



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:23 AM UTC

PDB ID : 6DZI / pdb_00006dzi
EMDB ID : EMD-8932
Title : Cryo-EM Structure of Mycobacterium smegmatis 70S C(minus) ribosome 70S-MPY complex
Authors : Sharma, M.R.; Li, Y.; Korripella, R.; Yang, Y.; Kaushal, P.S.; Lin, Q.; Wade, J.T.; Gray, A.G.; Derbyshire, K.M.; Agrawal, R.K.; Ojha, A.
Deposited on : 2018-07-05
Resolution : 3.46 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
MolProbity : 4-5-2 with Phenix2.0
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

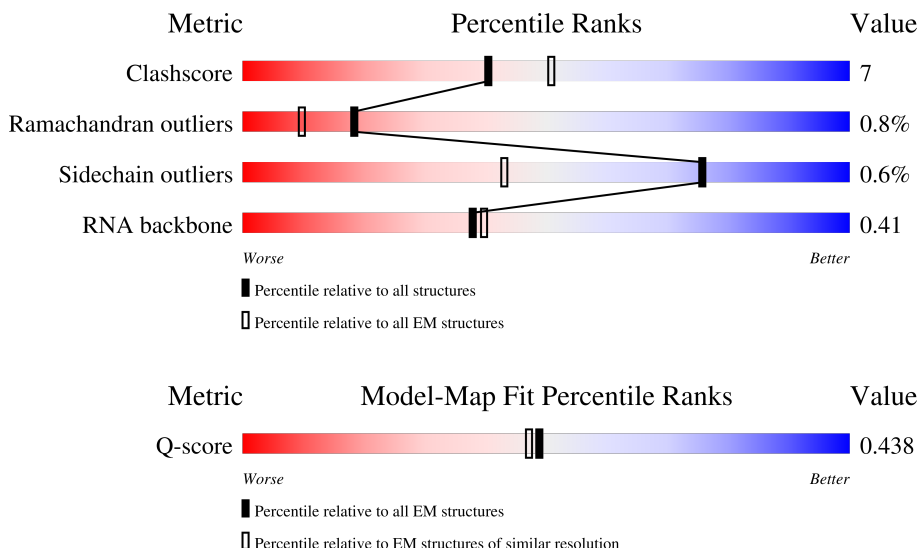
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 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.



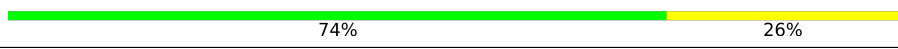
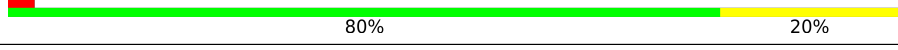
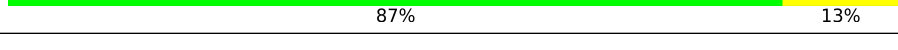
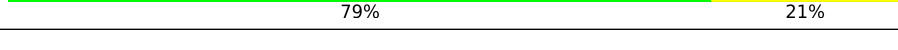
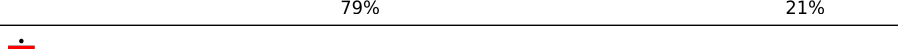
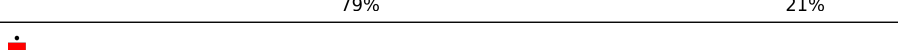
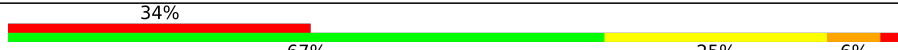
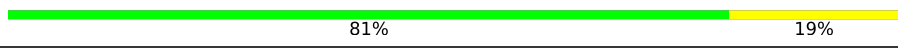
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13788 (2.96 - 3.96)

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	h	1511	
2	j	32	
3	k	208	

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Mol	Chain	Length	Quality of chain
4	l	200	
5	m	180	
6	n	96	
7	p	155	
8	q	131	
9	4	126	
10	s	99	
11	t	115	
12	u	122	
13	v	116	
14	x	88	
15	z	113	
16	5	94	
17	6	82	
18	7	85	
19	8	228	
20	r	84	
21	Y	103	
22	9	100	
23	A	3119	
24	B	118	
25	C	275	
26	D	214	
27	E	209	
28	F	182	

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Mol	Chain	Length	Quality of chain
29	G	176	
30	H	151	
31	I	126	
32	J	133	
33	K	146	
34	L	122	
35	M	145	
36	N	136	
37	O	118	
38	P	126	
39	Q	113	
40	R	124	
41	S	100	
42	T	114	
43	U	97	
44	V	105	
45	W	192	
46	X	79	
47	Z	64	
48	a	59	
49	b	54	
50	c	53	
51	d	46	
52	e	63	
53	f	37	

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Mol	Chain	Length	Quality of chain
54	g	82	
55	y	77	
56	3	23	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 150868 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	h	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called CONSERVED PROTEIN DOMAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	j	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	k	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	l	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	n	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	p	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	q	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	4	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	s	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	t	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	u	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	v	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	x	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	z	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	5	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 17 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	6	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 18 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	7	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	8	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 20 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r	84	Total	C	N	O	S	0	0
			659	408	131	116	4		

- Molecule 21 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	103	Total	C	N	O	S	0	0
			861	529	175	155	2		

- Molecule 22 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	9	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 23 is a RNA chain called 23 S rRNA (3119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 24 is a RNA chain called 5S RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	151	Total	C	N	O	S	0	0
			1119	695	209	214	1		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 48 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 50 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	c	53	Total	C	N	O	S	0	0
			456	281	97	78			

- Molecule 51 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	e	63	Total	C	N	O	S	0	0
			502	302	115	85			

- Molecule 53 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	g	75	Total	C	N	O	S	0	0
			593	379	103	110	1		

- Molecule 55 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	77	Total	C	N	O	S	0	0
			617	377	132	106	2		

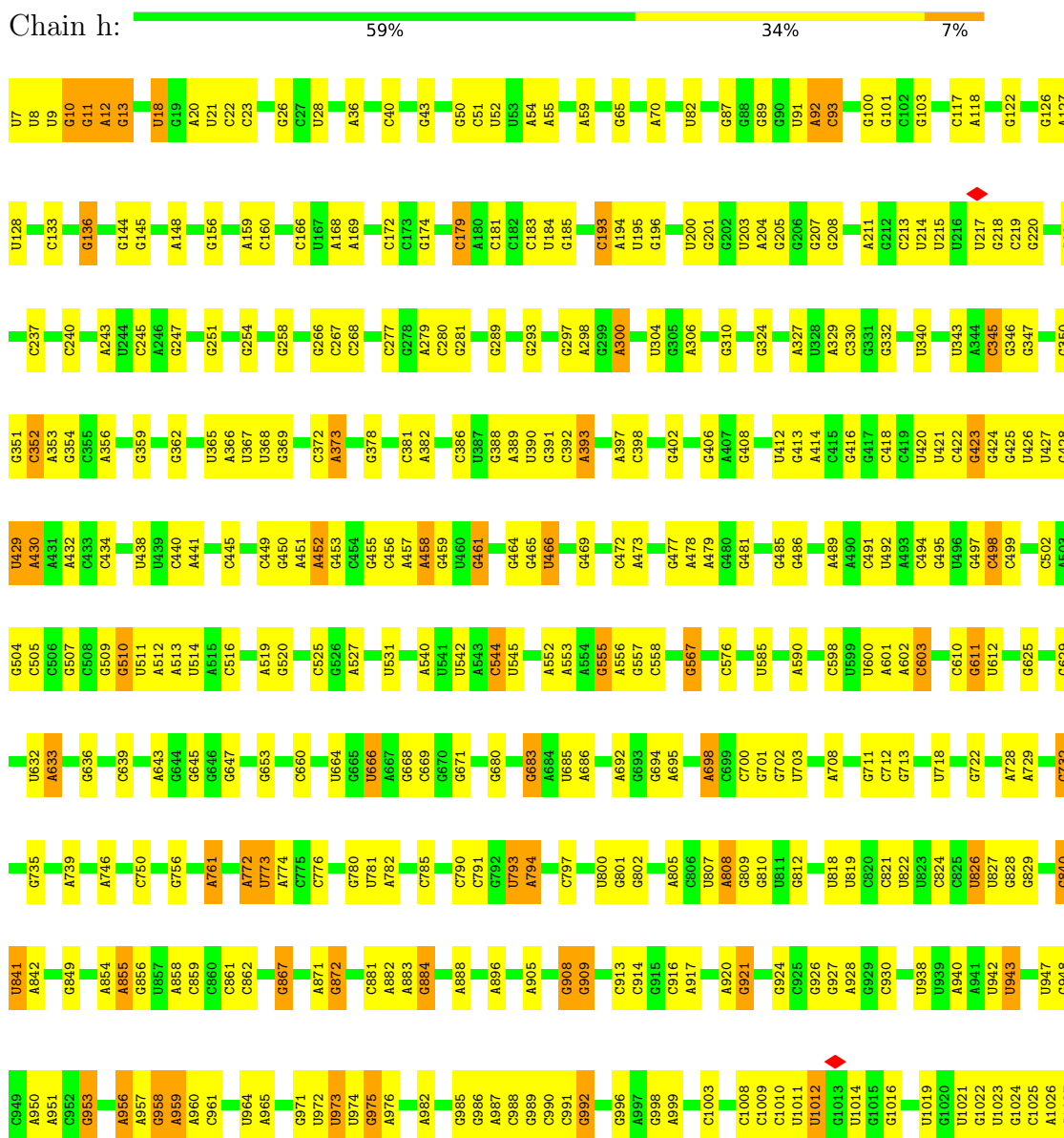
- Molecule 56 is a protein called Uncharacterized protein.

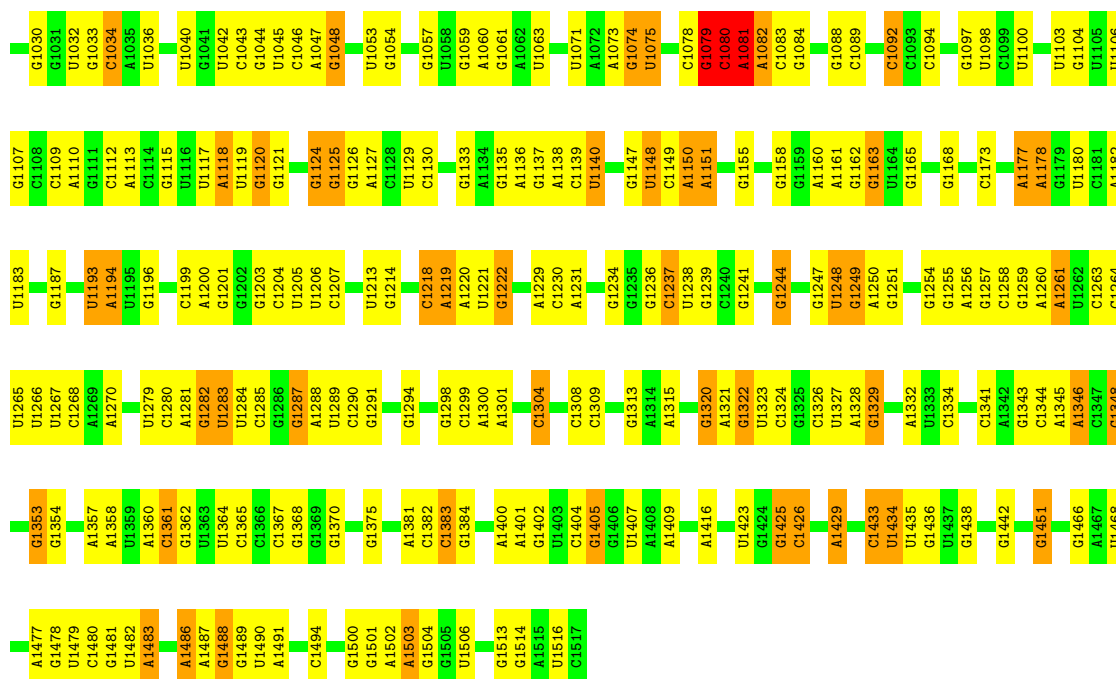
Mol	Chain	Residues	Atoms				AltConf	Trace
56	3	23	Total	C	N	O	0	0
			189	111	50	28		

3 Residue-property plots

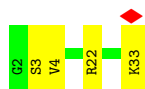
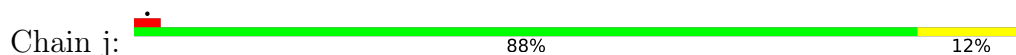
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA

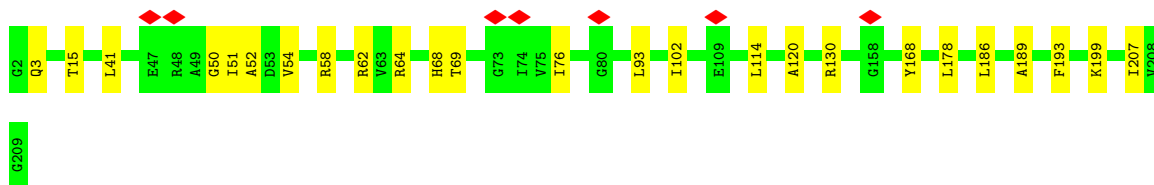
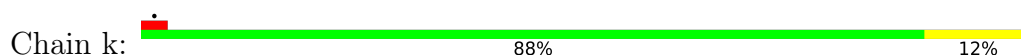




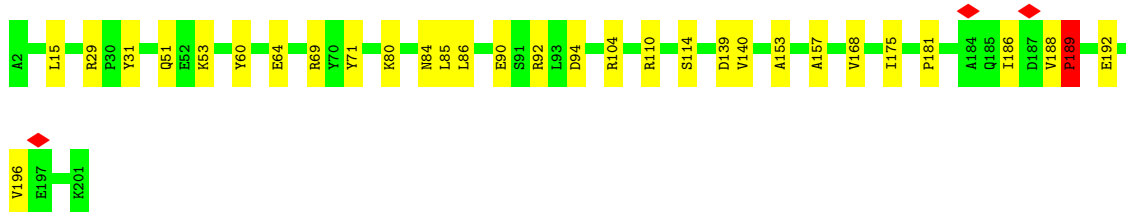
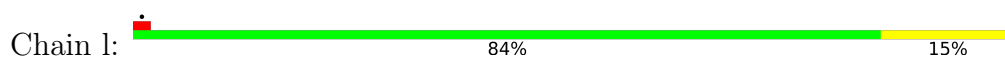
• Molecule 2: CONSERVED PROTEIN DOMAIN



• Molecule 3: 30S ribosomal protein S3

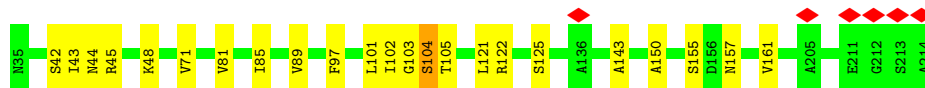


• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

Chain m:  87% 12%



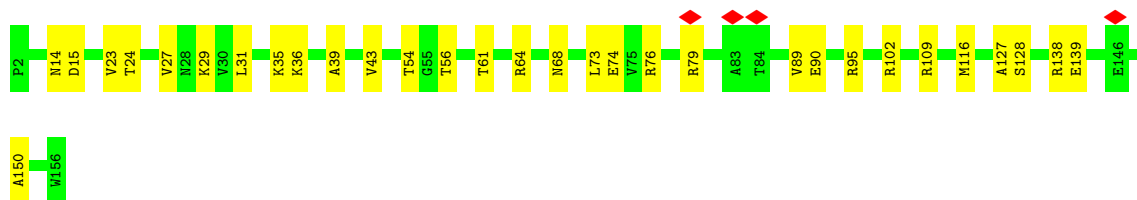
- Molecule 6: 30S ribosomal protein S6

Chain n:  74% 26%



- Molecule 7: 30S ribosomal protein S7

Chain p:  80% 20%



- Molecule 8: 30S ribosomal protein S8

Chain q:  80% 19%



- Molecule 9: 30S ribosomal protein S9

Chain 4:  78% 21%



- Molecule 10: 30S ribosomal protein S10

Chain s:  87% 13%

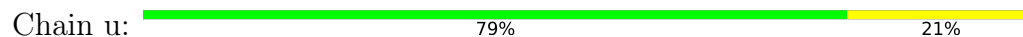


- Molecule 11: 30S ribosomal protein S11

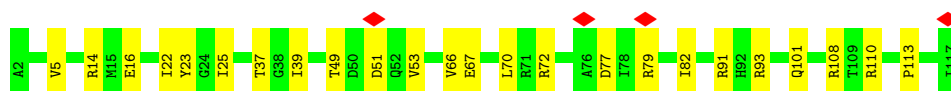
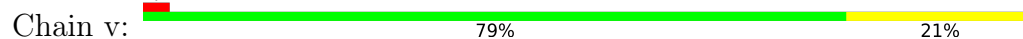
Chain t:  79% 21%



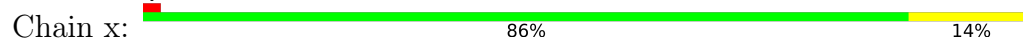
- Molecule 12: 30S ribosomal protein S12



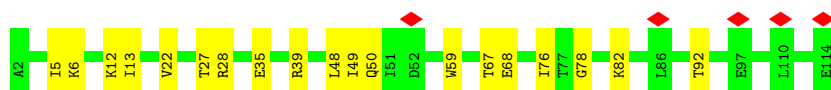
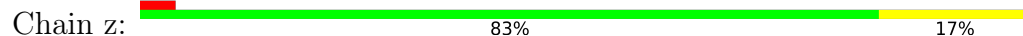
- Molecule 13: 30S ribosomal protein S13



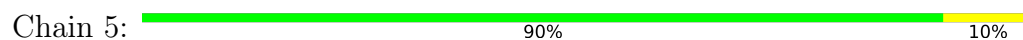
- Molecule 14: 30S ribosomal protein S15



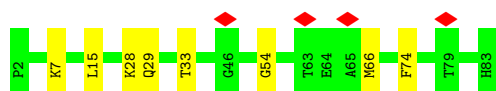
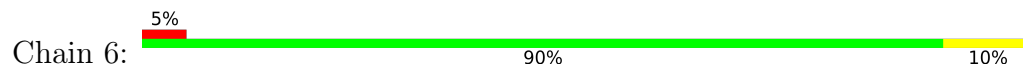
- Molecule 15: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S17



- Molecule 17: 30S ribosomal protein S19



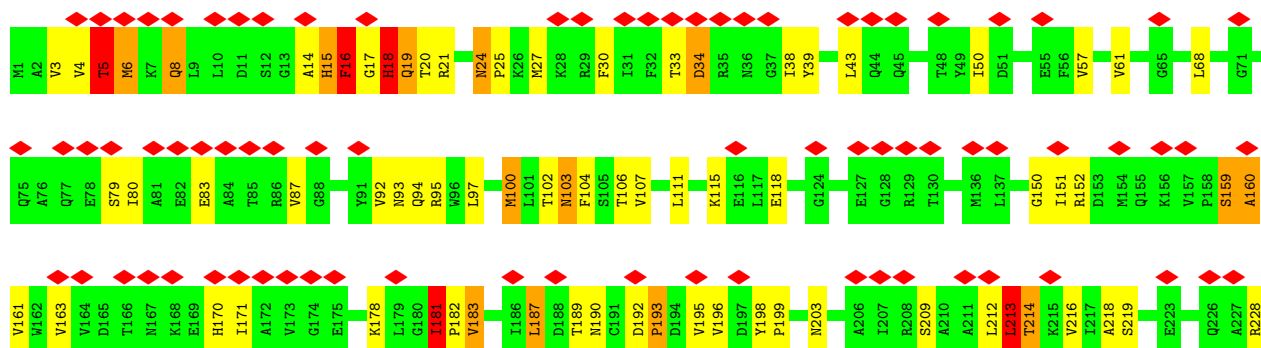
- Molecule 18: 30S ribosomal protein S20

Chain 7:  82% 16% .



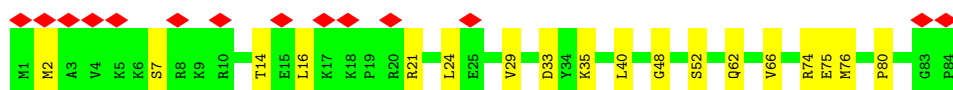
- Molecule 19: 30S ribosomal protein S2

Chain 8:  34% 67% 25% 6% .



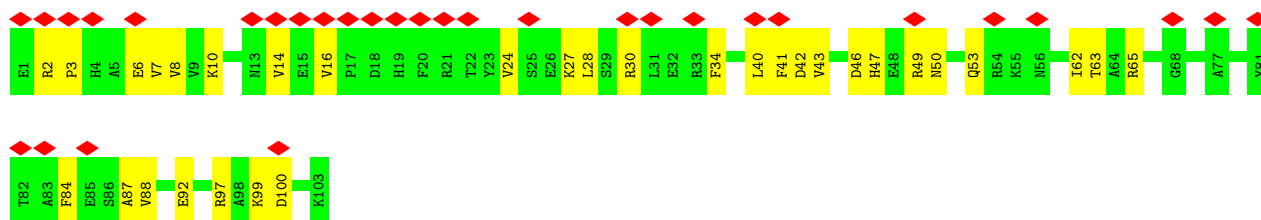
- Molecule 20: 30S ribosomal protein S18 1

Chain r:  17% 79% 21%



- Molecule 21: Ribosome hibernation promoting factor

Chain Y:  30% 69% 31%



- Molecule 22: 30S ribosomal protein S14

Chain 9:  77% 23%



- Molecule 23: 23 S rRNA (3119-MER)

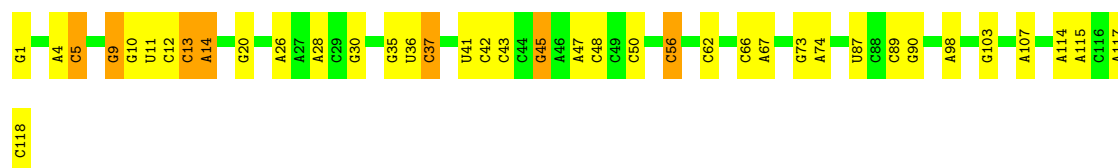
Chain A:  64% 29% 6%

U1544	C1440	C1287	A1195	C1103	U995	A897	U641	U544	U444	U337	C250	C126	A2
C1545	C1445	C1290	U1199	C1104	U996	A898	C642	G551	U445	C338	A251	C127	A3
G1546	U1444	G1291	U1200	C1105	G997	G899	G643	G552	G446	U339	A255	G128	U7
C1548	C1445	U1292	G1201	G1107	G997	G904	G644	G553	U448	C341	C259	U136	A11
G1549	C1449	U1293	A1202	C1112	C1001	A904	G645	G554	U449	C342	A265	G137	A11
G1550	C1450	U1294	A1203	C1113	C1002	G905	G646	G555	G450	U343	U266	A138	U19
U1551	C1456	U1551	A1204	C1114	C1003	A907	A648	G556	U451	G348	G267	U139	G20
A1552	C1457	G1302	G1205	C1115	C1004	A908	U654	G561	C455	G351	G271	A148	G23
C1553	U1503	U1303	A1206	G1116	A1005	A909	G655	G562	U452	G352	A271	C150	G24
U1554	C1462	A1504	G1207	C1117	A1006	G910	G656	U563	G460	G352	G272	A151	A25
A1555	C1462	G1305	U1208	U1117	G1007	U911	U658	G564	G467	A355	A273	A159	C28
A1556	C1465	U1320	G1209	A1118	C1008	U915	U661	A565	C467	G356	A279	A160	C29
C1557	C1468	U1320	U1212	G1121	A1011	G916	G662	A566	C472	U357	U279	U161	U30
A1558	C1478	U1325	A1213	C1125	C1012	G920	A663	A567	C473	A361	A282	U163	U31
U1560	C1479	G1332	U1215	U1126	A1013	G920	G664	A568	G474	A362	U285	U164	G32
C1562	A1480	U1337	A1216	A1127	A1015	G924	G665	G569	U475	A363	G286	A180	C43
A1563	C1482	G1338	U1219	G1128	A1025	U926	A667	C574	U482	U370	A287	U47	U47
A1564	G1483	G1339	C1222	G1129	C1027	C927	C676	G578	G483	A364	U288	G183	G48
A1565	C1484	G1343	U1223	G1130	U1028	G933	G679	G585	C484	U370	A289	G188	A49
C1566	A1493	A1344	G1224	U1141	C1029	A934	G683	A588	U489	A376	G292	A195	U56
C1567	G1494	G1345	G1225	G1142	C1030	A935	G684	A589	A490	C377	G298	A198	A57
A1568	U1499	A1352	C1227	G1143	U1034	U941	G685	A590	U491	A381	G299	A203	G58
A1569	C1495	G1353	U1228	A1144	U1034	U942	A696	A591	U492	A382	G300	G204	G59
C1570	A1500	U1359	A1229	G1148	G1038	U943	G697	A592	C492	A383	U301	A204	A60
G1572	C1501	G1362	G1230	U1151	C1046	A944	U700	U594	U493	A384	G302	G188	A63
U1573	G1507	G1365	U1234	U1152	A1047	G946	A701	A595	G494	U383	U304	G210	A71
A1574	C1508	U1370	U1235	U1153	A1048	U947	G706	A596	G499	G384	G305	U211	G72
C1576	U1509	G1371	G1238	G1157	G1049	G948	G707	C603	C505	A389	G306	G213	A81
C1577	U1511	U1371	C1239	U1157	U1058	U954	G708	C604	C506	A391	U307	G214	G82
G1578	A1518	C1376	G1240	G1162	G1059	U959	G713	G605	G507	A392	G314	A215	C83
C1579	C1522	A1377	A1244	A1163	G1061	G960	U714	C610	G508	U393	U315	A216	U84
A1580	U1523	U1380	A1245	G1165	G1062	U961	A715	C614	U509	A404	U316	A220	G85
C1581	G1524	G1381	G1251	G1173	G1063	C964	G717	U617	G512	A412	U317	A221	G84
U1582	U1525	U1387	G1252	U1178	U1075	U965	G718	U618	C513	G413	U318	A222	C95
U1584	U1529	G1386	C1253	U1179	A1076	C969	G724	C619	C514	U417	U319	A223	G96
U1585	G1530	U1388	C1258	G1180	G1077	G970	A725	G620	U515	A428	U327	A227	U97
C1586	C1531	U1389	U1259	U1183	C1079	G971	A726	G621	G516	A428	U328	A228	G98
G1587	G1532	C1404	C1260	U1184	U1080	A972	A727	A625	A517	A428	U329	U229	G99
U1588	U1533	C1404	A1261	U1184	C1081	G973	G730	A633	U523	C433	U330	G230	G107
C1589	C1534	C1408	A1267	A1185	U1084	G974	A731	A634	C530	G434	U331	U231	A108
U1590	C1535	A1415	G1270	G1186	G1085	U975	A736	A635	A531	A435	U332	A233	U109
U1591	U1537	A1416	A1271	A1187	C1086	A976	A737	G635	C532	C436	U333	A241	G114
G1592	C1538	C1272	C1271	G1188	A1091	G977	A738	U636	C533	G437	C332	A241	A115
U1593	A1539	C1435	A1275	C1190	G1092	A978	U739	U637	C539	U440	C333	G247	A116
C1594	U1540	C1436	A1275	G1191	A1101	U981	A740	U638	C539	G441	G334	G248	U117
G1595	A1543	A1437	A1275	G1192	G1102	C983	G741	G640	U543		C336	C249	C125

G3068	G3070	A3071	G3078	U3079	A3080	A3081	U3082	G3087	C3088	A3089	G3092	A3093	A3094	C3095	U3096	A3100	C3101	U3102	A3103	A3104	C3105	G3106	G3107	A3112	A3115	C3116	U3117	U3118	A3119	C3120
U2963	A2964	C2965	C2966	C2967	C2968	C2969	C2970	C2971	C2972	C2973	C2974	C2975	C2976	C2977	C2978	C2979	C2980	C2981	C2982	C2983	C2984	C2985	C2986	C2987	C2988	C2989	C2990	C2991	C2992	C2993
C2830	C2833	C2834	C2835	C2836	C2837	C2838	C2839	C2840	C2841	C2842	C2843	C2844	C2845	C2846	C2847	C2848	C2849	C2850	C2851	C2852	C2853	C2854	C2855	C2856	C2857	C2858	C2859	C2860	C2861	C2862
C2720	C2721	C2722	C2723	C2724	C2725	C2726	C2727	C2728	C2729	C2730	C2731	C2732	C2733	C2734	C2735	C2736	C2737	C2738	C2739	C2740	C2741	C2742	C2743	C2744	C2745	C2746	C2747	C2748	C2749	C2750
G2596	A2597	A2598	A2599	A2600	A2601	A2602	A2603	A2604	A2605	A2606	A2607	A2608	A2609	A2610	A2611	A2612	A2613	A2614	A2615	A2616	A2617	A2618	A2619	A2620	A2621	A2622	A2623	A2624	A2625	A2626
G2475	G2476	G2477	G2478	G2479	G2480	G2481	G2482	G2483	G2484	G2485	G2486	G2487	G2488	G2489	G2490	G2491	G2492	G2493	G2494	G2495	G2496	G2497	G2498	G2499	G2500	G2501	G2502	G2503	G2504	G2505
G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409
G2285	A2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315
G2178	U2179	U2180	A2181	C2182	C2183	C2184	C2185	C2186	C2187	C2188	C2189	C2190	C2191	C2192	C2193	C2194	C2195	C2196	C2197	C2198	C2199	C2200	C2201	C2202	C2203	C2204	C2205	C2206	C2207	C2208
G2064	A2065	G2066	A2067	A2068	A2069	A2070	A2071	A2072	A2073	A2074	A2075	A2076	A2077	A2078	A2079	A2080	A2081	A2082	A2083	A2084	A2085	A2086	A2087	A2088	A2089	A2090	A2091	A2092	A2093	A2094
U1947	A1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977
C1830	A1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	C1840	C1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	C1850	C1851	C1852	C1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860
A1715	A1716	C1717	C1718	C1719	C1720	C1721	C1722	C1723	C1724	C1725	C1726	C1727	C1728	C1729	C1730	C1731	C1732	C1733	C1734	C1735	C1736	C1737	C1738	C1739	C1740	C1741	C1742	C1743	C1744	C1745
U1604	A1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634
G1604	U1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634

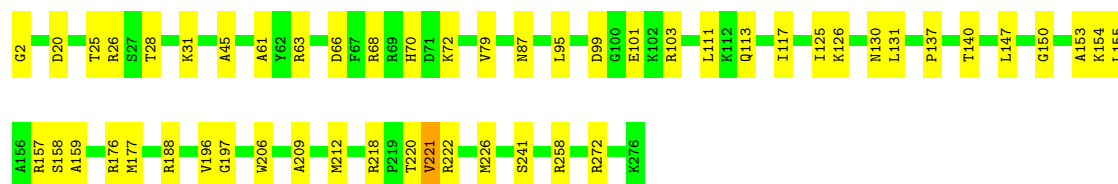
- Molecule 24: 5S RNA (118-MER)

Chain B:  67% 27% 6%



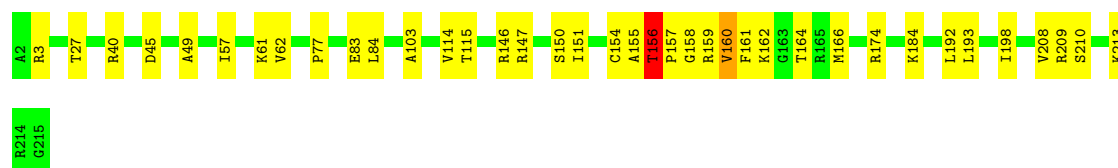
- Molecule 25: 50S ribosomal protein L2

Chain C:  81% 19%



- Molecule 26: 50S ribosomal protein L3

Chain D:  82% 17%



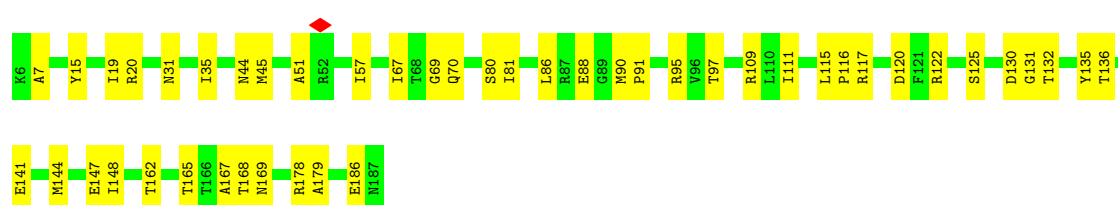
- Molecule 27: 50S ribosomal protein L4

Chain E:  88% 12%



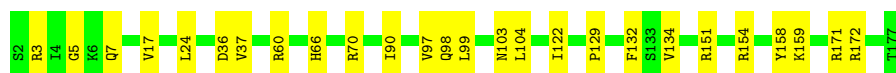
- Molecule 28: 50S ribosomal protein L5

Chain F:  75% 25%

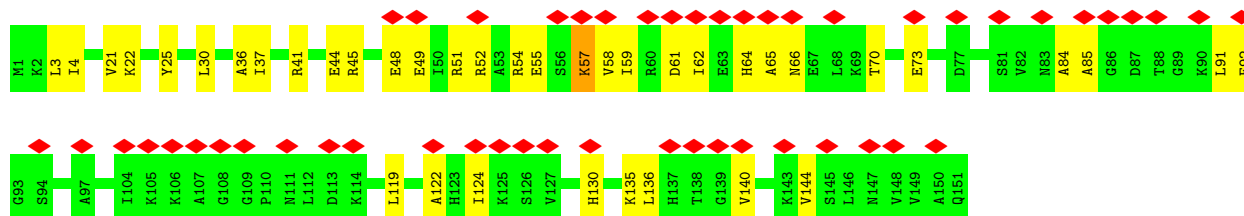
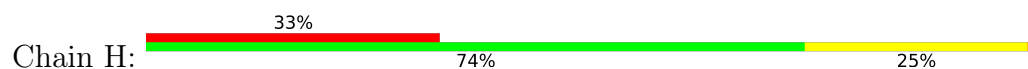


- Molecule 29: 50S ribosomal protein L6

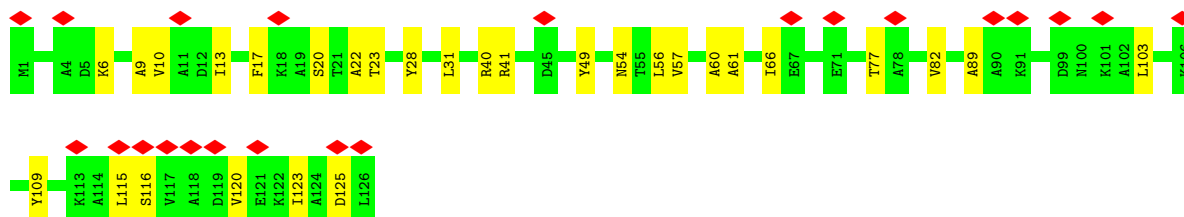
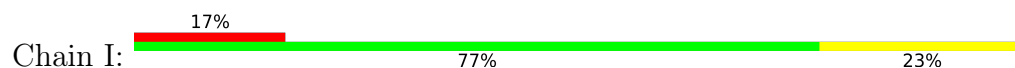
Chain G:  85% 15%



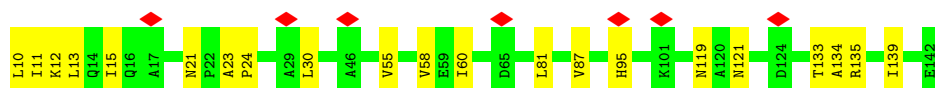
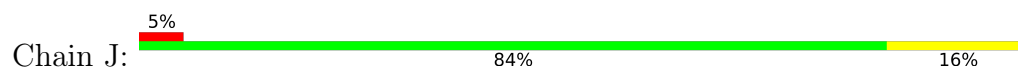
- Molecule 30: 50S ribosomal protein L9



- Molecule 31: 50S ribosomal protein L10



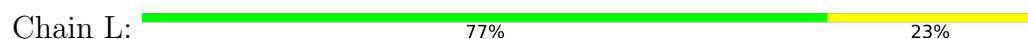
- Molecule 32: 50S ribosomal protein L11



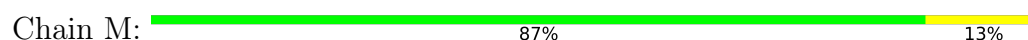
- Molecule 33: 50S ribosomal protein L13



- Molecule 34: 50S ribosomal protein L14



- Molecule 35: 50S ribosomal protein L15





- Molecule 36: 50S ribosomal protein L16



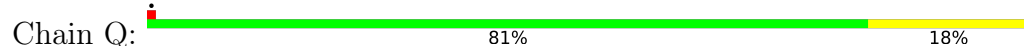
- Molecule 37: 50S ribosomal protein L17



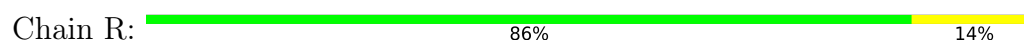
- Molecule 38: 50S ribosomal protein L18



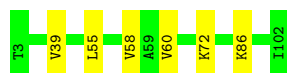
- Molecule 39: 50S ribosomal protein L19



- Molecule 40: 50S ribosomal protein L20



- Molecule 41: 50S ribosomal protein L21

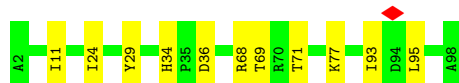
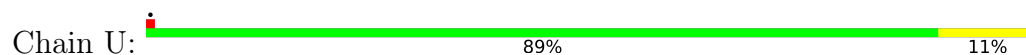


- Molecule 42: 50S ribosomal protein L22

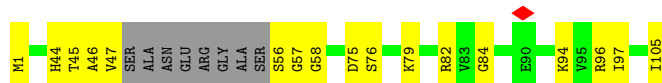
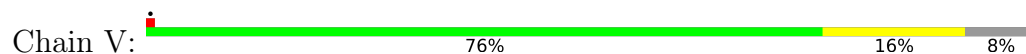




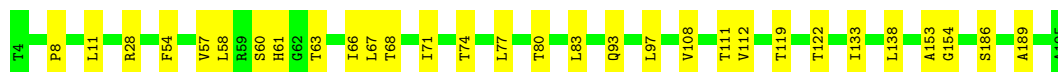
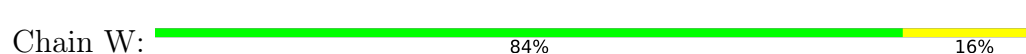
- Molecule 43: 50S ribosomal protein L23



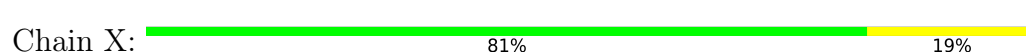
- Molecule 44: 50S ribosomal protein L24



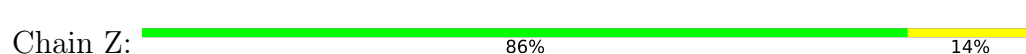
- Molecule 45: 50S ribosomal protein L25



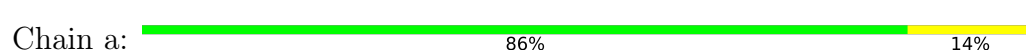
- Molecule 46: 50S ribosomal protein L27



- Molecule 47: 50S ribosomal protein L29

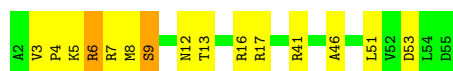


- Molecule 48: 50S ribosomal protein L30

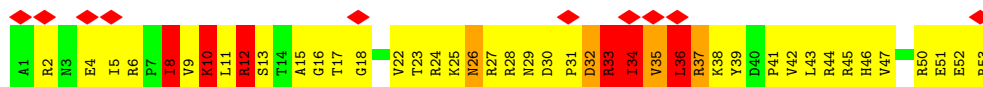


- Molecule 49: 50S ribosomal protein L32

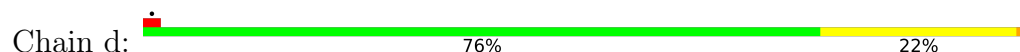




- Molecule 50: 50S ribosomal protein L33 2



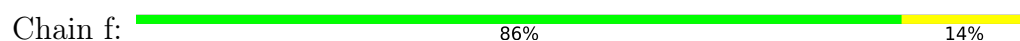
- Molecule 51: 50S ribosomal protein L34



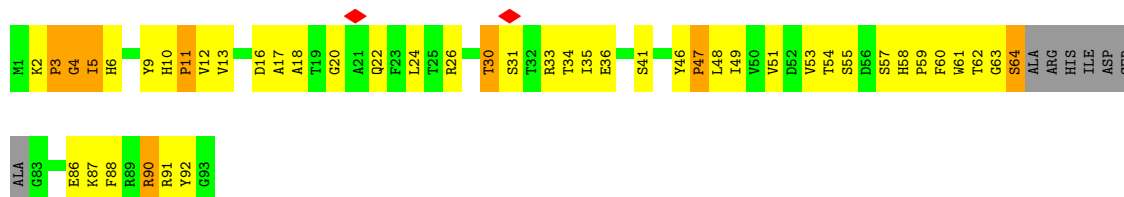
- Molecule 52: 50S ribosomal protein L35



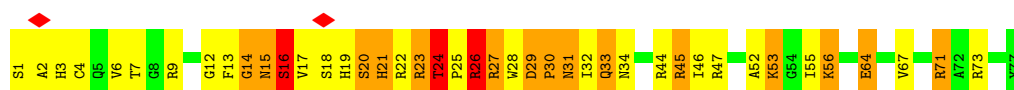
- Molecule 53: 50S ribosomal protein L36



- Molecule 54: 50S ribosomal protein L31



- Molecule 55: 50S ribosomal protein L28



- Molecule 56: Uncharacterized protein

Chain 3:  61% 35% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	66840	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 ($e^-/\text{\AA}^2$)	67.10	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.313	Depositor
Minimum map value	-0.175	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	485.78003, 485.78003, 485.78003	wwPDB
Map dimensions	454, 454, 454	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	h	0.34	0/36309	0.43	9/56657 (0.0%)
2	j	0.56	0/280	0.66	0/359
3	k	0.31	0/1684	0.50	0/2261
4	l	0.32	0/1672	0.55	0/2251
5	m	0.36	0/1312	0.55	0/1772
6	n	0.37	0/782	0.54	0/1059
7	p	0.30	0/1252	0.56	0/1690
8	q	0.39	0/1025	0.53	0/1385
9	4	0.30	0/1012	0.57	0/1362
10	s	0.31	0/802	0.50	0/1086
11	t	0.39	0/873	0.55	0/1180
12	u	0.42	0/969	0.64	0/1294
13	v	0.31	0/942	0.55	0/1260
14	x	0.45	0/729	0.52	0/977
15	z	0.36	0/908	0.64	0/1226
16	5	0.37	0/759	0.55	0/1016
17	6	0.31	0/680	0.53	0/915
18	7	0.42	0/663	0.52	0/882
19	8	0.50	0/1822	1.51	40/2457 (1.6%)
20	r	0.38	0/665	0.60	0/889
21	Y	0.34	0/875	0.56	0/1169
22	9	0.32	0/830	0.54	0/1106
23	A	0.57	0/75001	0.51	11/117027 (0.0%)
24	B	0.44	0/2821	0.43	0/4396
25	C	0.74	1/2153 (0.0%)	0.68	3/2895 (0.1%)
26	D	0.74	0/1609	0.75	3/2165 (0.1%)
27	E	0.64	0/1592	0.57	0/2153
28	F	0.45	0/1467	0.55	0/1973
29	G	0.47	0/1369	0.60	0/1848
30	H	0.40	0/1129	0.65	0/1524
31	I	0.29	0/925	0.50	0/1246
32	J	0.32	0/1006	0.58	0/1364
33	K	0.67	0/1157	0.58	0/1567
34	L	0.73	0/946	0.63	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.65	0/1091	0.65	0/1457
36	N	0.67	0/1118	0.62	0/1506
37	O	0.75	0/945	0.64	0/1267
38	P	0.55	0/966	0.58	0/1298
39	Q	0.74	1/921 (0.1%)	0.72	2/1236 (0.2%)
40	R	0.83	0/1000	0.63	0/1341
41	S	0.63	0/764	0.55	0/1030
42	T	0.74	0/887	0.62	0/1204
43	U	0.62	0/766	0.57	0/1030
44	V	0.48	0/738	0.58	0/987
45	W	0.49	0/1443	0.55	0/1970
46	X	0.75	0/595	0.59	0/798
47	Z	0.57	0/534	0.57	0/713
48	a	0.69	0/477	0.56	0/640
49	b	0.69	0/427	0.78	0/572
50	c	0.57	0/463	1.16	4/621 (0.6%)
51	d	0.86	0/380	0.90	3/500 (0.6%)
52	e	0.70	0/507	0.59	0/672
53	f	0.77	0/303	0.55	0/401
54	g	0.45	0/613	1.02	2/835 (0.2%)
55	y	0.56	0/629	1.09	7/843 (0.8%)
56	3	0.76	0/191	0.73	1/247 (0.4%)
All	All	0.52	2/163778 (0.0%)	0.54	85/244847 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	l	0	1
19	8	0	10
26	D	0	1
32	J	0	1
45	W	0	1
All	All	0	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	Q	50	GLN	CA-CB	-10.13	1.35	1.53
25	C	45	ALA	CA-C	-5.51	1.45	1.52

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	8	187	LEU	CA-C-N	16.06	144.38	121.42
19	8	187	LEU	C-N-CA	16.06	144.38	121.42
54	g	90	ARG	N-CA-C	-12.06	97.28	112.72
19	8	18	HIS	CA-C-N	10.36	141.60	122.02
19	8	18	HIS	C-N-CA	10.36	141.60	122.02
19	8	159	SER	CA-C-N	10.15	136.04	122.84
19	8	159	SER	C-N-CA	10.15	136.04	122.84
19	8	100	MET	CA-C-N	9.90	136.57	120.63
19	8	100	MET	C-N-CA	9.90	136.57	120.63
19	8	178	LYS	CA-C-N	9.87	139.03	121.66
19	8	178	LYS	C-N-CA	9.87	139.03	121.66
19	8	213	LEU	CA-CB-CG	9.45	149.37	116.30
19	8	5	THR	CA-C-N	9.38	133.20	120.44
19	8	5	THR	C-N-CA	9.38	133.20	120.44
39	Q	93	ARG	CA-C-N	8.71	138.14	122.46
39	Q	93	ARG	C-N-CA	8.71	138.14	122.46
25	C	221	VAL	CA-C-N	8.68	137.39	121.06
25	C	221	VAL	C-N-CA	8.68	137.39	121.06
19	8	103	ASN	CA-C-N	8.64	133.44	120.31
19	8	103	ASN	C-N-CA	8.64	133.44	120.31
19	8	195	VAL	CA-C-N	8.47	133.07	120.95
19	8	195	VAL	C-N-CA	8.47	133.07	120.95
50	c	8	ILE	N-CA-C	-8.43	97.72	108.84
19	8	218	ALA	CA-C-N	8.24	131.16	120.44
19	8	218	ALA	C-N-CA	8.24	131.16	120.44
19	8	170	HIS	CA-C-N	8.13	134.44	120.86
19	8	170	HIS	C-N-CA	8.13	134.44	120.86
55	y	24	THR	CA-C-N	8.05	127.94	120.21
55	y	24	THR	C-N-CA	8.05	127.94	120.21
26	D	158	GLY	N-CA-C	-7.73	103.34	116.01
51	d	9	GLN	N-CA-C	-7.23	95.29	109.10
26	D	156	THR	C-N-CD	7.20	136.43	120.60
50	c	26	ASN	N-CA-C	6.83	119.79	109.41
23	A	897	A	C4'-C3'-O3'	6.82	119.64	109.40
26	D	160	VAL	N-CA-CB	-6.71	100.16	111.23
55	y	71	ARG	N-CA-C	-6.61	104.15	111.36
1	h	1080	C	C2'-C3'-O3'	6.59	123.59	113.70
1	h	1082	A	C1'-C2'-O2'	6.56	118.24	108.40
23	A	2510	A	C4'-C3'-O3'	6.56	119.24	109.40
54	g	4	GLY	N-CA-C	-6.54	97.68	113.18
19	8	43	LEU	N-CA-C	6.53	118.08	110.97
23	A	2510	A	C3'-C2'-O2'	6.40	124.19	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	h	1082	A	C3'-C2'-O2'	6.39	120.28	110.70
55	y	24	THR	O-C-N	6.39	128.66	121.32
19	8	214	THR	OG1-CB-CG2	6.28	121.86	109.30
23	A	2510	A	C1'-C2'-O2'	6.23	121.15	111.80
19	8	198	TYR	N-CA-C	6.21	123.11	108.40
55	y	64	GLU	N-CA-C	-6.09	104.33	110.97
23	A	2512	A	C4'-C3'-O3'	6.05	118.47	109.40
19	8	79	SER	CA-C-N	5.99	128.67	120.46
19	8	79	SER	C-N-CA	5.99	128.67	120.46
23	A	2003	A	C5'-C4'-C3'	5.89	124.03	115.20
51	d	9	GLN	CA-C-N	-5.87	113.91	120.14
51	d	9	GLN	C-N-CA	-5.87	113.91	120.14
1	h	1081	A	O4'-C1'-N9	5.87	117.00	108.20
23	A	2004	A	C1'-C2'-O2'	5.71	116.96	108.40
19	8	213	LEU	CB-CG-CD2	5.65	127.64	110.70
56	3	11	ARG	N-CA-C	-5.64	105.13	112.23
19	8	106	THR	OG1-CB-CG2	5.62	120.53	109.30
19	8	8	GLN	CA-CB-CG	5.59	125.29	114.10
23	A	2004	A	C3'-C2'-O2'	5.57	119.05	110.70
55	y	16	SER	N-CA-C	5.53	122.57	110.80
23	A	2509	C	O4'-C1'-N1	5.51	116.77	108.50
1	h	841	U	C5'-C4'-O4'	5.46	117.99	109.80
50	c	10	LYS	N-CA-C	5.44	122.39	110.80
19	8	102	THR	OG1-CB-CG2	5.40	120.10	109.30
55	y	20	SER	N-CA-C	-5.38	99.34	110.80
19	8	92	VAL	CG1-CB-CG2	5.32	122.51	110.80
25	C	220	THR	OG1-CB-CG2	5.31	119.93	109.30
19	8	6	MET	N-CA-C	5.29	116.86	111.14
1	h	1081	A	N9-C1'-C2'	5.29	121.94	114.00
1	h	1080	C	C4'-C3'-O3'	5.27	120.91	113.00
23	A	2003	A	C4'-C3'-O3'	5.24	117.26	109.40
19	8	50	ILE	CG1-CB-CG2	5.23	126.39	110.70
19	8	183	VAL	CG1-CB-CG2	5.14	122.12	110.80
1	h	1079	G	C2'-C3'-O3'	5.14	121.41	113.70
19	8	214	THR	CA-CB-CG2	5.14	119.23	110.50
19	8	106	THR	CA-CB-CG2	5.13	119.22	110.50
23	A	2005	C	C4'-C3'-O3'	5.11	120.67	113.00
19	8	228	ARG	N-CA-C	5.08	125.23	111.00
1	h	842	A	C5'-C4'-C3'	5.07	123.60	116.00
19	8	80	ILE	CG1-CB-CG2	5.06	125.88	110.70
19	8	181	ILE	CG1-CB-CG2	5.06	125.88	110.70
50	c	36	LEU	N-CA-C	5.05	121.57	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	8	3	VAL	CG1-CB-CG2	5.01	121.82	110.80

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	8	159	SER	Peptide
19	8	160	ALA	Peptide
19	8	181	ILE	Peptide
19	8	192	ASP	Peptide
19	8	193	PRO	Peptide
19	8	24	ASN	Peptide
19	8	34	ASP	Peptide
19	8	4	VAL	Peptide
19	8	5	THR	Peptide
19	8	8	GLN	Peptide
26	D	147	ARG	Peptide
32	J	21	ASN	Peptide
45	W	153	ALA	Peptide
4	l	189	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	h	32439	0	16321	272	0
2	j	280	0	342	3	0
3	k	1660	0	1707	36	0
4	l	1641	0	1668	18	0
5	m	1296	0	1360	18	0
6	n	771	0	797	29	0
7	p	1232	0	1281	30	0
8	q	1010	0	1042	27	0
9	4	994	0	1050	37	0
10	s	788	0	819	13	0
11	t	855	0	863	15	0
12	u	958	0	1045	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	v	935	0	986	18	0
14	x	720	0	760	9	0
15	z	891	0	935	14	0
16	5	748	0	795	8	0
17	6	662	0	677	5	0
18	7	660	0	712	18	0
19	8	1793	0	1839	61	0
20	r	659	0	717	17	0
21	Y	861	0	862	25	0
22	9	819	0	866	17	0
23	A	66981	0	33700	396	0
24	B	2522	0	1285	15	0
25	C	2110	0	2165	45	0
26	D	1587	0	1630	32	0
27	E	1569	0	1607	18	0
28	F	1445	0	1476	40	0
29	G	1348	0	1399	20	0
30	H	1119	0	1165	54	0
31	I	918	0	959	20	0
32	J	990	0	1021	18	0
33	K	1130	0	1167	7	0
34	L	938	0	1000	22	0
35	M	1078	0	1151	26	0
36	N	1092	0	1128	10	0
37	O	928	0	972	17	0
38	P	956	0	991	12	0
39	Q	907	0	938	13	0
40	R	988	0	1038	13	0
41	S	754	0	802	4	0
42	T	873	0	909	12	0
43	U	756	0	802	10	0
44	V	732	0	782	20	0
45	W	1428	0	1443	17	0
46	X	586	0	601	10	0
47	Z	531	0	541	8	0
48	a	474	0	500	6	0
49	b	423	0	460	23	0
50	c	456	0	474	109	0
51	d	377	0	411	12	0
52	e	502	0	541	32	0
53	f	299	0	324	6	0
54	g	593	0	568	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	y	617	0	625	77	0
56	3	189	0	205	15	0
All	All	150868	0	102224	1615	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 7.

All (1615) 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)
55:y:14:GLY:HA3	55:y:28:TRP:CZ3	1.28	1.66
54:g:35:ILE:CD1	54:g:49:ILE:HG23	1.12	1.58
19:8:16:PHE:CD2	19:8:203:ASN:ND2	1.72	1.54
7:p:61:THR:CB	7:p:64:ARG:NH2	1.69	1.50
55:y:14:GLY:CA	55:y:28:TRP:CZ3	1.97	1.47
54:g:60:PHE:HE1	54:g:62:THR:CG2	1.12	1.45
1:h:808:A:H2	19:8:24:ASN:ND2	1.20	1.40
55:y:14:GLY:CA	55:y:28:TRP:HZ3	1.29	1.40
7:p:61:THR:HB	7:p:64:ARG:NH2	1.11	1.39
1:h:808:A:C2	19:8:24:ASN:ND2	1.92	1.37
54:g:35:ILE:CD1	54:g:49:ILE:CG2	2.03	1.36
54:g:35:ILE:HD13	54:g:49:ILE:CG2	1.56	1.32
19:8:16:PHE:HD2	19:8:203:ASN:ND2	0.83	1.31
23:A:2279:C:OP1	49:b:5:LYS:NZ	1.61	1.31
50:c:15:ALA:HB3	50:c:18:GLY:O	1.14	1.30
54:g:60:PHE:CE1	54:g:62:THR:HG23	1.27	1.28
30:H:55:GLU:O	30:H:59:ILE:HG23	1.21	1.28
1:h:1097:G:O3'	9:4:126:ARG:NE	1.63	1.26
50:c:6:ARG:HG3	50:c:8:ILE:O	1.23	1.26
55:y:14:GLY:HA3	55:y:28:TRP:CH2	1.68	1.25
44:V:47:VAL:HB	44:V:56:SER:N	1.51	1.24
50:c:10:LYS:O	50:c:11:LEU:HD23	1.34	1.23
49:b:8:MET:CE	49:b:16:ARG:HH12	1.50	1.23
55:y:44:ARG:NH1	55:y:46:ILE:HD11	1.52	1.23
55:y:23:ARG:O	55:y:24:THR:OG1	1.55	1.21
44:V:45:THR:O	44:V:57:GLY:HA3	1.41	1.21
23:A:2442:U:OP1	55:y:45:ARG:NH1	1.73	1.21
50:c:27:ARG:NH1	50:c:29:ASN:HB2	1.53	1.20
50:c:10:LYS:NZ	50:c:53:ARG:CD	2.05	1.20
55:y:26:ARG:O	55:y:27:ARG:O	1.61	1.19
54:g:60:PHE:CE1	54:g:62:THR:CG2	1.89	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:k:62:ARG:NH1	3:k:64:ARG:HB2	1.60	1.16
19:8:16:PHE:CD2	19:8:203:ASN:CG	2.23	1.16
54:g:10:HIS:HB3	54:g:30:THR:CG2	1.74	1.16
28:F:122:ARG:O	54:g:61:TRP:NE1	1.80	1.15
50:c:5:ILE:HG23	50:c:28:ARG:NH2	1.62	1.14
44:V:45:THR:O	44:V:57:GLY:CA	1.94	1.14
50:c:36:LEU:O	50:c:37:ARG:HG3	1.46	1.14
50:c:37:ARG:HE	50:c:51:GLU:HG3	1.02	1.13
30:H:4:ILE:HG13	30:H:45:ARG:CD	1.79	1.12
35:M:64:LEU:HD13	52:e:15:ARG:HE	1.11	1.12
19:8:16:PHE:CD2	19:8:203:ASN:CB	2.33	1.12
23:A:2314:U:H1'	55:y:33:GLN:HE22	1.08	1.12
50:c:6:ARG:O	50:c:9:VAL:CG1	1.97	1.11
55:y:14:GLY:N	55:y:28:TRP:HZ3	1.47	1.10
3:k:62:ARG:HH12	3:k:64:ARG:HD2	0.96	1.10
49:b:8:MET:HE1	49:b:16:ARG:HH12	1.14	1.10
50:c:10:LYS:NZ	50:c:53:ARG:HD2	1.65	1.10
50:c:25:LYS:HD2	52:e:34:GLU:CD	1.76	1.10
35:M:64:LEU:HD13	52:e:15:ARG:NE	1.67	1.09
49:b:8:MET:CE	49:b:16:ARG:NH1	2.15	1.08
30:H:4:ILE:HG13	30:H:45:ARG:HD3	1.09	1.08
3:k:62:ARG:NH1	3:k:64:ARG:HD2	1.68	1.08
50:c:10:LYS:HZ2	50:c:53:ARG:CD	1.61	1.08
19:8:16:PHE:CD2	19:8:203:ASN:HB2	1.88	1.07
50:c:27:ARG:HH11	50:c:29:ASN:HB2	1.08	1.07
54:g:87:LYS:HB3	54:g:91:ARG:NH1	1.69	1.07
7:p:61:THR:OG1	7:p:64:ARG:NH2	1.88	1.06
50:c:44:ARG:HG3	50:c:45:ARG:H	0.93	1.06
50:c:10:LYS:HZ2	50:c:53:ARG:HD2	0.94	1.05
54:g:86:GLU:O	54:g:90:ARG:CG	2.03	1.05
55:y:14:GLY:N	55:y:28:TRP:CZ3	2.20	1.05
3:k:62:ARG:HH12	3:k:64:ARG:CD	1.69	1.05
25:C:155:LEU:HD13	25:C:177:MET:HE1	1.37	1.05
55:y:26:ARG:HB2	55:y:26:ARG:HH21	1.21	1.05
1:h:1097:G:H5''	9:4:126:ARG:NH2	1.70	1.04
5:m:102:ILE:O	5:m:104:SER:N	1.90	1.04
44:V:47:VAL:CB	44:V:56:SER:N	2.21	1.03
49:b:8:MET:HE1	49:b:16:ARG:NH1	1.68	1.03
54:g:35:ILE:HD13	54:g:49:ILE:CB	1.88	1.03
44:V:47:VAL:C	44:V:56:SER:N	2.16	1.03
7:p:61:THR:CB	7:p:64:ARG:CZ	2.37	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:g:86:GLU:O	54:g:90:ARG:HG3	1.55	1.02
55:y:26:ARG:HD2	55:y:28:TRP:CH2	1.94	1.02
50:c:15:ALA:CB	50:c:18:GLY:O	2.07	1.01
54:g:10:HIS:CB	54:g:30:THR:HG21	1.90	1.01
54:g:35:ILE:HD13	54:g:49:ILE:HG23	1.00	1.00
54:g:35:ILE:HD11	54:g:49:ILE:HG23	1.02	1.00
50:c:6:ARG:O	50:c:9:VAL:HG13	1.60	0.99
7:p:61:THR:HA	7:p:64:ARG:CZ	1.92	0.99
50:c:44:ARG:HG3	50:c:45:ARG:N	1.69	0.99
1:h:1097:G:C3'	9:4:126:ARG:HE	1.73	0.99
50:c:37:ARG:NE	50:c:51:GLU:HG3	1.75	0.99
3:k:62:ARG:CZ	3:k:64:ARG:HB2	1.93	0.98
7:p:27:VAL:HG12	7:p:43:VAL:HG21	1.45	0.98
50:c:13:SER:HB2	50:c:22:VAL:O	1.63	0.98
54:g:35:ILE:HB	54:g:48:LEU:O	1.64	0.97
54:g:10:HIS:CB	54:g:30:THR:CG2	2.41	0.97
23:A:306:U:H4'	30:H:44:GLU:HG3	1.46	0.97
7:p:61:THR:HB	7:p:64:ARG:CZ	1.93	0.97
50:c:6:ARG:CG	50:c:8:ILE:O	2.13	0.97
50:c:6:ARG:NE	50:c:8:ILE:HG22	1.78	0.97
50:c:44:ARG:O	50:c:45:ARG:NH2	1.98	0.97
54:g:35:ILE:HD13	54:g:49:ILE:HA	1.47	0.96
50:c:2:ARG:HD3	50:c:4:GLU:OE2	1.65	0.96
23:A:2314:U:H1'	55:y:33:GLN:NE2	1.80	0.95
54:g:30:THR:HA	54:g:34:THR:CG2	1.95	0.95
6:n:77:ARG:NH2	25:C:126:LYS:HG2	1.81	0.95
50:c:9:VAL:HG21	50:c:28:ARG:HD3	1.49	0.95
8:q:11:LEU:HD22	8:q:77:LEU:HD21	1.48	0.95
55:y:44:ARG:NH1	55:y:46:ILE:CD1	2.29	0.94
50:c:5:ILE:HG23	50:c:28:ARG:HH21	1.19	0.94
19:8:14:ALA:O	19:8:15:HIS:CG	2.20	0.94
54:g:10:HIS:HB2	54:g:30:THR:HG21	1.50	0.94
30:H:55:GLU:O	30:H:59:ILE:CG2	2.15	0.93
54:g:35:ILE:HD13	54:g:49:ILE:CA	1.98	0.93
7:p:61:THR:CA	7:p:64:ARG:CZ	2.46	0.92
55:y:26:ARG:HB2	55:y:26:ARG:NH2	1.84	0.92
3:k:62:ARG:NH2	3:k:64:ARG:HG3	1.82	0.92
50:c:44:ARG:CG	50:c:45:ARG:H	1.81	0.92
28:F:132:THR:OG1	28:F:168:THR:C	2.12	0.92
50:c:10:LYS:NZ	50:c:53:ARG:HD3	1.83	0.92
50:c:5:ILE:CG2	50:c:28:ARG:HH21	1.83	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:M:63:LYS:HA	52:e:13:ARG:HG3	1.49	0.91
54:g:87:LYS:HB3	54:g:91:ARG:HH12	1.25	0.91
18:7:15:GLU:O	18:7:18:ARG:HG3	1.70	0.91
54:g:10:HIS:N	54:g:30:THR:OG1	2.05	0.90
54:g:10:HIS:HB3	54:g:30:THR:HG23	1.54	0.90
50:c:36:LEU:O	50:c:37:ARG:CG	2.20	0.89
54:g:30:THR:HA	54:g:34:THR:HG21	1.53	0.89
1:h:794:A:HO2'	1:h:1494:C:HO2'	1.15	0.88
35:M:64:LEU:CD1	52:e:15:ARG:HE	1.87	0.88
26:D:155:ALA:O	26:D:156:THR:OG1	1.92	0.87
50:c:9:VAL:HG21	50:c:28:ARG:CD	2.05	0.87
50:c:2:ARG:HB2	50:c:4:GLU:OE1	1.74	0.87
30:H:4:ILE:CG1	30:H:45:ARG:HD3	2.02	0.87
6:n:77:ARG:NH2	25:C:126:LYS:CG	2.38	0.87
54:g:46:TYR:HB2	54:g:47:PRO:HD2	1.55	0.87
55:y:26:ARG:O	55:y:27:ARG:C	2.18	0.86
50:c:27:ARG:NH1	50:c:29:ASN:CB	2.38	0.86
3:k:62:ARG:NH1	3:k:64:ARG:CB	2.38	0.86
50:c:27:ARG:HG2	50:c:28:ARG:H	1.40	0.86
56:3:8:LYS:O	56:3:11:ARG:HG2	1.76	0.86
55:y:44:ARG:HH11	55:y:46:ILE:HD11	1.35	0.86
55:y:9:ARG:HD2	55:y:53:LYS:HZ1	1.38	0.86
1:h:808:A:H2	19:8:24:ASN:HD22	1.22	0.86
23:A:801:U:O2	51:d:9:GLN:O	1.94	0.85
3:k:41:LEU:HD12	3:k:93:LEU:HD11	1.58	0.85
5:m:102:ILE:HB	5:m:105:THR:O	1.77	0.85
54:g:5:ILE:HG22	54:g:6:HIS:O	1.76	0.85
54:g:2:LYS:O	54:g:3:PRO:O	1.94	0.85
50:c:10:LYS:HZ1	50:c:53:ARG:CD	1.86	0.85
26:D:57:ILE:HG21	26:D:62:VAL:HG13	1.59	0.85
50:c:33:ARG:O	50:c:34:ILE:HG23	1.76	0.84
19:8:183:VAL:HB	19:8:196:VAL:HG11	1.60	0.84
30:H:70:THR:HG21	30:H:140:VAL:CG1	2.06	0.84
50:c:10:LYS:O	50:c:11:LEU:CD2	2.25	0.84
23:A:282:A:H1'	30:H:51:ARG:HD2	1.59	0.84
50:c:6:ARG:O	50:c:9:VAL:HG12	1.78	0.83
24:B:1:G:O6	24:B:115:A:N6	2.12	0.82
54:g:87:LYS:O	54:g:90:ARG:HB2	1.79	0.82
54:g:24:LEU:HD22	54:g:41:SER:HB3	1.59	0.82
55:y:44:ARG:HH12	55:y:46:ILE:HD11	1.41	0.82
23:A:2454:G:H2'	23:A:2455:C:C6	2.14	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:481:G:OP1	12:u:114:ARG:NH2	2.13	0.82
35:M:64:LEU:HD11	52:e:15:ARG:HG3	1.61	0.82
54:g:60:PHE:CE1	54:g:62:THR:N	2.48	0.81
23:A:1825:C:N4	23:A:1840:G:OP2	2.13	0.81
54:g:87:LYS:CB	54:g:91:ARG:HH12	1.93	0.81
50:c:5:ILE:CG2	50:c:28:ARG:NH2	2.41	0.81
23:A:1302:G:OP1	41:S:86:LYS:NZ	2.13	0.81
1:h:1097:G:C5'	9:4:126:ARG:NH2	2.44	0.81
3:k:62:ARG:NH2	3:k:64:ARG:CG	2.44	0.81
54:g:60:PHE:CD1	54:g:62:THR:N	2.45	0.81
50:c:37:ARG:HE	50:c:51:GLU:CG	1.90	0.80
1:h:808:A:N3	19:8:24:ASN:ND2	2.27	0.80
23:A:2127:G:OP1	25:C:241:SER:OG	1.98	0.80
54:g:60:PHE:O	54:g:63:GLY:O	2.00	0.80
55:y:6:VAL:HG23	55:y:7:THR:HG23	1.64	0.80
6:n:77:ARG:HH21	25:C:126:LYS:HG2	1.47	0.80
55:y:6:VAL:O	55:y:73:ARG:NH2	2.15	0.79
1:h:1203:G:OP2	1:h:1304:C:N4	2.15	0.79
23:A:2570:A:C6	50:c:24:ARG:NH1	2.50	0.79
1:h:50:G:N2	1:h:366:A:O4'	2.14	0.79
1:h:237:C:O3'	16:5:44:LYS:NZ	2.14	0.79
54:g:10:HIS:HB3	54:g:30:THR:OG1	1.81	0.79
23:A:2975:G:OP2	29:G:3:ARG:NH1	2.16	0.79
23:A:663:A:N6	23:A:2724:U:OP1	2.15	0.79
1:h:1329:G:O6	9:4:32:ARG:NH2	2.16	0.79
3:k:120:ALA:HB1	3:k:189:ALA:HB2	1.65	0.79
1:h:1219:A:N6	1:h:1283:U:O2	2.15	0.78
54:g:60:PHE:N	54:g:63:GLY:O	2.17	0.78
23:A:1479:G:N2	23:A:1482:A:OP2	2.16	0.78
6:n:17:ARG:NH1	23:A:1612:U:O2	2.16	0.78
8:q:5:ASP:OD1	8:q:79:ARG:NH1	2.17	0.78
23:A:333:C:N4	23:A:348:G:O6	2.15	0.78
23:A:2018:G:OP2	25:C:154:LYS:NZ	2.17	0.78
50:c:10:LYS:CE	50:c:53:ARG:HD3	2.14	0.78
12:u:5:GLN:OE1	16:5:51:LYS:NZ	2.17	0.78
19:8:16:PHE:CE2	19:8:203:ASN:HB2	2.19	0.78
23:A:2339:G:O6	23:A:2394:A:N6	2.16	0.78
23:A:1079:C:HO2'	23:A:2720:C:HO2'	1.15	0.78
1:h:807:U:O2	1:h:856:G:N2	2.16	0.77
23:A:81:A:N1	23:A:96:G:O2'	2.17	0.77
23:A:324:C:N4	23:A:450:G:O6	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:485:U:C5'	55:y:30:PRO:O	2.32	0.77
23:A:2160:A:OP2	23:A:2186:C:N4	2.18	0.77
23:A:2727:A:O2'	23:A:2729:G:OP2	2.00	0.77
54:g:87:LYS:HA	54:g:90:ARG:HG3	1.64	0.77
23:A:2882:C:OP1	29:G:159:LYS:NZ	2.18	0.77
23:A:610:C:O2	23:A:646:U:O2'	2.02	0.77
3:k:62:ARG:HH22	3:k:64:ARG:CD	1.98	0.77
1:h:1214:G:OP1	9:4:139:LYS:NZ	2.18	0.77
1:h:1057:G:N2	1:h:1060:A:OP2	2.16	0.77
44:V:47:VAL:H	44:V:57:GLY:H	1.32	0.77
1:h:457:A:O2'	1:h:458:A:O5'	2.02	0.76
23:A:3102:U:O2	37:O:45:ARG:NH2	2.19	0.76
1:h:352:C:O2'	1:h:354:G:OP1	2.01	0.76
1:h:408:G:O2'	4:l:104:ARG:NH1	2.18	0.76
23:A:1201:G:N2	23:A:1204:A:OP2	2.17	0.76
23:A:2800:G:O2'	23:A:2803:C:OP2	2.03	0.76
54:g:24:LEU:HD22	54:g:41:SER:CB	2.13	0.76
50:c:35:VAL:O	50:c:36:LEU:O	2.03	0.76
1:h:953:G:O2'	1:h:1348:G:O2'	2.03	0.76
19:8:160:ALA:O	19:8:182:PRO:O	2.03	0.76
50:c:36:LEU:C	50:c:37:ARG:HG3	2.10	0.76
23:A:285:U:O2'	23:A:286:G:O3'	2.03	0.76
23:A:533:C:OP1	40:R:2:ALA:N	2.18	0.76
23:A:1164:A:O2'	31:I:6:LYS:NZ	2.19	0.76
54:g:18:ALA:HB1	54:g:57:SER:HB3	1.65	0.76
54:g:86:GLU:O	54:g:90:ARG:HG2	1.83	0.76
23:A:291:C:O2'	23:A:338:C:OP1	2.03	0.76
1:h:193:C:N4	16:5:18:GLY:O	2.19	0.76
1:h:666:U:O4	1:h:683:G:O2'	2.04	0.76
39:Q:100:ARG:O	39:Q:103:ARG:NH1	2.19	0.76
55:y:26:ARG:HD2	55:y:28:TRP:CZ3	2.21	0.76
8:q:41:LYS:NZ	8:q:48:ASP:OD1	2.16	0.75
44:V:45:THR:O	44:V:57:GLY:HA2	1.86	0.75
37:O:7:GLY:O	37:O:9:ARG:NH1	2.19	0.75
39:Q:33:GLU:OE1	39:Q:38:ARG:NH2	2.19	0.75
50:c:37:ARG:HG3	50:c:37:ARG:HH21	1.49	0.75
54:g:35:ILE:HD11	54:g:49:ILE:CG2	1.93	0.75
54:g:10:HIS:HB3	54:g:30:THR:CB	2.17	0.75
23:A:2224:C:O2'	23:A:2913:U:OP2	2.04	0.75
1:h:1257:G:N3	1:h:1263:C:O2'	2.19	0.75
23:A:2389:U:O4	23:A:2393:A:N6	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:65:G:N7	18:7:6:SER:OG	2.19	0.75
19:8:16:PHE:CG	19:8:203:ASN:HB2	2.23	0.74
23:A:1186:G:O2'	23:A:1187:A:OP1	2.05	0.74
23:A:1493:A:O2'	23:A:1495:G:N7	2.19	0.74
21:Y:34:PHE:O	21:Y:99:LYS:NZ	2.19	0.74
35:M:84:ASN:ND2	35:M:117:LYS:O	2.18	0.74
1:h:1249:G:N2	1:h:1308:C:O2	2.19	0.74
3:k:62:ARG:CZ	3:k:64:ARG:CB	2.65	0.74
6:n:77:ARG:NH2	25:C:126:LYS:HD3	2.01	0.74
1:h:122:G:OP1	1:h:585:U:O2'	2.05	0.74
23:A:485:U:H5'	55:y:30:PRO:O	1.88	0.74
45:W:66:ILE:HD11	45:W:77:LEU:HD11	1.69	0.74
1:h:1103:U:O4	1:h:1130:C:N4	2.19	0.74
1:h:1177:A:O2'	1:h:1178:A:OP1	2.05	0.74
30:H:57:LYS:HE2	30:H:57:LYS:HA	1.70	0.74
23:A:1162:G:O2'	23:A:1229:A:N6	2.21	0.74
23:A:1827:A:N7	23:A:1865:A:N6	2.35	0.74
50:c:11:LEU:O	50:c:12:ARG:O	2.05	0.74
1:h:567:G:OP1	8:q:86:ARG:NH2	2.20	0.74
23:A:28:C:O2'	23:A:1353:G:OP1	2.06	0.74
30:H:62:ILE:HG13	30:H:65:ALA:H	1.53	0.74
1:h:664:U:O2'	11:t:50:VAL:O	2.03	0.73
23:A:306:U:H4'	30:H:44:GLU:CG	2.15	0.73
21:Y:50:ASN:O	21:Y:53:GLN:NE2	2.21	0.73
23:A:896:A:OP1	25:C:218:ARG:NH2	2.21	0.73
54:g:24:LEU:HD12	54:g:24:LEU:O	1.89	0.73
31:I:10:VAL:HG22	31:I:60:ALA:HB2	1.71	0.73
1:h:297:G:N2	1:h:300:A:OP2	2.22	0.73
1:h:465:G:O2'	1:h:466:U:O5'	2.07	0.73
1:h:1097:G:O3'	9:4:126:ARG:CZ	2.36	0.73
23:A:2348:G:N2	23:A:2394:A:OP1	2.22	0.73
30:H:119:LEU:HD11	30:H:124:ILE:HD12	1.68	0.73
44:V:46:ALA:HA	44:V:57:GLY:HA3	1.70	0.73
23:A:159:A:OP2	23:A:164:A:N6	2.22	0.73
23:A:1480:A:O5'	55:y:1:SER:N	2.22	0.72
23:A:2630:A:OP2	23:A:2635:A:N6	2.21	0.72
30:H:70:THR:HG21	30:H:140:VAL:HG11	1.71	0.72
23:A:318:U:O2'	23:A:319:G:O5'	2.04	0.72
23:A:2750:G:OP1	29:G:154:ARG:NH1	2.22	0.72
1:h:1034:C:O2'	21:Y:50:ASN:ND2	2.22	0.72
29:G:158:TYR:O	29:G:172:ARG:NH2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:948:G:O3'	52:e:57:ARG:NH2	2.22	0.72
54:g:10:HIS:CB	54:g:30:THR:OG1	2.37	0.72
23:A:1533:U:O2	23:A:1803:A:O2'	2.07	0.72
23:A:2239:A:C2	49:b:3:VAL:HG12	2.24	0.72
23:A:249:C:O2	52:e:12:LYS:NZ	2.22	0.72
37:O:87:TYR:OH	37:O:116:VAL:O	2.08	0.72
44:V:47:VAL:CA	44:V:56:SER:N	2.52	0.72
23:A:2:A:N6	23:A:3118:U:O4	2.19	0.72
23:A:56:U:OP1	43:U:77:LYS:NZ	2.22	0.72
50:c:38:LYS:O	50:c:39:TYR:CG	2.42	0.72
35:M:64:LEU:CD1	52:e:15:ARG:HG3	2.20	0.72
23:A:369:G:O2'	23:A:371:G:O5'	2.08	0.72
23:A:2016:G:OP1	25:C:258:ARG:NH1	2.23	0.71
23:A:2908:U:O2'	34:L:68:GLU:OE1	2.07	0.71
30:H:55:GLU:HA	30:H:58:VAL:HG22	1.70	0.71
54:g:60:PHE:HD1	54:g:61:TRP:N	1.86	0.71
54:g:54:THR:HG23	54:g:55:SER:N	2.03	0.71
1:h:1479:U:OP1	21:Y:27:LYS:NZ	2.23	0.71
1:h:926:G:N2	1:h:1321:A:OP2	2.24	0.71
14:x:89:ARG:NH1	23:A:830:A:OP2	2.22	0.71
19:8:16:PHE:CE2	19:8:203:ASN:CB	2.74	0.71
55:y:34:ASN:OD1	55:y:47:ARG:NH2	2.22	0.71
1:h:1094:C:O2	22:9:100:SER:OG	2.08	0.71
23:A:2088:C:O2'	23:A:2089:C:OP1	2.07	0.71
31:I:54:ASN:OD1	31:I:77:THR:OG1	2.06	0.71
28:F:130:ASP:O	28:F:132:THR:N	2.23	0.71
49:b:8:MET:HE3	49:b:16:ARG:NH1	2.04	0.71
54:g:30:THR:CA	54:g:34:THR:HG23	2.21	0.71
56:3:8:LYS:HA	56:3:11:ARG:HE	1.54	0.71
4:l:92:ARG:NH2	4:l:94:ASP:OD2	2.23	0.71
9:4:125:THR:HG22	9:4:126:ARG:O	1.90	0.71
1:h:908:G:N2	21:Y:100:ASP:OD2	2.24	0.71
24:B:28:A:OP1	38:P:71:ARG:NH2	2.24	0.71
1:h:136:G:N2	16:5:8:LYS:O	2.24	0.71
6:n:77:ARG:NH2	25:C:126:LYS:CD	2.54	0.71
23:A:499:G:OP2	23:A:2630:A:O2'	2.08	0.71
23:A:2015:U:OP2	25:C:272:ARG:NH2	2.24	0.71
24:B:117:A:O2'	24:B:118:C:O4'	2.05	0.71
35:M:63:LYS:HG2	52:e:13:ARG:HD2	1.71	0.70
1:h:639:C:OP2	14:x:8:LYS:NZ	2.23	0.70
1:h:598:C:O2	15:z:12:LYS:NZ	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:772:A:O2'	1:h:774:A:N7	2.22	0.70
19:8:14:ALA:O	19:8:15:HIS:CD2	2.44	0.70
23:A:2043:C:O2'	23:A:2195:U:OP2	2.09	0.70
23:A:2332:U:O2	23:A:2404:G:N2	2.24	0.70
1:h:992:G:OP2	22:9:24:ARG:NH1	2.25	0.70
10:s:35:SER:OG	10:s:78:ASP:OD2	2.09	0.70
23:A:1046:C:O2'	23:A:1287:C:O2	2.07	0.70
4:l:53:LYS:NZ	4:l:64:GLU:OE2	2.22	0.70
8:q:78:ARG:HD2	8:q:78:ARG:C	2.17	0.70
19:8:183:VAL:HB	19:8:196:VAL:CG1	2.21	0.70
45:W:119:THR:OG1	45:W:122:THR:OG1	2.09	0.70
1:h:671:G:OP2	11:t:37:ASN:ND2	2.25	0.69
1:h:1180:U:O2'	1:h:1183:U:OP2	2.09	0.69
23:A:1165:G:O2'	23:A:1228:A:N6	2.23	0.69
23:A:2977:A:O2'	53:f:15:ARG:NH1	2.25	0.69
50:c:27:ARG:HG2	50:c:28:ARG:N	2.05	0.69
54:g:87:LYS:CB	54:g:91:ARG:NH1	2.50	0.69
1:h:996:G:N2	1:h:999:A:OP2	2.25	0.69
23:A:1084:U:O2'	23:A:1085:G:OP1	2.08	0.69
8:q:11:LEU:CD2	8:q:77:LEU:HD21	2.21	0.69
1:h:1320:G:O2'	1:h:1321:A:O4'	2.09	0.69
1:h:1433:C:N4	1:h:1434:U:O2	2.26	0.69
20:r:24:LEU:HD12	20:r:62:GLN:HB3	1.75	0.69
23:A:684:G:O2'	23:A:685:G:OP1	2.10	0.69
23:A:2503:G:N7	46:X:14:ARG:NH2	2.39	0.69
49:b:5:LYS:C	49:b:6:ARG:HD3	2.17	0.69
23:A:1481:C:OP1	55:y:3:HIS:CE1	2.46	0.69
23:A:1907:A:OP2	23:A:1916:A:N6	2.25	0.69
23:A:2351:A:O2'	23:A:2352:C:O4'	2.11	0.69
24:B:56:C:O2'	28:F:31:ASN:ND2	2.25	0.69
54:g:24:LEU:CD2	54:g:41:SER:OG	2.41	0.69
54:g:30:THR:HA	54:g:34:THR:HG23	1.73	0.69
23:A:2490:A:N6	23:A:2497:A:OP2	2.26	0.69
25:C:26:ARG:NE	25:C:28:THR:O	2.26	0.69
1:h:1468:U:HO2'	23:A:2184:A:HO2'	1.36	0.69
23:A:1320:U:OP1	27:E:152:LYS:NZ	2.21	0.69
1:h:277:C:OP2	16:5:58:LYS:NZ	2.26	0.68
3:k:62:ARG:HH22	3:k:64:ARG:HG3	1.58	0.68
50:c:27:ARG:CG	50:c:28:ARG:H	2.06	0.68
23:A:1292:U:O2'	23:A:1293:G:OP2	2.11	0.68
1:h:356:A:N3	1:h:368:U:O2'	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:1365:C:O2'	7:p:79:ARG:NH1	2.27	0.68
50:c:36:LEU:O	50:c:37:ARG:CB	2.41	0.68
51:d:6:ARG:O	51:d:9:GLN:NE2	2.27	0.68
55:y:30:PRO:O	55:y:31:ASN:CB	2.42	0.68
23:A:959:U:OP2	23:A:960:G:N2	2.27	0.68
26:D:157:PRO:HB2	26:D:159:ARG:HG2	1.74	0.68
55:y:23:ARG:C	55:y:24:THR:OG1	2.37	0.68
55:y:44:ARG:HH12	55:y:46:ILE:CD1	2.02	0.68
1:h:185:G:O6	1:h:203:U:O2	2.11	0.68
1:h:986:G:N2	1:h:1016:G:O6	2.27	0.68
50:c:9:VAL:HG23	50:c:10:LYS:HG2	1.76	0.68
50:c:25:LYS:HD2	52:e:34:GLU:CG	2.23	0.68
50:c:27:ARG:HH11	50:c:29:ASN:CB	1.96	0.68
22:9:38:PRO:O	22:9:42:ALA:N	2.27	0.67
23:A:1531:C:O2'	23:A:1532:G:O4'	2.10	0.67
30:H:70:THR:CG2	30:H:140:VAL:CG1	2.71	0.67
1:h:598:C:N4	1:h:601:A:OP2	2.22	0.67
23:A:484:C:O2'	55:y:29:ASP:O	2.11	0.67
28:F:70:GLN:NE2	28:F:97:THR:O	2.27	0.67
28:F:7:ALA:CB	54:g:26:ARG:HE	2.07	0.67
1:h:1078:C:N4	1:h:1079:G:O6	2.28	0.67
23:A:1770:G:OP1	23:A:1937:U:O2'	2.11	0.67
1:h:1097:G:C5'	9:4:126:ARG:HH21	2.06	0.67
23:A:2570:A:C5	50:c:24:ARG:NH1	2.63	0.67
1:h:179:C:O2'	1:h:181:C:N4	2.27	0.67
23:A:730:G:N7	35:M:111:LYS:NZ	2.37	0.67
23:A:2083:A:N6	23:A:2099:G:O2'	2.28	0.67
54:g:60:PHE:CD1	54:g:61:TRP:N	2.63	0.67
1:h:647:G:OP1	1:h:712:C:O2'	2.10	0.67
30:H:54:ARG:O	30:H:58:VAL:HG13	1.95	0.67
1:h:1109:C:N4	1:h:1120:G:O2'	2.28	0.67
1:h:1158:G:OP2	9:4:119:LYS:NZ	2.25	0.67
3:k:62:ARG:HH22	3:k:64:ARG:CG	2.08	0.67
18:7:18:ARG:HG2	18:7:18:ARG:HH11	1.58	0.67
23:A:619:C:N4	23:A:2244:A:N3	2.43	0.67
23:A:1530:G:N2	23:A:1531:C:O4'	2.27	0.66
23:A:2006:A:OP2	25:C:222:ARG:NH2	2.28	0.66
20:r:48:GLY:O	20:r:74:ARG:NH2	2.28	0.66
23:A:1543:A:O2'	23:A:1544:U:O4'	2.10	0.66
1:h:416:G:N2	1:h:427:U:O2	2.23	0.66
1:h:1187:G:O2'	3:k:193:PHE:O	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:k:62:ARG:CZ	3:k:64:ARG:HD2	2.24	0.66
20:r:2:MET:SD	20:r:7:SER:OG	2.52	0.66
23:A:1947:U:O2'	23:A:1948:A:O4'	2.14	0.66
25:C:68:ARG:NH1	25:C:150:GLY:O	2.28	0.66
1:h:498:C:O2	12:u:47:SER:OG	2.12	0.66
23:A:891:G:N7	23:A:908:A:O2'	2.25	0.66
30:H:41:ARG:HB3	30:H:44:GLU:HB3	1.76	0.66
37:O:70:ILE:HD11	37:O:76:VAL:HG12	1.77	0.66
23:A:885:G:OP1	51:d:11:ASN:ND2	2.29	0.66
23:A:1449:C:OP1	43:U:68:ARG:NH1	2.28	0.66
50:c:2:ARG:CD	50:c:4:GLU:OE2	2.42	0.66
23:A:2600:A:N3	38:P:121:ARG:NH2	2.44	0.66
50:c:10:LYS:HE3	50:c:53:ARG:HD3	1.77	0.66
54:g:10:HIS:CA	54:g:30:THR:OG1	2.44	0.66
55:y:9:ARG:HD2	55:y:53:LYS:NZ	2.10	0.66
1:h:1213:U:OP1	9:4:148:SER:OG	2.12	0.66
8:q:77:LEU:CD1	8:q:131:VAL:HG22	2.24	0.66
24:B:9:G:OP1	38:P:37:ARG:NH2	2.29	0.66
46:X:11:ARG:O	46:X:14:ARG:NH1	2.28	0.66
23:A:2244:A:O2'	23:A:2246:U:OP2	2.12	0.66
23:A:866:G:N2	23:A:904:A:O2'	2.29	0.66
23:A:965:U:O2'	48:a:22:SER:OG	2.12	0.66
24:B:5:C:OP1	24:B:62:C:O2'	2.13	0.66
50:c:37:ARG:HG3	50:c:37:ARG:NH2	2.07	0.66
32:J:81:LEU:HD13	32:J:139:ILE:HD13	1.78	0.65
35:M:64:LEU:CD1	52:e:15:ARG:NE	2.49	0.65
3:k:62:ARG:NH1	3:k:64:ARG:CD	2.41	0.65
23:A:641:U:O2'	23:A:642:G:OP1	2.14	0.65
55:y:26:ARG:HH21	55:y:26:ARG:CB	2.05	0.65
21:Y:28:LEU:HD11	21:Y:41:PHE:CG	2.31	0.65
23:A:1886:A:O2'	23:A:1892:G:N7	2.28	0.65
35:M:48:VAL:O	52:e:57:ARG:NH1	2.29	0.65
54:g:30:THR:O	54:g:34:THR:HG23	1.96	0.65
1:h:1361:C:O2	7:p:76:ARG:NH2	2.29	0.65
23:A:2693:A:N6	23:A:2705:G:O2'	2.30	0.65
1:h:1289:U:O2'	13:v:110:ARG:NH2	2.29	0.65
23:A:1480:A:O4'	55:y:27:ARG:NH1	2.28	0.65
50:c:42:VAL:C	50:c:44:ARG:H	2.05	0.65
56:3:8:LYS:HA	56:3:11:ARG:NE	2.11	0.65
1:h:402:G:OP1	4:l:69:ARG:NH1	2.30	0.65
3:k:62:ARG:CZ	3:k:64:ARG:CG	2.75	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:D:3:ARG:NE	26:D:210:SER:O	2.28	0.65
50:c:16:GLY:O	50:c:17:THR:HG22	1.97	0.65
54:g:59:PRO:HB3	54:g:64:SER:C	2.22	0.65
1:h:148:A:OP2	1:h:166:C:N4	2.28	0.65
1:h:1367:C:N4	1:h:1368:G:O6	2.30	0.65
6:n:30:ILE:HG22	6:n:36:THR:HG21	1.78	0.65
23:A:485:U:H5''	55:y:30:PRO:O	1.95	0.65
23:A:1125:C:OP1	33:K:37:ARG:NH1	2.30	0.65
38:P:78:LYS:O	38:P:82:VAL:HG23	1.96	0.65
1:h:1147:G:O2'	1:h:1151:A:N6	2.30	0.64
23:A:292:G:O2'	23:A:293:G:O4'	2.16	0.64
23:A:2219:U:O2	34:L:3:GLN:NE2	2.29	0.64
23:A:2455:C:O5'	23:A:2455:C:H6	1.79	0.64
55:y:67:VAL:O	55:y:71:ARG:HG3	1.97	0.64
23:A:1548:C:N4	23:A:1622:G:O6	2.30	0.64
25:C:66:ASP:OD2	25:C:103:ARG:NH1	2.31	0.64
30:H:37:ILE:HD11	30:H:49:GLU:OE1	1.98	0.64
55:y:2:ALA:O	55:y:3:HIS:HB2	1.95	0.64
19:8:19:GLN:HG3	19:8:20:THR:H	1.63	0.64
19:8:68:LEU:HD21	19:8:150:GLY:HA3	1.79	0.64
23:A:2076:A:OP2	23:A:2107:G:N2	2.29	0.64
43:U:34:HIS:ND1	43:U:36:ASP:OD1	2.31	0.64
1:h:1402:G:O2'	23:A:2173:G:O2'	2.15	0.63
23:A:2300:A:N3	23:A:2658:A:O2'	2.31	0.63
25:C:25:THR:HG21	25:C:113:GLN:OE1	1.97	0.63
1:h:7:U:O2'	1:h:8:U:O4'	2.16	0.63
26:D:157:PRO:HB2	26:D:159:ARG:CG	2.28	0.63
1:h:809:G:O2'	1:h:810:G:H5'	1.99	0.63
12:u:63:VAL:HG11	12:u:95:TYR:CD2	2.33	0.63
19:8:18:HIS:CD2	19:8:189:THR:HG21	2.34	0.63
23:A:377:C:O3'	44:V:94:LYS:NZ	2.30	0.63
23:A:1832:A:N6	42:T:99:ARG:O	2.25	0.63
1:h:1298:G:N7	17:6:7:LYS:NZ	2.47	0.63
23:A:162:A:O4'	30:H:135:LYS:NZ	2.27	0.63
1:h:1080:C:H3'	19:8:95:ARG:NH2	2.13	0.63
3:k:62:ARG:NH2	3:k:64:ARG:CD	2.62	0.63
12:u:27:SER:OG	12:u:29:GLN:O	2.09	0.63
23:A:331:U:OP1	23:A:446:G:N2	2.30	0.63
23:A:1188:A:N7	23:A:1214:A:O2'	2.32	0.63
23:A:1536:A:O2'	23:A:1537:U:O5'	2.16	0.63
55:y:22:ARG:O	55:y:23:ARG:O	2.17	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:v:82:ILE:HD11	13:v:93:ARG:HG3	1.80	0.63
50:c:25:LYS:HD2	52:e:34:GLU:OE2	1.98	0.63
23:A:911:U:OP1	27:E:63:LYS:NZ	2.28	0.62
23:A:1258:C:OP2	33:K:68:LYS:NZ	2.29	0.62
36:N:43:THR:HG22	36:N:94:VAL:HG12	1.80	0.62
23:A:2587:U:OP2	52:e:43:ARG:NH2	2.32	0.62
19:8:16:PHE:CG	19:8:203:ASN:CG	2.77	0.62
20:r:24:LEU:HD11	20:r:66:VAL:CG2	2.29	0.62
28:F:132:THR:OG1	28:F:168:THR:CA	2.46	0.62
31:I:41:ARG:NH2	32:J:119:ASN:OD1	2.32	0.62
37:O:56:LYS:NZ	37:O:94:TYR:OH	2.25	0.62
23:A:2916:C:O2	23:A:3068:U:O2'	2.17	0.62
23:A:2390:U:N3	23:A:2393:A:OP2	2.32	0.62
50:c:6:ARG:CZ	50:c:8:ILE:HG22	2.28	0.62
1:h:1022:G:O2'	1:h:1023:U:O4'	2.15	0.62
3:k:76:ILE:HG22	3:k:102:ILE:HD13	1.80	0.62
23:A:885:G:OP2	51:d:14:ARG:NH2	2.33	0.62
28:F:122:ARG:O	54:g:61:TRP:CD1	2.52	0.62
54:g:18:ALA:CB	54:g:57:SER:HB3	2.30	0.62
1:h:502:C:OP2	12:u:66:TYR:OH	2.16	0.62
23:A:251:A:OP1	52:e:7:HIS:NE2	2.33	0.62
23:A:1114:G:OP2	40:R:93:LYS:NZ	2.32	0.62
1:h:884:G:OP1	2:j:22:ARG:NH1	2.33	0.62
23:A:860:G:O2'	23:A:863:G:O2'	2.15	0.62
23:A:2456:C:OP2	55:y:26:ARG:NH1	2.33	0.62
1:h:956:A:OP1	22:9:69:ARG:NH2	2.31	0.61
4:l:80:LYS:N	4:l:84:ASN:OD1	2.32	0.61
19:8:5:THR:HG22	19:8:6:MET:H	1.65	0.61
31:I:20:SER:OG	31:I:82:VAL:O	2.17	0.61
50:c:2:ARG:HB2	50:c:4:GLU:CD	2.24	0.61
1:h:947:U:O2	21:Y:10:LYS:NZ	2.33	0.61
8:q:78:ARG:HG2	8:q:78:ARG:HH11	1.64	0.61
9:4:126:ARG:HH11	9:4:126:ARG:CG	2.13	0.61
18:7:18:ARG:HB2	18:7:18:ARG:CZ	2.30	0.61
23:A:2029:A:OP2	23:A:2426:C:N4	2.33	0.61
8:q:78:ARG:CZ	8:q:130:TYR:HB2	2.30	0.61
23:A:2357:A:N6	23:A:2381:A:O4'	2.33	0.61
1:h:698:A:OP2	1:h:700:C:N4	2.33	0.61
1:h:1261:A:OP1	10:s:9:ARG:NH2	2.33	0.61
23:A:808:A:O2'	23:A:809:U:H5'	2.01	0.61
23:A:2870:C:OP2	23:A:2956:G:O2'	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:975:G:N7	1:h:1194:A:N6	2.49	0.61
7:p:89:VAL:HG12	7:p:90:GLU:O	2.01	0.61
9:4:135:LYS:NZ	9:4:141:ALA:O	2.29	0.61
23:A:109:U:OP1	47:Z:62:ARG:NH2	2.33	0.61
23:A:2521:C:N4	23:A:2544:U:O2	2.34	0.61
1:h:1082:A:H2'	1:h:1083:C:C6	2.36	0.61
8:q:35:ASN:HB3	8:q:112:LEU:HD12	1.82	0.61
19:8:16:PHE:CG	19:8:203:ASN:ND2	2.60	0.61
50:c:27:ARG:NH2	50:c:30:ASP:HB2	2.16	0.61
23:A:552:U:O2	51:d:19:HIS:NE2	2.34	0.61
54:g:16:ASP:OD2	54:g:20:GLY:N	2.34	0.61
23:A:2442:U:P	55:y:45:ARG:HH12	2.23	0.61
35:M:63:LYS:HG2	52:e:13:ARG:CD	2.30	0.61
1:h:1291:G:O2'	13:v:77:ASP:OD2	2.19	0.60
23:A:1671:U:O2	23:A:1673:A:N6	2.34	0.60
23:A:2859:C:O2'	26:D:83:GLU:OE1	2.11	0.60
31:I:115:LEU:HD13	31:I:123:ILE:HD11	1.83	0.60
46:X:70:GLY:O	46:X:77:THR:OG1	2.18	0.60
54:g:2:LYS:C	54:g:3:PRO:O	2.43	0.60
23:A:2707:C:N3	36:N:124:LYS:NZ	2.45	0.60
23:A:2899:A:O3'	34:L:31:ARG:NH1	2.33	0.60
28:F:141:GLU:O	28:F:144:MET:HE3	2.01	0.60
29:G:171:ARG:NH2	53:f:28:SER:O	2.33	0.60
23:A:1639:G:O2'	23:A:1799:A:N6	2.34	0.60
1:h:156:G:N2	1:h:159:A:N7	2.48	0.60
1:h:1480:C:OP2	21:Y:30:ARG:NH2	2.35	0.60
6:n:77:ARG:HH22	25:C:126:LYS:HG2	1.66	0.60
23:A:2223:C:O2	23:A:2911:U:O2'	2.19	0.60
1:h:1249:G:O2'	1:h:1250:A:O4'	2.19	0.60
19:8:18:HIS:O	19:8:38:ILE:HD11	2.02	0.60
25:C:2:GLY:N	25:C:20:ASP:O	2.35	0.60
1:h:805:A:O2'	8:q:13:ARG:NH2	2.33	0.60
8:q:78:ARG:HD2	8:q:78:ARG:O	2.01	0.60
28:F:111:ILE:HD13	28:F:115:LEU:HD12	1.83	0.60
15:z:78:GLY:O	15:z:82:LYS:N	2.33	0.60
23:A:336:C:O2'	23:A:337:U:OP1	2.18	0.60
23:A:551:G:N2	23:A:554:A:OP2	2.34	0.60
1:h:1425:G:OP2	1:h:1426:C:N4	2.34	0.60
23:A:2331:U:O4	23:A:2404:G:N1	2.34	0.60
42:T:44:ARG:NH2	49:b:53:ASP:O	2.35	0.60
47:Z:13:LEU:HD13	47:Z:17:GLU:HG3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:722:G:OP2	14:x:35:ARG:NH2	2.35	0.60
20:r:24:LEU:HD11	20:r:66:VAL:HG23	1.83	0.60
35:M:55:MET:SD	35:M:59:MET:HE2	2.41	0.60
1:h:393:A:OP2	15:z:13:ILE:HD11	2.02	0.59
7:p:68:ASN:ND2	7:p:128:SER:O	2.34	0.59
23:A:1648:A:O2'	25:C:31:LYS:NZ	2.24	0.59
23:A:926:U:O4	35:M:24:ARG:NH1	2.34	0.59
23:A:2204:G:O2'	23:A:2206:C:OP2	2.16	0.59
50:c:5:ILE:O	50:c:5:ILE:HG22	2.01	0.59
35:M:126:ALA:HB3	35:M:129:PHE:HE1	1.68	0.59
3:k:15:THR:HG23	3:k:207:ILE:HD12	1.84	0.59
18:7:18:ARG:HH11	18:7:18:ARG:CG	2.16	0.59
19:8:95:ARG:NH1	19:8:97:LEU:HD23	2.17	0.59
23:A:1305:G:OP1	35:M:32:THR:OG1	2.11	0.59
28:F:116:PRO:HA	54:g:58:HIS:CD2	2.37	0.59
1:h:973:U:O2	1:h:1194:A:N7	2.35	0.59
23:A:2375:G:N2	23:A:2376:G:N7	2.50	0.59
23:A:2482:U:O2'	23:A:2651:C:OP2	2.21	0.59
52:e:10:ALA:O	52:e:14:PHE:HB2	2.01	0.59
54:g:35:ILE:CD1	54:g:49:ILE:HA	2.28	0.59
6:n:77:ARG:HH21	25:C:126:LYS:CD	2.16	0.59
54:g:24:LEU:HD22	54:g:41:SER:OG	2.02	0.59
10:s:29:VAL:HG13	10:s:76:ILE:HD12	1.84	0.59
11:t:97:GLY:O	11:t:102:ARG:NH2	2.35	0.59
54:g:18:ALA:HB1	54:g:57:SER:CB	2.31	0.59
1:h:1044:G:N3	1:h:1046:C:N4	2.50	0.59
54:g:35:ILE:HG22	54:g:36:GLU:N	2.17	0.59
4:l:188:VAL:HG22	4:l:189:PRO:HD2	1.86	0.58
23:A:964:C:O2	48:a:24:ARG:NH2	2.36	0.58
1:h:761:A:O2'	1:h:1506:U:O2	2.20	0.58
14:x:47:LYS:O	14:x:53:ARG:NH2	2.37	0.58
24:B:47:A:H5''	38:P:10:ILE:HD11	1.84	0.58
28:F:81:ILE:HG22	28:F:86:LEU:HD23	1.84	0.58
1:h:636:G:O2'	14:x:28:GLN:NE2	2.36	0.58
23:A:2557:A:OP2	46:X:75:ARG:NH2	2.35	0.58
50:c:9:VAL:HG21	50:c:28:ARG:CG	2.32	0.58
23:A:1178:U:O4	32:J:133:THR:HG23	2.03	0.58
28:F:7:ALA:HB1	54:g:26:ARG:HE	1.68	0.58
50:c:27:ARG:HH12	50:c:29:ASN:HB2	1.59	0.58
1:h:1249:G:O2'	1:h:1250:A:O5'	2.21	0.58
1:h:625:G:O2'	16:5:43:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:382:A:OP2	44:V:82:ARG:NH2	2.37	0.58
23:A:451:U:N3	23:A:452:G:O6	2.37	0.58
23:A:886:G:OP2	51:d:14:ARG:NH1	2.36	0.58
30:H:62:ILE:O	30:H:66:ASN:ND2	2.37	0.58
32:J:95:HIS:NE2	32:J:135:ARG:O	2.36	0.58
35:M:64:LEU:HD13	52:e:15:ARG:CZ	2.34	0.58
4:l:192:GLU:O	4:l:196:VAL:HG23	2.04	0.58
21:Y:84:PHE:O	21:Y:88:VAL:HG23	2.04	0.58
23:A:1605:G:N2	23:A:1606:G:N7	2.52	0.58
23:A:2968:G:O5'	29:G:151:ARG:NH2	2.36	0.58
25:C:61:ALA:O	25:C:87:ASN:ND2	2.36	0.58
28:F:15:TYR:HA	28:F:19:ILE:HD12	1.85	0.58
1:h:100:G:N7	18:7:9:LYS:NZ	2.43	0.58
1:h:531:U:O2'	12:u:83:ARG:NH1	2.37	0.58
1:h:1287:G:O2'	1:h:1288:A:O4'	2.21	0.58
6:n:10:LEU:HD23	6:n:85:VAL:HA	1.85	0.58
23:A:1078:G:O6	56:3:8:LYS:NZ	2.36	0.58
1:h:194:A:O2'	1:h:195:U:O4'	2.21	0.58
1:h:1042:U:O4	3:k:3:GLN:NE2	2.37	0.58
7:p:39:ALA:O	7:p:43:VAL:HG23	2.04	0.58
23:A:3043:G:O2'	23:A:3045:C:OP2	2.12	0.58
1:h:1043:C:OP2	1:h:1044:G:O2'	2.15	0.58
1:h:1207:C:OP1	13:v:91:ARG:NH1	2.37	0.58
1:h:1341:C:OP2	22:9:75:ARG:NE	2.36	0.58
7:p:61:THR:HA	7:p:64:ARG:NE	2.19	0.58
7:p:138:ARG:NH1	7:p:139:GLU:OE2	2.36	0.58
23:A:389:G:O2'	23:A:391:G:O6	2.21	0.58
23:A:619:C:OP2	40:R:38:GLN:NE2	2.36	0.58
23:A:2178:G:O2'	23:A:2180:U:O4	2.19	0.58
50:c:10:LYS:HZ1	50:c:53:ARG:NE	2.02	0.58
16:5:23:ALA:HB1	16:5:40:LEU:HD22	1.86	0.57
23:A:473:C:O2'	23:A:476:G:N2	2.37	0.57
34:L:13:ASN:OD1	34:L:97:ARG:N	2.34	0.57
50:c:27:ARG:HH12	50:c:29:ASN:C	2.12	0.57
1:h:1137:G:O2'	1:h:1161:A:N6	2.37	0.57
9:4:108:ILE:HD12	9:4:115:ARG:HB2	1.87	0.57
31:I:40:ARG:NH2	31:I:49:TYR:O	2.37	0.57
49:b:16:ARG:HG3	49:b:17:ARG:N	2.19	0.57
1:h:426:U:OP2	4:l:29:ARG:NH2	2.38	0.57
12:u:54:ARG:HH11	12:u:64:THR:HG23	1.69	0.57
43:U:11:ILE:O	47:Z:33:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:791:C:O2'	1:h:883:A:N1	2.38	0.57
28:F:132:THR:O	28:F:169:ASN:C	2.47	0.57
29:G:99:LEU:HD12	29:G:103:ASN:O	2.04	0.57
50:c:36:LEU:C	50:c:37:ARG:CG	2.69	0.57
55:y:21:HIS:CD2	55:y:21:HIS:N	2.72	0.57
23:A:1107:G:OP2	48:a:11:SER:OG	2.14	0.57
23:A:2570:A:N6	50:c:24:ARG:HH11	2.01	0.57
23:A:2764:C:O2'	23:A:2964:A:N3	2.34	0.57
34:L:24:VAL:CG1	34:L:33:ALA:HB2	2.34	0.57
1:h:343:U:O2'	1:h:346:G:O6	2.21	0.57
1:h:457:A:HO2'	1:h:458:A:P	2.25	0.57
7:p:74:GLU:OE1	7:p:95:ARG:NH1	2.38	0.57
21:Y:6:GLU:O	21:Y:40:LEU:HD12	2.05	0.57
23:A:325:U:O2	23:A:450:G:C6	2.58	0.57
23:A:747:A:N6	23:A:768:G:O2'	2.37	0.57
54:g:35:ILE:CD1	54:g:49:ILE:CB	2.66	0.57
5:m:85:ILE:O	5:m:89:VAL:HG23	2.05	0.57
23:A:2753:G:N7	53:f:31:ARG:NH2	2.53	0.57
12:u:22:ALA:O	12:u:25:LYS:NZ	2.36	0.56
19:8:16:PHE:N	19:8:16:PHE:CD1	2.73	0.56
19:8:97:LEU:HD12	19:8:100:MET:HE3	1.87	0.56
22:9:74:LEU:O	22:9:78:GLY:N	2.38	0.56
28:F:136:THR:HG23	28:F:162:THR:HB	1.86	0.56
30:H:73:GLU:OE1	30:H:73:GLU:HA	2.03	0.56
1:h:310:G:OP1	15:z:28:ARG:NH1	2.37	0.56
1:h:1148:U:OP2	1:h:1150:A:N6	2.34	0.56
7:p:109:ARG:HA	7:p:116:MET:HE1	1.87	0.56
12:u:71:GLY:O	12:u:99:ARG:NH1	2.37	0.56
23:A:2756:G:O2'	23:A:2881:A:N1	2.38	0.56
37:O:33:ARG:NH1	49:b:51:LEU:HD21	2.20	0.56
40:R:47:TYR:OH	40:R:51:ARG:NH2	2.37	0.56
4:l:15:LEU:HD22	4:l:51:GLN:HG3	1.87	0.56
23:A:2454:G:C6	23:A:2455:C:N4	2.73	0.56
37:O:70:ILE:HD11	37:O:76:VAL:CG1	2.36	0.56
39:Q:57:THR:OG1	39:Q:73:PHE:O	2.13	0.56
43:U:29:TYR:CD2	43:U:93:ILE:HD12	2.41	0.56
55:y:26:ARG:O	55:y:26:ARG:NH2	2.37	0.56
29:G:90:ILE:HD11	29:G:132:PHE:CE1	2.40	0.56
18:7:20:ARG:O	18:7:24:VAL:HG23	2.05	0.56
23:A:282:A:O2'	30:H:51:ARG:HD2	2.05	0.56
23:A:2453:U:C2'	23:A:2454:G:H5'	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:3096:U:O2'	39:Q:1:MET:N	2.39	0.56
23:A:3105:C:N4	49:b:41:ARG:O	2.38	0.56
29:G:5:GLY:O	29:G:66:HIS:NE2	2.38	0.56
32:J:10:LEU:N	32:J:60:ILE:O	2.39	0.56
1:h:451:A:N6	1:h:461:G:OP2	2.38	0.56
1:h:921:G:OP2	7:p:102:ARG:NH1	2.38	0.56
23:A:159:A:N3	23:A:2431:C:O2'	2.37	0.56
28:F:178:ARG:NH2	28:F:186:GLU:OE2	2.38	0.56
56:3:12:LYS:HA	56:3:21:ARG:HD2	1.88	0.56
1:h:1482:U:O2'	1:h:1483:A:OP2	2.19	0.56
5:m:71:VAL:HG21	5:m:143:ALA:HB2	1.88	0.56
23:A:84:U:O2	47:Z:45:ARG:NH2	2.38	0.56
23:A:2475:G:OP2	36:N:82:ARG:NH1	2.38	0.56
24:B:37:C:N3	24:B:50:C:O2'	2.38	0.56
30:H:55:GLU:HA	30:H:58:VAL:CG2	2.35	0.56
39:Q:2:ASN:O	39:Q:5:ASP:N	2.38	0.56
45:W:66:ILE:HD13	45:W:138:LEU:HD23	1.88	0.56
1:h:1218:C:OP1	1:h:1285:C:O2'	2.23	0.56
23:A:2165:C:O2'	23:A:2166:C:OP1	2.24	0.56
23:A:2453:U:H2'	23:A:2454:G:H5'	1.88	0.56
38:P:38:LEU:HD23	38:P:102:PHE:HD1	1.71	0.56
23:A:1144:A:OP2	23:A:1252:G:O2'	2.15	0.56
49:b:5:LYS:O	49:b:6:ARG:CD	2.54	0.56
1:h:452:A:O2'	15:z:76:ILE:HD11	2.05	0.55
1:h:1097:G:H4'	9:4:126:ARG:NE	2.20	0.55
3:k:62:ARG:NH1	3:k:64:ARG:CG	2.69	0.55
20:r:16:LEU:HD22	20:r:21:ARG:HA	1.88	0.55
23:A:724:G:N2	23:A:727:A:OP2	2.36	0.55
23:A:1078:G:OP1	56:3:9:ARG:NH2	2.40	0.55
25:C:147:LEU:HD21	25:C:155:LEU:HD11	1.87	0.55
1:h:632:U:O4	1:h:732:G:O2'	2.18	0.55
8:q:77:LEU:HG	8:q:78:ARG:N	2.20	0.55
23:A:1203:A:O2'	23:A:1222:C:O2	2.24	0.55
23:A:1996:U:OP2	23:A:2001:A:N6	2.38	0.55
27:E:20:LEU:HD22	27:E:25:PHE:HE2	1.70	0.55
30:H:3:LEU:HD13	30:H:36:ALA:HB1	1.88	0.55
37:O:38:GLU:OE2	37:O:42:ARG:NH2	2.40	0.55
23:A:1183:U:H3	23:A:1187:A:HO2'	1.51	0.55
25:C:68:ARG:O	25:C:70:HIS:ND1	2.39	0.55
25:C:101:GLU:OE2	25:C:103:ARG:NH2	2.39	0.55
26:D:184:LYS:HB3	26:D:193:LEU:HD12	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:P:70:VAL:HG22	38:P:87:LEU:HD11	1.87	0.55
3:k:130:ARG:NH1	3:k:168:TYR:OH	2.39	0.55
4:l:71:TYR:HA	4:l:85:LEU:HD13	1.87	0.55
5:m:102:ILE:C	5:m:104:SER:N	2.59	0.55
11:t:91:VAL:HG12	11:t:92:ASP:O	2.06	0.55
18:7:51:LEU:HD22	18:7:83:LEU:HD22	1.89	0.55
23:A:1640:A:N6	23:A:1714:A:N1	2.54	0.55
1:h:555:G:N2	1:h:862:C:O2	2.33	0.55
19:8:83:GLU:O	19:8:87:VAL:HG23	2.07	0.55
26:D:27:THR:HG21	26:D:198:ILE:HG12	1.89	0.55
31:I:17:PHE:CE1	31:I:23:THR:HG21	2.41	0.55
14:x:59:LEU:HD23	14:x:62:ARG:HE	1.71	0.55
26:D:62:VAL:HG11	26:D:77:PRO:CB	2.36	0.55
31:I:82:VAL:HG11	31:I:89:ALA:HB2	1.88	0.55
54:g:11:PRO:O	54:g:12:VAL:HG13	2.06	0.55
54:g:30:THR:CA	54:g:34:THR:CG2	2.73	0.55
14:x:3:LEU:HD12	14:x:35:ARG:HH11	1.71	0.55
23:A:1116:C:O2	48:a:32:ARG:NH2	2.38	0.55
23:A:1478:C:O2'	23:A:2026:A:N3	2.35	0.55
3:k:62:ARG:NH2	3:k:64:ARG:HD2	2.21	0.55
12:u:79:MET:N	12:u:103:ASP:OD2	2.38	0.55
23:A:625:A:N6	23:A:647:G:O2'	2.39	0.55
23:A:1129:G:OP2	40:R:66:ASN:ND2	2.40	0.55
23:A:2967:C:O2'	29:G:151:ARG:NE	2.36	0.55
34:L:24:VAL:HG13	34:L:33:ALA:HB2	1.88	0.55
1:h:1358:A:O3'	7:p:29:LYS:NZ	2.33	0.55
10:s:42:LEU:CD1	10:s:73:LEU:HD12	2.36	0.55
23:A:362:A:N7	23:A:363:A:N6	2.53	0.55
23:A:3008:C:O2'	26:D:45:ASP:OD1	2.10	0.55
31:I:61:ALA:HA	31:I:66:ILE:HD11	1.89	0.55
54:g:60:PHE:CD1	54:g:60:PHE:C	2.85	0.55
1:h:958:G:O2'	1:h:1344:C:N4	2.41	0.54
13:v:22:ILE:HB	13:v:25:ILE:HD12	1.89	0.54
22:9:64:ASP:OD1	22:9:65:VAL:N	2.39	0.54
27:E:58:VAL:HG21	27:E:80:ARG:HB3	1.88	0.54
37:O:98:ILE:HD12	37:O:114:GLU:OE2	2.06	0.54
55:y:53:LYS:O	55:y:56:LYS:HB2	2.07	0.54
9:4:26:ILE:HG21	9:4:41:LEU:O	2.07	0.54
22:9:31:ILE:O	22:9:37:SER:OG	2.09	0.54
23:A:2026:A:O2'	23:A:2027:A:O5'	2.23	0.54
23:A:3038:C:OP1	37:O:42:ARG:NH2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:W:60:SER:OG	45:W:61:HIS:ND1	2.41	0.54
1:h:959:A:N6	1:h:1205:U:O5'	2.40	0.54
4:l:168:VAL:HG22	4:l:175:ILE:HG12	1.90	0.54
6:n:4:TYR:CD2	6:n:72:VAL:HG11	2.42	0.54
53:f:2:LYS:NZ	53:f:31:ARG:O	2.36	0.54
1:h:40:C:OP1	12:u:120:LYS:NZ	2.32	0.54
12:u:14:ASP:OD1	12:u:15:LYS:N	2.40	0.54
23:A:1510:A:O2'	23:A:1511:U:O5'	2.22	0.54
23:A:2956:G:OP1	26:D:213:LYS:NZ	2.28	0.54
25:C:68:ARG:O	25:C:70:HIS:N	2.40	0.54
50:c:27:ARG:HH22	50:c:30:ASP:HB2	1.73	0.54
56:3:8:LYS:O	56:3:11:ARG:CG	2.53	0.54
56:3:12:LYS:HD2	56:3:20:LYS:HA	1.89	0.54
1:h:718:U:OP1	6:n:2:ARG:NH1	2.40	0.54
1:h:826:U:O4'	20:r:14:THR:HG23	2.08	0.54
12:u:68:PRO:O	12:u:99:ARG:NH2	2.40	0.54
20:r:33:ASP:O	20:r:40:LEU:HD11	2.06	0.54
22:9:80:SER:O	22:9:84:VAL:HG23	2.08	0.54
36:N:16:GLU:O	36:N:96:ASN:ND2	2.39	0.54
1:h:429:U:O2'	1:h:430:A:OP2	2.21	0.54
30:H:51:ARG:HG3	30:H:52:ARG:N	2.23	0.54
42:T:75:THR:O	42:T:117:ARG:N	2.39	0.54
1:h:1082:A:H2'	1:h:1083:C:H6	1.71	0.54
21:Y:6:GLU:OE1	21:Y:65:ARG:NH2	2.41	0.54
23:A:49:A:OP2	23:A:116:A:N6	2.40	0.54
23:A:725:A:OP1	52:e:47:ARG:NH1	2.41	0.54
23:A:1564:A:O2'	23:A:1565:A:O4'	2.26	0.54
23:A:2980:U:OP2	53:f:19:ARG:NE	2.40	0.54
1:h:1092:C:C4	3:k:178:LEU:HD12	2.43	0.54
1:h:1193:U:O2'	1:h:1194:A:O4'	2.25	0.54
4:l:181:PRO:HB2	4:l:186:ILE:HD11	1.90	0.54
19:8:83:GLU:OE1	19:8:214:THR:HB	2.08	0.54
1:h:168:A:O2'	1:h:169:A:O4'	2.11	0.54
19:8:14:ALA:C	19:8:15:HIS:CG	2.83	0.54
19:8:187:LEU:HD21	19:8:199:PRO:HB3	1.90	0.54
24:B:13:C:O2'	24:B:14:A:OP2	2.24	0.54
54:g:30:THR:C	54:g:34:THR:HG23	2.33	0.54
1:h:1400:A:C6	1:h:1466:G:C6	2.97	0.53
19:8:14:ALA:O	19:8:15:HIS:ND1	2.41	0.53
28:F:20:ARG:HE	28:F:35:ILE:HG21	1.72	0.53
34:L:16:ALA:HB2	34:L:52:VAL:HG11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:L:102:VAL:HG22	34:L:121:VAL:HG22	1.90	0.53
55:y:14:GLY:N	55:y:28:TRP:CE3	2.69	0.53
13:v:23:TYR:HD2	13:v:70:LEU:HD13	1.72	0.53
23:A:58:G:OP1	47:Z:48:ARG:NE	2.41	0.53
23:A:2474:G:OP1	23:A:2499:C:O2'	2.18	0.53
1:h:145:G:N2	1:h:172:C:O2	2.41	0.53
9:4:45:THR:HG22	9:4:46:GLY:H	1.71	0.53
23:A:97:U:OP1	23:A:98:U:O2'	2.27	0.53
26:D:115:THR:HG21	26:D:174:ARG:HE	1.73	0.53
26:D:157:PRO:HG2	26:D:161:PHE:CZ	2.43	0.53
32:J:13:LEU:HD21	32:J:30:LEU:HD22	1.90	0.53
6:n:41:ASP:OD1	6:n:42:ILE:N	2.42	0.53
21:Y:42:ASP:OD1	21:Y:63:THR:N	2.41	0.53
23:A:1113:C:O2	33:K:3:THR:OG1	2.20	0.53
36:N:34:ILE:HD12	36:N:104:PHE:HB2	1.89	0.53
50:c:2:ARG:NH2	50:c:4:GLU:OE2	2.42	0.53
55:y:9:ARG:CD	55:y:53:LYS:NZ	2.72	0.53
23:A:2456:C:P	55:y:26:ARG:HH11	2.32	0.53
23:A:2615:G:OP2	52:e:32:LEU:HD13	2.08	0.53
8:q:78:ARG:HH11	8:q:78:ARG:CG	2.22	0.53
10:s:12:ALA:CB	10:s:18:ILE:HD13	2.38	0.53
13:v:82:ILE:HD11	13:v:93:ARG:CG	2.38	0.53
19:8:83:GLU:OE2	19:8:214:THR:HG22	2.08	0.53
23:A:2240:U:O2	49:b:4:PRO:HG2	2.09	0.53
30:H:119:LEU:HD11	30:H:124:ILE:CD1	2.36	0.53
1:h:943:U:OP2	1:h:1204:C:O2'	2.16	0.53
1:h:1442:G:OP1	18:7:30:THR:OG1	2.15	0.53
23:A:2303:A:OP1	55:y:19:HIS:CD2	2.62	0.53
56:3:8:LYS:HA	56:3:11:ARG:CD	2.38	0.53
1:h:1231:A:N3	1:h:1353:G:O2'	2.35	0.53
6:n:77:ARG:HH21	25:C:126:LYS:CG	2.09	0.53
8:q:11:LEU:HB3	8:q:77:LEU:HD21	1.91	0.53
23:A:1480:A:H5''	55:y:27:ARG:NH1	2.24	0.53
30:H:61:ASP:C	30:H:61:ASP:OD1	2.51	0.53
44:V:47:VAL:H	44:V:57:GLY:N	2.05	0.53
1:h:362:G:N1	1:h:365:U:OP2	2.41	0.53
21:Y:30:ARG:NH1	21:Y:92:GLU:OE2	2.42	0.53
29:G:122:ILE:HD11	29:G:134:VAL:HG12	1.89	0.53
1:h:1244:G:O6	1:h:1254:G:N2	2.41	0.53
1:h:1290:C:OP2	13:v:101:GLN:NE2	2.42	0.53
15:z:35:GLU:OE1	15:z:59:TRP:NE1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1480:A:H5''	55:y:27:ARG:HH12	1.72	0.53
23:A:2338:G:O2'	23:A:2340:A:N7	2.33	0.53
32:J:81:LEU:HD13	32:J:139:ILE:CD1	2.39	0.53
33:K:76:ARG:O	33:K:84:LEU:HD12	2.08	0.53
34:L:5:GLU:HA	34:L:20:LEU:HD11	1.91	0.53
1:h:920:A:O2'	1:h:921:G:OP1	2.26	0.52
1:h:1404:C:O2'	1:h:1405:G:OP1	2.21	0.52
23:A:658:U:O2'	23:A:924:G:OP2	2.25	0.52
23:A:789:G:OP1	27:E:55:ARG:NH2	2.41	0.52
23:A:1186:G:N2	23:A:1213:A:O2'	2.42	0.52
35:M:80:VAL:HG13	35:M:118:LEU:HD13	1.90	0.52
45:W:186:SER:OG	45:W:189:ALA:N	2.41	0.52
23:A:292:G:H22	23:A:343:U:H2'	1.75	0.52
23:A:2316:G:H21	23:A:2421:A:N6	2.06	0.52
8:q:11:LEU:HB3	8:q:77:LEU:CD2	2.38	0.52
23:A:1737:A:O2'	23:A:1776:C:O2	2.27	0.52
23:A:2387:U:O2	23:A:2394:A:N6	2.41	0.52
28:F:44:ASN:OD1	28:F:45:MET:N	2.42	0.52
50:c:37:ARG:CD	50:c:51:GLU:HG3	2.38	0.52
1:h:1080:C:OP2	19:8:95:ARG:NE	2.40	0.52
1:h:1097:G:C4'	9:4:126:ARG:HE	2.23	0.52
10:s:32:THR:HG21	10:s:83:THR:OG1	2.09	0.52
34:L:14:THR:HG21	34:L:86:ILE:HD12	1.92	0.52
38:P:9:ASN:OD1	38:P:10:ILE:N	2.42	0.52
44:V:84:GLY:N	44:V:97:ILE:O	2.37	0.52
23:A:1153:U:O3'	29:G:60:ARG:NH2	2.42	0.52
23:A:3055:G:H2'	23:A:3100:A:H61	1.73	0.52
34:L:102:VAL:CG2	34:L:121:VAL:HG22	2.40	0.52
7:p:31:LEU:HD13	7:p:36:LYS:HA	1.92	0.52
23:A:2233:G:OP1	42:T:26:ARG:NH2	2.42	0.52
32:J:15:ILE:HD12	32:J:58:VAL:HG11	1.92	0.52
42:T:17:VAL:O	42:T:107:THR:OG1	2.12	0.52
45:W:57:VAL:O	45:W:60:SER:OG	2.25	0.52
50:c:12:ARG:HB3	50:c:52:GLU:O	2.10	0.52
54:g:60:PHE:HE1	54:g:62:THR:HG23	0.36	0.52
9:4:126:ARG:HH11	9:4:126:ARG:HG2	1.75	0.52
54:g:30:THR:HG22	54:g:31:SER:N	2.25	0.52
23:A:114:G:OP2	23:A:116:A:O2'	2.28	0.52
23:A:1252:G:OP2	56:3:3:LYS:NZ	2.28	0.52
23:A:1849:G:N2	23:A:1852:A:OP2	2.32	0.52
2:j:33:LYS:NZ	23:A:2199:G:O2'	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:k:62:ARG:HH22	3:k:64:ARG:HD2	1.73	0.52
51:d:27:THR:O	51:d:31:ARG:NH1	2.43	0.52
54:g:22:GLN:HE22	54:g:24:LEU:HD23	1.74	0.52
1:h:653:G:O2'	20:r:75:GLU:OE1	2.14	0.52
1:h:1256:A:H61	1:h:1264:C:H5'	1.75	0.52
5:m:71:VAL:O	5:m:97:PHE:N	2.42	0.52
23:A:2358:A:O5'	23:A:2379:G:N2	2.43	0.52
40:R:26:GLY:O	40:R:30:ARG:NH1	2.42	0.52
55:y:17:VAL:HG23	55:y:18:SER:O	2.09	0.52
1:h:92:A:O2'	1:h:93:C:O5'	2.24	0.51
6:n:62:VAL:HG21	20:r:35:LYS:NZ	2.25	0.51
23:A:544:U:H1'	43:U:71:THR:HG23	1.92	0.51
23:A:2500:G:OP2	36:N:86:GLY:N	2.42	0.51
49:b:5:LYS:O	49:b:6:ARG:HD3	2.10	0.51
54:g:35:ILE:CD1	54:g:49:ILE:CG1	2.87	0.51
7:p:150:ALA:HB1	11:t:68:THR:HG21	1.91	0.51
23:A:563:U:H3	23:A:567:A:H62	1.58	0.51
24:B:48:C:OP2	38:P:14:ARG:NH2	2.43	0.51
49:b:9:SER:OG	49:b:12:ASN:ND2	2.42	0.51
55:y:14:GLY:CA	55:y:28:TRP:CH2	2.61	0.51
23:A:736:G:N2	23:A:739:U:OP2	2.43	0.51
45:W:54:PHE:CE2	45:W:58:LEU:HD11	2.46	0.51
50:c:42:VAL:O	50:c:44:ARG:N	2.42	0.51
32:J:12:LYS:O	32:J:13:LEU:HD12	2.09	0.51
1:h:1097:G:C4'	9:4:126:ARG:NE	2.73	0.51
6:n:21:PRO:O	6:n:25:THR:HG23	2.10	0.51
21:Y:7:VAL:HG22	21:Y:28:LEU:CD2	2.41	0.51
23:A:2245:C:OP1	40:R:25:ARG:NH1	2.43	0.51
26:D:40:ARG:HB2	26:D:49:ALA:HB3	1.92	0.51
26:D:157:PRO:HG2	26:D:161:PHE:CE1	2.46	0.51
19:8:189:THR:HG23	19:8:190:ASN:CG	2.36	0.51
23:A:265:A:O2'	23:A:516:G:O6	2.27	0.51
23:A:603:C:O2'	23:A:1376:C:O2'	2.29	0.51
23:A:2445:A:O2'	25:C:188:ARG:NH1	2.43	0.51
28:F:51:ALA:HB2	28:F:90:MET:HE1	1.92	0.51
36:N:42:ILE:HD12	36:N:97:VAL:HG21	1.93	0.51
1:h:544:C:OP2	12:u:12:ARG:NH2	2.43	0.51
8:q:78:ARG:NE	8:q:130:TYR:HB2	2.26	0.51
18:7:18:ARG:HD3	18:7:19:LEU:N	2.26	0.51
23:A:2442:U:P	55:y:45:ARG:NH1	2.78	0.51
39:Q:13:ARG:NH1	39:Q:80:ILE:O	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:g:18:ALA:CB	54:g:57:SER:CB	2.89	0.51
54:g:88:PHE:O	54:g:92:TYR:N	2.36	0.51
21:Y:14:VAL:O	21:Y:16:VAL:HG23	2.11	0.51
23:A:2473:U:N3	23:A:2477:G:OP2	2.41	0.51
23:A:3012:U:O2'	23:A:3030:A:N3	2.37	0.51
31:I:31:LEU:HD11	31:I:103:LEU:HB2	1.93	0.51
54:g:35:ILE:HD12	54:g:49:ILE:CG1	2.41	0.51
1:h:1098:U:P	9:4:126:ARG:NE	2.81	0.51
1:h:1468:U:O2'	23:A:2184:A:O2'	2.12	0.51
23:A:255:A:O2'	23:A:472:C:OP2	2.28	0.51
23:A:2054:C:O2'	23:A:2151:A:N3	2.42	0.51
29:G:122:ILE:HD11	29:G:134:VAL:CG1	2.41	0.51
9:4:69:LYS:O	9:4:73:VAL:HG23	2.11	0.50
19:8:68:LEU:HD21	19:8:150:GLY:CA	2.41	0.50
23:A:1112:C:OP1	40:R:53:ARG:NH2	2.43	0.50
23:A:3071:A:OP2	23:A:3087:G:N1	2.40	0.50
32:J:12:LYS:C	32:J:13:LEU:HD12	2.35	0.50
35:M:118:LEU:HD21	35:M:137:ILE:HD13	1.93	0.50
55:y:12:GLY:C	55:y:13:PHE:CD1	2.89	0.50
1:h:345:C:OP2	39:Q:38:ARG:NH1	2.44	0.50
1:h:602:A:OP2	1:h:603:C:N4	2.41	0.50
23:A:136:U:N3	23:A:139:U:OP2	2.41	0.50
23:A:210:G:OP2	51:d:28:ARG:NH2	2.44	0.50
23:A:316:U:O2'	23:A:317:G:OP1	2.22	0.50
23:A:1712:G:H1	23:A:1718:C:H42	1.59	0.50
26:D:160:VAL:O	26:D:164:THR:OG1	2.26	0.50
30:H:37:ILE:HD11	30:H:49:GLU:HB2	1.92	0.50
46:X:65:GLY:HA2	46:X:83:VAL:HG13	1.94	0.50
55:y:26:ARG:CD	55:y:28:TRP:CZ3	2.94	0.50
1:h:324:G:N1	1:h:327:A:OP2	2.38	0.50
7:p:14:ASN:OD1	7:p:15:ASP:N	2.44	0.50
23:A:286:G:N1	23:A:300:G:OP2	2.44	0.50
45:W:11:LEU:HD12	45:W:67:LEU:HD22	1.93	0.50
50:c:25:LYS:HD2	52:e:34:GLU:HG2	1.92	0.50
1:h:1118:A:O2'	1:h:1119:U:O4'	2.29	0.50
32:J:15:ILE:HD12	32:J:58:VAL:CG1	2.41	0.50
5:m:81:VAL:HG12	5:m:85:ILE:HD12	1.94	0.50
6:n:77:ARG:HH22	25:C:126:LYS:CG	2.19	0.50
11:t:77:GLU:OE2	11:t:81:ARG:NH2	2.44	0.50
31:I:23:THR:HG23	31:I:109:TYR:HD2	1.76	0.50
45:W:67:LEU:O	45:W:77:LEU:HD12	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:c:31:PRO:O	50:c:32:ASP:HB2	2.11	0.50
4:l:153:ALA:O	4:l:157:ALA:HB2	2.12	0.50
21:Y:8:VAL:CG2	21:Y:40:LEU:HD11	2.41	0.50
23:A:807:C:H2'	23:A:808:A:H8	1.76	0.50
23:A:1564:A:O2'	23:A:1565:A:O5'	2.29	0.50
23:A:2510:A:N7	50:c:36:LEU:HD22	2.26	0.50
28:F:57:ILE:HD13	28:F:91:PRO:HB2	1.94	0.50
1:h:610:C:O2'	1:h:611:G:OP1	2.28	0.50
1:h:1124:G:N1	1:h:1125:G:O6	2.45	0.50
3:k:62:ARG:CZ	3:k:64:ARG:CD	2.89	0.50
23:A:282:A:O2'	30:H:51:ARG:HB2	2.12	0.50
28:F:122:ARG:C	54:g:61:TRP:HE1	2.11	0.50
29:G:36:ASP:OD1	29:G:37:VAL:N	2.45	0.50
35:M:63:LYS:HG2	52:e:13:ARG:NE	2.27	0.50
1:h:510:G:N1	21:Y:53:GLN:O	2.44	0.50
11:t:32:ILE:HG23	11:t:41:VAL:HG12	1.94	0.50
23:A:2454:G:C5	23:A:2455:C:N4	2.79	0.50
50:c:33:ARG:NH2	50:c:50:ARG:NH2	2.60	0.50
1:h:183:C:H42	1:h:205:G:H1	1.58	0.50
21:Y:62:ILE:HD12	21:Y:87:ALA:HB1	1.94	0.50
23:A:2702:A:OP1	53:f:31:ARG:NH1	2.44	0.50
42:T:12:ALA:CB	42:T:61:ALA:HB2	2.41	0.50
55:y:13:PHE:CD1	55:y:13:PHE:N	2.80	0.50
23:A:700:U:O3'	27:E:101:ARG:NH2	2.44	0.49
23:A:1105:C:O2'	23:A:1118:A:N3	2.42	0.49
49:b:8:MET:HE2	49:b:16:ARG:HH12	1.64	0.49
1:h:1109:C:O2'	1:h:1110:A:N7	2.44	0.49
8:q:39:ILE:HD11	8:q:112:LEU:HB2	1.93	0.49
34:L:42:THR:OG1	34:L:56:ASP:O	2.22	0.49
50:c:6:ARG:HE	50:c:8:ILE:HG22	1.72	0.49
54:g:24:LEU:HD13	54:g:46:TYR:OH	2.12	0.49
1:h:1097:G:C3'	9:4:126:ARG:NE	2.55	0.49
37:O:10:LEU:HD21	37:O:40:LYS:HG2	1.94	0.49
54:g:54:THR:HG23	54:g:55:SER:H	1.77	0.49
13:v:72:ARG:NE	28:F:120:ASP:OD2	2.45	0.49
23:A:604:C:O2'	42:T:25:ARG:NH2	2.45	0.49
23:A:1275:A:O4'	40:R:51:ARG:NH1	2.46	0.49
26:D:157:PRO:CG	26:D:161:PHE:CZ	2.95	0.49
27:E:97:ASP:OD1	27:E:98:TYR:N	2.44	0.49
28:F:117:ARG:NH1	28:F:144:MET:O	2.43	0.49
39:Q:20:SER:N	39:Q:23:ASP:OD2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:998:G:N3	1:h:1199:C:O2'	2.38	0.49
23:A:369:G:HO2'	23:A:371:G:C5'	2.25	0.49
23:A:2176:A:OP1	34:L:44:LYS:NZ	2.21	0.49
29:G:90:ILE:HD11	29:G:132:PHE:HE1	1.77	0.49
55:y:19:HIS:C	55:y:20:SER:O	2.53	0.49
23:A:436:C:N4	23:A:437:G:O6	2.46	0.49
23:A:1788:G:OP1	25:C:63:ARG:NH2	2.45	0.49
1:h:991:C:OP1	22:9:20:TYR:OH	2.26	0.49
50:c:25:LYS:CD	52:e:34:GLU:OE2	2.61	0.49
54:g:3:PRO:HA	54:g:5:ILE:HD13	1.94	0.49
15:z:48:LEU:HD12	15:z:49:ILE:H	1.78	0.49
48:a:6:ILE:HG21	48:a:28:LEU:HD11	1.94	0.49
1:h:184:U:H3	1:h:204:A:H61	1.60	0.49
6:n:9:ILE:HG22	6:n:86:LEU:HD12	1.94	0.49
10:s:25:ILE:O	10:s:29:VAL:HG23	2.13	0.49
23:A:357:U:O4	23:A:364:A:N6	2.46	0.49
23:A:532:C:OP1	27:E:46:ARG:NH2	2.40	0.49
29:G:17:VAL:CG1	29:G:24:LEU:HD11	2.43	0.49
54:g:2:LYS:HB2	54:g:3:PRO:HD2	1.95	0.49
1:h:23:C:OP1	5:m:155:SER:OG	2.26	0.48
1:h:1097:G:H5''	9:4:126:ARG:CZ	2.39	0.48
23:A:974:G:O2'	23:A:1031:G:O6	2.31	0.48
30:H:66:ASN:OD1	30:H:136:LEU:O	2.31	0.48
1:h:1119:U:O2'	1:h:1120:G:OP1	2.30	0.48
23:A:587:G:N1	23:A:590:A:OP2	2.43	0.48
23:A:2454:G:O2'	23:A:2455:C:H5'	2.12	0.48
26:D:154:CYS:O	26:D:155:ALA:HB3	2.12	0.48
1:h:450:G:OP2	1:h:451:A:O2'	2.27	0.48
1:h:756:G:N1	1:h:782:A:OP1	2.45	0.48
1:h:1383:C:OP2	21:Y:97:ARG:NH2	2.46	0.48
23:A:1885:G:O2'	23:A:2215:U:O4	2.32	0.48
49:b:5:LYS:O	49:b:6:ARG:HD2	2.14	0.48
19:8:95:ARG:HH11	19:8:97:LEU:HD23	1.78	0.48
23:A:978:A:O2'	24:B:98:A:N3	2.46	0.48
50:c:42:VAL:C	50:c:44:ARG:N	2.69	0.48
12:u:63:VAL:HG12	12:u:64:THR:O	2.13	0.48
13:v:14:ARG:NH1	13:v:16:GLU:OE2	2.46	0.48
23:A:2313:A:N6	23:A:2454:G:O6	2.45	0.48
31:I:120:VAL:HA	31:I:123:ILE:HD12	1.95	0.48
1:h:145:G:HO2'	1:h:1429:A:HO2'	1.58	0.48
1:h:1081:A:H5'	19:8:171:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:1236:G:O2'	1:h:1237:C:O5'	2.30	0.48
18:7:15:GLU:O	18:7:18:ARG:CG	2.54	0.48
26:D:103:ALA:HB1	26:D:192:LEU:HD11	1.94	0.48
37:O:98:ILE:CG2	49:b:46:ALA:HB2	2.43	0.48
55:y:30:PRO:HG2	55:y:32:ILE:HG23	1.95	0.48
3:k:58:ARG:O	10:s:94:ALA:HB1	2.14	0.48
23:A:2819:G:N2	23:A:2822:A:OP2	2.42	0.48
26:D:161:PHE:O	26:D:164:THR:OG1	2.31	0.48
46:X:25:ARG:NE	46:X:35:GLU:OE2	2.47	0.48
9:4:126:ARG:CG	9:4:126:ARG:NH1	2.73	0.48
19:8:16:PHE:HD2	19:8:203:ASN:HD22	0.50	0.48
32:J:87:VAL:O	32:J:87:VAL:HG23	2.14	0.48
36:N:19:GLY:O	36:N:39:HIS:NE2	2.45	0.48
50:c:38:LYS:O	50:c:39:TYR:CD1	2.67	0.48
1:h:1074:G:O2'	1:h:1075:U:OP2	2.32	0.48
1:h:1098:U:P	9:4:126:ARG:NH2	2.87	0.48
1:h:1404:C:OP1	34:L:54:ARG:NH2	2.47	0.48
25:C:137:PRO:O	25:C:140:THR:HG23	2.14	0.48
31:I:6:LYS:O	31:I:10:VAL:HG23	2.14	0.48
50:c:11:LEU:CD2	50:c:25:LYS:HG2	2.44	0.48
55:y:30:PRO:O	55:y:31:ASN:HB2	2.12	0.48
6:n:7:MET:HG2	20:r:76:MET:HE2	1.95	0.48
23:A:1148:G:OP2	36:N:128:LYS:NZ	2.33	0.48
28:F:7:ALA:HB2	54:g:26:ARG:HE	1.77	0.48
44:V:47:VAL:N	44:V:57:GLY:H	2.08	0.48
1:h:972:U:O2	1:h:1196:G:O6	2.32	0.47
15:z:48:LEU:HD12	15:z:49:ILE:N	2.28	0.47
23:A:2907:C:O2	34:L:76:TYR:OH	2.32	0.47
24:B:73:G:O2'	24:B:74:A:O4'	2.28	0.47
27:E:27:VAL:O	27:E:120:ARG:NH2	2.47	0.47
31:I:17:PHE:HE1	31:I:23:THR:HG21	1.78	0.47
32:J:23:ALA:HB3	32:J:24:PRO:HD3	1.96	0.47
43:U:95:LEU:HD13	47:Z:31:ASN:OD1	2.14	0.47
50:c:33:ARG:HH21	50:c:50:ARG:NH2	2.12	0.47
1:h:700:C:OP1	20:r:52:SER:OG	2.31	0.47
1:h:1500:G:N1	1:h:1503:A:OP2	2.47	0.47
23:A:543:U:H3'	23:A:544:U:H5''	1.96	0.47
28:F:69:GLY:O	54:g:9:TYR:OH	2.30	0.47
6:n:62:VAL:HG21	20:r:35:LYS:CE	2.44	0.47
7:p:61:THR:CA	7:p:64:ARG:NH1	2.77	0.47
20:r:24:LEU:HA	20:r:29:VAL:HG21	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:380:A:N1	23:A:404:A:O2'	2.43	0.47
23:A:935:A:N3	23:A:1060:U:O2'	2.45	0.47
23:A:1377:A:N3	49:b:7:ARG:NH2	2.62	0.47
23:A:1381:G:N7	42:T:22:THR:OG1	2.42	0.47
30:H:55:GLU:CA	30:H:58:VAL:HG22	2.40	0.47
1:h:750:C:H1'	1:h:881:C:H42	1.79	0.47
6:n:76:ASP:OD2	6:n:90:VAL:HG21	2.14	0.47
19:8:209:SER:O	19:8:213:LEU:HD23	2.15	0.47
23:A:228:A:H3'	23:A:229:U:H5''	1.96	0.47
23:A:1081:C:O2'	23:A:2497:A:N3	2.47	0.47
23:A:1869:G:OP1	37:O:40:LYS:NZ	2.43	0.47
23:A:2255:A:O2'	23:A:2678:G:N2	2.46	0.47
26:D:84:LEU:HD22	26:D:209:ARG:NH1	2.30	0.47
30:H:21:VAL:HG22	30:H:22:LYS:H	1.79	0.47
50:c:22:VAL:HG11	50:c:39:TYR:CE2	2.49	0.47
1:h:502:C:OP1	12:u:69:GLY:N	2.42	0.47
1:h:1053:U:H3	1:h:1082:A:H61	1.62	0.47
1:h:1100:U:O4	1:h:1135:G:N1	2.48	0.47
5:m:71:VAL:CG2	5:m:143:ALA:HB2	2.45	0.47
19:8:104:PHE:HA	19:8:107:VAL:HG22	1.96	0.47
23:A:1002:C:O2'	23:A:1003:A:OP1	2.19	0.47
23:A:1252:G:O6	56:3:6:ARG:NH2	2.44	0.47
27:E:50:HIS:NE2	27:E:98:TYR:OH	2.44	0.47
39:Q:5:ASP:OD1	39:Q:6:PHE:N	2.47	0.47
50:c:27:ARG:NH1	50:c:29:ASN:CA	2.76	0.47
1:h:20:A:N3	1:h:1060:A:O2'	2.44	0.47
6:n:30:ILE:HD11	6:n:75:LEU:HD22	1.96	0.47
7:p:61:THR:O	7:p:64:ARG:HB2	2.14	0.47
3:k:52:ALA:HB2	3:k:114:LEU:HD11	1.97	0.47
4:l:60:TYR:OH	4:l:90:GLU:OE2	2.29	0.47
15:z:92:THR:O	15:z:92:THR:HG22	2.15	0.47
23:A:701:A:OP2	23:A:713:G:N1	2.43	0.47
23:A:752:C:H42	23:A:763:G:H1	1.61	0.47
23:A:1112:C:O2'	23:A:1114:G:OP1	2.29	0.47
23:A:1481:C:H5'	55:y:3:HIS:HE1	1.80	0.47
29:G:7:GLN:OE1	29:G:70:ARG:NH2	2.47	0.47
30:H:57:LYS:HE2	30:H:57:LYS:CA	2.43	0.47
30:H:84:ALA:HB1	30:H:91:LEU:HA	1.95	0.47
34:L:107:ARG:NH1	39:Q:33:GLU:OE2	2.47	0.47
54:g:87:LYS:HA	54:g:90:ARG:CG	2.39	0.47
1:h:909:G:H21	1:h:1516:U:H4'	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:x:78:TYR:CZ	14:x:82:ILE:HD11	2.50	0.47
25:C:111:LEU:HD11	25:C:117:ILE:HD11	1.95	0.47
39:Q:48:ARG:NH1	39:Q:97:TYR:OH	2.44	0.47
44:V:75:ASP:OD1	44:V:76:SER:N	2.48	0.47
9:4:74:THR:HG21	9:4:118:LEU:HD23	1.97	0.47
23:A:1942:G:H1	23:A:1952:C:H42	1.63	0.47
23:A:3066:C:H42	23:A:3092:G:H1	1.62	0.47
30:H:70:THR:CG2	30:H:140:VAL:HG11	2.41	0.47
38:P:74:ASP:OD1	38:P:75:GLY:N	2.48	0.47
1:h:1063:U:O2'	1:h:1082:A:OP2	2.22	0.47
1:h:1324:C:OP1	9:4:149:LYS:NZ	2.45	0.47
15:z:48:LEU:HD11	15:z:50:GLN:HG3	1.96	0.47
40:R:106:PHE:O	40:R:110:VAL:HG23	2.15	0.47
50:c:23:THR:HG22	50:c:24:ARG:N	2.29	0.47
11:t:43:ILE:HG21	11:t:51:ILE:HD11	1.96	0.46
12:u:39:THR:HG22	12:u:51:LYS:HG2	1.96	0.46
23:A:1968:U:O2'	23:A:3082:U:O2'	2.34	0.46
23:A:3056:A:N6	23:A:3100:A:O5'	2.48	0.46
54:g:35:ILE:HB	54:g:49:ILE:HA	1.96	0.46
54:g:35:ILE:CB	54:g:48:LEU:O	2.51	0.46
5:m:157:ASN:O	5:m:161:VAL:HG23	2.15	0.46
15:z:5:ILE:HG12	15:z:22:VAL:HG22	1.96	0.46
23:A:808:A:O2'	23:A:1468:A:N3	2.42	0.46
23:A:2648:C:O2	23:A:2653:G:O2'	2.22	0.46
26:D:155:ALA:C	26:D:156:THR:HG1	2.07	0.46
54:g:30:THR:HG22	54:g:31:SER:H	1.78	0.46
23:A:361:A:N1	23:A:440:U:O2'	2.29	0.46
1:h:208:G:O2'	18:7:63:SER:OG	2.30	0.46
1:h:465:G:HO2'	1:h:466:U:P	2.35	0.46
1:h:819:U:H3	1:h:829:G:H22	1.62	0.46
7:p:24:THR:HA	7:p:27:VAL:HG22	1.96	0.46
8:q:35:ASN:CB	8:q:112:LEU:HD12	2.46	0.46
21:Y:28:LEU:HD11	21:Y:41:PHE:CD2	2.49	0.46
23:A:1720:G:N2	25:C:99:ASP:O	2.28	0.46
35:M:80:VAL:CG1	35:M:118:LEU:HD13	2.45	0.46
47:Z:13:LEU:HD13	47:Z:17:GLU:CG	2.46	0.46
50:c:9:VAL:HG21	50:c:28:ARG:HG2	1.97	0.46
1:h:441:A:H61	1:h:473:A:H61	1.63	0.46
1:h:1201:G:H21	17:6:54:GLY:HA2	1.80	0.46
9:4:149:LYS:O	9:4:150:ARG:NE	2.44	0.46
14:x:3:LEU:HD11	14:x:35:ARG:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:9:74:LEU:HD12	22:9:84:VAL:HG21	1.97	0.46
23:A:1381:G:O2'	23:A:2236:G:O6	2.30	0.46
30:H:73:GLU:HG3	30:H:73:GLU:O	2.16	0.46
32:J:55:VAL:HG23	32:J:55:VAL:O	2.16	0.46
1:h:1040:U:OP1	22:9:85:ARG:NH2	2.49	0.46
1:h:1140:U:O4'	1:h:1163:G:N2	2.49	0.46
23:A:2538:A:OP1	28:F:95:ARG:NH1	2.49	0.46
34:L:77:ILE:HD13	39:Q:71:ARG:HD2	1.98	0.46
54:g:13:VAL:HG13	54:g:24:LEU:HB3	1.96	0.46
55:y:26:ARG:HD2	55:y:28:TRP:CZ2	2.49	0.46
1:h:10:G:O6	5:m:125:SER:N	2.48	0.46
1:h:22:C:OP1	5:m:157:ASN:ND2	2.48	0.46
1:h:692:A:O2'	25:C:176:ARG:NH2	2.49	0.46
1:h:928:A:O2'	1:h:1315:A:N3	2.43	0.46
1:h:1125:G:N2	1:h:1127:A:H62	2.12	0.46
3:k:52:ALA:HB2	3:k:114:LEU:HD21	1.97	0.46
8:q:37:ALA:O	8:q:46:ILE:HD11	2.16	0.46
21:Y:24:VAL:HG11	21:Y:43:VAL:HG11	1.97	0.46
50:c:37:ARG:O	50:c:38:LYS:HG3	2.14	0.46
1:h:194:A:HO2'	1:h:195:U:C5'	2.27	0.46
9:4:125:THR:HG22	9:4:126:ARG:N	2.31	0.46
19:8:16:PHE:CB	19:8:203:ASN:CG	2.89	0.46
19:8:93:ASN:OD1	19:8:94:GLN:N	2.49	0.46
25:C:153:ALA:O	25:C:157:ARG:NH2	2.47	0.46
1:h:862:C:OP2	12:u:3:THR:OG1	2.34	0.46
1:h:1248:U:N3	1:h:1309:C:O2'	2.48	0.46
23:A:383:U:O4	44:V:79:LYS:NZ	2.30	0.46
45:W:60:SER:OG	45:W:61:HIS:N	2.49	0.46
4:l:110:ARG:O	4:l:114:SER:OG	2.30	0.46
23:A:271:A:OP2	23:A:314:G:N1	2.43	0.46
23:A:2018:G:N1	23:A:2028:G:OP2	2.49	0.46
23:A:2456:C:P	55:y:26:ARG:NH1	2.89	0.46
55:y:29:ASP:HB3	55:y:30:PRO:CD	2.46	0.46
7:p:68:ASN:ND2	7:p:127:ALA:O	2.45	0.45
22:9:65:VAL:HG13	22:9:66:VAL:HG23	1.99	0.45
23:A:1259:U:OP2	33:K:65:SER:OG	2.31	0.45
25:C:125:ILE:O	25:C:125:ILE:HG22	2.16	0.45
50:c:30:ASP:OD1	50:c:31:PRO:HD2	2.15	0.45
1:h:12:A:O2'	1:h:13:G:O4'	2.34	0.45
1:h:1248:U:O2'	1:h:1249:G:O5'	2.29	0.45
19:8:19:GLN:HG3	19:8:20:THR:N	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:872:G:O2'	1:h:888:A:N6	2.49	0.45
3:k:50:GLY:O	3:k:69:THR:HG23	2.16	0.45
8:q:115:ASP:OD1	8:q:116:ARG:N	2.48	0.45
15:z:39:ARG:NH1	15:z:50:GLN:OE1	2.49	0.45
23:A:282:A:H1'	30:H:51:ARG:CD	2.39	0.45
23:A:2528:G:O2'	28:F:136:THR:HG22	2.17	0.45
23:A:2967:C:OP2	23:A:2979:C:N4	2.49	0.45
35:M:55:MET:O	35:M:60:ARG:NH1	2.45	0.45
50:c:32:ASP:OD1	50:c:33:ARG:N	2.50	0.45
1:h:867:G:OP2	12:u:15:LYS:NZ	2.36	0.45
18:7:18:ARG:CZ	18:7:18:ARG:CB	2.94	0.45
23:A:740:A:O2'	23:A:741:G:OP2	2.29	0.45
23:A:940:A:H61	23:A:947:U:H3	1.65	0.45
45:W:71:ILE:N	45:W:74:THR:O	2.49	0.45
1:h:183:C:H42	1:h:205:G:H22	1.64	0.45
1:h:1053:U:O2'	19:8:103:ASN:OD1	2.31	0.45
6:n:18:THR:HG22	6:n:18:THR:O	2.17	0.45
30:H:51:ARG:CG	30:H:52:ARG:N	2.80	0.45
31:I:28:TYR:HA	31:I:31:LEU:HD12	1.99	0.45
50:c:6:ARG:CZ	50:c:8:ILE:CG2	2.93	0.45
51:d:9:GLN:OE1	51:d:9:GLN:HA	2.17	0.45
1:h:28:U:O2'	1:h:504:G:O2'	2.34	0.45
23:A:306:U:H5''	30:H:44:GLU:HB2	1.98	0.45
25:C:158:SER:OG	25:C:159:ALA:N	2.43	0.45
30:H:45:ARG:C	30:H:45:ARG:HD2	2.41	0.45
47:Z:53:GLU:O	47:Z:57:VAL:HG23	2.17	0.45
18:7:15:GLU:HA	18:7:18:ARG:HG2	1.99	0.45
23:A:2007:C:O2'	25:C:209:ALA:HB2	2.17	0.45
23:A:2509:C:OP1	50:c:27:ARG:HD3	2.17	0.45
27:E:178:ILE:HD11	27:E:187:ASP:OD2	2.16	0.45
28:F:80:SER:OG	28:F:88:GLU:N	2.50	0.45
35:M:63:LYS:CG	52:e:13:ARG:NE	2.80	0.45
41:S:39:VAL:CG2	41:S:60:VAL:HG23	2.47	0.45
1:h:1256:A:H61	1:h:1264:C:C5'	2.29	0.45
13:v:49:THR:HG22	13:v:51:ASP:H	1.82	0.45
23:A:1184:U:O2'	23:A:1187:A:N7	2.50	0.45
23:A:2813:A:N1	23:A:2830:C:N4	2.65	0.45
30:H:4:ILE:HG13	30:H:45:ARG:NE	2.30	0.45
32:J:134:ALA:HB1	32:J:139:ILE:HB	1.99	0.45
40:R:91:ASP:OD1	40:R:94:ASN:ND2	2.49	0.45
1:h:1384:G:O6	1:h:1488:G:N2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:v:23:TYR:N	13:v:67:GLU:OE2	2.45	0.45
13:v:79:ARG:HA	13:v:82:ILE:HG22	1.99	0.45
19:8:216:VAL:O	19:8:219:SER:OG	2.30	0.45
23:A:749:C:H42	23:A:766:G:H1	1.65	0.45
23:A:2454:G:C5	23:A:2455:C:C4	3.05	0.45
23:A:2474:G:N2	23:A:2500:G:OP1	2.44	0.45
23:A:2530:C:OP2	23:A:2531:G:O2'	2.27	0.45
35:M:63:LYS:HG3	52:e:13:ARG:HE	1.82	0.45
1:h:669:C:O2'	1:h:685:U:O2'	2.35	0.45
1:h:1044:G:H1	1:h:1173:C:H41	1.65	0.45
1:h:1097:G:O3'	9:4:126:ARG:NH2	2.50	0.45
1:h:1229:A:O2'	1:h:1230:C:O4'	2.21	0.45
23:A:1191:A:O2'	23:A:2699:C:OP1	2.35	0.45
24:B:35:G:O2'	24:B:45:G:N7	2.49	0.45
24:B:47:A:C5'	38:P:10:ILE:HD11	2.46	0.45
45:W:63:THR:HG23	45:W:83:LEU:HD11	1.99	0.45
1:h:802:G:O6	1:h:861:C:N4	2.49	0.44
1:h:826:U:C1'	20:r:14:THR:HG23	2.47	0.44
19:8:111:LEU:HD22	19:8:151:ILE:O	2.17	0.44
23:A:2345:U:OP1	23:A:2391:G:N2	2.46	0.44
33:K:18:ILE:HG21	33:K:28:LEU:CD1	2.47	0.44
50:c:44:ARG:C	50:c:45:ARG:HG2	2.42	0.44
54:g:10:HIS:CG	54:g:11:PRO:HD2	2.53	0.44
9:4:118:LEU:O	9:4:122:GLY:N	2.50	0.44
15:z:6:LYS:NZ	15:z:27:THR:OG1	2.50	0.44
21:Y:8:VAL:HG23	21:Y:40:LEU:HD11	1.98	0.44
23:A:552:U:O2'	23:A:553:G:OP1	2.32	0.44
23:A:569:G:OP2	44:V:44:HIS:ND1	2.44	0.44
23:A:1698:A:N6	23:A:1736:G:O2'	2.45	0.44
27:E:184:ASN:ND2	27:E:187:ASP:OD2	2.47	0.44
29:G:98:GLN:O	29:G:104:LEU:HD12	2.17	0.44
43:U:29:TYR:HD2	43:U:93:ILE:HD12	1.80	0.44
54:g:13:VAL:HG23	54:g:47:PRO:O	2.17	0.44
54:g:35:ILE:CG2	54:g:36:GLU:N	2.79	0.44
1:h:144:G:H1	1:h:172:C:H42	1.65	0.44
19:8:111:LEU:HD13	19:8:152:ARG:HA	1.99	0.44
23:A:2230:C:O2'	23:A:3044:A:N3	2.49	0.44
50:c:41:PRO:HG2	50:c:44:ARG:HB3	2.00	0.44
55:y:30:PRO:O	55:y:31:ASN:HB3	2.14	0.44
55:y:52:ALA:HA	55:y:55:ILE:HD12	1.99	0.44
1:h:1075:U:OP2	1:h:1088:G:N1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:t:95:VAL:HG12	11:t:120:SER:O	2.17	0.44
19:8:111:LEU:HD11	19:8:115:LYS:HE3	1.98	0.44
23:A:2750:G:OP2	29:G:154:ARG:NH2	2.50	0.44
23:A:2786:U:H4'	34:L:25:LEU:HD21	1.98	0.44
54:g:10:HIS:ND1	54:g:11:PRO:HD2	2.33	0.44
23:A:920:G:N2	23:A:944:A:OP1	2.50	0.44
23:A:2616:A:N1	35:M:55:MET:HE3	2.33	0.44
23:A:2681:U:OP2	56:3:2:ALA:N	2.51	0.44
50:c:26:ASN:CG	50:c:27:ARG:N	2.75	0.44
50:c:44:ARG:O	50:c:45:ARG:CZ	2.65	0.44
54:g:54:THR:CG2	54:g:55:SER:N	2.73	0.44
1:h:1247:G:N2	1:h:1251:G:N7	2.66	0.44
8:q:55:ARG:HG3	8:q:56:VAL:HG23	1.99	0.44
10:s:12:ALA:HB2	10:s:18:ILE:HD13	1.99	0.44
10:s:12:ALA:HB3	10:s:18:ILE:HD13	2.00	0.44
17:6:15:LEU:HD23	17:6:33:THR:HG21	2.00	0.44
18:7:18:ARG:CG	18:7:18:ARG:NH1	2.73	0.44
23:A:1673:A:O2'	23:A:2926:A:OP2	2.27	0.44
23:A:2454:G:H2'	23:A:2455:C:H6	1.77	0.44
27:E:119:ALA:HB2	27:E:124:ILE:HD12	2.00	0.44
30:H:70:THR:HG21	30:H:140:VAL:HG13	1.92	0.44
46:X:69:PHE:CD1	46:X:78:VAL:HG22	2.53	0.44
52:e:13:ARG:O	52:e:14:PHE:CG	2.70	0.44
1:h:18:U:N3	1:h:21:U:OP2	2.44	0.44
1:h:300:A:C2'	1:h:544:C:H42	2.29	0.44
23:A:676:C:OP2	40:R:6:ARG:NE	2.49	0.44
23:A:1530:G:N2	23:A:1805:G:H22	2.16	0.44
26:D:151:ILE:HD11	26:D:166:MET:CE	2.47	0.44
52:e:26:LYS:NZ	52:e:43:ARG:O	2.30	0.44
1:h:441:A:N6	1:h:473:A:H61	2.16	0.44
1:h:953:G:N1	1:h:1346:A:OP2	2.50	0.44
23:A:2339:G:N1	23:A:2388:G:O6	2.51	0.44
25:C:221:VAL:HG12	25:C:222:ARG:O	2.17	0.44
26:D:62:VAL:HG11	26:D:77:PRO:HB3	2.00	0.44
26:D:150:SER:OG	26:D:151:ILE:N	2.51	0.44
27:E:130:LEU:CD1	27:E:158:ILE:HD11	2.48	0.44
49:b:9:SER:O	49:b:13:THR:OG1	2.20	0.44
54:g:60:PHE:H	54:g:63:GLY:C	2.21	0.44
1:h:669:C:OP2	11:t:66:LYS:NZ	2.51	0.43
1:h:1249:G:HO2'	1:h:1250:A:C5'	2.29	0.43
9:4:45:THR:O	9:4:82:ASP:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:8:17:GLY:O	19:8:18:HIS:CB	2.66	0.43
23:A:325:U:C2	23:A:450:G:O6	2.71	0.43
23:A:2222:A:OP2	26:D:146:ARG:NH1	2.50	0.43
25:C:130:ASN:OD1	25:C:131:LEU:N	2.51	0.43
55:y:16:SER:C	55:y:17:VAL:HG13	2.43	0.43
17:6:28:LYS:O	17:6:29:GLN:NE2	2.51	0.43
23:A:2018:G:O4'	23:A:2426:C:O2'	2.37	0.43
55:y:24:THR:HA	55:y:25:PRO:HD3	1.64	0.43
1:h:293:G:O6	1:h:304:U:O2	2.36	0.43
1:h:746:A:N7	1:h:793:U:O4	2.51	0.43
8:q:108:THR:HG22	8:q:109:SER:N	2.33	0.43
23:A:1292:U:HO2'	23:A:1293:G:P	2.38	0.43
23:A:2537:C:O4'	28:F:44:ASN:ND2	2.51	0.43
27:E:131:VAL:HG21	27:E:164:VAL:HG23	2.00	0.43
30:H:61:ASP:OD1	30:H:61:ASP:O	2.35	0.43
31:I:13:ILE:HD13	31:I:57:VAL:HG22	2.01	0.43
45:W:8:PRO:HB2	45:W:68:THR:HG23	2.00	0.43
55:y:30:PRO:HD2	55:y:31:ASN:H	1.82	0.43
1:h:194:A:O2'	1:h:195:U:O5'	2.23	0.43
17:6:66:MET:HE3	17:6:74:PHE:CE1	2.54	0.43
23:A:247:G:OP2	23:A:249:C:N4	2.49	0.43
23:A:1563:A:O2'	23:A:1564:A:OP2	2.31	0.43
26:D:62:VAL:HG11	26:D:77:PRO:HB2	2.01	0.43
55:y:22:ARG:C	55:y:23:ARG:O	2.61	0.43
1:h:1098:U:P	9:4:126:ARG:CZ	3.07	0.43
6:n:82:ASN:OD1	6:n:83:GLU:N	2.51	0.43
25:C:206:TRP:CG	25:C:212:MET:HE3	2.54	0.43
48:a:15:ALA:O	48:a:20:ARG:NH2	2.52	0.43
50:c:25:LYS:CD	52:e:34:GLU:HG2	2.48	0.43
30:H:119:LEU:O	30:H:122:ALA:HB3	2.18	0.43
1:h:686:A:H2	11:t:50:VAL:HG21	1.84	0.43
1:h:849:G:O2'	1:h:855:A:N1	2.47	0.43
6:n:7:MET:CG	20:r:76:MET:HE2	2.49	0.43
45:W:80:THR:HA	45:W:97:LEU:HD23	2.00	0.43
55:y:32:ILE:C	55:y:33:GLN:HG2	2.43	0.43
13:v:108:ARG:NH2	13:v:113:PRO:O	2.42	0.43
23:A:1337:G:N7	41:S:72:LYS:NZ	2.67	0.43
30:H:62:ILE:H	30:H:65:ALA:HB3	1.83	0.43
42:T:12:ALA:HB3	42:T:61:ALA:HB2	2.01	0.43
50:c:5:ILE:HG23	50:c:28:ARG:HH22	1.69	0.43
54:g:60:PHE:O	54:g:63:GLY:N	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:t:43:ILE:HG22	11:t:44:THR:N	2.34	0.43
22:9:92:GLU:O	22:9:93:LEU:HD23	2.19	0.43
23:A:2084:A:N6	23:A:2099:G:N3	2.66	0.43
23:A:2086:U:H3	23:A:2096:G:H22	1.67	0.43
30:H:55:GLU:HG3	30:H:59:ILE:CG2	2.49	0.43
51:d:27:THR:OG1	51:d:28:ARG:N	2.43	0.43
55:y:64:GLU:O	55:y:67:VAL:HG22	2.19	0.43
3:k:41:LEU:HD12	3:k:93:LEU:CD1	2.37	0.43
13:v:49:THR:O	13:v:53:VAL:HG23	2.18	0.43
19:8:163:VAL:CG2	19:8:183:VAL:HG13	2.49	0.43
22:9:24:ARG:NH2	22:9:51:LEU:HD21	2.34	0.43
23:A:3:A:O2'	33:K:132:HIS:ND1	2.52	0.43
43:U:24:ILE:HG23	43:U:29:TYR:HE1	1.84	0.43
54:g:30:THR:O	54:g:33:ARG:N	2.51	0.43
1:h:418:C:N4	1:h:425:G:O6	2.49	0.42
1:h:1222:G:OP1	7:p:35:LYS:NZ	2.52	0.42
3:k:186:LEU:HD13	3:k:199:LYS:HG2	2.01	0.42
18:7:47:ALA:HB1	18:7:83:LEU:HD13	2.00	0.42
23:A:273:A:O2'	23:A:455:C:O2'	2.26	0.42
23:A:1886:A:N3	23:A:1888:C:N4	2.67	0.42
25:C:196:VAL:HG12	25:C:197:GLY:N	2.33	0.42
30:H:25:TYR:CE2	30:H:30:LEU:HD11	2.54	0.42
46:X:56:ASP:OD1	46:X:58:THR:OG1	2.37	0.42
1:h:426:U:OP1	4:l:31:TYR:OH	2.26	0.42
1:h:1250:A:H2	1:h:1294:G:H21	1.65	0.42
3:k:51:ILE:HG21	3:k:54:VAL:CG2	2.49	0.42
23:A:223:A:OP2	23:A:507:G:N2	2.50	0.42
23:A:1484:G:H21	23:A:2027:A:H2	1.67	0.42
23:A:1830:C:O2'	51:d:8:PHE:O	2.31	0.42
23:A:2518:C:OP1	38:P:104:ARG:NH2	2.52	0.42
25:C:72:LYS:NZ	25:C:101:GLU:OE1	2.43	0.42
40:R:77:ASN:OD1	40:R:78:ARG:N	2.50	0.42
1:h:378:G:O6	1:h:386:C:N4	2.52	0.42
1:h:1400:A:N6	1:h:1466:G:C6	2.87	0.42
1:h:1486:A:H2	1:h:1489:G:H22	1.67	0.42
19:8:33:THR:HG22	19:8:34:ASP:H	1.84	0.42
23:A:807:C:H2'	23:A:808:A:C8	2.54	0.42
23:A:1195:A:N6	23:A:1206:A:O2'	2.49	0.42
26:D:114:VAL:HG12	26:D:208:VAL:HG12	2.01	0.42
30:H:48:GLU:HA	30:H:51:ARG:HE	1.84	0.42
1:h:1032:U:OP1	21:Y:49:ARG:NE	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:m:102:ILE:N	5:m:105:THR:O	2.52	0.42
6:n:30:ILE:CD1	6:n:75:LEU:HD22	2.49	0.42
23:A:259:C:O2	23:A:715:A:O2'	2.36	0.42
34:L:35:ILE:O	34:L:69:ARG:NH1	2.52	0.42
43:U:69:THR:HG22	43:U:71:THR:H	1.83	0.42
55:y:15:ASN:HB3	55:y:16:SER:H	1.50	0.42
6:n:30:ILE:CG2	6:n:36:THR:HG21	2.48	0.42
9:4:68:ILE:HG23	9:4:99:LEU:HD23	2.01	0.42
15:z:67:THR:HG22	15:z:68:GLU:H	1.85	0.42
21:Y:46:ASP:OD1	21:Y:47:HIS:N	2.44	0.42
23:A:1598:U:O2'	23:A:1600:G:N7	2.47	0.42
28:F:132:THR:OG1	28:F:169:ASN:N	2.52	0.42
44:V:45:THR:O	44:V:58:GLY:N	2.53	0.42
8:q:78:ARG:CG	8:q:78:ARG:NH1	2.78	0.42
18:7:28:LEU:HD11	18:7:58:LEU:HD21	2.00	0.42
23:A:1756:G:O2'	23:A:1757:U:O2	2.35	0.42
23:A:2107:G:O2'	23:A:2108:A:O4'	2.33	0.42
35:M:57:ILE:H	35:M:57:ILE:HD12	1.83	0.42
1:h:494:C:N4	1:h:495:G:O6	2.53	0.42
1:h:558:C:O2'	1:h:708:A:N3	2.46	0.42
1:h:1048:G:N7	1:h:1074:G:O2'	2.32	0.42
19:8:118:GLU:OE1	19:8:152:ARG:NH1	2.53	0.42
23:A:738:A:O2'	23:A:740:A:OP1	2.36	0.42
26:D:157:PRO:HB2	26:D:159:ARG:HG3	2.02	0.42
28:F:7:ALA:CB	54:g:26:ARG:NE	2.78	0.42
29:G:97:VAL:N	29:G:129:PRO:O	2.50	0.42
50:c:36:LEU:O	50:c:37:ARG:HB2	2.19	0.42
54:g:3:PRO:O	54:g:4:GLY:C	2.60	0.42
6:n:49:ALA:HB1	20:r:80:PRO:HA	2.02	0.42
19:8:57:VAL:O	19:8:61:VAL:HG23	2.19	0.42
21:Y:2:ARG:HB2	21:Y:3:PRO:HD3	2.02	0.42
30:H:48:GLU:HA	30:H:51:ARG:NE	2.35	0.42
30:H:85:ALA:HB2	30:H:92:PHE:CE1	2.54	0.42
44:V:96:ARG:NE	44:V:105:ILE:OXT	2.44	0.42
50:c:33:ARG:O	50:c:34:ILE:CG2	2.59	0.42
1:h:1281:A:O2'	1:h:1282:G:O5'	2.33	0.42
4:l:86:LEU:HD23	4:l:192:GLU:OE2	2.20	0.42
4:l:139:ASP:OD1	4:l:140:VAL:N	2.48	0.42
23:A:530:G:O4'	27:E:47:GLN:NE2	2.53	0.42
23:A:1882:A:H61	23:A:2220:C:H42	1.67	0.42
23:A:2019:A:OP2	23:A:2031:G:N1	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2912:A:N6	23:A:2944:U:OP2	2.45	0.42
28:F:67:ILE:HD11	28:F:148:ILE:HD11	2.01	0.42
55:y:12:GLY:O	55:y:27:ARG:HA	2.19	0.42
1:h:633:A:OP1	8:q:56:VAL:HG21	2.20	0.42
1:h:773:U:O2'	1:h:774:A:OP1	2.37	0.42
23:A:1648:A:N6	23:A:1791:A:OP2	2.47	0.42
41:S:55:LEU:HA	41:S:58:VAL:HG12	2.01	0.42
45:W:28:ARG:NH2	45:W:93:GLN:O	2.51	0.42
1:h:961:C:H42	22:9:58:VAL:HG22	1.85	0.41
7:p:73:LEU:HD12	7:p:89:VAL:O	2.19	0.41
19:8:33:THR:HG22	19:8:34:ASP:N	2.35	0.41
19:8:97:LEU:CD1	19:8:100:MET:HE3	2.49	0.41
23:A:2642:G:OP1	52:e:29:ARG:NH2	2.52	0.41
28:F:125:SER:O	28:F:135:TYR:OH	2.23	0.41
45:W:111:THR:HG22	45:W:112:VAL:O	2.20	0.41
1:h:808:A:H62	1:h:840:G:H21	1.68	0.41
10:s:29:VAL:CG1	10:s:76:ILE:HD12	2.49	0.41
10:s:42:LEU:HD11	10:s:73:LEU:HD12	2.00	0.41
19:8:18:HIS:O	19:8:38:ILE:CD1	2.69	0.41
25:C:79:VAL:HG22	25:C:95:LEU:HD23	2.02	0.41
30:H:48:GLU:O	30:H:51:ARG:HG2	2.21	0.41
55:y:22:ARG:O	55:y:23:ARG:HB2	2.20	0.41
1:h:780:G:N2	1:h:781:U:O4	2.53	0.41
1:h:973:U:C2	1:h:1194:A:N7	2.88	0.41
1:h:1071:U:O2'	1:h:1073:A:N7	2.46	0.41
1:h:1260:A:O2'	1:h:1263:C:N4	2.53	0.41
9:4:127:ASP:OD1	9:4:129:ARG:NH2	2.48	0.41
28:F:132:THR:HA	28:F:169:ASN:HA	2.01	0.41
1:h:373:A:H61	1:h:391:G:H1'	1.85	0.41
1:h:455:G:N2	1:h:457:A:N3	2.69	0.41
23:A:969:C:H42	23:A:1038:G:H1	1.67	0.41
23:A:1195:A:O3'	32:J:95:HIS:ND1	2.53	0.41
23:A:1832:A:N6	42:T:95:ARG:O	2.53	0.41
27:E:135:THR:O	27:E:135:THR:HG23	2.19	0.41
51:d:37:ARG:NE	51:d:45:LEU:O	2.53	0.41
1:h:1061:G:OP1	5:m:48:LYS:N	2.53	0.41
30:H:122:ALA:O	30:H:130:HIS:ND1	2.54	0.41
50:c:33:ARG:HD2	50:c:33:ARG:HA	1.82	0.41
50:c:37:ARG:O	50:c:38:LYS:CG	2.69	0.41
1:h:809:G:C6	1:h:840:G:N2	2.88	0.41
1:h:1416:A:OP2	1:h:1451:G:N1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:1486:A:N3	1:h:1486:A:O2'	2.51	0.41
3:k:52:ALA:HB3	3:k:68:HIS:O	2.21	0.41
23:A:355:A:O2'	23:A:358:G:N2	2.54	0.41
23:A:897:A:N1	25:C:226:MET:HE2	2.35	0.41
23:A:1481:C:OP1	55:y:3:HIS:HE1	2.00	0.41
23:A:1676:G:H1	23:A:2928:C:H42	1.68	0.41
23:A:3014:A:O2'	23:A:3015:C:O5'	2.29	0.41
34:L:24:VAL:HG11	34:L:33:ALA:HB2	2.02	0.41
34:L:71:ARG:CZ	34:L:77:ILE:HD11	2.51	0.41
50:c:32:ASP:O	50:c:33:ARG:CB	2.68	0.41
54:g:10:HIS:CB	54:g:30:THR:HG23	2.34	0.41
55:y:26:ARG:O	55:y:26:ARG:HD3	2.20	0.41
1:h:1334:C:N4	1:h:1354:G:O6	2.54	0.41
19:8:160:ALA:HB3	19:8:181:ILE:HG22	2.02	0.41
23:A:1127:A:N3	23:A:1272:C:O2'	2.51	0.41
23:A:1187:A:OP1	23:A:1214:A:O2'	2.38	0.41
23:A:2226:U:OP1	37:O:9:ARG:N	2.49	0.41
24:B:20:G:O6	24:B:66:C:N4	2.53	0.41
28:F:132:THR:OG1	28:F:168:THR:HA	2.21	0.41
50:c:16:GLY:C	50:c:18:GLY:H	2.27	0.41
50:c:44:ARG:HE	50:c:47:VAL:HG11	1.86	0.41
1:h:1322:G:H2'	1:h:1323:U:O4'	2.21	0.41
23:A:975:U:OP2	23:A:1031:G:N1	2.42	0.41
23:A:2528:G:O2'	28:F:136:THR:O	2.37	0.41
26:D:57:ILE:HG23	26:D:61:LYS:HB2	2.03	0.41
28:F:165:THR:HG22	28:F:167:ALA:H	1.85	0.41
31:I:116:SER:O	31:I:120:VAL:HG23	2.21	0.41
45:W:108:VAL:N	45:W:133:ILE:O	2.44	0.41
54:g:35:ILE:HD12	54:g:49:ILE:HG13	2.03	0.41
54:g:55:SER:C	54:g:57:SER:H	2.28	0.41
55:y:15:ASN:O	55:y:16:SER:O	2.38	0.41
1:h:103:G:N7	18:7:10:ARG:NH2	2.69	0.41
1:h:1048:G:OP1	1:h:1370:G:O2'	2.38	0.41
1:h:1425:G:P	1:h:1426:C:H41	2.44	0.41
7:p:23:VAL:O	7:p:27:VAL:HG13	2.21	0.41
11:t:54:ALA:HB3	11:t:79:ALA:HB2	2.03	0.41
13:v:66:VAL:C	13:v:70:LEU:HD12	2.46	0.41
23:A:565:A:N6	23:A:588:A:OP1	2.53	0.41
23:A:683:G:N2	52:e:2:PRO:O	2.39	0.41
23:A:971:G:H2'	23:A:972:A:C8	2.56	0.41
23:A:974:G:O2'	23:A:975:U:OP2	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1199:U:O3'	32:J:121:ASN:ND2	2.46	0.41
23:A:2741:C:N3	23:A:2766:A:N6	2.69	0.41
23:A:3078:G:N2	23:A:3081:A:OP2	2.48	0.41
26:D:84:LEU:HD22	26:D:209:ARG:HH11	1.85	0.41
30:H:73:GLU:OE2	30:H:144:VAL:CG2	2.69	0.41
34:L:88:LYS:O	34:L:91:ASN:N	2.53	0.41
36:N:15:PRO:HG3	36:N:72:ARG:HE	1.85	0.41
44:V:47:VAL:N	44:V:57:GLY:N	2.68	0.41
50:c:9:VAL:CG2	50:c:28:ARG:HG2	2.50	0.41
56:3:12:LYS:HG3	56:3:20:LYS:C	2.46	0.41
2:j:3:SER:OG	2:j:4:VAL:N	2.53	0.41
5:m:42:SER:O	5:m:43:ILE:HD13	2.20	0.41
10:s:32:THR:HG22	10:s:32:THR:O	2.20	0.41
13:v:5:VAL:O	13:v:5:VAL:HG12	2.21	0.41
19:8:5:THR:CG2	19:8:6:MET:H	2.31	0.41
23:A:271:A:OP2	23:A:314:G:N2	2.52	0.41
23:A:774:G:OP1	27:E:101:ARG:NH1	2.54	0.41
23:A:819:G:O2'	23:A:841:G:N2	2.51	0.41
31:I:22:ALA:HB3	31:I:82:VAL:HG22	2.02	0.41
32:J:11:ILE:HD13	32:J:30:LEU:HB3	2.02	0.41
37:O:45:ARG:HD2	37:O:97:ILE:HD12	2.03	0.41
37:O:98:ILE:HG23	49:b:46:ALA:HB2	2.03	0.41
54:g:54:THR:O	54:g:58:HIS:HB2	2.20	0.41
1:h:1011:U:O2'	1:h:1012:U:O5'	2.31	0.40
5:m:44:ASN:OD1	5:m:45:ARG:N	2.53	0.40
6:n:10:LEU:HD21	6:n:85:VAL:HG12	2.03	0.40
8:q:12:THR:HG22	8:q:15:ARG:HH12	1.85	0.40
23:A:1013:U:H2'	23:A:1014:G:O4'	2.21	0.40
52:e:6:THR:HG22	52:e:7:HIS:N	2.36	0.40
54:g:10:HIS:CB	54:g:30:THR:CB	2.90	0.40
1:h:905:A:N6	1:h:1375:G:O6	2.54	0.40
11:t:56:SER:OG	11:t:71:ALA:HB1	2.22	0.40
22:9:94:PRO:O	22:9:96:VAL:HG23	2.21	0.40
23:A:574:C:O2'	42:T:67:ASN:OD1	2.39	0.40
23:A:2521:C:H42	23:A:2545:G:H1	1.69	0.40
25:C:158:SER:O	25:C:196:VAL:HG11	2.21	0.40
31:I:9:ALA:CB	31:I:56:LEU:HD21	2.50	0.40
39:Q:32:ILE:HD12	39:Q:32:ILE:O	2.21	0.40
56:3:12:LYS:HE2	56:3:12:LYS:HB3	1.95	0.40
1:h:11:G:H22	5:m:122:ARG:NH1	2.19	0.40
19:8:27:MET:HE2	19:8:30:PHE:HE2	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2384:C:HO2'	23:A:2385:G:P	2.43	0.40
23:A:2879:G:O2'	23:A:2888:G:O6	2.35	0.40
28:F:19:ILE:HG23	28:F:179:ALA:CB	2.52	0.40
42:T:87:PRO:O	42:T:107:THR:HG22	2.21	0.40
50:c:36:LEU:O	50:c:37:ARG:NH2	2.49	0.40
54:g:17:ALA:HB3	54:g:51:VAL:O	2.21	0.40
56:3:8:LYS:C	56:3:11:ARG:HG2	2.43	0.40
1:h:1401:A:N6	1:h:1466:G:O2'	2.54	0.40
7:p:54:THR:O	7:p:56:THR:HG23	2.21	0.40
11:t:80:ALA:HB1	11:t:114:LEU:HD11	2.03	0.40
23:A:933:G:N1	23:A:1303:U:OP2	2.46	0.40
26:D:155:ALA:O	26:D:156:THR:CB	2.70	0.40
37:O:33:ARG:HH12	49:b:51:LEU:HD21	1.87	0.40
46:X:37:LEU:HD13	46:X:78:VAL:HG11	2.02	0.40
1:h:420:U:O2'	1:h:423:G:O6	2.33	0.40
1:h:808:A:H62	1:h:840:G:N2	2.20	0.40
5:m:121:LEU:HD23	5:m:150:ALA:HB2	2.02	0.40
8:q:52:GLU:N	8:q:59:SER:O	2.55	0.40
9:4:75:VAL:HG12	9:4:75:VAL:O	2.21	0.40
13:v:37:THR:HG21	13:v:39:ILE:HD12	2.03	0.40
16:5:85:THR:O	16:5:85:THR:HG22	2.21	0.40
23:A:183:G:O2'	23:A:216:A:N3	2.53	0.40
23:A:759:G:O6	46:X:33:ALA:N	2.55	0.40
23:A:1630:U:O4	23:A:1631:A:N6	2.54	0.40
28:F:109:ARG:NE	28:F:147:GLU:OE2	2.55	0.40
30:H:64:HIS:HD1	30:H:64:HIS:C	2.27	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	j	30/32 (94%)	29 (97%)	1 (3%)	0	100	100
3	k	206/208 (99%)	182 (88%)	24 (12%)	0	100	100
4	l	198/200 (99%)	178 (90%)	19 (10%)	1 (0%)	24	57
5	m	178/180 (99%)	154 (86%)	22 (12%)	2 (1%)	11	42
6	n	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
7	p	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
8	q	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
9	4	124/126 (98%)	111 (90%)	12 (10%)	1 (1%)	16	49
10	s	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
11	t	113/115 (98%)	100 (88%)	13 (12%)	0	100	100
12	u	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
13	v	114/116 (98%)	100 (88%)	14 (12%)	0	100	100
14	x	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
15	z	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
16	5	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
17	6	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
18	7	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
19	8	226/228 (99%)	196 (87%)	23 (10%)	7 (3%)	3	25
20	r	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
21	Y	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
22	9	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
25	C	273/275 (99%)	232 (85%)	41 (15%)	0	100	100
26	D	212/214 (99%)	182 (86%)	28 (13%)	2 (1%)	14	46
27	E	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
28	F	180/182 (99%)	165 (92%)	14 (8%)	1 (1%)	21	53
29	G	174/176 (99%)	157 (90%)	17 (10%)	0	100	100
30	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
31	I	124/126 (98%)	117 (94%)	6 (5%)	1 (1%)	16	49
32	J	131/133 (98%)	116 (88%)	15 (12%)	0	100	100
33	K	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
34	L	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
35	M	143/145 (99%)	120 (84%)	21 (15%)	2 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	N	134/136 (98%)	119 (89%)	15 (11%)	0	100	100
37	O	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
38	P	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
39	Q	111/113 (98%)	94 (85%)	15 (14%)	2 (2%)	6	34
40	R	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
41	S	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
42	T	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
43	U	95/97 (98%)	81 (85%)	14 (15%)	0	100	100
44	V	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
45	W	190/192 (99%)	169 (89%)	20 (10%)	1 (0%)	24	57
46	X	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
47	Z	62/64 (97%)	62 (100%)	0	0	100	100
48	a	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
49	b	52/54 (96%)	47 (90%)	4 (8%)	1 (2%)	6	33
50	c	51/53 (96%)	26 (51%)	15 (29%)	10 (20%)	0	1
51	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
52	e	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
53	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
54	g	71/82 (87%)	50 (70%)	16 (22%)	5 (7%)	1	10
55	y	75/77 (97%)	56 (75%)	8 (11%)	11 (15%)	0	3
56	3	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
All	All	6173/6298 (98%)	5524 (90%)	602 (10%)	47 (1%)	18	49

All (47) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	m	103	GLY
19	8	16	PHE
19	8	25	PRO
19	8	161	VAL
26	D	156	THR
28	F	131	GLY
49	b	9	SER
50	c	10	LYS
50	c	12	ARG

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Mol	Chain	Res	Type
50	c	33	ARG
50	c	34	ILE
50	c	36	LEU
54	g	3	PRO
55	y	16	SER
55	y	24	THR
55	y	27	ARG
55	y	31	ASN
9	4	147	TYR
19	8	15	HIS
50	c	32	ASP
50	c	37	ARG
50	c	46	HIS
55	y	23	ARG
55	y	30	PRO
19	8	18	HIS
19	8	193	PRO
31	I	125	ASP
54	g	47	PRO
55	y	14	GLY
55	y	15	ASN
5	m	104	SER
35	M	45	ASN
50	c	43	LEU
54	g	30	THR
26	D	162	LYS
35	M	70	ARG
39	Q	93	ARG
50	c	35	VAL
55	y	4	CYS
55	y	26	ARG
55	y	29	ASP
19	8	21	ARG
39	Q	3	THR
54	g	5	ILE
4	l	189	PRO
45	W	154	GLY
54	g	11	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	j	30/30 (100%)	30 (100%)	0	100	100
3	k	170/170 (100%)	170 (100%)	0	100	100
4	l	175/175 (100%)	175 (100%)	0	100	100
5	m	127/127 (100%)	126 (99%)	1 (1%)	73	77
6	n	85/85 (100%)	84 (99%)	1 (1%)	63	74
7	p	131/131 (100%)	131 (100%)	0	100	100
8	q	107/107 (100%)	106 (99%)	1 (1%)	70	76
9	4	102/102 (100%)	101 (99%)	1 (1%)	68	76
10	s	89/89 (100%)	89 (100%)	0	100	100
11	t	89/89 (100%)	88 (99%)	1 (1%)	65	75
12	u	103/103 (100%)	103 (100%)	0	100	100
13	v	99/99 (100%)	99 (100%)	0	100	100
14	x	76/76 (100%)	75 (99%)	1 (1%)	61	73
15	z	92/92 (100%)	92 (100%)	0	100	100
16	5	80/80 (100%)	80 (100%)	0	100	100
17	6	73/73 (100%)	73 (100%)	0	100	100
18	7	69/69 (100%)	68 (99%)	1 (1%)	59	72
19	8	191/191 (100%)	184 (96%)	7 (4%)	30	57
20	r	70/70 (100%)	70 (100%)	0	100	100
21	Y	91/91 (100%)	91 (100%)	0	100	100
22	9	85/85 (100%)	85 (100%)	0	100	100
25	C	215/215 (100%)	215 (100%)	0	100	100
26	D	160/160 (100%)	160 (100%)	0	100	100
27	E	169/169 (100%)	169 (100%)	0	100	100
28	F	151/151 (100%)	151 (100%)	0	100	100
29	G	148/148 (100%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	H	116/116 (100%)	115 (99%)	1 (1%)	70	76
31	I	89/89 (100%)	89 (100%)	0	100	100
32	J	102/102 (100%)	102 (100%)	0	100	100
33	K	119/119 (100%)	118 (99%)	1 (1%)	73	77
34	L	100/100 (100%)	100 (100%)	0	100	100
35	M	112/112 (100%)	112 (100%)	0	100	100
36	N	114/114 (100%)	114 (100%)	0	100	100
37	O	97/97 (100%)	97 (100%)	0	100	100
38	P	93/93 (100%)	93 (100%)	0	100	100
39	Q	100/100 (100%)	100 (100%)	0	100	100
40	R	97/97 (100%)	97 (100%)	0	100	100
41	S	81/81 (100%)	81 (100%)	0	100	100
42	T	90/90 (100%)	89 (99%)	1 (1%)	65	75
43	U	83/83 (100%)	83 (100%)	0	100	100
44	V	81/86 (94%)	80 (99%)	1 (1%)	63	74
45	W	155/155 (100%)	155 (100%)	0	100	100
46	X	58/58 (100%)	58 (100%)	0	100	100
47	Z	58/58 (100%)	58 (100%)	0	100	100
48	a	52/52 (100%)	52 (100%)	0	100	100
49	b	43/43 (100%)	42 (98%)	1 (2%)	44	65
50	c	49/49 (100%)	45 (92%)	4 (8%)	10	35
51	d	35/35 (100%)	35 (100%)	0	100	100
52	e	53/53 (100%)	52 (98%)	1 (2%)	50	68
53	f	35/35 (100%)	35 (100%)	0	100	100
54	g	64/70 (91%)	62 (97%)	2 (3%)	35	61
55	y	64/64 (100%)	58 (91%)	6 (9%)	8	31
56	3	18/18 (100%)	18 (100%)	0	100	100
All	All	5135/5146 (100%)	5103 (99%)	32 (1%)	76	80

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	m	101	LEU

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Mol	Chain	Res	Type
6	n	47	ARG
8	q	78	ARG
9	4	126	ARG
11	t	137	ARG
14	x	88	ARG
18	7	18	ARG
19	8	5	THR
19	8	16	PHE
19	8	18	HIS
19	8	19	GLN
19	8	39	TYR
19	8	212	LEU
19	8	213	LEU
30	H	57	LYS
33	K	80	TYR
42	T	104	ARG
44	V	1	MET
49	b	6	ARG
50	c	8	ILE
50	c	12	ARG
50	c	33	ARG
50	c	34	ILE
52	e	13	ARG
54	g	53	VAL
54	g	64	SER
55	y	21	HIS
55	y	26	ARG
55	y	33	GLN
55	y	45	ARG
55	y	53	LYS
55	y	56	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
3	k	101	ASN
5	m	163	HIS
6	n	96	HIS
7	p	148	ASN
8	q	93	ASN
8	q	121	GLN
10	s	70	HIS

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Mol	Chain	Res	Type
11	t	49	ASN
14	x	51	HIS
17	6	29	GLN
18	7	74	ASN
21	Y	58	GLN
25	C	38	HIS
25	C	53	HIS
25	C	91	ASN
25	C	143	HIS
26	D	130	HIS
27	E	125	HIS
27	E	151	ASN
27	E	182	GLN
28	F	31	ASN
30	H	102	ASN
32	J	33	HIS
33	K	77	HIS
38	P	41	ASN
41	S	90	HIS
44	V	4	HIS
44	V	70	ASN
50	c	46	HIS
54	g	58	HIS
55	y	5	GLN
55	y	19	HIS
55	y	21	HIS
55	y	33	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	h	1510/1511 (99%)	391 (25%)	0
23	A	3118/3119 (99%)	771 (24%)	32 (1%)
24	B	117/118 (99%)	23 (19%)	1 (0%)
All	All	4745/4748 (99%)	1185 (24%)	33 (0%)

All (1185) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	h	9	U
1	h	10	G

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Mol	Chain	Res	Type
1	h	11	G
1	h	12	A
1	h	13	G
1	h	18	U
1	h	26	G
1	h	36	A
1	h	43	G
1	h	51	C
1	h	52	U
1	h	54	A
1	h	55	A
1	h	59	A
1	h	70	A
1	h	82	U
1	h	87	G
1	h	89	G
1	h	91	U
1	h	92	A
1	h	93	C
1	h	101	G
1	h	117	C
1	h	118	A
1	h	126	G
1	h	127	A
1	h	128	U
1	h	133	C
1	h	136	G
1	h	160	C
1	h	174	G
1	h	179	C
1	h	193	C
1	h	196	G
1	h	200	U
1	h	201	G
1	h	207	G
1	h	211	A
1	h	213	C
1	h	214	U
1	h	215	U
1	h	217	U
1	h	218	G
1	h	219	C

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Mol	Chain	Res	Type
1	h	220	G
1	h	231	G
1	h	240	C
1	h	243	A
1	h	245	C
1	h	247	G
1	h	251	G
1	h	254	G
1	h	258	G
1	h	266	G
1	h	267	C
1	h	268	C
1	h	279	A
1	h	280	C
1	h	281	G
1	h	289	G
1	h	298	A
1	h	300	A
1	h	306	A
1	h	329	A
1	h	330	C
1	h	332	G
1	h	340	U
1	h	345	C
1	h	347	G
1	h	350	G
1	h	351	G
1	h	352	C
1	h	353	A
1	h	359	G
1	h	367	U
1	h	369	G
1	h	372	C
1	h	373	A
1	h	381	C
1	h	382	A
1	h	388	G
1	h	389	A
1	h	390	U
1	h	392	C
1	h	393	A
1	h	397	A

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Mol	Chain	Res	Type
1	h	398	C
1	h	406	G
1	h	412	U
1	h	413	G
1	h	414	A
1	h	421	U
1	h	422	C
1	h	423	G
1	h	424	G
1	h	428	G
1	h	429	U
1	h	430	A
1	h	432	A
1	h	434	C
1	h	438	U
1	h	440	C
1	h	445	C
1	h	449	C
1	h	452	A
1	h	453	G
1	h	456	C
1	h	458	A
1	h	459	G
1	h	461	G
1	h	464	G
1	h	466	U
1	h	469	G
1	h	472	C
1	h	477	G
1	h	478	A
1	h	479	A
1	h	485	G
1	h	486	G
1	h	489	A
1	h	491	C
1	h	492	U
1	h	497	G
1	h	498	C
1	h	499	C
1	h	505	C
1	h	507	G
1	h	509	G

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Mol	Chain	Res	Type
1	h	510	G
1	h	511	U
1	h	512	A
1	h	513	A
1	h	514	U
1	h	516	C
1	h	519	A
1	h	520	G
1	h	525	C
1	h	527	A
1	h	540	A
1	h	542	U
1	h	544	C
1	h	545	U
1	h	552	A
1	h	553	A
1	h	555	G
1	h	556	A
1	h	557	G
1	h	567	G
1	h	576	C
1	h	590	A
1	h	600	U
1	h	603	C
1	h	611	G
1	h	612	U
1	h	629	G
1	h	633	A
1	h	643	A
1	h	645	G
1	h	660	C
1	h	666	U
1	h	668	G
1	h	680	G
1	h	683	G
1	h	694	G
1	h	695	A
1	h	698	A
1	h	701	G
1	h	702	G
1	h	703	U
1	h	711	G

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Mol	Chain	Res	Type
1	h	713	G
1	h	728	A
1	h	729	A
1	h	732	G
1	h	735	G
1	h	739	A
1	h	761	A
1	h	772	A
1	h	773	U
1	h	776	C
1	h	785	C
1	h	790	C
1	h	793	U
1	h	794	A
1	h	797	C
1	h	800	U
1	h	801	G
1	h	808	A
1	h	812	G
1	h	818	U
1	h	821	C
1	h	822	U
1	h	824	C
1	h	826	U
1	h	827	U
1	h	828	G
1	h	840	G
1	h	841	U
1	h	854	A
1	h	855	A
1	h	858	A
1	h	859	C
1	h	867	G
1	h	871	A
1	h	872	G
1	h	882	A
1	h	884	G
1	h	896	A
1	h	908	G
1	h	909	G
1	h	913	C
1	h	914	C

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Mol	Chain	Res	Type
1	h	916	C
1	h	917	A
1	h	921	G
1	h	924	G
1	h	927	G
1	h	930	C
1	h	938	U
1	h	940	A
1	h	942	U
1	h	943	U
1	h	948	G
1	h	950	A
1	h	951	A
1	h	953	G
1	h	956	A
1	h	957	A
1	h	958	G
1	h	959	A
1	h	960	A
1	h	964	U
1	h	965	A
1	h	971	G
1	h	973	U
1	h	974	U
1	h	975	G
1	h	976	A
1	h	982	A
1	h	985	G
1	h	987	A
1	h	988	C
1	h	989	G
1	h	990	C
1	h	992	G
1	h	1003	C
1	h	1008	C
1	h	1009	C
1	h	1010	C
1	h	1012	U
1	h	1014	U
1	h	1019	U
1	h	1021	U
1	h	1024	G

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Mol	Chain	Res	Type
1	h	1025	C
1	h	1026	A
1	h	1027	G
1	h	1030	G
1	h	1033	G
1	h	1034	C
1	h	1036	U
1	h	1045	U
1	h	1047	A
1	h	1048	G
1	h	1054	G
1	h	1059	G
1	h	1074	G
1	h	1075	U
1	h	1079	G
1	h	1080	C
1	h	1081	A
1	h	1084	G
1	h	1089	C
1	h	1092	C
1	h	1104	G
1	h	1106	U
1	h	1107	G
1	h	1112	C
1	h	1113	A
1	h	1115	G
1	h	1117	U
1	h	1118	A
1	h	1120	G
1	h	1121	G
1	h	1124	G
1	h	1125	G
1	h	1126	G
1	h	1129	U
1	h	1133	G
1	h	1136	A
1	h	1138	A
1	h	1139	C
1	h	1140	U
1	h	1148	U
1	h	1149	C
1	h	1150	A

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Mol	Chain	Res	Type
1	h	1151	A
1	h	1155	G
1	h	1160	A
1	h	1162	G
1	h	1163	G
1	h	1165	G
1	h	1168	G
1	h	1177	A
1	h	1178	A
1	h	1182	A
1	h	1193	U
1	h	1194	A
1	h	1200	A
1	h	1206	U
1	h	1218	C
1	h	1219	A
1	h	1220	A
1	h	1221	U
1	h	1222	G
1	h	1234	G
1	h	1237	C
1	h	1238	U
1	h	1239	G
1	h	1241	G
1	h	1244	G
1	h	1248	U
1	h	1249	G
1	h	1255	G
1	h	1258	C
1	h	1259	G
1	h	1261	A
1	h	1265	U
1	h	1266	U
1	h	1267	U
1	h	1268	C
1	h	1270	A
1	h	1279	U
1	h	1280	C
1	h	1282	G
1	h	1283	U
1	h	1284	U
1	h	1287	G

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Mol	Chain	Res	Type
1	h	1299	C
1	h	1300	A
1	h	1301	A
1	h	1304	C
1	h	1313	G
1	h	1320	G
1	h	1322	G
1	h	1326	C
1	h	1327	U
1	h	1328	A
1	h	1329	G
1	h	1332	A
1	h	1343	G
1	h	1345	A
1	h	1346	A
1	h	1348	G
1	h	1353	G
1	h	1357	A
1	h	1360	A
1	h	1361	C
1	h	1362	G
1	h	1364	U
1	h	1381	A
1	h	1382	C
1	h	1383	C
1	h	1405	G
1	h	1407	U
1	h	1409	A
1	h	1423	U
1	h	1425	G
1	h	1426	C
1	h	1429	A
1	h	1433	C
1	h	1434	U
1	h	1435	U
1	h	1436	G
1	h	1438	G
1	h	1451	G
1	h	1477	A
1	h	1478	G
1	h	1481	G
1	h	1483	A

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Mol	Chain	Res	Type
1	h	1486	A
1	h	1487	A
1	h	1488	G
1	h	1490	U
1	h	1491	A
1	h	1501	G
1	h	1502	A
1	h	1503	A
1	h	1504	G
1	h	1513	G
1	h	1514	G
23	A	7	U
23	A	11	A
23	A	19	U
23	A	20	G
23	A	23	G
23	A	25	A
23	A	29	C
23	A	31	U
23	A	32	G
23	A	43	C
23	A	47	U
23	A	60	A
23	A	68	A
23	A	71	A
23	A	72	G
23	A	81	A
23	A	82	G
23	A	85	G
23	A	94	G
23	A	98	U
23	A	99	G
23	A	107	G
23	A	115	A
23	A	117	U
23	A	125	C
23	A	126	C
23	A	128	G
23	A	136	U
23	A	138	A
23	A	148	A
23	A	150	C

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Mol	Chain	Res	Type
23	A	151	A
23	A	159	A
23	A	161	U
23	A	162	A
23	A	180	A
23	A	188	G
23	A	195	A
23	A	198	A
23	A	203	A
23	A	204	G
23	A	212	A
23	A	214	G
23	A	215	A
23	A	220	A
23	A	221	A
23	A	227	A
23	A	229	U
23	A	230	G
23	A	232	G
23	A	233	A
23	A	241	A
23	A	248	G
23	A	265	A
23	A	267	G
23	A	279	U
23	A	282	A
23	A	285	U
23	A	286	G
23	A	287	A
23	A	288	U
23	A	289	A
23	A	290	C
23	A	291	C
23	A	292	G
23	A	298	G
23	A	299	G
23	A	300	G
23	A	301	U
23	A	303	G
23	A	305	G
23	A	315	U
23	A	316	U

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Mol	Chain	Res	Type
23	A	317	G
23	A	318	U
23	A	319	G
23	A	323	C
23	A	324	C
23	A	327	U
23	A	329	U
23	A	330	U
23	A	331	U
23	A	335	G
23	A	336	C
23	A	337	U
23	A	338	C
23	A	340	A
23	A	342	C
23	A	348	G
23	A	351	G
23	A	352	G
23	A	357	U
23	A	358	G
23	A	361	A
23	A	363	A
23	A	369	G
23	A	370	U
23	A	376	G
23	A	383	U
23	A	384	G
23	A	391	G
23	A	393	U
23	A	404	A
23	A	412	A
23	A	413	G
23	A	417	C
23	A	428	A
23	A	433	C
23	A	434	G
23	A	437	G
23	A	441	G
23	A	444	U
23	A	445	U
23	A	446	G
23	A	448	U

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Mol	Chain	Res	Type
23	A	449	G
23	A	450	G
23	A	452	G
23	A	460	G
23	A	467	C
23	A	474	G
23	A	475	U
23	A	482	U
23	A	489	A
23	A	491	U
23	A	493	U
23	A	494	G
23	A	500	A
23	A	505	C
23	A	509	U
23	A	512	G
23	A	514	C
23	A	517	A
23	A	523	U
23	A	531	A
23	A	539	C
23	A	543	U
23	A	544	U
23	A	552	U
23	A	553	G
23	A	556	G
23	A	561	G
23	A	562	G
23	A	563	U
23	A	565	A
23	A	566	A
23	A	567	A
23	A	569	G
23	A	578	G
23	A	585	G
23	A	589	A
23	A	591	G
23	A	592	A
23	A	594	U
23	A	595	A
23	A	596	C
23	A	597	C

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Mol	Chain	Res	Type
23	A	605	G
23	A	614	C
23	A	617	U
23	A	618	C
23	A	619	C
23	A	620	G
23	A	633	A
23	A	634	C
23	A	636	U
23	A	637	G
23	A	638	U
23	A	639	C
23	A	640	G
23	A	642	G
23	A	644	G
23	A	646	U
23	A	648	A
23	A	654	U
23	A	655	G
23	A	661	U
23	A	665	G
23	A	666	A
23	A	667	A
23	A	679	G
23	A	684	G
23	A	685	G
23	A	696	A
23	A	697	G
23	A	706	G
23	A	707	G
23	A	708	G
23	A	714	U
23	A	721	A
23	A	725	A
23	A	731	A
23	A	740	A
23	A	747	A
23	A	756	A
23	A	757	G
23	A	758	A
23	A	760	U
23	A	763	G

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Mol	Chain	Res	Type
23	A	764	U
23	A	766	G
23	A	767	U
23	A	768	G
23	A	784	G
23	A	801	U
23	A	830	A
23	A	832	G
23	A	845	C
23	A	862	U
23	A	863	G
23	A	868	C
23	A	880	G
23	A	890	G
23	A	897	A
23	A	898	A
23	A	899	G
23	A	905	U
23	A	907	A
23	A	909	A
23	A	915	U
23	A	916	G
23	A	920	G
23	A	927	C
23	A	942	U
23	A	943	U
23	A	945	G
23	A	954	U
23	A	960	G
23	A	961	U
23	A	973	G
23	A	974	G
23	A	975	U
23	A	976	A
23	A	981	U
23	A	982	A
23	A	983	C
23	A	995	U
23	A	997	G
23	A	1001	C
23	A	1002	C
23	A	1003	A

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Mol	Chain	Res	Type
23	A	1004	C
23	A	1005	A
23	A	1006	G
23	A	1007	G
23	A	1008	G
23	A	1011	A
23	A	1012	C
23	A	1013	U
23	A	1015	A
23	A	1025	A
23	A	1027	C
23	A	1028	U
23	A	1029	C
23	A	1030	C
23	A	1034	U
23	A	1046	C
23	A	1047	A
23	A	1049	G
23	A	1058	A
23	A	1062	A
23	A	1063	G
23	A	1075	U
23	A	1076	A
23	A	1078	G
23	A	1084	U
23	A	1085	G
23	A	1091	A
23	A	1092	G
23	A	1101	A
23	A	1103	C
23	A	1114	G
23	A	1121	G
23	A	1130	C
23	A	1131	G
23	A	1140	G
23	A	1141	U
23	A	1143	G
23	A	1144	A
23	A	1151	U
23	A	1152	G
23	A	1153	U
23	A	1157	G

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Mol	Chain	Res	Type
23	A	1164	A
23	A	1165	G
23	A	1173	G
23	A	1178	U
23	A	1179	U
23	A	1180	G
23	A	1184	U
23	A	1185	A
23	A	1186	G
23	A	1187	A
23	A	1188	A
23	A	1189	G
23	A	1190	C
23	A	1191	A
23	A	1192	G
23	A	1200	U
23	A	1201	G
23	A	1202	A
23	A	1203	A
23	A	1205	G
23	A	1206	A
23	A	1207	G
23	A	1208	U
23	A	1209	G
23	A	1212	U
23	A	1213	A
23	A	1214	A
23	A	1215	U
23	A	1216	A
23	A	1219	U
23	A	1223	U
23	A	1224	G
23	A	1226	U
23	A	1230	G
23	A	1234	U
23	A	1235	U
23	A	1238	G
23	A	1240	G
23	A	1244	A
23	A	1246	A
23	A	1251	A
23	A	1253	C

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Mol	Chain	Res	Type
23	A	1260	C
23	A	1261	A
23	A	1267	A
23	A	1270	G
23	A	1290	C
23	A	1292	U
23	A	1293	G
23	A	1294	U
23	A	1320	U
23	A	1325	U
23	A	1332	G
23	A	1339	G
23	A	1343	G
23	A	1344	A
23	A	1345	G
23	A	1352	A
23	A	1353	G
23	A	1359	G
23	A	1362	A
23	A	1365	G
23	A	1370	U
23	A	1371	G
23	A	1380	A
23	A	1386	G
23	A	1387	A
23	A	1389	U
23	A	1404	C
23	A	1408	C
23	A	1415	A
23	A	1416	A
23	A	1435	C
23	A	1437	A
23	A	1440	C
23	A	1444	U
23	A	1445	C
23	A	1456	G
23	A	1457	A
23	A	1462	G
23	A	1465	C
23	A	1480	A
23	A	1481	C
23	A	1499	A

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Mol	Chain	Res	Type
23	A	1501	C
23	A	1507	G
23	A	1508	A
23	A	1510	A
23	A	1511	U
23	A	1518	A
23	A	1522	G
23	A	1524	G
23	A	1525	U
23	A	1529	U
23	A	1530	G
23	A	1531	C
23	A	1534	C
23	A	1536	A
23	A	1537	U
23	A	1538	G
23	A	1540	U
23	A	1544	U
23	A	1546	A
23	A	1547	G
23	A	1550	G
23	A	1551	U
23	A	1552	A
23	A	1553	C
23	A	1554	U
23	A	1555	A
23	A	1556	A
23	A	1558	C
23	A	1559	A
23	A	1561	C
23	A	1564	A
23	A	1565	A
23	A	1567	C
23	A	1570	C
23	A	1571	C
23	A	1572	G
23	A	1574	G
23	A	1579	C
23	A	1580	A
23	A	1584	U
23	A	1587	G
23	A	1588	G

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Mol	Chain	Res	Type
23	A	1589	G
23	A	1595	G
23	A	1598	U
23	A	1599	U
23	A	1600	G
23	A	1604	G
23	A	1605	G
23	A	1607	C
23	A	1608	U
23	A	1611	A
23	A	1616	A
23	A	1617	C
23	A	1623	U
23	A	1625	G
23	A	1627	U
23	A	1629	G
23	A	1630	U
23	A	1631	A
23	A	1632	G
23	A	1637	G
23	A	1638	C
23	A	1639	G
23	A	1640	A
23	A	1648	A
23	A	1649	C
23	A	1650	G
23	A	1658	G
23	A	1674	G
23	A	1679	A
23	A	1680	A
23	A	1681	U
23	A	1688	G
23	A	1696	G
23	A	1703	G
23	A	1710	A
23	A	1711	G
23	A	1713	U
23	A	1716	A
23	A	1717	U
23	A	1720	G
23	A	1724	G
23	A	1727	A

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Mol	Chain	Res	Type
23	A	1728	U
23	A	1730	U
23	A	1731	A
23	A	1736	G
23	A	1737	A
23	A	1738	G
23	A	1746	G
23	A	1751	G
23	A	1754	G
23	A	1755	A
23	A	1756	G
23	A	1757	U
23	A	1760	G
23	A	1767	U
23	A	1778	A
23	A	1787	A
23	A	1789	A
23	A	1791	A
23	A	1801	C
23	A	1802	G
23	A	1803	A
23	A	1813	C
23	A	1820	U
23	A	1825	C
23	A	1834	A
23	A	1835	C
23	A	1852	A
23	A	1857	U
23	A	1864	U
23	A	1865	A
23	A	1866	C
23	A	1871	G
23	A	1872	A
23	A	1878	G
23	A	1890	C
23	A	1892	G
23	A	1895	A
23	A	1909	C
23	A	1912	C
23	A	1916	A
23	A	1917	G
23	A	1918	A

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Mol	Chain	Res	Type
23	A	1921	G
23	A	1925	A
23	A	1931	A
23	A	1946	U
23	A	1947	U
23	A	1948	A
23	A	1950	G
23	A	1973	C
23	A	1975	A
23	A	1979	A
23	A	1980	G
23	A	1981	U
23	A	1990	A
23	A	1998	C
23	A	2003	A
23	A	2004	A
23	A	2017	C
23	A	2018	G
23	A	2024	G
23	A	2025	C
23	A	2026	A
23	A	2027	A
23	A	2033	U
23	A	2036	A
23	A	2046	A
23	A	2047	C
23	A	2050	C
23	A	2052	G
23	A	2064	A
23	A	2065	A
23	A	2066	G
23	A	2086	U
23	A	2088	C
23	A	2089	C
23	A	2090	U
23	A	2092	U
23	A	2093	G
23	A	2094	G
23	A	2095	G
23	A	2096	G
23	A	2106	A
23	A	2107	G

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Mol	Chain	Res	Type
23	A	2112	U
23	A	2130	G
23	A	2136	A
23	A	2138	C
23	A	2140	A
23	A	2141	U
23	A	2152	A
23	A	2153	G
23	A	2154	G
23	A	2155	U
23	A	2161	A
23	A	2162	A
23	A	2163	U
23	A	2164	U
23	A	2165	C
23	A	2166	C
23	A	2167	U
23	A	2178	G
23	A	2179	U
23	A	2191	C
23	A	2194	A
23	A	2195	U
23	A	2196	G
23	A	2197	G
23	A	2199	G
23	A	2215	U
23	A	2217	U
23	A	2221	A
23	A	2241	U
23	A	2246	U
23	A	2255	A
23	A	2256	G
23	A	2257	A
23	A	2267	C
23	A	2276	G
23	A	2279	C
23	A	2280	G
23	A	2284	A
23	A	2285	G
23	A	2286	A
23	A	2293	G
23	A	2300	A

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Mol	Chain	Res	Type
23	A	2315	U
23	A	2316	G
23	A	2325	U
23	A	2327	C
23	A	2329	G
23	A	2331	U
23	A	2334	U
23	A	2335	G
23	A	2336	U
23	A	2338	G
23	A	2339	G
23	A	2341	U
23	A	2342	A
23	A	2343	G
23	A	2346	G
23	A	2347	G
23	A	2348	G
23	A	2350	G
23	A	2351	A
23	A	2352	C
23	A	2353	U
23	A	2354	G
23	A	2355	U
23	A	2356	G
23	A	2358	A
23	A	2359	G
23	A	2363	A
23	A	2367	G
23	A	2368	C
23	A	2373	G
23	A	2375	G
23	A	2380	G
23	A	2381	A
23	A	2382	G
23	A	2383	U
23	A	2384	C
23	A	2385	G
23	A	2387	U
23	A	2388	G
23	A	2389	U
23	A	2390	U
23	A	2392	A

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Mol	Chain	Res	Type
23	A	2394	A
23	A	2395	U
23	A	2399	A
23	A	2401	U
23	A	2402	C
23	A	2403	U
23	A	2407	C
23	A	2408	G
23	A	2411	U
23	A	2413	G
23	A	2421	A
23	A	2434	A
23	A	2436	A
23	A	2437	U
23	A	2449	A
23	A	2450	C
23	A	2454	G
23	A	2462	G
23	A	2463	G
23	A	2490	A
23	A	2492	A
23	A	2503	G
23	A	2507	C
23	A	2508	C
23	A	2510	A
23	A	2511	A
23	A	2520	U
23	A	2521	C
23	A	2528	G
23	A	2529	A
23	A	2530	C
23	A	2532	G
23	A	2534	A
23	A	2549	G
23	A	2559	A
23	A	2566	C
23	A	2571	C
23	A	2574	C
23	A	2585	U
23	A	2596	G
23	A	2601	A
23	A	2607	G

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Mol	Chain	Res	Type
23	A	2609	A
23	A	2626	U
23	A	2627	C
23	A	2639	G
23	A	2643	U
23	A	2647	U
23	A	2649	A
23	A	2653	G
23	A	2654	A
23	A	2655	U
23	A	2658	A
23	A	2659	A
23	A	2664	C
23	A	2665	C
23	A	2672	A
23	A	2673	U
23	A	2693	A
23	A	2694	G
23	A	2699	C
23	A	2707	C
23	A	2715	U
23	A	2722	C
23	A	2726	G
23	A	2728	U
23	A	2729	G
23	A	2730	U
23	A	2742	A
23	A	2749	G
23	A	2750	G
23	A	2753	G
23	A	2755	A
23	A	2759	G
23	A	2767	G
23	A	2778	U
23	A	2788	A
23	A	2790	A
23	A	2791	G
23	A	2796	A
23	A	2797	C
23	A	2802	G
23	A	2806	G
23	A	2810	U

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Mol	Chain	Res	Type
23	A	2826	A
23	A	2827	G
23	A	2833	U
23	A	2835	U
23	A	2837	U
23	A	2853	C
23	A	2854	A
23	A	2857	A
23	A	2860	U
23	A	2862	G
23	A	2870	C
23	A	2871	U
23	A	2878	A
23	A	2884	A
23	A	2893	G
23	A	2906	U
23	A	2912	A
23	A	2913	U
23	A	2926	A
23	A	2929	A
23	A	2936	C
23	A	2937	G
23	A	2938	G
23	A	2957	A
23	A	2959	A
23	A	2963	U
23	A	2968	G
23	A	2972	A
23	A	2974	A
23	A	2979	C
23	A	2982	A
23	A	2985	G
23	A	2989	A
23	A	2990	A
23	A	3002	A
23	A	3013	C
23	A	3014	A
23	A	3015	C
23	A	3020	U
23	A	3021	A
23	A	3023	G
23	A	3024	A

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Mol	Chain	Res	Type
23	A	3029	U
23	A	3039	C
23	A	3042	A
23	A	3047	A
23	A	3053	U
23	A	3054	U
23	A	3055	G
23	A	3068	U
23	A	3070	G
23	A	3079	U
23	A	3080	A
23	A	3082	U
23	A	3087	G
23	A	3088	C
23	A	3089	A
23	A	3093	A
23	A	3095	C
23	A	3100	A
23	A	3101	C
23	A	3104	A
23	A	3105	C
23	A	3106	C
23	A	3107	G
23	A	3112	A
23	A	3115	A
23	A	3117	U
24	B	4	A
24	B	5	C
24	B	9	G
24	B	11	U
24	B	12	C
24	B	13	C
24	B	14	A
24	B	26	A
24	B	30	G
24	B	36	U
24	B	37	C
24	B	41	U
24	B	42	C
24	B	43	C
24	B	45	G
24	B	56	C

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Mol	Chain	Res	Type
24	B	67	A
24	B	87	U
24	B	89	C
24	B	90	G
24	B	103	G
24	B	107	A
24	B	114	A

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	81	A
23	A	97	U
23	A	228	A
23	A	316	U
23	A	336	C
23	A	357	U
23	A	445	U
23	A	552	U
23	A	641	U
23	A	643	G
23	A	899	G
23	A	974	G
23	A	1002	C
23	A	1004	C
23	A	1006	G
23	A	1014	G
23	A	1046	C
23	A	1084	U
23	A	1186	G
23	A	1293	G
23	A	1436	C
23	A	1510	A
23	A	2003	A
23	A	2005	C
23	A	2088	C
23	A	2094	G
23	A	2139	U
23	A	2165	C
23	A	2350	G
23	A	2384	C
23	A	2389	U

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Mol	Chain	Res	Type
23	A	2626	U
24	B	10	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](#)

There are no ligands in this entry.

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.

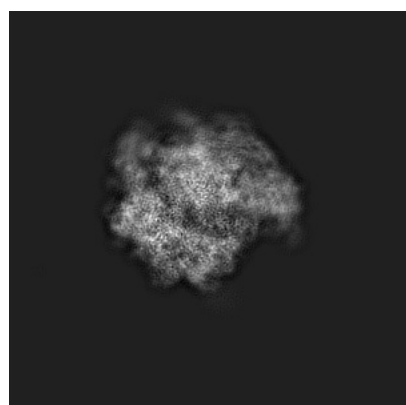
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8932. These allow visual inspection of the internal detail of the map and identification of artifacts.

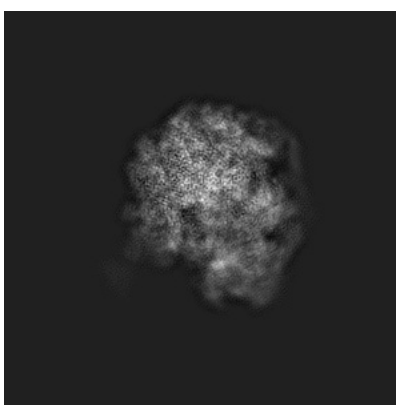
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

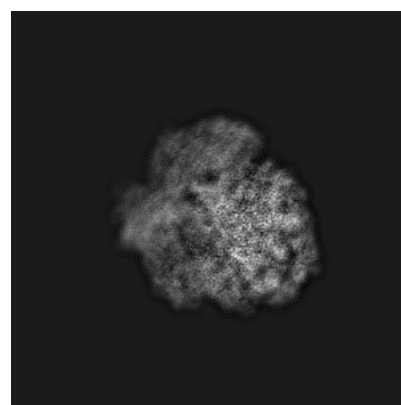
6.1.1 Primary map



X



Y

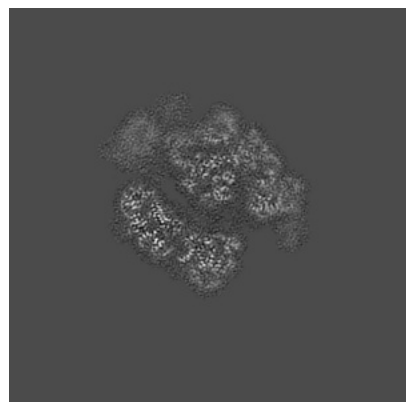


Z

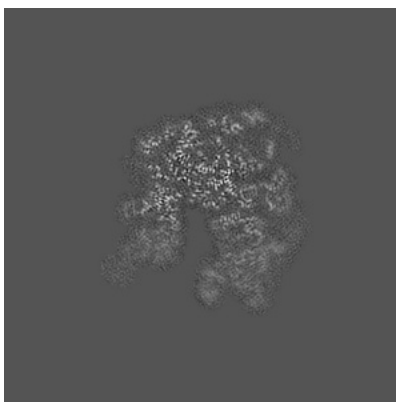
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

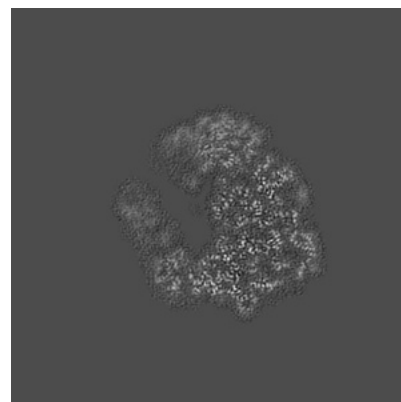
6.2.1 Primary map



X Index: 227



Y Index: 227

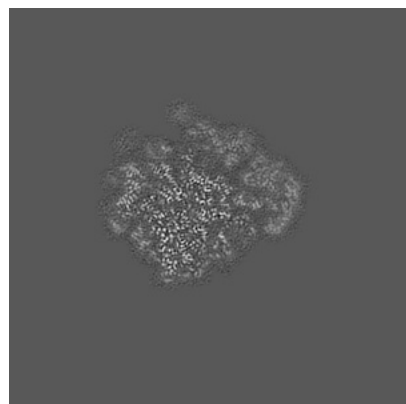


Z Index: 227

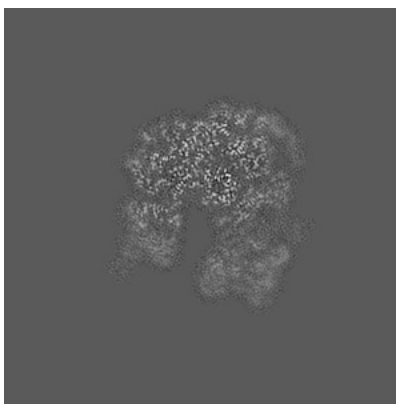
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

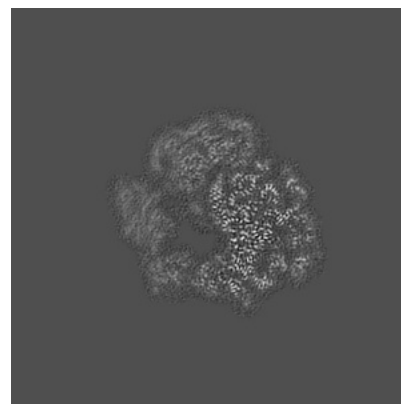
6.3.1 Primary map



X Index: 255



Y Index: 216

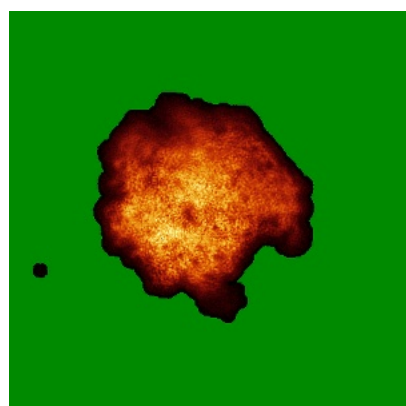


Z Index: 238

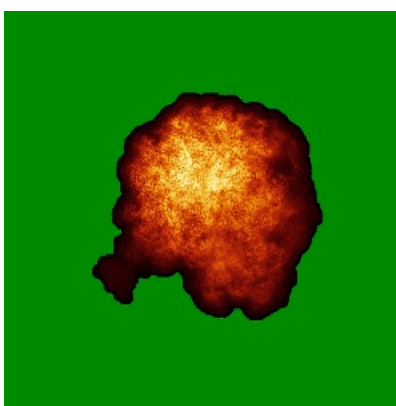
The images above show the largest variance slices of the map in three orthogonal directions.

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

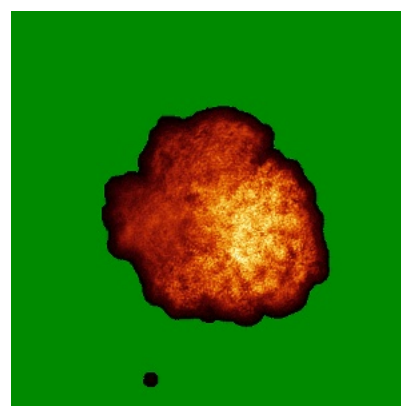
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

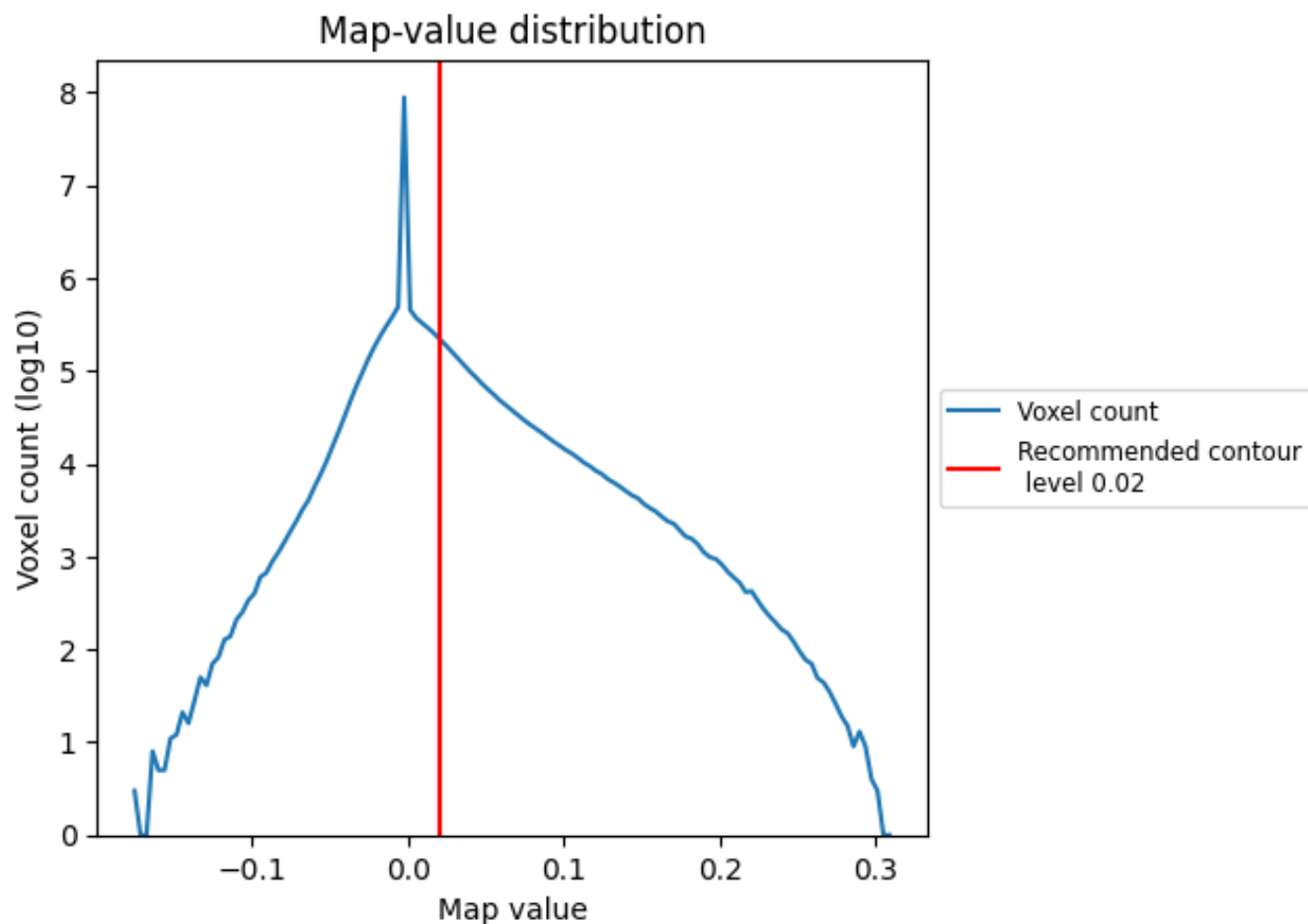
6.6 Mask visualisation

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

7 Map analysis [i](#)

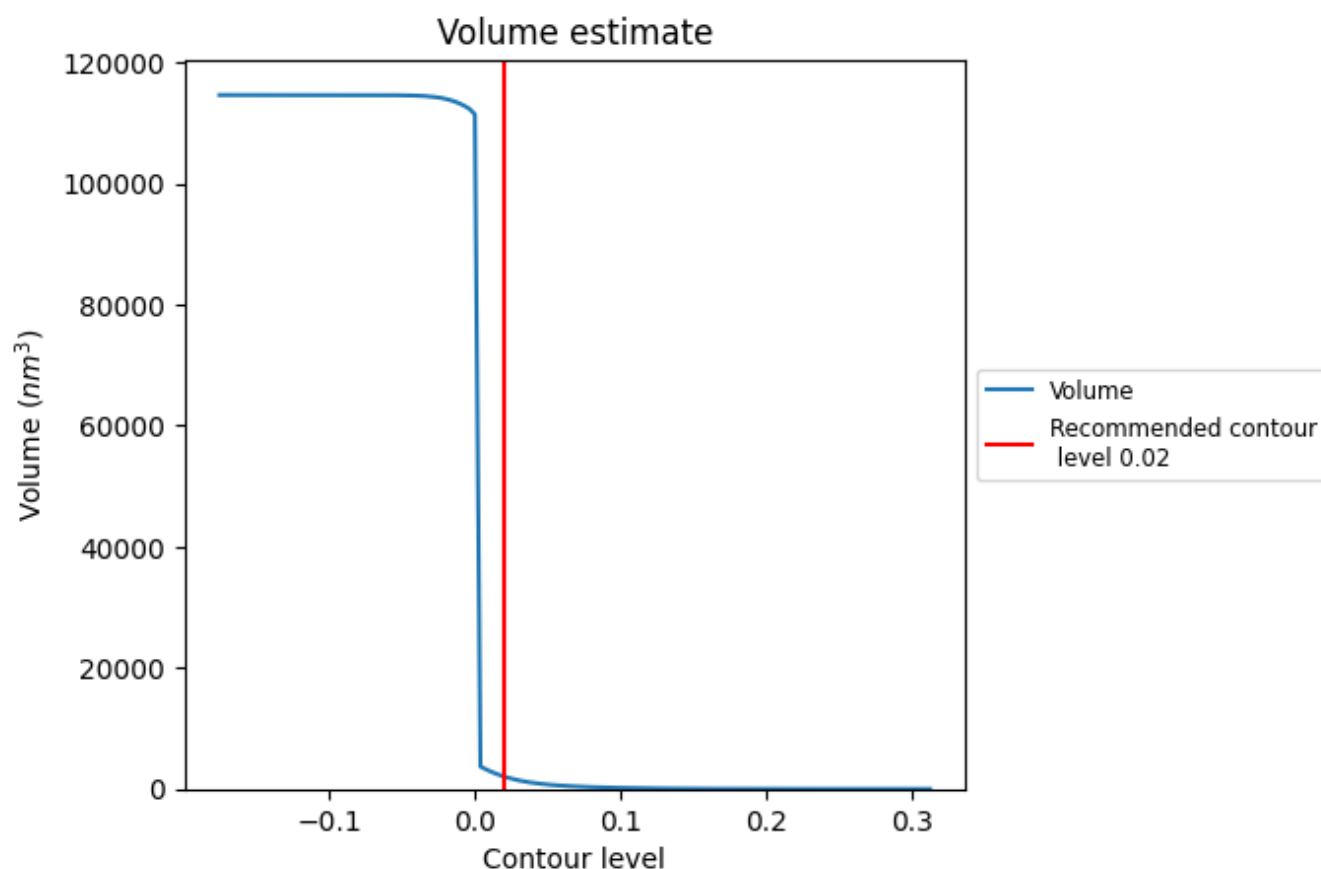
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

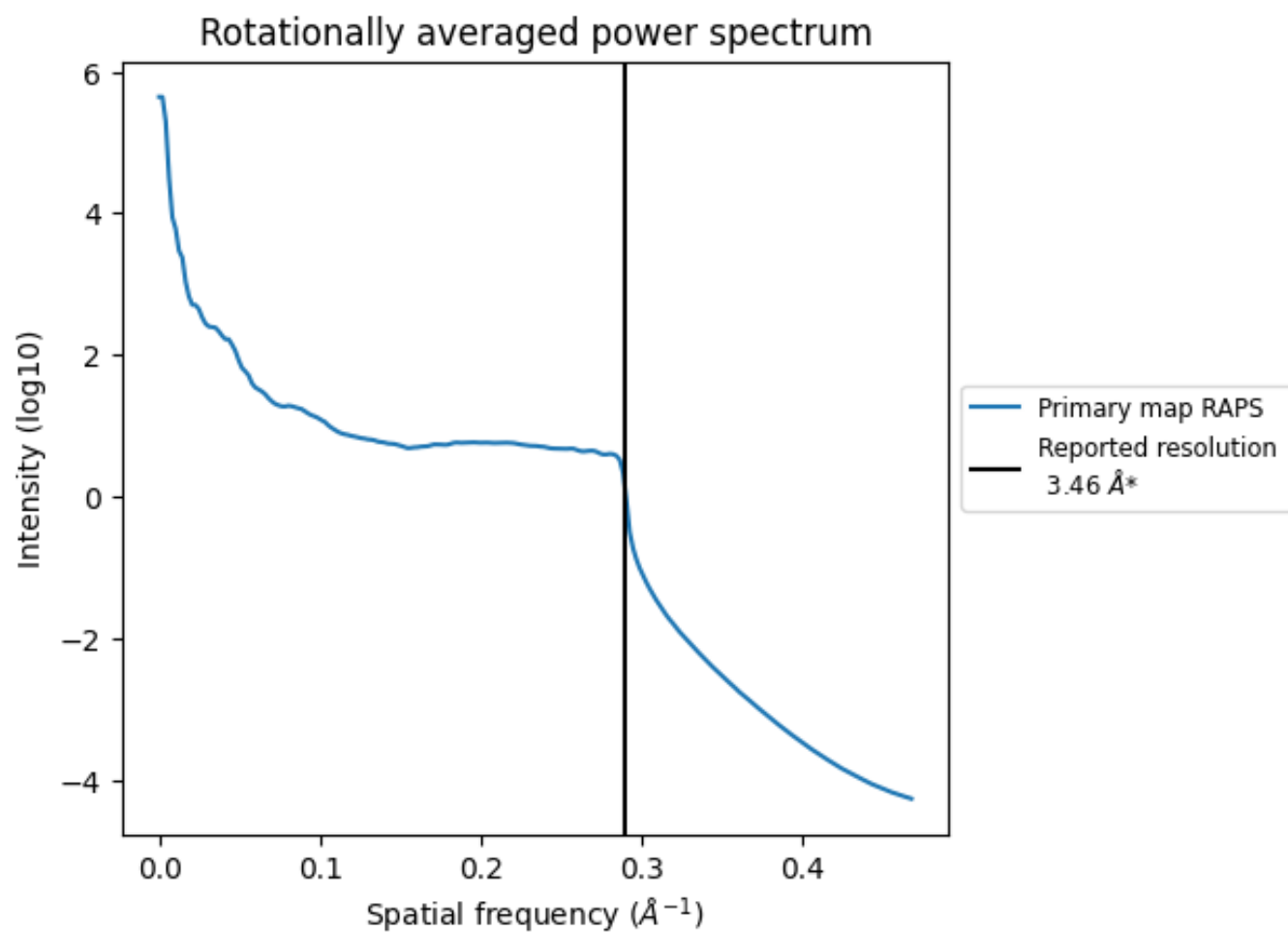
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2059 nm³; this corresponds to an approximate mass of 1860 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 ⓘ

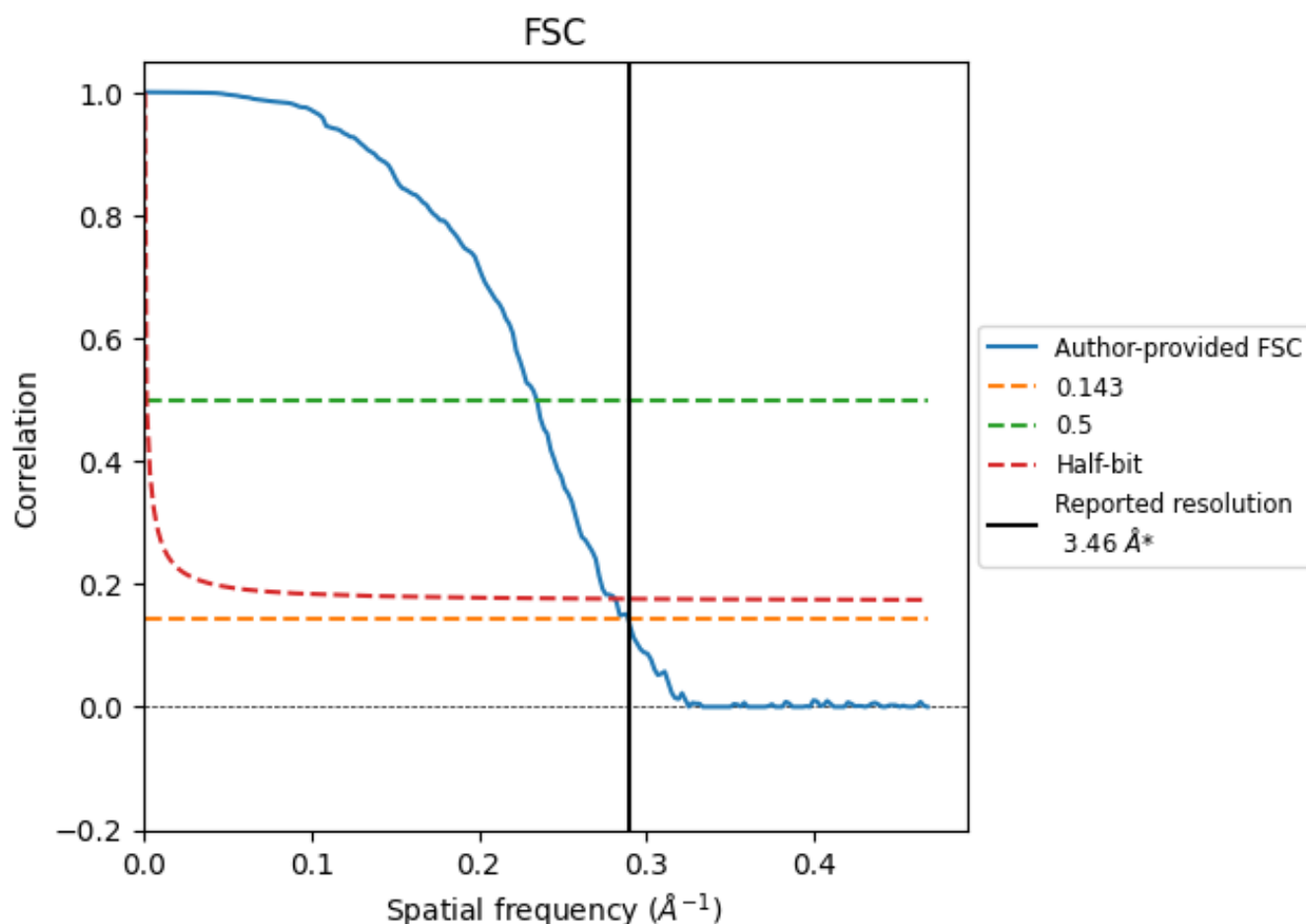


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

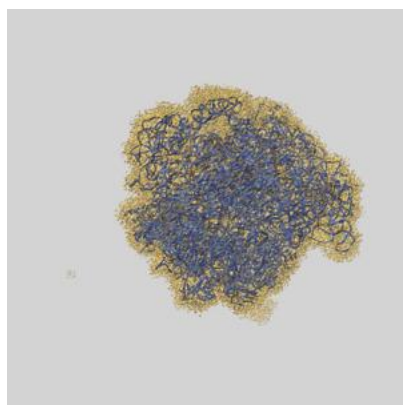
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.46	4.27	3.56
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

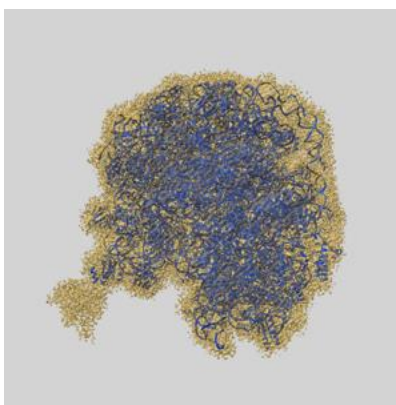
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8932 and PDB model 6DZI. Per-residue inclusion information can be found in section [3](#) on page [15](#).

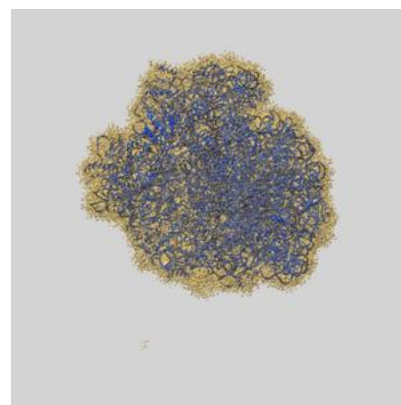
9.1 Map-model overlay [i](#)



X



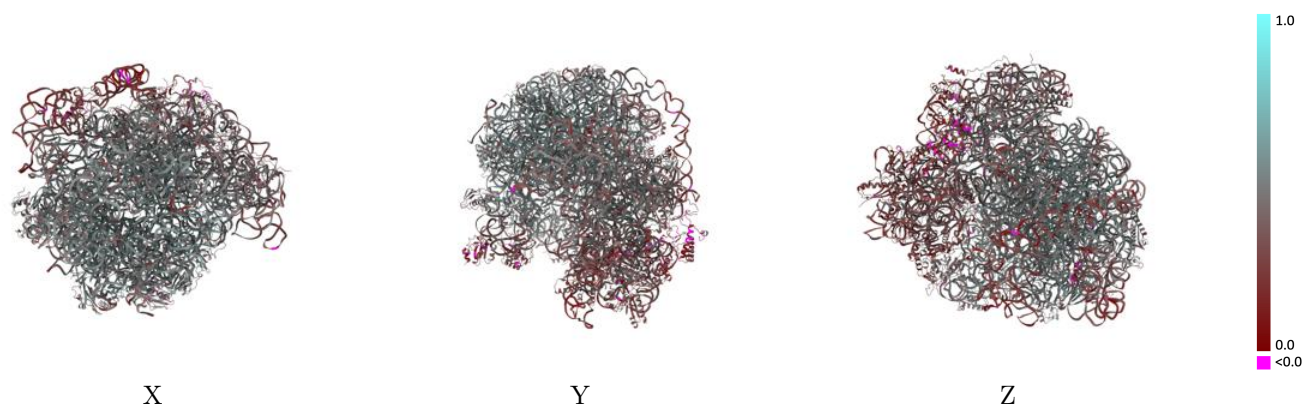
Y



Z

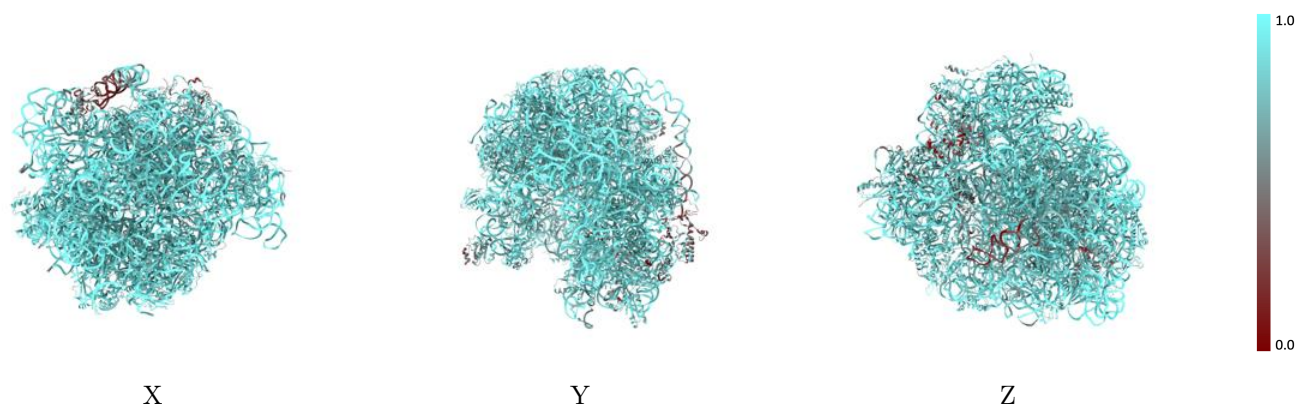
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



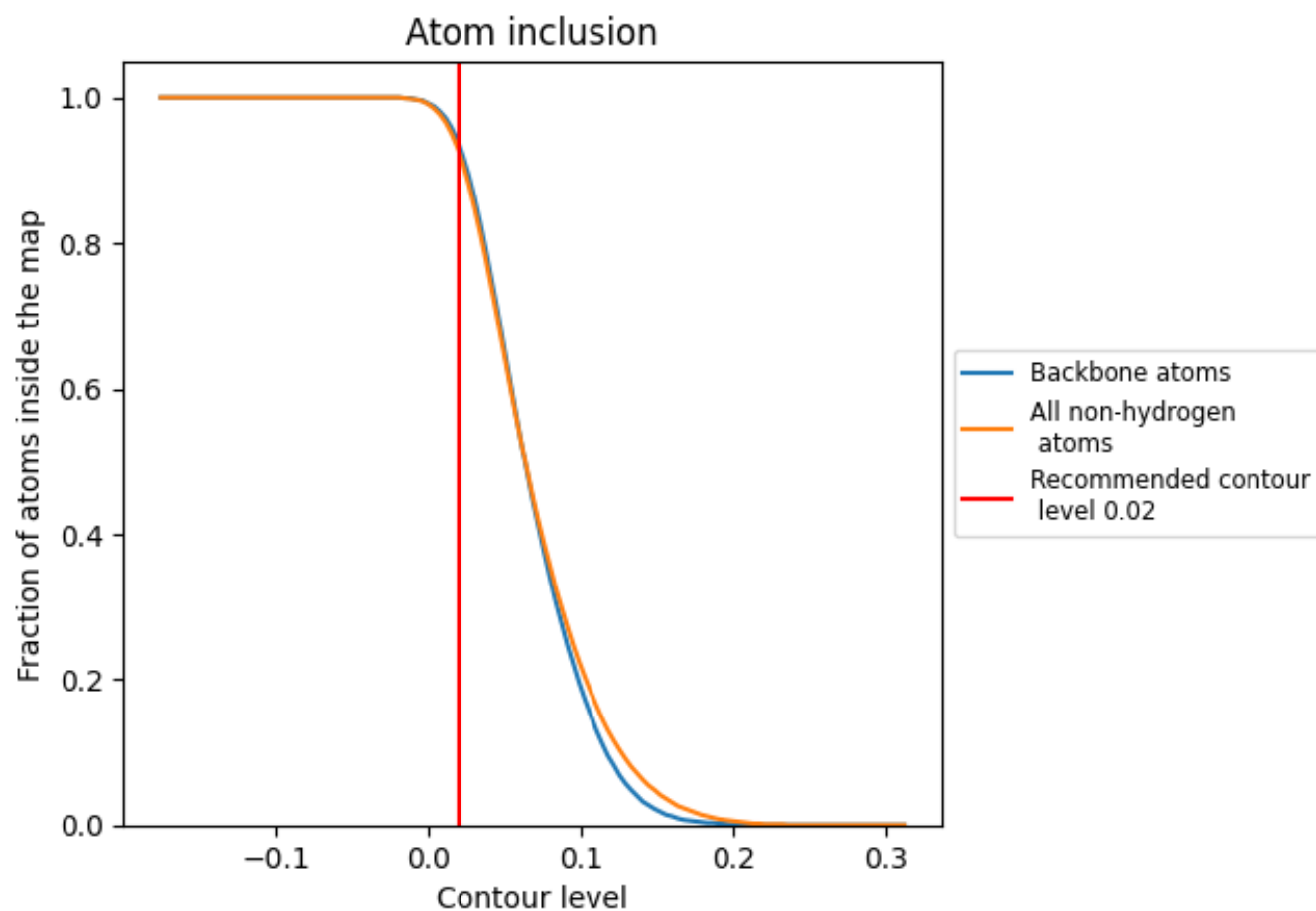
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.4380
3	 0.9110	 0.5190
4	 0.8930	 0.3240
5	 0.8730	 0.4370
6	 0.7960	 0.3270
7	 0.8870	 0.3630
8	 0.5220	 0.1690
9	 0.8690	 0.3250
A	 0.9620	 0.4760
B	 0.9830	 0.4620
C	 0.8920	 0.5100
D	 0.9330	 0.5100
E	 0.9210	 0.4830
F	 0.9160	 0.4010
G	 0.9260	 0.4290
H	 0.5670	 0.2940
I	 0.6280	 0.2350
J	 0.7940	 0.2780
K	 0.9380	 0.5090
L	 0.8930	 0.5020
M	 0.9290	 0.4940
N	 0.9110	 0.5050
O	 0.9250	 0.5030
P	 0.9470	 0.4560
Q	 0.8920	 0.4730
R	 0.9120	 0.5060
S	 0.9500	 0.5090
T	 0.9110	 0.4950
U	 0.9110	 0.4620
V	 0.9030	 0.4270
W	 0.8950	 0.4510
X	 0.9330	 0.5160
Y	 0.5180	 0.2720
Z	 0.9330	 0.4440
a	 0.9350	 0.4990



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Chain	Atom inclusion	Q-score
b	 0.9350	 0.4940
c	 0.7620	 0.3500
d	 0.9000	 0.5200
e	 0.9150	 0.5140
f	 0.9370	 0.5230
g	 0.8480	 0.2800
h	 0.9640	 0.4050
j	 0.7820	 0.4360
k	 0.8210	 0.3330
l	 0.8410	 0.3100
m	 0.8560	 0.3790
n	 0.8550	 0.3930
p	 0.8080	 0.3130
q	 0.9250	 0.4160
r	 0.7210	 0.3310
s	 0.8310	 0.3250
t	 0.8560	 0.4150
u	 0.8750	 0.4180
v	 0.8500	 0.3210
x	 0.8850	 0.4130
y	 0.8740	 0.4340
z	 0.8540	 0.3830