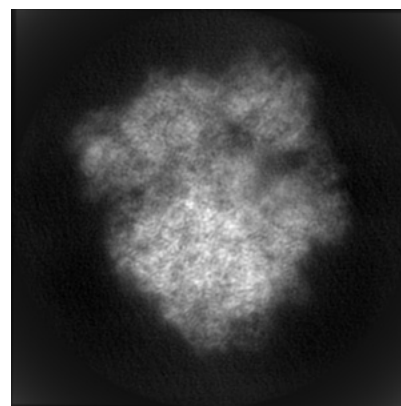
6.1.1 Primary map



X

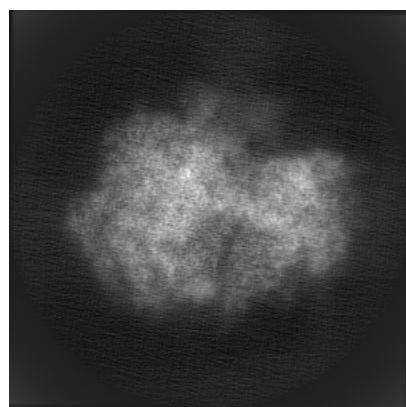


Y

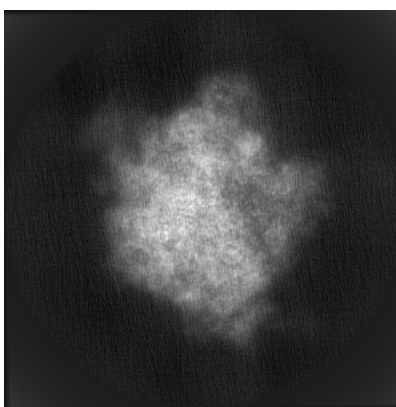


Z

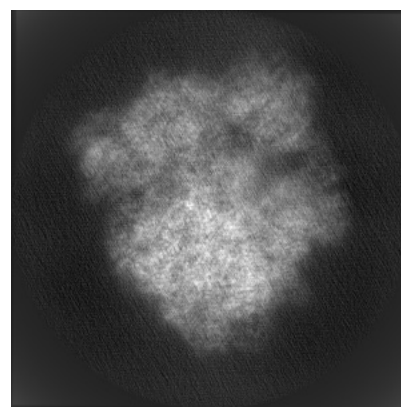
6.1.2 Raw map



X



Y

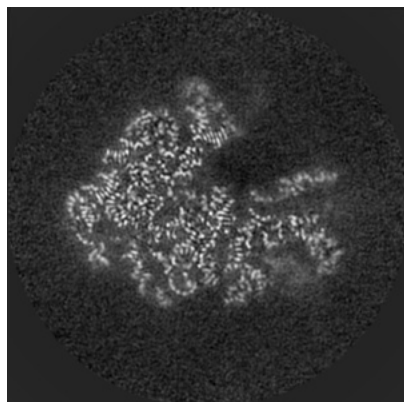


Z

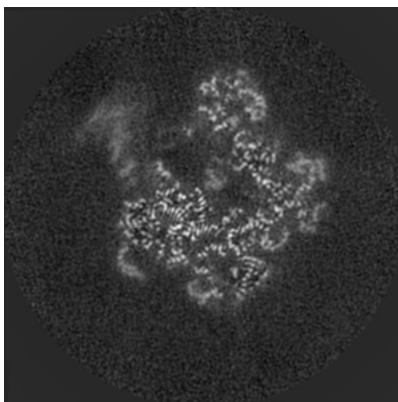
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

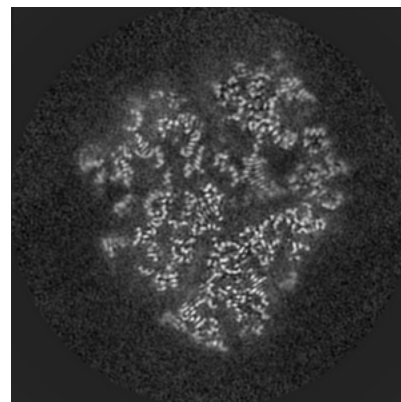
6.2.1 Primary map



X Index: 210

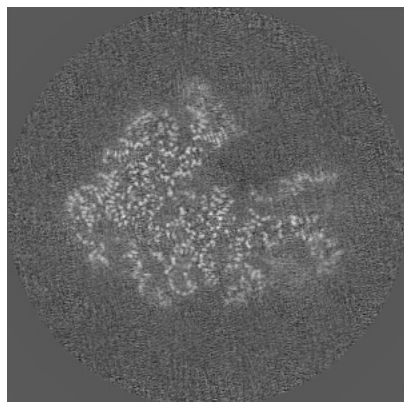


Y Index: 210

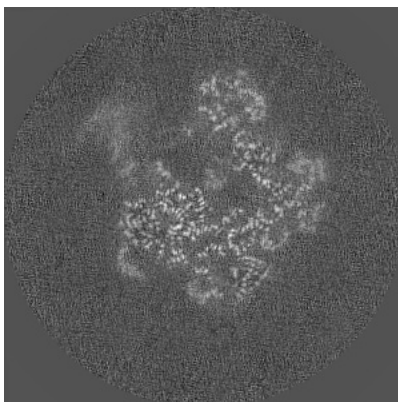


Z Index: 210

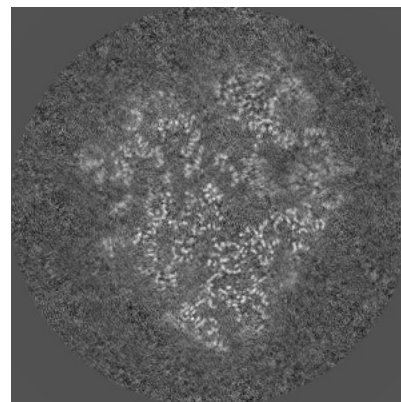
6.2.2 Raw map



X Index: 210



Y Index: 210

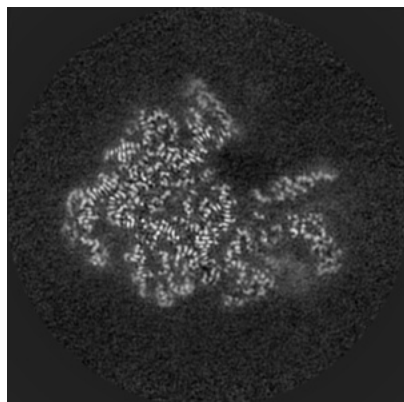


Z Index: 210

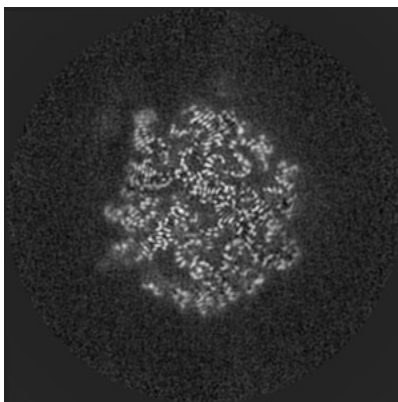
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

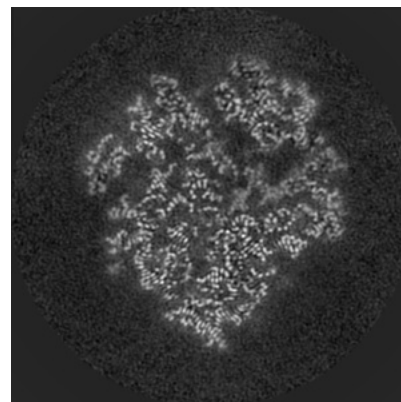
6.3.1 Primary map



X Index: 207

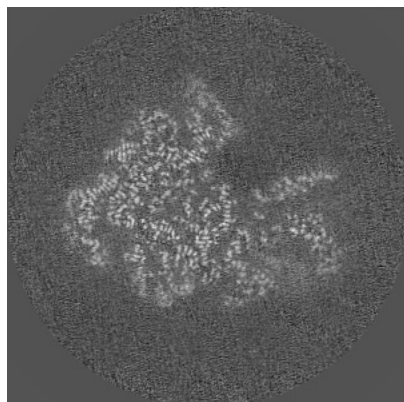


Y Index: 170

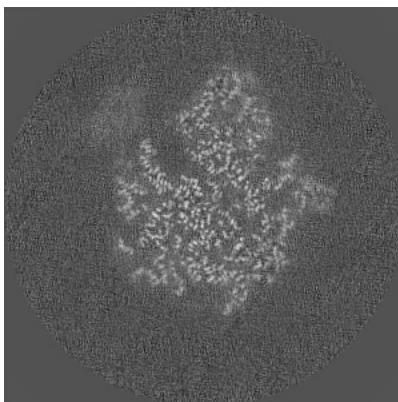


Z Index: 218

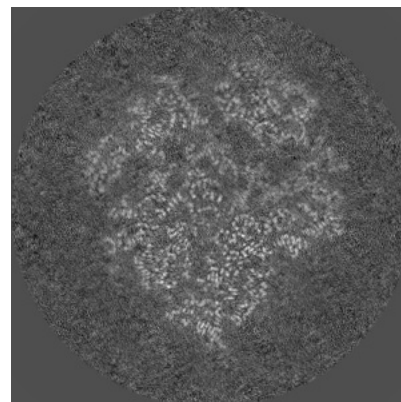
6.3.2 Raw map



X Index: 207



Y Index: 191

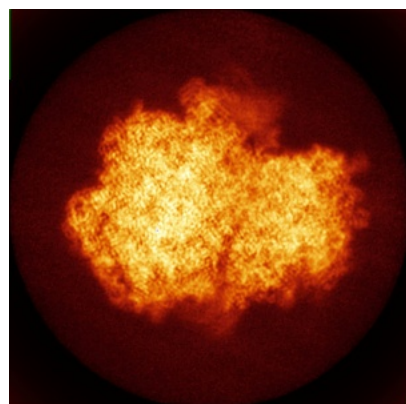


Z Index: 217

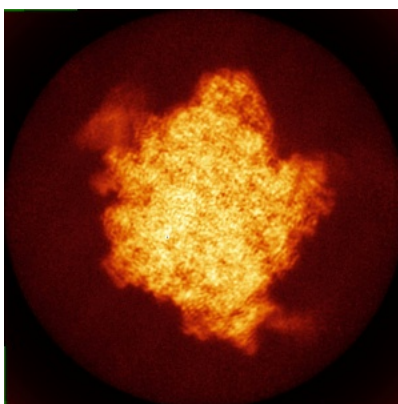
The images above show the largest variance slices of the map in three orthogonal directions.

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

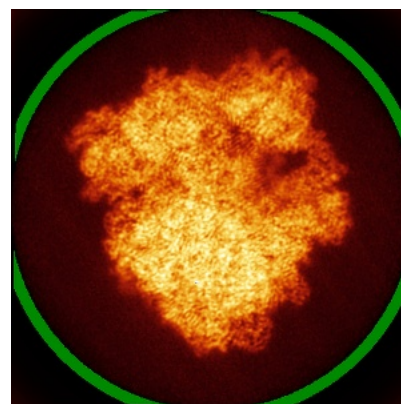
6.4.1 Primary map



X

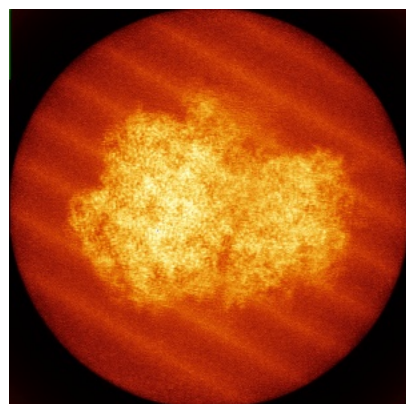


Y

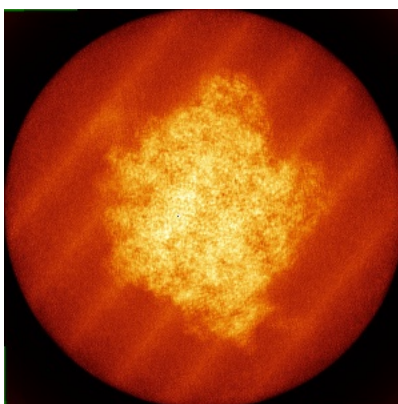


Z

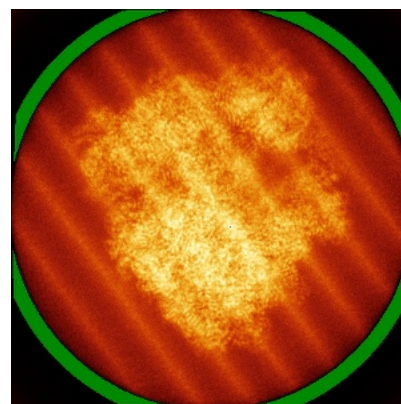
6.4.2 Raw map



X



Y

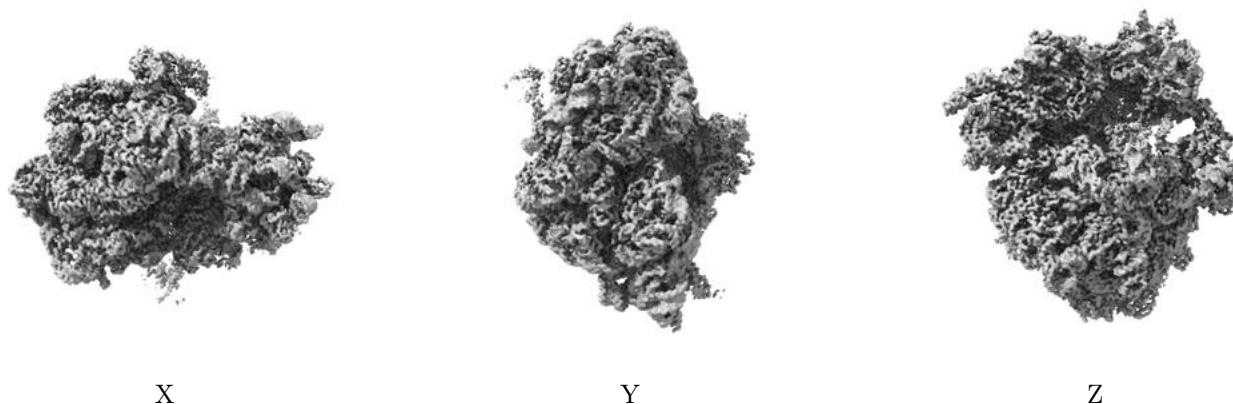


Z

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.

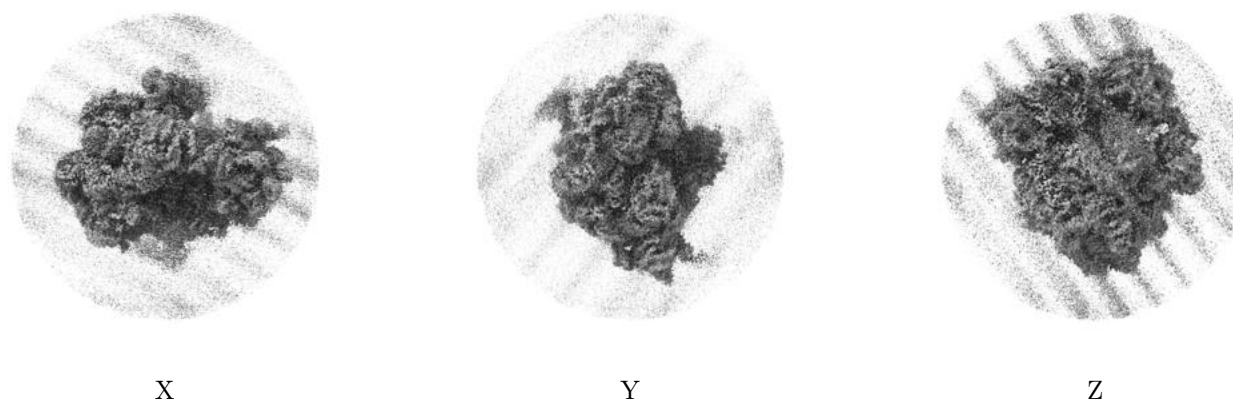
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

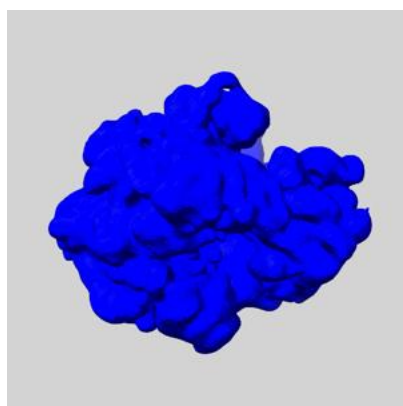
6.6 Mask visualisation [i](#)

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

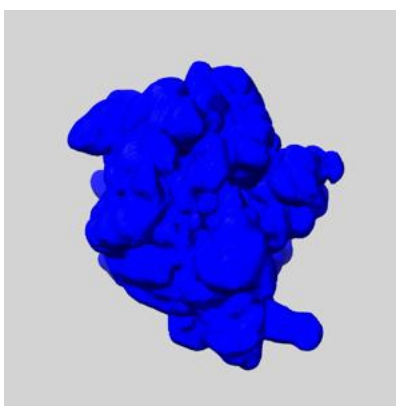
A mask typically either:

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

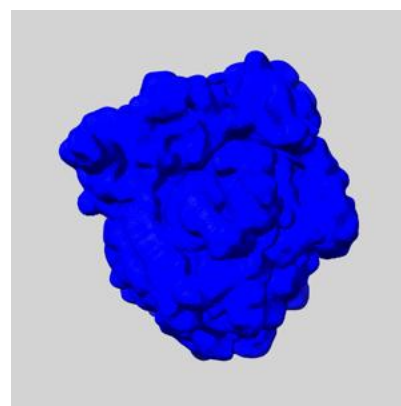
6.6.1 emd_13245_msk_1.map [i](#)



X



Y

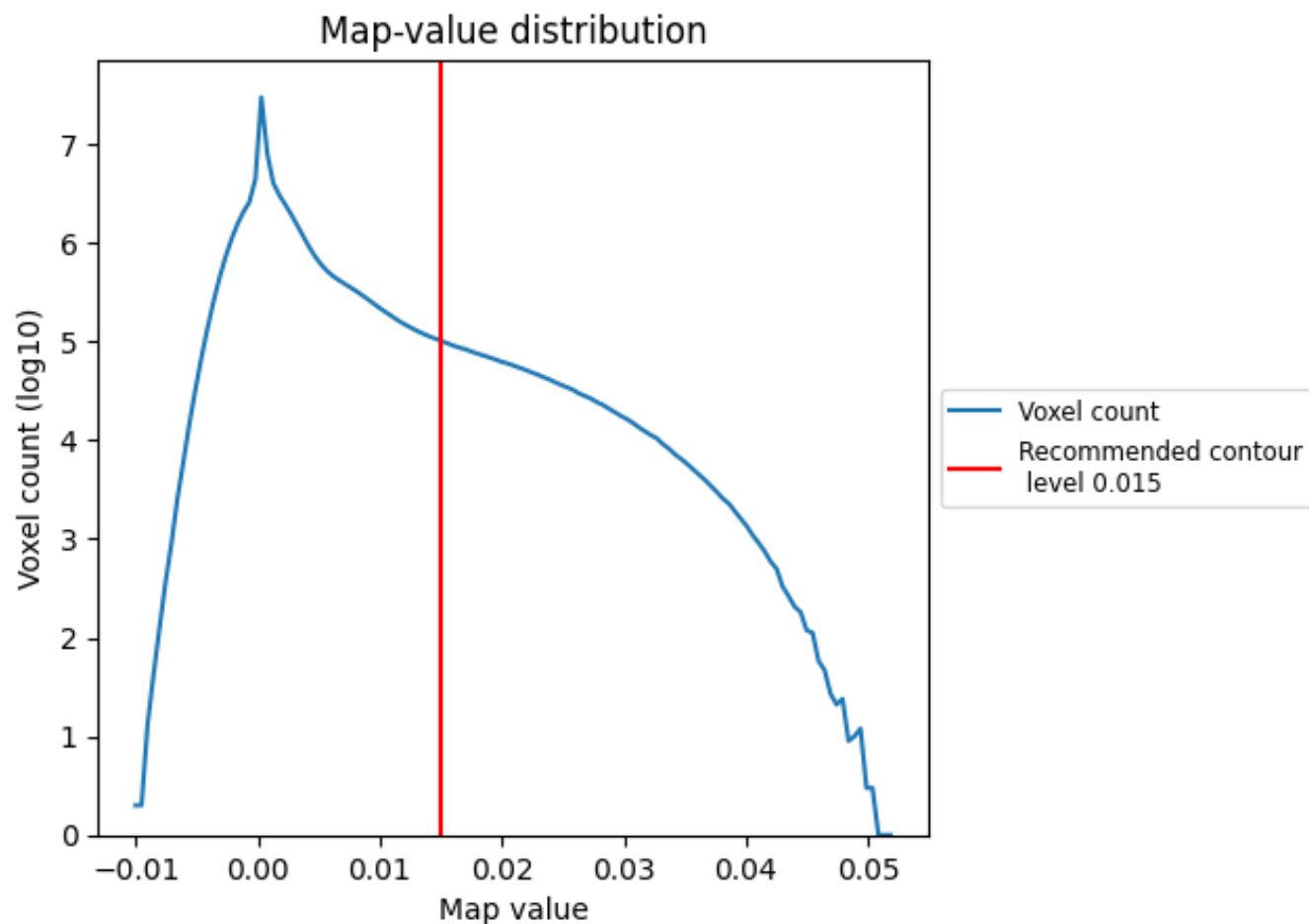


Z

7 Map analysis [i](#)

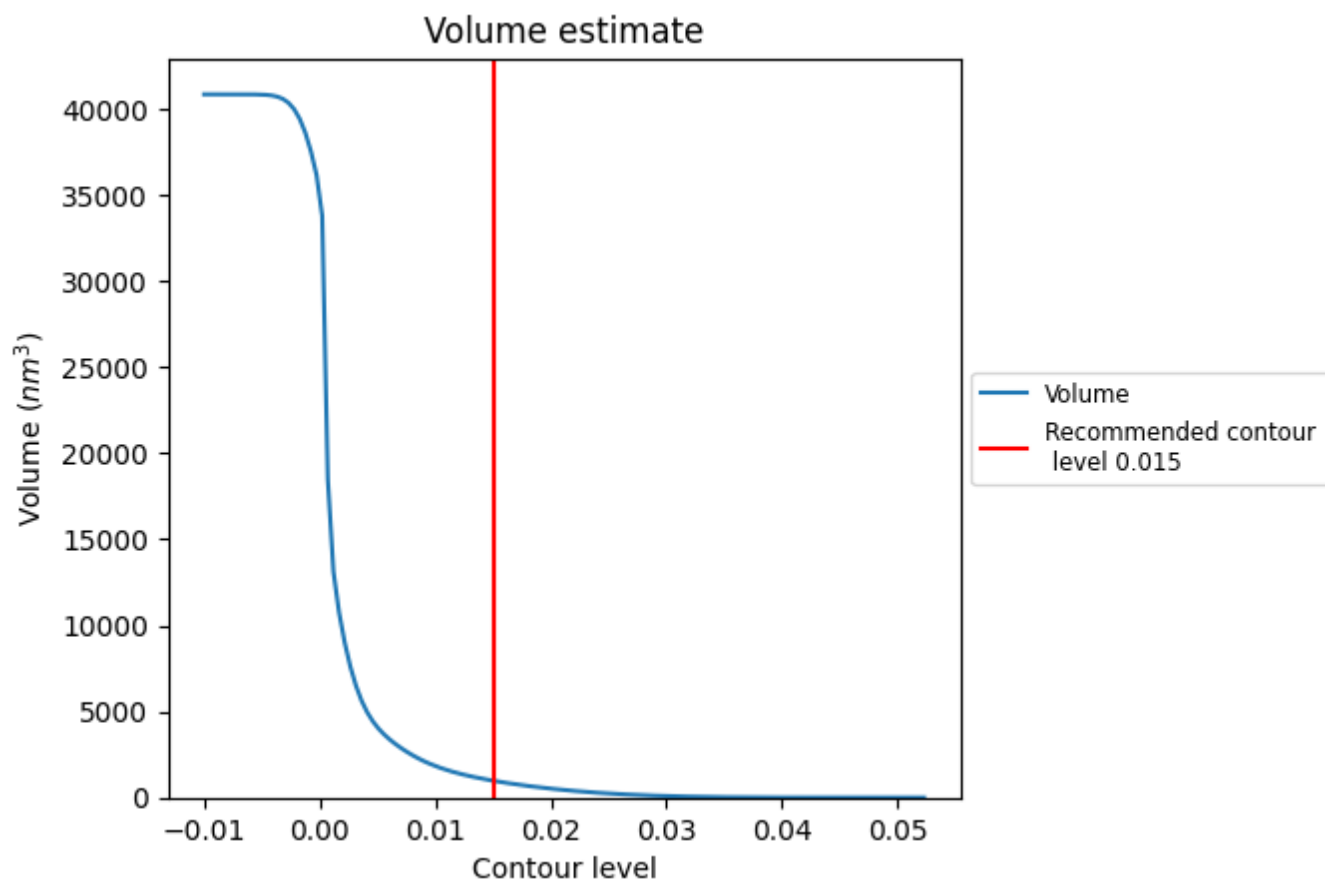
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

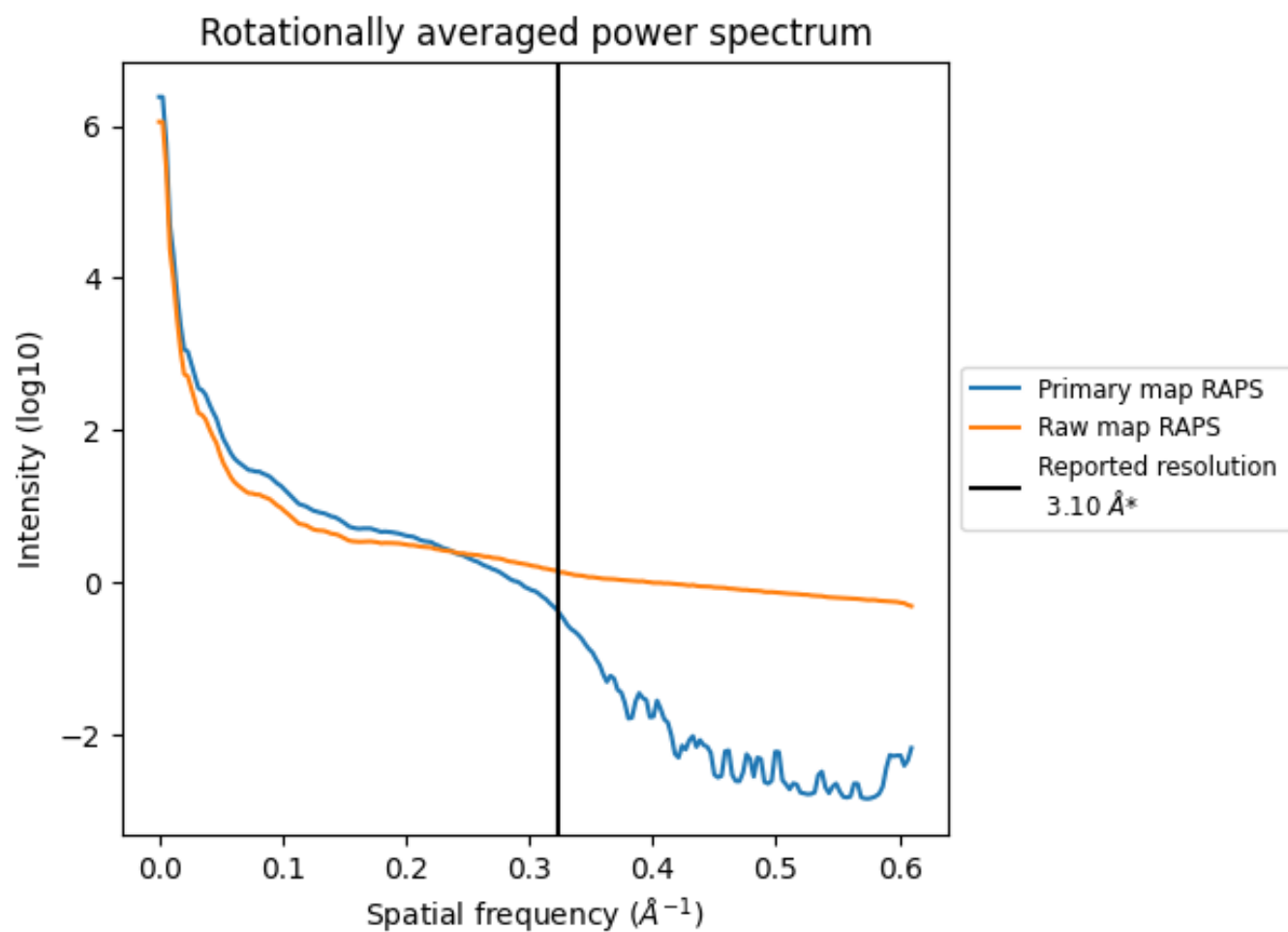
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 980 nm³; this corresponds to an approximate mass of 885 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 ⓘ

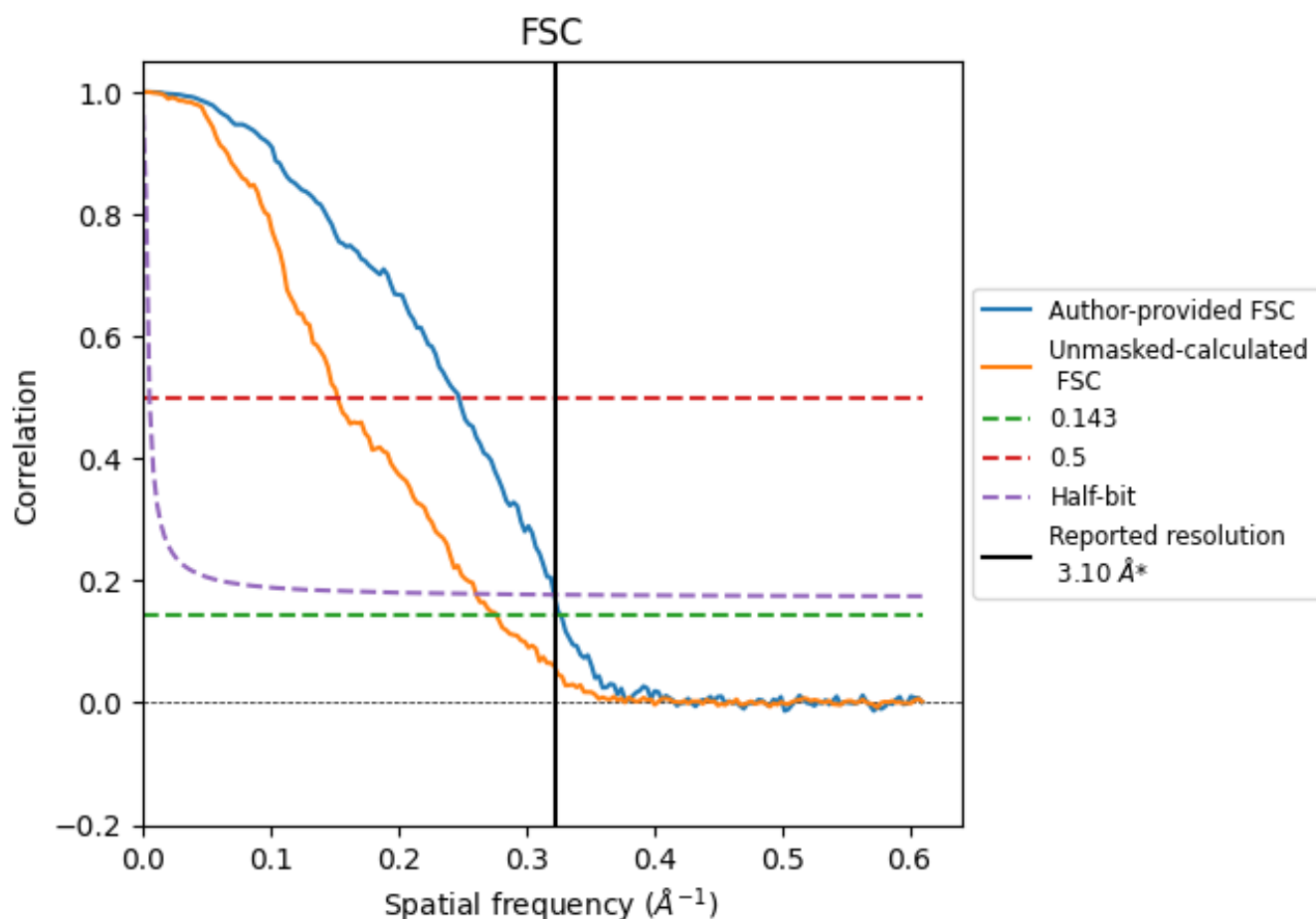


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

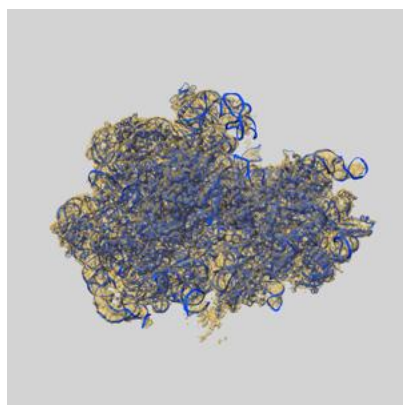
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	4.04	3.10
Unmasked-calculated*	3.61	6.54	3.83

*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 3.61 differs from the reported value 3.1 by more than 10 %

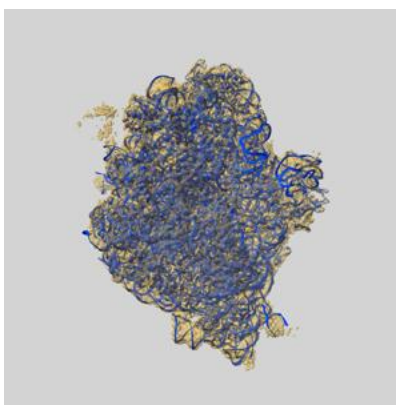
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13245 and PDB model 7P7U. Per-residue inclusion information can be found in section 3 on page 15.

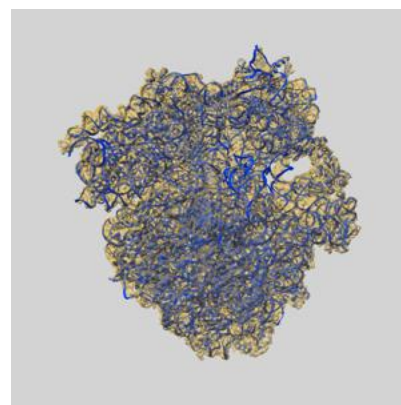
9.1 Map-model overlay [i](#)



X



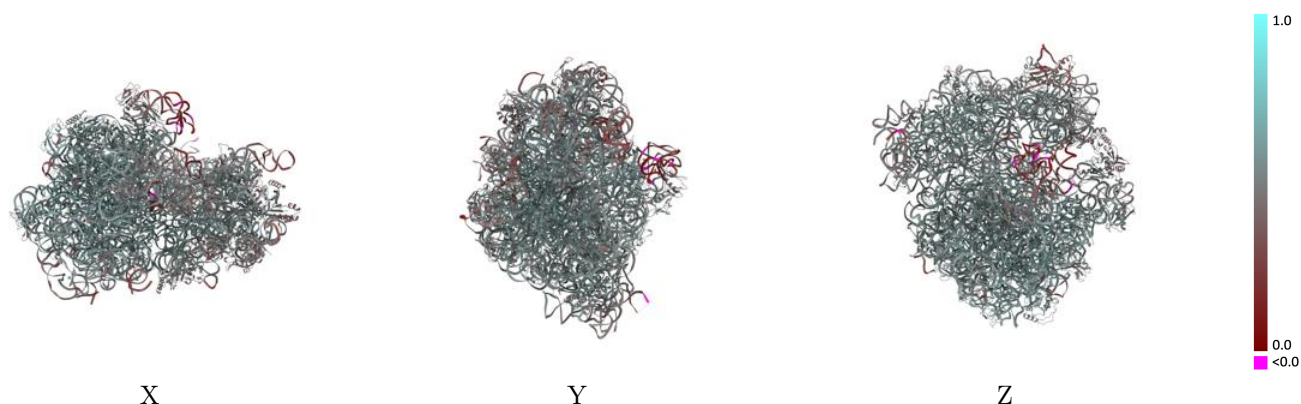
Y



Z

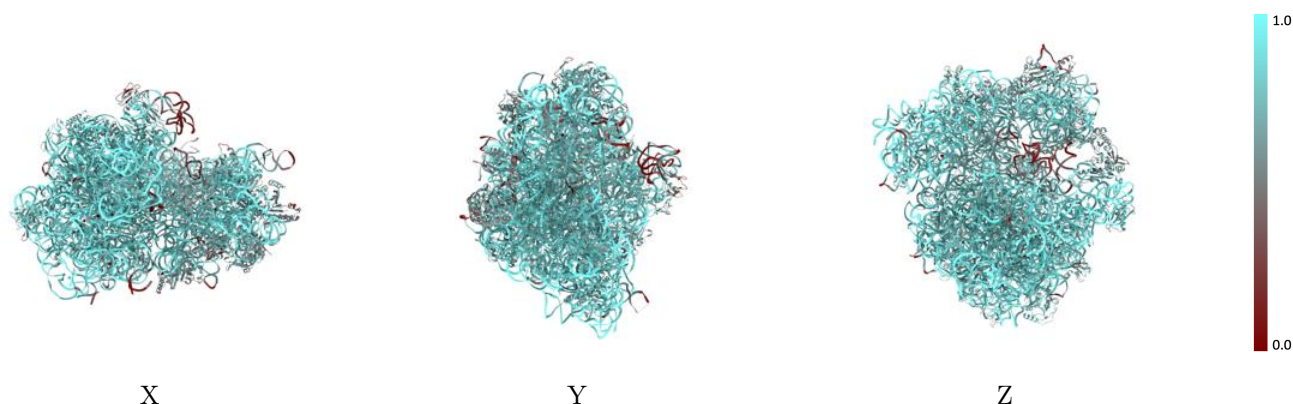
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



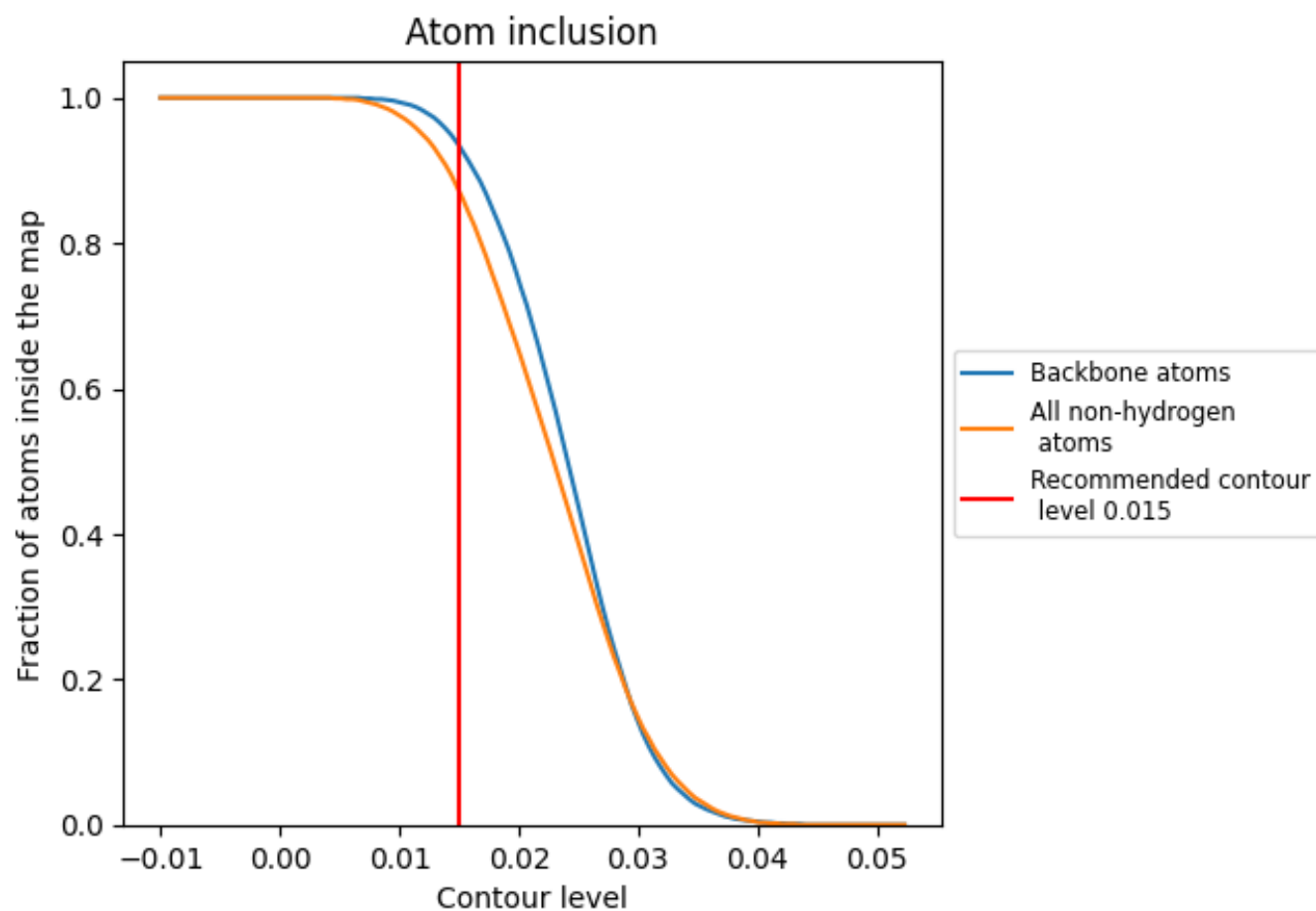
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 87% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8710	 0.5260
1	 0.7450	 0.4960
2	 0.7820	 0.5350
3	 0.5840	 0.4450
4	 0.8490	 0.5610
5	 0.8430	 0.5540
6	 0.9120	 0.5940
7	 0.9240	 0.5910
8	 0.8550	 0.5530
A	 0.9340	 0.5400
B	 0.9320	 0.4990
D	 0.6920	 0.4210
G	 0.8470	 0.5780
H	 0.7800	 0.5550
I	 0.8260	 0.5580
J	 0.6620	 0.4610
K	 0.6070	 0.4530
M	 0.8470	 0.5520
N	 0.7470	 0.5540
O	 0.8090	 0.5580
P	 0.7890	 0.5520
Q	 0.8010	 0.5290
R	 0.7350	 0.4940
S	 0.7540	 0.5350
T	 0.8580	 0.5580
U	 0.8090	 0.5700
V	 0.8190	 0.5500
W	 0.8020	 0.5230
X	 0.6740	 0.4990
Y	 0.8730	 0.5730
Z	 0.6650	 0.5470
a	 0.9210	 0.5180
b	 0.2840	 0.3380
c	 0.6020	 0.4510
d	 0.6970	 0.4970



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Chain	Atom inclusion	Q-score
e	 0.7420	 0.4990
f	 0.7850	 0.5310
g	 0.6510	 0.5050
h	 0.5890	 0.4600
i	 0.8190	 0.5320
j	 0.6870	 0.4700
k	 0.6450	 0.4590
l	 0.6660	 0.4800
m	 0.7080	 0.5400
n	 0.6540	 0.4690
o	 0.8550	 0.5330
p	 0.7450	 0.5150
q	 0.8010	 0.5110
r	 0.7870	 0.5350
s	 0.6800	 0.4910
t	 0.6630	 0.4770
u	 0.7070	 0.4800