



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 08:04 PM UTC

PDB ID : 8WIC / pdb_00008wic
EMDB ID : EMD-37563
Title : Cryo- EM structure of Mycobacterium smegmatis 50S ribosomal subunit (body 1) of 70S ribosome, E- tRNA and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

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:

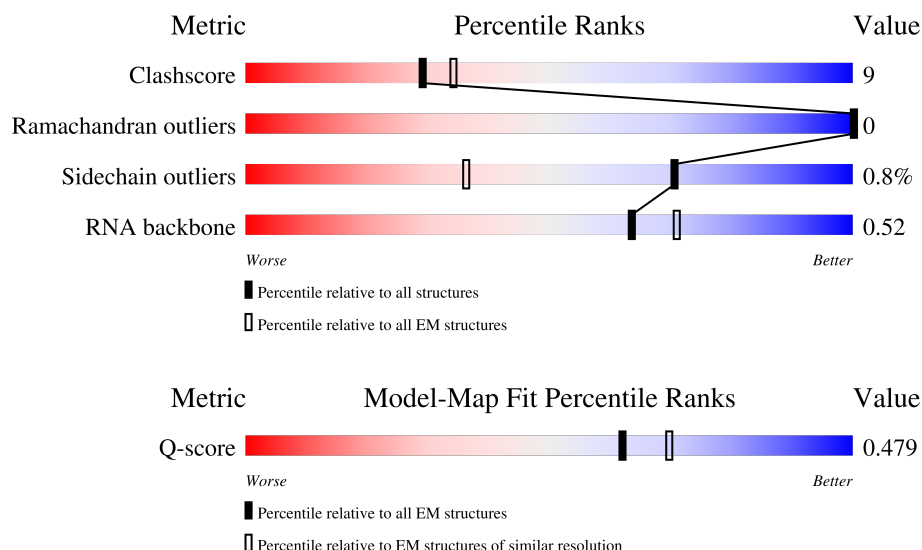
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 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.



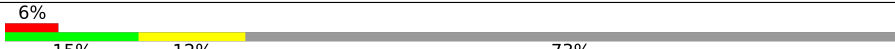
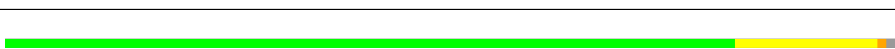
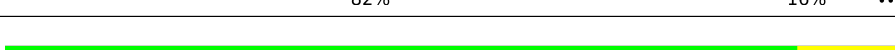
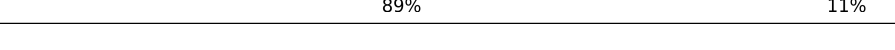
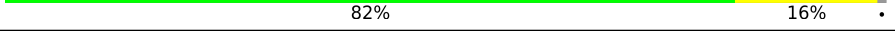
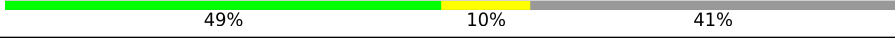
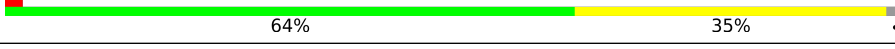
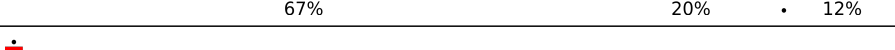
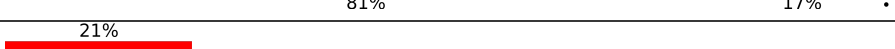
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	E	278	 86% 13%
2	F	217	 77% 18%
3	G	215	 78% 19%

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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

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Mol	Chain	Length	Quality of chain
29	C	76	36% 46% 18%

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 91332 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	209	Total	C	N	O	S	0	0
			1563	969	305	285	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	208	Total	C	N	O	S	0	0
			1562	965	294	301	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	180	Total	C	N	O	S	0	0
			1428	897	267	258	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

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

- Molecule 8 is a protein called 50S ribosomal protein L14.

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

- Molecule 9 is a protein called 50S ribosomal protein L15.

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

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	125	Total	C	N	O	0	0
			951	583	198	170		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	S	112	Total	C	N	O	0	0
			899	565	170	164		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	123	Total	C	N	O	0	0
			982	610	202	170		

- Molecule 14 is a protein called 50S ribosomal protein L21.

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

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	113	Total	C	N	O	0	0
			864	538	170	156		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	96	Total	C	N	O	0	0
			751	476	137	138		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	92	Total	C	N	O	S	0	0
			706	441	132	131	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	77	Total	C	N	O	0	0
			574	355	121	98		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	62	Total	C	N	O	S	0	0
			465	280	102	79	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	58	Total	C	N	O	0	0
			470	290	94	86		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3022	Total	C	N	O	P	0	0
			64906	28929	11938	21017	3022		

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	117	Total	C	N	O	P	0	0
			2502	1117	465	803	117		

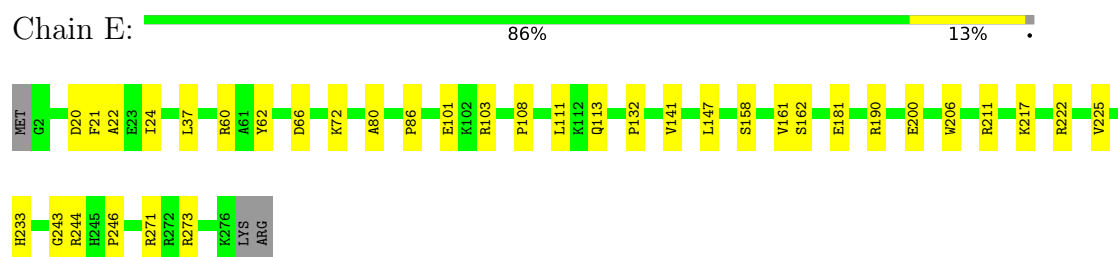
- Molecule 29 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	C	76	Total	C	N	O	P	0	0
			1622	723	294	529	76		

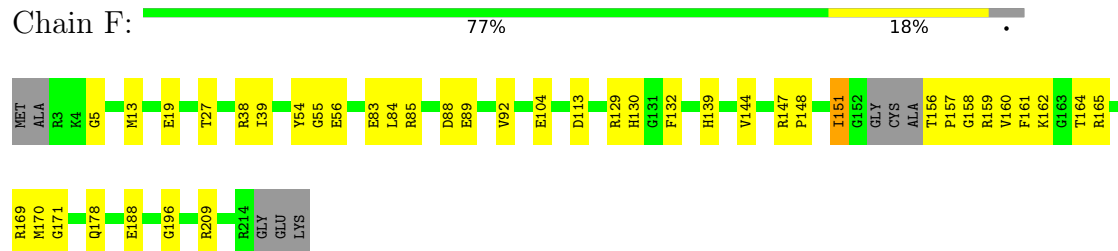
3 Residue-property plots [i](#)

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

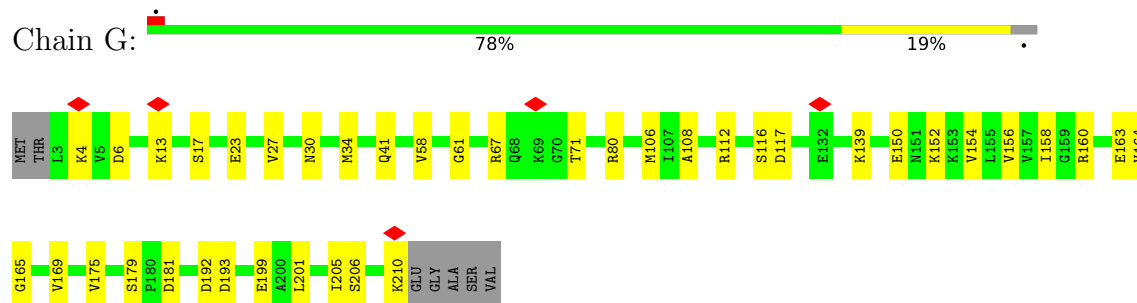
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

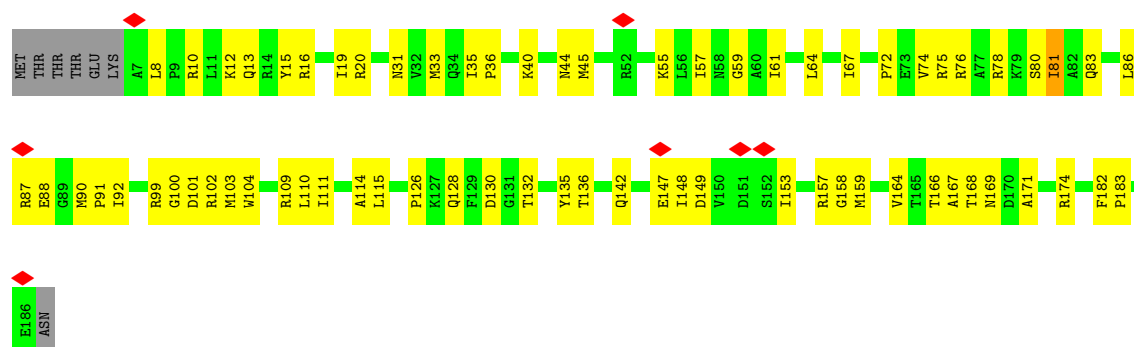


• Molecule 3: 50S ribosomal protein L4

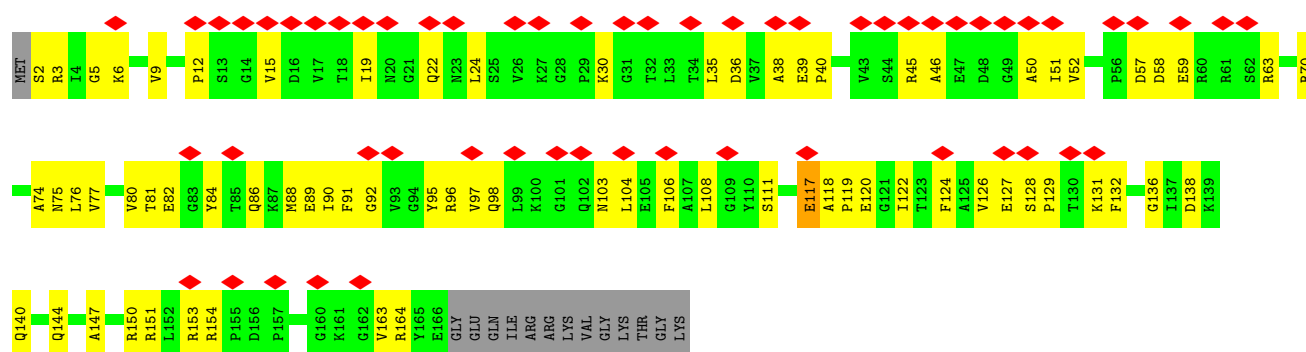


• Molecule 4: 50S ribosomal protein L5

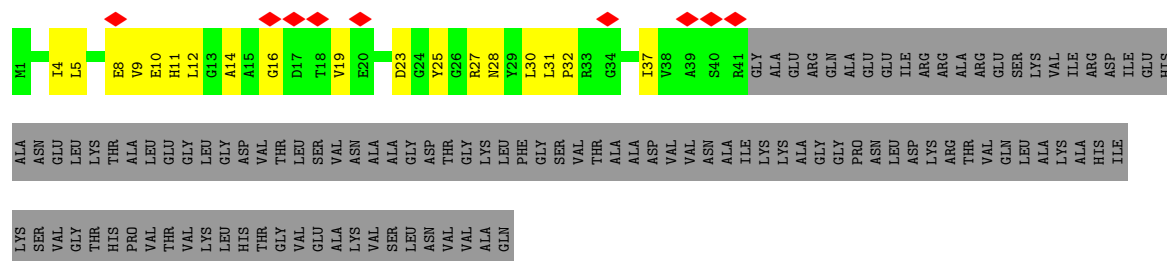




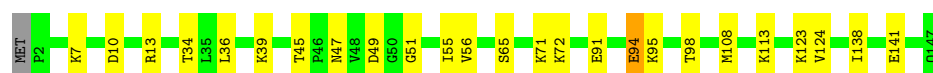
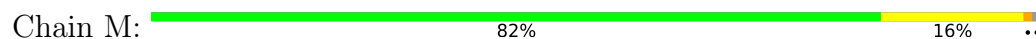
• Molecule 5: 50S ribosomal protein L6



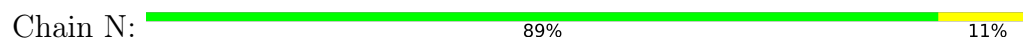
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L13



• Molecule 8: 50S ribosomal protein L14





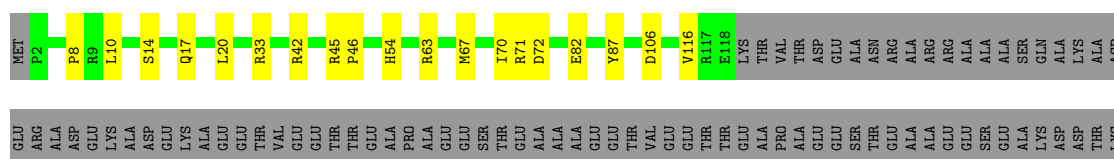
- Molecule 9: 50S ribosomal protein L15

Chain O: 82% 16%



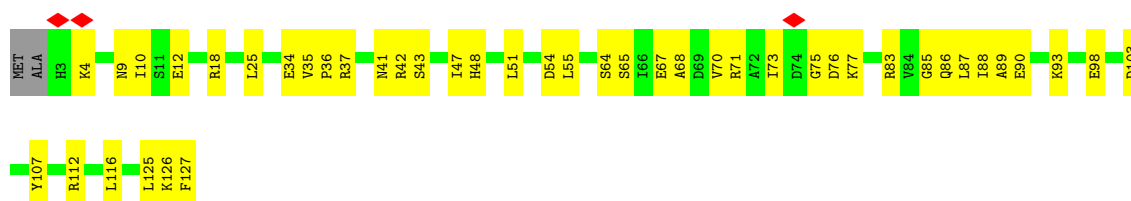
- Molecule 10: 50S ribosomal protein L17

Chain Q: 49% 10% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R: 64% 35%



- Molecule 12: 50S ribosomal protein L19

Chain S: 83% 16%



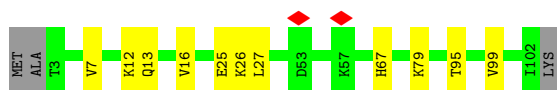
- Molecule 13: 50S ribosomal protein L20

Chain T: 76% 19% 5%



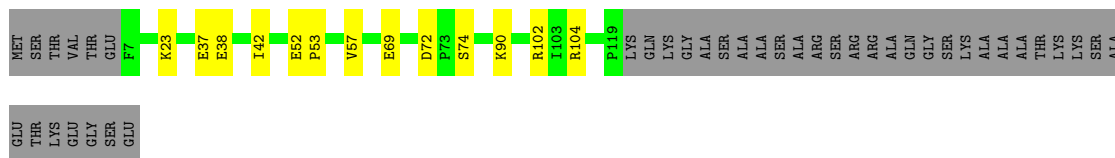
- Molecule 14: 50S ribosomal protein L21

Chain U: 86% 11%



- Molecule 15: 50S ribosomal protein L22

Chain V: 65% 8% 26%



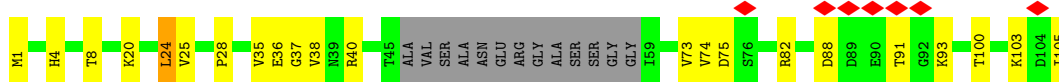
- Molecule 16: 50S ribosomal protein L23

Chain W: 83% 13% .



- Molecule 17: 50S ribosomal protein L24

Chain X: 7% 67% 20% . 12%



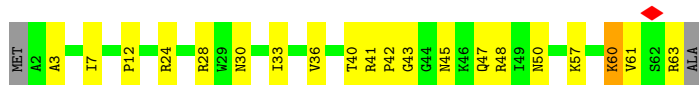
- Molecule 18: 50S ribosomal protein L27

Chain Z: 74% 14% 13%



- Molecule 19: 50S ribosomal protein L28

Chain 1: 66% 30% . .

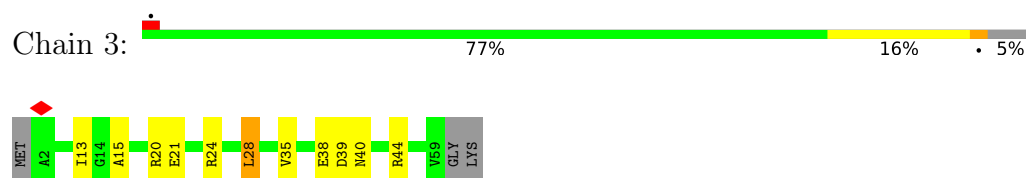


- Molecule 20: 50S ribosomal protein L29

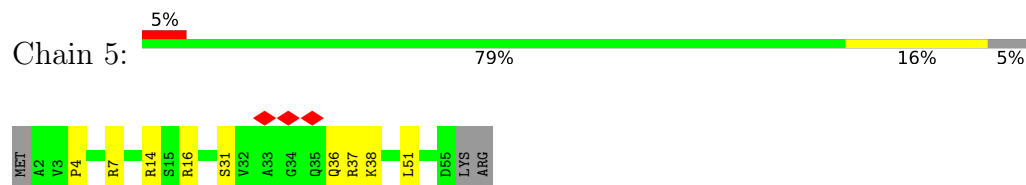
Chain 2: 58% 23% 18%



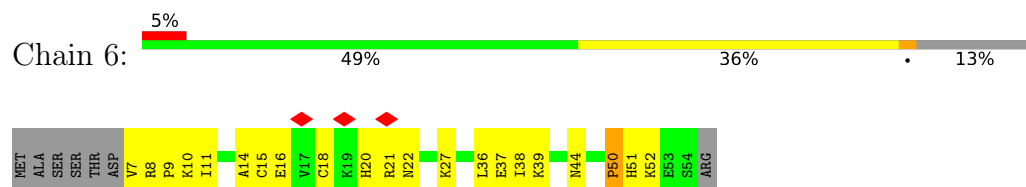
- Molecule 21: 50S ribosomal protein L30



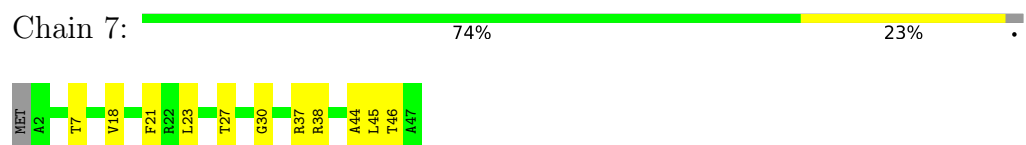
- Molecule 22: 50S ribosomal protein L32



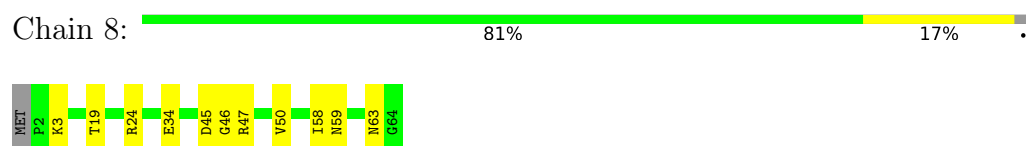
- Molecule 23: 50S ribosomal protein L33A



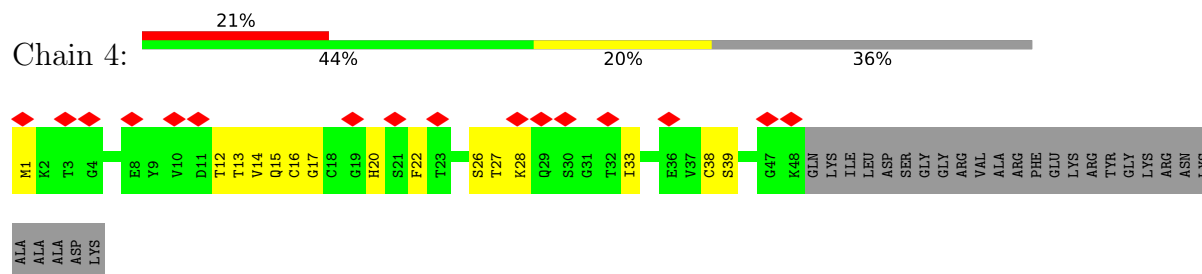
- Molecule 24: 50S ribosomal protein L34



- Molecule 25: 50S ribosomal protein L35



- Molecule 26: 50S ribosomal protein L31

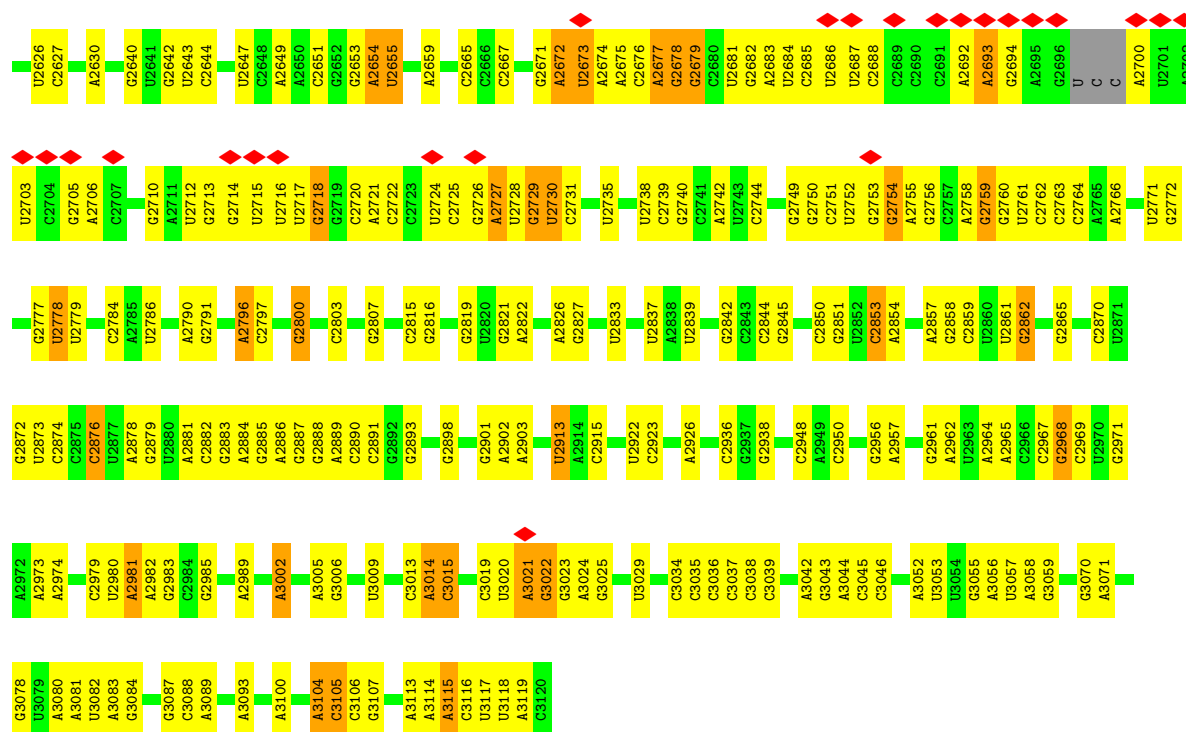


- Molecule 27: 23S rRNA



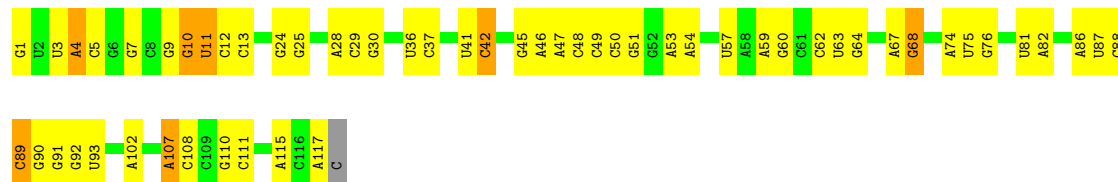
U1223	G1078	G986	G880	U764	U674	U586	A489	U388	C310	U234	A2
G1224	U1084	A987	G883	G765	A678	G887	U493	G389	G311	U235	A3
G1225	G1085	G988	G766	G766	G679	A589	G313	A589	G312	G242	G4
A1228	G1086	G989	G890	U767	U680	A590	A392	U393	G314	G247	U5
A1229	U1088	C991	G891	G768	C681	G591	U393	U315	G314	G248	G6
G1230	U1088	C992	G892	U769	A682	A592	G394	U316	U317	G249	U7
U1231	G1092	A993	A897	U772	G683	G893	C502	G399	U318	C250	U8
U1232	G1093	A994	A898	G773	G684	A594	A503	G400	G319	G251	U9
U1233	A1099	U995	G899	G776	G685	A595	C504	C401	G324	A256	G12
U1234	C1100	A903	A903	G776	G686	C596	C505	C401	U325	A257	G13
U1235	A1101	G997	A903	U780	U690	C597	G508	A412	U326	G254	G20
G1236	A1101	G998	U911	C781	C692	A601	U509	G413	A326	A256	G21
U1237	G1105	C999	C912	U782	C693	A602	G512	G419	C149	A257	U22
G1238	A1106	C1000	G783	G783	C694	A616	U515	G420	C149	G263	G23
G1239	G1107	A919	G784	U785	A695	U617	U516	G424	C150	G264	G24
G1240	A1108	G920	A785	A785	A696	C618	G516	U425	C151	A265	A25
G1241	G1111	G924	G789	G789	G706	C619	G520	U426	C332	U266	U26
C1242	C1112	C927	A790	A790	G707	G620	A520	G426	C333	U270	G27
G1243	G1113	U928	U794	U794	G708	U621	U523	A429	C334	A271	C28
A1244	G1114	C929	G794	G794	U709	C622	U523	A430	C335	A272	C29
U1245	G1118	G933	U801	U801	C718	A625	G534	G434	C336	A273	U30
U1248	A1119	A934	C813	C813	A721	G632	C539	G437	C341	U277	G31
G1249	G1120	A935	A814	A814	G724	G635	A542	U440	C342	U279	G32
A1251	G1121	U942	G815	G815	G728	U636	A543	U440	C343	G280	A41
C1253	C1122	U943	G815	G815	A729	G637	U544	U440	C344	G281	G42
G1254	G1123	A944	U944	U944	C729	U638	A545	U440	C345	C282	G85
U1257	G1124	U945	U945	U945	G730	C639	G546	U444	C346	A282	A60
G1258	A1127	U947	U947	U947	A731	G640	G551	U447	C347	U285	G61
U1259	G1128	G948	U948	U948	G732	U641	A554	U448	C348	U286	G62
C1260	C1130	G949	U949	U949	A733	G642	G555	U449	C349	A287	A68
A1261	G1131	G951	G951	G951	U735	U643	G556	U450	C350	U288	G72
C1272	U1132	U961	U961	U961	G736	G644	G557	U451	C351	A289	A71
A1284	G1133	U966	U966	U966	A737	U645	G561	U452	C352	C290	G82
G1285	U1137	C967	C967	C967	G738	U646	G562	U453	C353	G291	A81
A1288	A1138	C968	C968	C968	A739	U647	G563	U454	C354	G292	G82
A1289	G1140	U971	U971	U971	G741	U654	G564	U454	C355	G293	A88
U1292	A1144	G972	G972	G972	G745	G655	A565	G460	C356	G294	A89
G1293	A1145	C981	C981	C981	U746	U655	A566	G469	C357	U295	C90
U1294	G1146	G973	G973	G973	A747	U660	A567	G470	C358	A296	C91
U1295	A1147	G974	G974	G974	U748	U661	A568	G470	C359	A297	G94
G1296	G1148	U975	U975	U975	C749	A662	A569	G471	C360	G298	G95
C1297	G1149	A976	A976	A976	C750	A663	G569	C473	C361	G299	U97
G1298	A1150	G977	G977	G977	A751	A664	G577	U474	C362	G300	G99
U1302	U1151	A878	A878	A878	C752	G665	G578	U475	C363	U301	A100
U1303	G1152	G979	G979	G979	A753	A666	A579	G476	C364	A222	G99
G1304	U1153	C980	C980	C980	C754	A667	G580	G476	C365	A227	U229
A1305	U1154	U981	U981	U981	A755	A668	G581	U479	C366	U302	G230
G1305	G1157	A882	A882	A882	G757	G669	G582	U480	C367	G303	U31
C1311	U1158	C983	C983	C983	U758	A670	G583	U481	C368	U304	G307
G1312	A1159	U984	U984	U984	G759	A671	G584	U487	C369	U305	U308
		G878	G878	G878	U760	C672	G585	G488	C370	U306	G309
		A879	A879	A879		C573			C371	U307	
									C372	U308	
									C373	U309	
									C374	U310	
									C375	U311	
									C376	U312	
									C377	U313	
									C378	U314	
									C379	U315	
									C380	U316	
									C381	U317	
									C382	U318	
									C383	U319	
									C384	U320	
									C385	U321	
									C386	U322	
									C387	U323	
									C388	U324	
									C389	U325	
									C390	U326	
									C391	U327	
									C392	U328	
									C393	U329	
									C394	U330	
									C395	U331	
									C396	U332	
									C397	U333	
									C398	U334	
									C399	U335	
									C400	U336	
									C401	U337	
									C402	U338	
									C403	U339	
									C404	U340	
									C405	U341	
									C406	U342	
									C407	U343	
									C408	U344	
									C409	U345	
									C410	U346	
									C411	U347	
									C412	U348	
									C413	U349	
									C414	U350	
									C415	U351	
									C416	U352	
									C417	U353	
									C418	U354	
									C419	U355	
									C420	U356	
									C421	U357	
									C422	U358	
									C423	U359	
									C424	U360	
									C425	U361	
									C426	U362	
									C427	U363	
									C428	U364	
									C429	U365	
									C430	U366	
									C431	U367	
									C432	U368	
									C433	U369	
									C434	U370	
									C435	U371	
									C436	U372	
									C437	U373	
									C438	U374	
									C439	U375	
									C440	U376	
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									C442	U378	
									C443	U379	
									C444	U380	
									C445	U381	
									C446	U382	
									C447	U383	
									C448	U384	
									C449	U385	
									C450	U386	
									C451	U387	
									C452	U388	
									C453	U389	
									C454	U390	
									C455	U391	
									C456	U392	
									C457	U393	
									C458	U394	
									C459	U395	
									C460	U396	
									C461	U397	
									C462	U398	
									C463	U399	
									C464	U400	
									C465	U401	
									C466	U402	
									C467	U403	
									C468	U404	
									C469	U405	
									C470	U406	
									C471	U407	
									C472	U408	
									C473	U409	
									C474	U410	
									C475	U411	
									C476	U412	
									C477	U413	
									C478	U414	





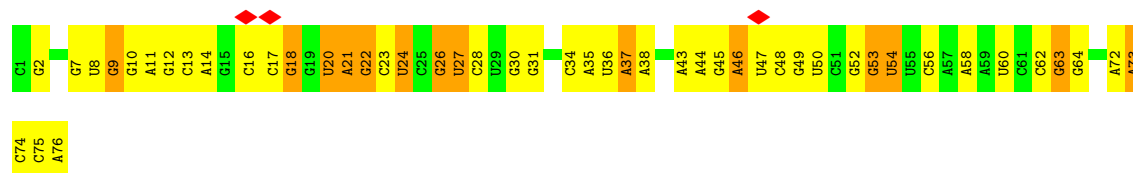
• Molecule 28: 5S rRNA

Chain B: 52% 42% 6% .



• Molecule 29: E-tRNA

Chain C: 36% 46% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44299	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE; CTF correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.218	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	E	0.32	0/2153	0.34	0/2895
2	F	0.31	0/1584	0.46	1/2130 (0.0%)
3	G	0.32	0/1585	0.47	0/2143
4	H	0.23	0/1450	0.40	0/1951
5	I	0.18	0/1281	0.45	0/1733
6	J	0.31	0/311	0.49	0/419
7	M	0.31	0/1157	0.35	0/1567
8	N	0.30	0/946	0.37	0/1268
9	O	0.29	0/1091	0.39	0/1457
10	Q	0.31	0/936	0.42	0/1256
11	R	0.27	0/961	0.53	0/1291
12	S	0.30	0/913	0.44	0/1226
13	T	0.33	0/994	0.38	0/1333
14	U	0.31	0/764	0.36	0/1030
15	V	0.30	0/878	0.38	0/1192
16	W	0.31	0/761	0.37	0/1023
17	X	0.27	0/712	0.45	0/952
18	Z	0.30	0/583	0.34	0/782
19	1	0.32	0/473	0.52	0/634
20	2	0.28	0/530	0.48	0/708
21	3	0.35	0/473	0.43	0/635
22	5	0.23	0/427	0.32	0/572
23	6	0.39	0/405	0.84	1/542 (0.2%)
24	7	0.35	0/380	0.38	0/500
25	8	0.26	0/507	0.31	0/672
26	4	0.23	0/372	0.47	0/503
27	A	0.31	0/72677	0.31	0/113395
28	B	0.28	0/2799	0.33	0/4362
29	C	0.16	0/1812	0.35	0/2821
All	All	0.30	0/99915	0.34	2/150992 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	6	50	PRO	CA-N-CD	-9.63	98.52	112.00
2	F	151	ILE	N-CA-C	-6.85	106.82	113.53

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	26	0
2	F	1563	0	1608	33	0
3	G	1562	0	1600	33	0
4	H	1428	0	1457	59	0
5	I	1260	0	1300	66	0
6	J	308	0	323	14	0
7	M	1130	0	1167	21	0
8	N	938	0	1000	11	0
9	O	1078	0	1151	20	0
10	Q	919	0	959	16	0
11	R	951	0	986	37	0
12	S	899	0	926	12	0
13	T	982	0	1033	19	0
14	U	754	0	802	9	0
15	V	864	0	903	10	0
16	W	751	0	797	10	0
17	X	706	0	757	15	0
18	Z	574	0	591	11	0
19	1	465	0	479	16	0
20	2	527	0	538	12	0
21	3	470	0	497	8	0
22	5	423	0	463	9	0
23	6	397	0	407	16	0
24	7	377	0	411	6	0
25	8	502	0	541	8	0
26	4	364	0	352	12	0
27	A	64906	0	32656	883	0
28	B	2502	0	1274	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	C	1622	0	825	31	0
All	All	91332	0	57968	1351	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1351) 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)
27:A:2971:G:H21	27:A:2981:A:N6	1.55	1.04
27:A:1550:G:H1	27:A:1620:U:H3	1.04	1.04
27:A:2086:U:H3	27:A:2096:G:H1	1.01	0.97
27:A:1754:G:H1	27:A:1759:A:H61	1.13	0.97
27:A:2971:G:N2	27:A:2981:A:H62	1.61	0.96
27:A:1754:G:H1	27:A:1759:A:N6	1.63	0.95
27:A:337:U:H3	27:A:344:G:H1	0.99	0.93
27:A:1754:G:N2	27:A:1759:A:N1	2.17	0.92
27:A:334:G:H1	27:A:347:U:H3	1.14	0.91
27:A:2971:G:H21	27:A:2981:A:H62	0.94	0.88
27:A:2674:A:N6	27:A:2725:C:O2	2.10	0.85
4:H:87:ARG:H	4:H:90:MET:HE2	1.42	0.84
29:C:50:U:H3	29:C:64:G:H1	1.26	0.84
27:A:1540:U:H3	27:A:1632:G:H1	1.26	0.82
2:F:160:VAL:HG21	27:A:2842:G:H21	1.42	0.82
18:Z:64:PRO:HB3	27:A:759:G:H1	1.47	0.80
27:A:337:U:O2	27:A:344:G:N2	2.15	0.79
27:A:1755:A:O2'	27:A:1758:G:N2	2.16	0.79
5:I:90:ILE:HD13	5:I:95:TYR:HB2	1.65	0.79
5:I:88:MET:HE3	5:I:89:GLU:H	1.47	0.78
27:A:1542:A:H61	27:A:1628:A:H1'	1.46	0.78
23:6:14:ALA:HB2	23:6:21:ARG:HE	1.47	0.78
27:A:329:U:O2	27:A:446:G:O6	2.01	0.78
27:A:2681:U:H3	27:A:2718:G:H1	1.31	0.78
3:G:34:MET:HE1	9:O:4:ILE:HD12	1.65	0.78
27:A:2386:U:OP1	27:A:2393:A:O2'	2.01	0.78
5:I:57:ASP:OD1	5:I:58:ASP:N	2.18	0.77
27:A:1147:A:N6	27:A:1243:G:O2'	2.17	0.77
4:H:44:ASN:ND2	27:A:2537:C:O4'	2.18	0.77
27:A:326:A:H61	27:A:449:G:H1	1.33	0.77
27:A:365:U:H3	27:A:437:G:H1	1.31	0.77
27:A:747:A:N6	27:A:768:G:O2'	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:2:62:ARG:NH1	20:2:65:GLU:OE2	2.19	0.76
27:A:1996:U:OP2	27:A:2001:A:N6	2.18	0.76
27:A:324:C:N4	27:A:451:U:O4	2.18	0.76
27:A:2756:G:O2'	27:A:2881:A:N1	2.18	0.75
10:Q:10:LEU:HB2	10:Q:17:GLN:HG3	1.68	0.75
27:A:279:U:H3	27:A:307:G:H1	1.34	0.75
1:E:72:LYS:NZ	1:E:101:GLU:OE1	2.18	0.75
27:A:1547:G:H1	27:A:1623:U:H3	0.79	0.75
21:3:38:GLU:OE1	21:3:38:GLU:N	2.18	0.75
27:A:1710:A:N6	27:A:1716:A:OP2	2.20	0.75
27:A:2674:A:OP1	27:A:2721:A:O2'	2.04	0.74
5:I:96:ARG:HH22	5:I:98:GLN:HB3	1.53	0.74
19:1:24:ARG:NH1	27:A:469:G:OP1	2.21	0.74
27:A:1530:G:H21	27:A:1805:G:H22	1.35	0.74
4:H:83:GLN:OE1	4:H:83:GLN:N	2.17	0.74
24:7:38:ARG:HG3	24:7:45:LEU:HD21	1.70	0.74
27:A:1540:U:O4	27:A:1632:G:O6	2.05	0.74
27:A:1533:U:OP2	27:A:1535:C:N4	2.20	0.73
27:A:1556:A:N1	27:A:1615:G:O6	2.22	0.73
27:A:1530:G:N2	27:A:1805:G:H1	1.87	0.73
5:I:104:LEU:HD21	5:I:132:PHE:HE2	1.53	0.73
27:A:2470:A:H2'	27:A:2471:A:H8	1.53	0.73
9:O:89:GLN:N	9:O:89:GLN:OE1	2.21	0.73
27:A:736:G:N2	27:A:739:U:OP2	2.18	0.72
27:A:499:G:OP2	27:A:2630:A:O2'	2.08	0.72
27:A:1532:G:O2'	27:A:1803:A:N1	2.21	0.72
27:A:334:G:N2	27:A:347:U:O2	2.20	0.72
19:1:47:GLN:OE1	19:1:47:GLN:N	2.23	0.72
27:A:217:G:H22	27:A:235:U:H4'	1.54	0.72
27:A:2339:G:H1	27:A:2387:U:H3	1.37	0.71
27:A:2357:A:N7	27:A:2379:G:N2	2.38	0.71
27:A:2883:G:N2	27:A:2886:A:OP2	2.17	0.71
27:A:1530:G:H22	27:A:1805:G:H1	1.37	0.71
3:G:150:GLU:N	3:G:150:GLU:OE1	2.23	0.71
23:6:18:CYS:SG	23:6:20:HIS:NE2	2.64	0.71
3:G:41:GLN:HG2	27:A:709:U:H1'	1.72	0.71
11:R:71:ARG:NH2	28:B:28:A:OP1	2.23	0.71
20:2:9:GLU:OE1	20:2:9:GLU:N	2.22	0.71
4:H:57:ILE:HG13	4:H:91:PRO:HB2	1.73	0.70
27:A:1018:U:O2	27:A:1019:C:N4	2.24	0.70
27:A:1554:U:H2'	27:A:1555:A:C8	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:W:18:GLU:OE2	16:W:18:GLU:N	2.22	0.70
27:A:2343:G:H2'	27:A:2344:G:C8	2.26	0.70
27:A:2372:U:H2'	27:A:2373:G:C8	2.27	0.70
24:7:37:ARG:NH1	24:7:44:ALA:O	2.25	0.70
17:X:4:HIS:NE2	27:A:81:A:OP1	2.25	0.69
27:A:2674:A:N6	27:A:2725:C:C2	2.58	0.69
27:A:2371:G:H2'	27:A:2372:U:C6	2.27	0.69
10:Q:14:SER:HG	27:A:2913:U:HO2'	1.38	0.69
5:I:35:LEU:HB2	5:I:76:LEU:HD13	1.74	0.69
5:I:151:ARG:NH2	27:A:2967:C:O2	2.21	0.69
8:N:93:PRO:HG3	8:N:114:ILE:HG12	1.75	0.69
27:A:2681:U:O4	27:A:2718:G:O6	2.11	0.69
5:I:88:MET:HE2	5:I:163:VAL:HB	1.74	0.69
22:5:16:ARG:NH2	27:A:1379:G:OP1	2.16	0.68
27:A:990:G:O6	27:A:1018:U:O4	2.10	0.68
27:A:1541:G:OP2	27:A:1629:G:N2	2.26	0.68
27:A:2342:A:N6	27:A:2390:U:O2'	2.26	0.68
5:I:58:ASP:O	5:I:63:ARG:NH1	2.26	0.68
27:A:1552:A:N6	27:A:1616:A:OP2	2.26	0.68
4:H:20:ARG:HG2	4:H:35:ILE:HG21	1.74	0.68
7:M:141:GLU:OE2	7:M:141:GLU:N	2.25	0.68
27:A:1547:G:O6	27:A:1623:U:O4	2.11	0.68
5:I:108:LEU:HD11	5:I:153:ARG:HB2	1.76	0.68
27:A:664:A:H3'	27:A:665:G:H8	1.56	0.68
27:A:1541:G:H2'	27:A:1542:A:H8	1.59	0.68
27:A:2394:A:O2'	27:A:2396:A:OP1	2.11	0.68
20:2:9:GLU:HA	20:2:12:GLU:HG2	1.75	0.68
13:T:73:ASP:O	13:T:114:ARG:NH2	2.27	0.67
27:A:2470:A:H2'	27:A:2471:A:C8	2.30	0.67
8:N:112:MET:HA	8:N:112:MET:HE3	1.77	0.67
27:A:567:A:H4'	27:A:568:A:H5'	1.76	0.67
29:C:62:C:H2'	29:C:63:G:H8	1.59	0.67
5:I:150:ARG:HD2	5:I:163:VAL:HG23	1.75	0.67
9:O:97:GLU:N	9:O:97:GLU:OE2	2.27	0.67
18:Z:49:VAL:HG22	18:Z:79:ASN:HB3	1.77	0.67
5:I:98:GLN:HA	5:I:126:VAL:HG11	1.77	0.67
12:S:48:ARG:NH1	12:S:97:TYR:OH	2.26	0.67
19:1:41:ARG:HG2	19:1:43:GLY:H	1.59	0.67
27:A:994:A:OP2	27:A:1014:G:N2	2.21	0.66
15:V:37:GLU:OE1	15:V:37:GLU:N	2.23	0.66
27:A:2323:G:H1	27:A:2412:U:H3	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:8:19:THR:OG1	27:A:745:G:OP1	2.14	0.66
27:A:3078:G:N2	27:A:3081:A:OP2	2.25	0.66
29:C:36:U:H3'	29:C:37:A:H5''	1.76	0.66
27:A:987:A:H2	27:A:1021:G:H22	1.44	0.66
27:A:2333:G:O2'	27:A:2343:G:OP2	2.13	0.66
27:A:470:G:N2	27:A:481:C:N3	2.44	0.66
11:R:126:LYS:N	11:R:126:LYS:HE2	2.11	0.66
19:1:40:THR:OG1	19:1:47:GLN:NE2	2.30	0.65
5:I:120:GLU:OE1	5:I:120:GLU:N	2.24	0.65
11:R:34:GLU:OE1	11:R:34:GLU:N	2.20	0.65
27:A:137:G:H21	27:A:1524:G:H1'	1.61	0.65
14:U:26:LYS:HA	14:U:95:THR:HG23	1.78	0.65
27:A:2364:C:H2'	27:A:2365:A:C8	2.32	0.65
27:A:2878:A:N6	27:A:2890:C:OP2	2.29	0.65
27:A:724:G:N2	27:A:727:A:OP2	2.26	0.65
27:A:2862:G:O2'	27:A:3002:A:N6	2.30	0.65
5:I:108:LEU:HD21	5:I:153:ARG:HD2	1.80	0.64
27:A:1018:U:H1'	27:A:1019:C:H41	1.62	0.64
27:A:2323:G:N2	27:A:2412:U:O2	2.22	0.64
3:G:199:GLU:OE1	3:G:199:GLU:N	2.21	0.64
10:Q:106:ASP:OD2	27:A:1867:G:O2'	2.15	0.64
27:A:1009:U:H2'	27:A:1010:U:C6	2.31	0.64
3:G:160:ARG:NH2	27:A:706:G:O2'	2.30	0.64
27:A:2677:A:O2'	27:A:2796:A:N3	2.31	0.64
26:4:1:MET:HE3	26:4:1:MET:HA	1.77	0.64
27:A:308:U:H2'	27:A:309:G:H8	1.61	0.64
27:A:1544:U:O4	27:A:1626:G:O6	2.16	0.64
27:A:326:A:N6	27:A:449:G:H1	1.96	0.64
27:A:989:G:O6	27:A:990:G:N2	2.31	0.64
27:A:2759:G:H2'	27:A:2760:G:H8	1.63	0.63
27:A:666:A:N6	27:A:2258:U:OP1	2.32	0.63
27:A:1426:G:OP2	27:A:1426:G:N2	2.30	0.63
27:A:1165:G:O2'	27:A:1228:A:N6	2.25	0.63
27:A:3014:A:O2'	27:A:3015:C:H5''	1.98	0.63
1:E:80:ALA:O	1:E:113:GLN:NE2	2.19	0.63
27:A:1229:A:H8	27:A:1230:G:H1'	1.64	0.63
15:V:52:GLU:OE2	15:V:52:GLU:N	2.31	0.63
27:A:1543:A:N1	27:A:1628:A:O2'	2.29	0.62
27:A:1754:G:N1	27:A:1759:A:N6	2.27	0.62
26:4:16:CYS:SG	26:4:17:GLY:N	2.71	0.62
10:Q:70:ILE:HG22	10:Q:72:ASP:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1165:G:HO2'	27:A:1228:A:H61	1.44	0.62
27:A:2482:U:O2'	27:A:2651:C:OP2	2.17	0.62
27:A:1223:U:H2'	27:A:1224:G:H8	1.64	0.62
27:A:2407:C:N4	27:A:2408:G:O6	2.32	0.62
27:A:933:G:N1	27:A:1303:U:OP2	2.25	0.62
27:A:2344:G:O3'	27:A:2391:G:N2	2.32	0.62
29:C:10:G:H2'	29:C:11:A:C8	2.34	0.62
12:S:52:GLY:H	12:S:56:GLU:HG2	1.64	0.62
27:A:664:A:H3'	27:A:665:G:C8	2.35	0.62
27:A:2329:G:O6	27:A:2406:U:O4	2.18	0.62
8:N:108:GLU:CD	8:N:108:GLU:H	2.08	0.61
10:Q:33:ARG:HH12	22:5:51:LEU:HD21	1.64	0.61
27:A:256:A:H2'	27:A:257:A:H8	1.63	0.61
27:A:640:G:O2'	27:A:642:G:OP2	2.15	0.61
27:A:993:G:N1	27:A:1015:A:OP2	2.22	0.61
2:F:5:GLY:HA3	2:F:84:LEU:HD21	1.83	0.61
11:R:90:GLU:HA	11:R:93:LYS:HG2	1.82	0.61
27:A:551:G:N2	27:A:554:A:OP2	2.33	0.61
27:A:2106:A:H3'	27:A:2107:G:H5''	1.82	0.61
27:A:2552:A:H2'	27:A:2553:G:C8	2.36	0.61
27:A:2599:G:N2	27:A:2602:A:OP2	2.31	0.61
27:A:2356:G:H2'	27:A:2380:G:H1	1.64	0.61
27:A:663:A:C5	27:A:2254:A:C6	2.88	0.61
27:A:2254:A:H4'	27:A:2255:A:C8	2.36	0.61
27:A:2329:G:N1	27:A:2406:U:N3	2.48	0.61
27:A:2363:A:H2'	27:A:2364:C:C6	2.36	0.61
27:A:1165:G:H4'	27:A:1166:A:H5'	1.83	0.60
11:R:12:GLU:CD	28:B:60:G:H4'	2.26	0.60
11:R:77:LYS:HB3	11:R:112:ARG:HD3	1.83	0.60
13:T:25:ARG:NH1	27:A:2245:C:OP1	2.34	0.60
23:6:38:ILE:O	23:6:51:HIS:N	2.29	0.60
27:A:1073:G:O2'	27:A:1076:A:N6	2.34	0.60
9:O:80:VAL:HA	9:O:83:ILE:HD12	1.83	0.60
27:A:681:C:H2'	27:A:682:A:H8	1.66	0.60
4:H:168:THR:OG1	4:H:169:ASN:OD1	2.18	0.60
4:H:147:GLU:OE2	26:4:26:SER:OG	2.18	0.60
6:J:23:ASP:N	6:J:23:ASP:OD1	2.34	0.60
15:V:53:PRO:O	15:V:57:VAL:HG23	2.02	0.60
27:A:2902:A:H2'	27:A:2903:A:C8	2.36	0.59
9:O:98:LEU:HD22	9:O:103:LEU:HD12	1.84	0.59
11:R:127:PHE:O	27:A:2601:A:O2'	2.19	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:C:62:C:H2'	29:C:63:G:C8	2.36	0.59
6:J:27:ARG:NH2	27:A:2315:U:OP2	2.33	0.59
27:A:271:A:OP2	27:A:314:G:N2	2.33	0.59
2:F:88:ASP:N	2:F:88:ASP:OD1	2.34	0.59
27:A:2279:C:N4	27:A:2724:U:H1'	2.18	0.59
27:A:2381:A:H4'	27:A:2382:G:O5'	2.02	0.59
1:E:200:GLU:OE1	1:E:200:GLU:N	2.31	0.59
4:H:15:TYR:HA	4:H:19:ILE:HB	1.84	0.59
4:H:55:LYS:HD2	4:H:55:LYS:O	2.03	0.59
20:2:36:MET:HE2	20:2:41:LEU:HD21	1.84	0.59
23:6:9:PRO:HD2	23:6:27:LYS:O	2.03	0.59
27:A:2211:C:H2'	27:A:2212:A:H8	1.66	0.59
5:I:39:GLU:OE1	5:I:39:GLU:N	2.35	0.59
27:A:994:A:H5''	27:A:1014:G:H21	1.68	0.59
27:A:2538:A:H2'	27:A:2539:G:H8	1.68	0.59
27:A:543:U:H3'	27:A:544:U:H5''	1.83	0.59
9:O:56:PRO:HD2	9:O:59:MET:HE3	1.83	0.58
13:T:83:LEU:HD22	13:T:88:VAL:HG11	1.85	0.58
27:A:176:G:OP2	27:A:176:G:N2	2.26	0.58
27:A:543:U:H5	27:A:561:G:H5'	1.68	0.58
4:H:126:PRO:HB2	4:H:174:ARG:NH1	2.18	0.58
11:R:68:ALA:HA	11:R:71:ARG:HB2	1.86	0.58
1:E:244:ARG:NH2	27:A:2463:G:OP1	2.28	0.58
4:H:126:PRO:HB2	4:H:174:ARG:HH12	1.68	0.58
29:C:23:C:H2'	29:C:24:U:C6	2.38	0.58
23:6:37:GLU:HG2	23:6:52:LYS:HD2	1.86	0.58
27:A:2902:A:H2'	27:A:2903:A:H8	1.68	0.58
2:F:19:GLU:N	2:F:19:GLU:OE2	2.35	0.58
10:Q:82:GLU:N	10:Q:82:GLU:OE2	2.36	0.58
17:X:24:LEU:HD12	17:X:25:VAL:HG23	1.85	0.58
27:A:284:G:H1'	27:A:303:G:C2	2.38	0.58
27:A:718:C:O2'	27:A:772:U:OP1	2.20	0.58
27:A:90:C:H2'	27:A:91:C:O4'	2.04	0.58
27:A:3055:G:H2'	27:A:3100:A:H61	1.68	0.58
27:A:1758:G:H2'	27:A:1759:A:C8	2.39	0.58
27:A:329:U:O2	27:A:446:G:C6	2.57	0.57
27:A:2249:G:H2'	27:A:2250:A:C8	2.39	0.57
5:I:96:ARG:NH1	5:I:98:GLN:OE1	2.37	0.57
10:Q:42:ARG:NH2	27:A:3038:C:OP1	2.37	0.57
27:A:72:G:H22	27:A:108:A:H2	1.51	0.57
27:A:138:A:H2'	27:A:139:U:O2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1500:A:O2'	27:A:1511:U:O2	2.22	0.57
27:A:2465:A:H2'	27:A:2466:G:C8	2.39	0.57
29:C:10:G:H2'	29:C:11:A:H8	1.69	0.57
7:M:13:ARG:NH1	7:M:49:ASP:O	2.37	0.57
27:A:1381:G:O2'	27:A:2236:G:O6	2.22	0.57
27:A:1675:U:O2'	27:A:1676:G:N7	2.36	0.57
27:A:1710:A:H61	27:A:1716:A:H5''	1.69	0.57
28:B:67:A:H4'	28:B:68:G:H5'	1.85	0.57
27:A:654:U:H1'	27:A:664:A:H1'	1.85	0.57
27:A:1076:A:HO2'	27:A:2681:U:HO2'	1.49	0.57
27:A:2751:C:H2'	27:A:2752:U:O4'	2.05	0.57
27:A:2764:C:O2'	27:A:2964:A:N3	2.31	0.57
7:M:71:LYS:NZ	27:A:1140:G:OP1	2.36	0.57
27:A:857:U:H2'	27:A:858:A:C8	2.40	0.57
5:I:119:PRO:HD2	5:I:122:ILE:HD11	1.87	0.57
19:1:28:ARG:NH1	19:1:30:ASN:OD1	2.37	0.57
5:I:39:GLU:OE1	5:I:40:PRO:HD3	2.04	0.57
24:7:27:THR:HG23	24:7:30:GLY:H	1.70	0.57
27:A:2671:G:O4'	27:A:2725:C:N4	2.37	0.57
7:M:34:THR:HG23	7:M:39:LYS:HB2	1.86	0.57
21:3:39:ASP:OD1	21:3:44:ARG:HD3	2.05	0.57
27:A:339:U:H2'	27:A:340:A:C8	2.40	0.57
27:A:1640:A:H2'	27:A:1642:G:N7	2.20	0.57
27:A:2682:G:H21	27:A:2683:A:H61	1.53	0.57
27:A:789:G:H2'	27:A:919:A:H61	1.70	0.56
27:A:2224:C:O2'	27:A:2913:U:OP2	2.22	0.56
25:8:47:ARG:NH2	27:A:724:G:OP1	2.37	0.56
27:A:191:G:OP2	27:A:191:G:N2	2.28	0.56
27:A:990:G:N2	27:A:1018:U:O2	2.28	0.56
3:G:58:VAL:HG21	3:G:80:ARG:HB3	1.85	0.56
15:V:69:GLU:OE2	15:V:69:GLU:N	2.38	0.56
27:A:389:G:N1	27:A:392:A:OP2	2.35	0.56
27:A:1025:A:N3	27:A:2488:C:O2'	2.34	0.56
27:A:1105:C:O2'	27:A:1118:A:N3	2.35	0.56
27:A:1705:C:H2'	27:A:1706:A:H8	1.69	0.56
27:A:935:A:H4'	27:A:951:G:N2	2.20	0.56
1:E:108:PRO:HD2	1:E:111:LEU:HD22	1.86	0.56
18:Z:11:ARG:O	18:Z:14:ARG:NH1	2.38	0.56
27:A:857:U:H2'	27:A:858:A:H8	1.70	0.56
27:A:1614:G:H2'	27:A:1615:G:H8	1.69	0.56
27:A:2286:A:N7	27:A:2727:A:N6	2.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2686:U:H2'	27:A:2687:U:C6	2.40	0.56
29:C:35:A:H2'	29:C:36:U:C6	2.41	0.56
7:M:98:THR:HB	7:M:124:VAL:HG23	1.88	0.56
27:A:357:U:H4'	27:A:358:G:O5'	2.06	0.56
27:A:2366:C:H2'	27:A:2367:G:O4'	2.06	0.56
27:A:2467:U:H2'	27:A:2468:U:C6	2.41	0.56
29:C:9:G:O2'	29:C:10:G:N7	2.37	0.56
4:H:67:ILE:O	4:H:109:ARG:NH2	2.38	0.56
27:A:1396:G:H2'	27:A:1397:U:C6	2.39	0.56
27:A:986:G:C2	27:A:987:A:H1'	2.39	0.56
29:C:43:A:H2'	29:C:44:A:C8	2.41	0.56
21:3:21:GLU:OE1	21:3:24:ARG:NH1	2.39	0.55
27:A:1476:G:H2'	27:A:1477:C:C6	2.41	0.55
27:A:2386:U:OP1	27:A:2394:A:H5''	2.06	0.55
28:B:41:U:N3	28:B:45:G:OP2	2.37	0.55
27:A:586:U:H2'	27:A:587:G:O4'	2.06	0.55
27:A:1122:C:H2'	27:A:1129:G:H2'	1.88	0.55
27:A:2384:C:H5''	27:A:2387:U:O4	2.06	0.55
16:W:68:ARG:NH2	27:A:1449:C:OP1	2.40	0.55
27:A:2343:G:H1	27:A:2401:U:H3	1.53	0.55
27:A:2457:U:H2'	27:A:2458:G:H8	1.70	0.55
29:C:21:A:O2'	29:C:46:A:N6	2.38	0.55
21:3:13:ILE:HD11	27:A:1107:G:C8	2.42	0.55
3:G:4:LYS:NZ	3:G:17:SER:HB3	2.22	0.55
13:T:33:ARG:NH2	27:A:672:C:OP1	2.39	0.55
15:V:90:LYS:HB3	15:V:102:ARG:HD2	1.88	0.55
27:A:242:G:O2'	27:A:254:G:O6	2.22	0.55
4:H:147:GLU:HA	26:4:28:LYS:HE3	1.88	0.55
9:O:32:THR:HG22	9:O:35:ARG:H	1.70	0.55
27:A:1706:A:H2'	27:A:1707:G:H8	1.72	0.55
27:A:2922:U:H2'	27:A:2923:C:C6	2.42	0.55
27:A:1690:A:H2'	27:A:1691:A:C8	2.42	0.55
27:A:2385:G:OP2	27:A:2387:U:N3	2.38	0.55
4:H:76:ARG:HH21	28:B:42:C:H42	1.53	0.55
27:A:1729:A:H2'	27:A:1731:A:C8	2.42	0.55
11:R:9:ASN:ND2	28:B:59:A:N3	2.55	0.55
27:A:2870:C:OP2	27:A:2956:G:O2'	2.23	0.55
27:A:3022:G:H2'	27:A:3023:G:O4'	2.06	0.55
28:B:10:G:O2'	28:B:11:U:OP1	2.21	0.55
27:A:265:A:N1	27:A:515:U:O2'	2.35	0.54
27:A:1236:G:H2'	27:A:1237:U:O4'	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1612:U:H2'	27:A:1613:G:H8	1.71	0.54
27:A:3071:A:N7	27:A:3089:A:O2'	2.39	0.54
2:F:89:GLU:HA	2:F:92:VAL:HG12	1.89	0.54
4:H:45:MET:HE1	4:H:157:ARG:HD2	1.89	0.54
18:Z:11:ARG:NH2	18:Z:12:ASN:OD1	2.41	0.54
3:G:179:SER:OG	3:G:181:ASP:OD1	2.21	0.54
16:W:62:ARG:NH2	27:A:1455:U:OP2	2.40	0.54
27:A:858:A:O2'	27:A:1877:U:OP1	2.25	0.54
27:A:1758:G:H2'	27:A:1759:A:H8	1.71	0.54
4:H:81:ILE:O	4:H:86:LEU:N	2.40	0.54
5:I:57:ASP:OD1	5:I:59:GLU:N	2.38	0.54
5:I:128:SER:HB2	5:I:131:LYS:HG2	1.88	0.54
27:A:1087:G:H2'	27:A:1088:U:C6	2.41	0.54
27:A:2088:C:H2'	27:A:2089:C:C6	2.43	0.54
27:A:2356:G:H2'	27:A:2380:G:H22	1.73	0.54
27:A:2528:G:H22	27:A:2536:U:H3	1.54	0.54
29:C:18:G:H5''	29:C:58:A:H2	1.71	0.54
22:5:4:PRO:HG2	27:A:2240:U:O2	2.07	0.54
4:H:10:ARG:NE	26:4:22:PHE:HZ	2.06	0.54
4:H:128:GLN:O	27:A:2527:G:O2'	2.24	0.54
11:R:90:GLU:OE1	11:R:90:GLU:N	2.37	0.54
27:A:920:G:N2	27:A:944:A:OP1	2.40	0.54
27:A:1099:A:OP2	27:A:1100:C:N4	2.34	0.54
28:B:81:U:H2'	28:B:82:A:C8	2.43	0.54
27:A:1684:C:H2'	27:A:1685:G:H8	1.73	0.54
29:C:44:A:H2'	29:C:45:G:O4'	2.07	0.54
1:E:86:PRO:HG3	27:A:1787:A:H2'	1.90	0.54
2:F:139:HIS:NE2	27:A:1888:C:O2	2.38	0.54
2:F:158:GLY:HA2	27:A:2276:G:O2'	2.07	0.54
27:A:2682:G:O2'	27:A:2684:U:O4	2.25	0.54
27:A:3034:C:H2'	27:A:3035:C:H6	1.73	0.54
3:G:206:SER:O	3:G:210:LYS:HB3	2.06	0.54
27:A:81:A:N1	27:A:96:G:O2'	2.37	0.54
27:A:337:U:O4	27:A:344:G:O6	2.26	0.54
27:A:1534:C:H3'	27:A:1535:C:O2	2.08	0.54
27:A:3020:U:H1'	27:A:3022:G:O6	2.08	0.54
23:6:8:ARG:HA	23:6:27:LYS:O	2.08	0.54
27:A:444:U:H5'	27:A:446:G:H4'	1.89	0.54
27:A:1284:A:H2'	27:A:1285:G:H8	1.72	0.54
27:A:2457:U:H2'	27:A:2458:G:C8	2.43	0.54
27:A:1553:C:H5'	27:A:1554:U:C5	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1611:A:H2'	27:A:1612:U:C6	2.43	0.53
27:A:2465:A:H2'	27:A:2466:G:H8	1.73	0.53
28:B:86:A:H2'	28:B:88:C:OP2	2.08	0.53
20:2:7:PRO:HA	20:2:10:LEU:HB3	1.90	0.53
27:A:2086:U:H2'	27:A:2087:C:C6	2.43	0.53
27:A:2675:A:OP1	27:A:2721:A:N6	2.41	0.53
29:C:11:A:H2'	29:C:12:G:C8	2.43	0.53
26:4:14:VAL:HB	26:4:22:PHE:HB3	1.89	0.53
27:A:2248:C:H2'	27:A:2249:G:H8	1.74	0.53
1:E:66:ASP:OD2	1:E:103:ARG:NH1	2.42	0.53
27:A:997:G:H2'	27:A:998:G:C8	2.43	0.53
27:A:1703:G:H2'	27:A:1704:U:C6	2.43	0.53
27:A:1804:G:H2'	27:A:1805:G:C8	2.43	0.53
3:G:23:GLU:OE1	3:G:23:GLU:N	2.28	0.53
9:O:125:THR:HG23	9:O:145:THR:HG23	1.90	0.53
13:T:26:GLY:O	13:T:30:ARG:NH1	2.41	0.53
27:A:2474:G:O2'	27:A:2720:C:OP1	2.21	0.53
27:A:2815:C:H2'	27:A:2816:G:H8	1.72	0.53
8:N:17:LYS:HE3	8:N:47:ILE:HG13	1.89	0.53
13:T:97:GLU:OE2	13:T:101:SER:OG	2.27	0.53
26:4:13:THR:HA	26:4:22:PHE:O	2.09	0.53
27:A:625:A:N6	27:A:647:G:O2'	2.41	0.53
27:A:2729:G:H2'	27:A:2800:G:N1	2.24	0.53
5:I:144:GLN:OE1	27:A:2968:G:N2	2.42	0.53
27:A:298:G:O2'	27:A:299:G:O4'	2.20	0.53
27:A:351:G:O6	27:A:444:U:O2	2.27	0.53
27:A:994:A:H5''	27:A:1014:G:N2	2.23	0.53
27:A:1704:U:H2'	27:A:1705:C:C6	2.44	0.53
27:A:1922:G:H2'	27:A:1923:G:H8	1.72	0.53
29:C:14:A:C6	29:C:22:G:C5	2.97	0.53
4:H:149:ASP:O	4:H:153:ILE:HG23	2.08	0.53
5:I:150:ARG:NE	5:I:163:VAL:O	2.42	0.53
19:1:60:LYS:HA	19:1:60:LYS:HE2	1.90	0.53
27:A:2074:G:O6	27:A:2075:G:N1	2.41	0.53
1:E:132:PRO:HA	1:E:190:ARG:HA	1.91	0.52
11:R:48:HIS:ND1	11:R:64:SER:OG	2.33	0.52
11:R:73:ILE:HD12	11:R:73:ILE:H	1.73	0.52
27:A:883:G:H22	27:A:1494:U:H1'	1.74	0.52
27:A:1001:C:C5	27:A:1002:C:H1'	2.44	0.52
27:A:1673:A:H5''	27:A:1674:G:H5''	1.92	0.52
27:A:2515:U:H2'	27:A:2516:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2879:G:O2'	27:A:2888:G:O6	2.22	0.52
27:A:316:U:O2'	27:A:317:G:OP1	2.26	0.52
27:A:928:U:H2'	27:A:929:C:C6	2.45	0.52
6:J:8:GLU:OE1	6:J:14:ALA:HA	2.09	0.52
13:T:119:GLU:OE1	13:T:119:GLU:N	2.33	0.52
27:A:1541:G:H1	27:A:1631:A:H62	1.58	0.52
27:A:2376:G:H2'	27:A:2377:G:H8	1.75	0.52
27:A:2819:G:N2	27:A:2822:A:OP2	2.32	0.52
28:B:50:C:H2'	28:B:51:G:H8	1.75	0.52
19:1:57:LYS:NZ	27:A:488:G:N7	2.49	0.52
27:A:1921:G:H2'	27:A:1922:G:H8	1.74	0.52
27:A:2750:G:H2'	27:A:2751:C:C6	2.45	0.52
2:F:85:ARG:NH1	27:A:2861:U:H5''	2.24	0.52
27:A:247:G:OP2	27:A:249:C:N4	2.39	0.52
27:A:296:A:N1	27:A:340:A:N6	2.58	0.52
27:A:2374:U:H2'	27:A:2375:G:H8	1.73	0.52
3:G:163:GLU:OE1	3:G:164:VAL:N	2.41	0.52
6:J:12:LEU:HD12	6:J:19:VAL:HG11	1.92	0.52
13:T:37:GLU:OE2	27:A:1367:G:N1	2.36	0.52
17:X:24:LEU:HD23	17:X:36:GLU:HG2	1.90	0.52
27:A:2378:U:H2'	27:A:2379:G:H8	1.75	0.52
4:H:61:ILE:HD12	4:H:72:PRO:HG2	1.92	0.52
23:6:36:LEU:HD23	23:6:37:GLU:N	2.25	0.52
27:A:114:G:OP2	27:A:116:A:O2'	2.25	0.52
23:6:20:HIS:HB2	23:6:22:ASN:OD1	2.09	0.52
27:A:351:G:O6	27:A:444:U:C2	2.63	0.52
27:A:392:A:C4	27:A:394:G:C8	2.98	0.52
27:A:1559:A:H2'	27:A:1560:U:C6	2.45	0.52
27:A:1621:C:H2'	27:A:1622:G:H8	1.74	0.52
27:A:1756:G:H1'	27:A:1758:G:C6	2.45	0.52
28:B:5:C:OP1	28:B:62:C:O2'	2.27	0.52
7:M:65:SER:OG	27:A:1259:U:OP2	2.19	0.52
20:2:5:THR:OG1	20:2:9:GLU:OE2	2.23	0.52
27:A:256:A:H2'	27:A:257:A:C8	2.43	0.52
27:A:782:U:H2'	27:A:783:G:O4'	2.09	0.52
27:A:2872:G:H2'	27:A:2873:U:C6	2.45	0.52
27:A:639:C:O2'	27:A:640:G:H8	1.93	0.51
27:A:681:C:H2'	27:A:682:A:C8	2.45	0.51
27:A:1621:C:H2'	27:A:1622:G:C8	2.45	0.51
5:I:117:GLU:OE2	5:I:118:ALA:N	2.43	0.51
5:I:140:GLN:NE2	27:A:2969:C:O2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:27:G:H2'	27:A:28:C:C6	2.46	0.51
27:A:1076:A:O2'	27:A:2681:U:O2'	2.21	0.51
27:A:1624:U:O2'	27:A:1625:G:N7	2.40	0.51
27:A:1790:A:H2'	27:A:1791:A:C8	2.44	0.51
27:A:2096:G:H2'	27:A:2097:G:H8	1.75	0.51
17:X:75:ASP:OD2	17:X:100:THR:OG1	2.26	0.51
27:A:636:U:H5''	27:A:637:G:C4	2.45	0.51
27:A:3020:U:O2'	27:A:3021:A:O5'	2.24	0.51
11:R:37:ARG:NH2	11:R:54:ASP:OD1	2.41	0.51
25:8:59:ASN:O	25:8:63:ASN:ND2	2.43	0.51
27:A:974:G:H4'	27:A:975:U:O5'	2.11	0.51
27:A:1540:U:C4	27:A:1632:G:O6	2.63	0.51
27:A:1544:U:C4	27:A:1626:G:O6	2.64	0.51
27:A:30:U:O4	27:A:534:G:O2'	2.22	0.51
27:A:1529:U:H3'	27:A:1530:G:C8	2.46	0.51
27:A:2176:A:N3	27:A:2784:C:O2'	2.37	0.51
27:A:3019:C:H2'	27:A:3020:U:O4'	2.11	0.51
5:I:5:GLY:HA2	5:I:70:ARG:HB2	1.92	0.51
27:A:966:U:H2'	27:A:967:G:H8	1.75	0.51
27:A:1435:C:C5	27:A:1444:U:H5''	2.45	0.51
27:A:1609:G:H2'	27:A:1610:C:C6	2.45	0.51
16:W:95:LEU:O	16:W:95:LEU:HD12	2.10	0.51
22:5:7:ARG:NH1	27:A:671:G:O2'	2.44	0.51
27:A:747:A:H2'	27:A:748:U:O4'	2.11	0.51
27:A:1294:U:H2'	27:A:1295:U:C6	2.45	0.51
28:B:10:G:O2'	28:B:11:U:H5'	2.11	0.51
27:A:473:C:O2'	27:A:476:G:N2	2.43	0.51
28:B:37:C:N4	28:B:50:C:O2	2.43	0.51
5:I:46:ALA:HB2	5:I:52:VAL:HG23	1.93	0.51
5:I:97:VAL:HG22	5:I:106:PHE:HD2	1.76	0.51
27:A:362:A:H2'	27:A:363:A:H8	1.75	0.51
27:A:1127:A:N3	27:A:1272:C:O2'	2.42	0.51
15:V:104:ARG:NH1	27:A:2237:A:H5'	2.26	0.51
27:A:996:G:H2'	27:A:997:G:C8	2.46	0.51
2:F:188:GLU:H	2:F:188:GLU:CD	2.14	0.50
27:A:277:U:H2'	27:A:278:A:C8	2.46	0.50
27:A:356:G:H5''	27:A:357:U:OP1	2.11	0.50
27:A:429:A:H2'	27:A:430:A:C8	2.46	0.50
27:A:2170:U:H2'	27:A:2171:C:C6	2.46	0.50
27:A:3005:A:H5''	27:A:3006:G:H5'	1.93	0.50
27:A:326:A:N1	27:A:449:G:N2	2.57	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:347:U:H2'	27:A:348:G:H8	1.77	0.50
14:U:12:LYS:NZ	27:A:1112:C:O2	2.42	0.50
27:A:991:C:H2'	27:A:992:C:C6	2.47	0.50
4:H:76:ARG:HE	28:B:42:C:H42	1.59	0.50
19:1:36:VAL:HG22	19:1:63:ARG:HH21	1.76	0.50
27:A:363:A:H2'	27:A:364:A:O4'	2.11	0.50
1:E:60:ARG:HA	27:A:1788:G:H5'	1.92	0.50
27:A:1076:A:H2'	27:A:1077:A:C8	2.47	0.50
18:Z:18:ALA:HB1	27:A:2495:G:OP1	2.12	0.50
27:A:1148:G:O6	27:A:1243:G:N2	2.45	0.50
1:E:271:ARG:NH2	27:A:2016:G:OP2	2.44	0.50
11:R:34:GLU:HG2	11:R:35:VAL:HG23	1.93	0.50
20:2:14:THR:OG1	20:2:15:ASP:N	2.44	0.50
27:A:665:G:N2	27:A:2255:A:OP1	2.45	0.50
27:A:1551:U:H3'	27:A:1552:A:C8	2.46	0.50
27:A:2671:G:C8	27:A:2724:U:H3'	2.47	0.50
1:E:181:GLU:HG3	1:E:271:ARG:HA	1.94	0.50
3:G:30:ASN:O	3:G:34:MET:HG3	2.12	0.50
6:J:4:ILE:HD11	6:J:16:GLY:HA2	1.94	0.50
9:O:77:VAL:HG11	27:A:730:G:N1	2.27	0.50
12:S:19:PHE:O	12:S:49:ARG:NH1	2.45	0.50
27:A:1556:A:N1	27:A:1615:G:C6	2.80	0.50
27:A:1938:G:N1	27:A:1955:A:OP2	2.38	0.50
27:A:2603:G:H2'	27:A:2604:U:C6	2.47	0.50
5:I:19:ILE:HG12	5:I:24:LEU:HG	1.94	0.50
8:N:30:ARG:HG3	27:A:2898:G:H4'	1.92	0.50
19:1:48:ARG:NH1	19:1:48:ARG:HB2	2.27	0.50
25:8:45:ASP:OD1	25:8:46:GLY:N	2.45	0.50
27:A:217:G:N2	27:A:235:U:H4'	2.26	0.50
27:A:2275:A:H8	27:A:2275:A:OP2	1.94	0.50
27:A:2752:U:O2'	27:A:2754:G:OP1	2.24	0.50
19:1:36:VAL:HG13	19:1:63:ARG:HE	1.77	0.49
27:A:2:A:H2'	27:A:3:A:C8	2.47	0.49
27:A:502:C:H2'	27:A:503:A:H8	1.76	0.49
27:A:1146:A:OP2	27:A:1244:A:N6	2.28	0.49
27:A:2029:A:H2'	27:A:2030:C:C6	2.47	0.49
27:A:2279:C:H41	27:A:2724:U:H1'	1.77	0.49
27:A:2342:A:C2	27:A:2392:A:H2'	2.47	0.49
27:A:2366:C:H3'	27:A:2367:G:C8	2.47	0.49
5:I:5:GLY:HA2	5:I:70:ARG:CB	2.41	0.49
5:I:46:ALA:N	5:I:50:ALA:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:92:GLY:HA3	5:I:95:TYR:HE2	1.78	0.49
18:Z:14:ARG:NH2	27:A:2503:G:N7	2.60	0.49
18:Z:41:ARG:NE	18:Z:41:ARG:HA	2.27	0.49
25:8:50:VAL:HG11	25:8:58:ILE:HD12	1.94	0.49
27:A:139:U:H2'	27:A:140:G:O4'	2.12	0.49
9:O:80:VAL:HG22	9:O:114:GLY:HA2	1.94	0.49
14:U:27:LEU:H	14:U:95:THR:HG21	1.77	0.49
27:A:356:G:H4'	27:A:358:G:C5	2.47	0.49
27:A:543:U:C5	27:A:561:G:H5'	2.47	0.49
28:B:46:A:C4	28:B:47:A:C8	3.00	0.49
2:F:13:MET:HG2	2:F:27:THR:HG23	1.93	0.49
27:A:2752:U:H3'	27:A:2754:G:C8	2.47	0.49
15:V:23:LYS:NZ	27:A:2236:G:N7	2.61	0.49
27:A:1003:A:H2'	27:A:1003:A:OP1	2.12	0.49
27:A:2420:U:H1'	27:A:2421:A:C8	2.47	0.49
27:A:2738:U:H2'	27:A:2739:C:C6	2.47	0.49
27:A:2873:U:H2'	27:A:2874:C:C6	2.48	0.49
27:A:564:G:N1	27:A:567:A:OP2	2.44	0.49
27:A:971:G:H2'	27:A:972:A:C8	2.47	0.49
27:A:1609:G:H2'	27:A:1610:C:H6	1.75	0.49
27:A:1791:A:H2'	27:A:1792:A:C8	2.48	0.49
27:A:2654:A:H5'	27:A:2655:U:OP2	2.13	0.49
29:C:53:G:O2'	29:C:54:U:O5'	2.22	0.49
1:E:273:ARG:HB3	1:E:273:ARG:CZ	2.43	0.49
5:I:22:GLN:NE2	5:I:38:ALA:O	2.46	0.49
5:I:104:LEU:HD22	5:I:124:PHE:CG	2.48	0.49
13:T:68:ALA:O	13:T:72:ASN:ND2	2.44	0.49
27:A:285:U:H3'	27:A:286:G:H4'	1.94	0.49
27:A:298:G:H22	27:A:338:C:N4	2.10	0.49
27:A:2800:G:O2'	27:A:2803:C:OP2	2.22	0.49
29:C:63:G:H2'	29:C:64:G:C8	2.47	0.49
17:X:35:VAL:HB	17:X:38:VAL:HG22	1.94	0.49
27:A:987:A:H2'	27:A:988:U:H5'	1.94	0.49
27:A:2327:C:H2'	27:A:2328:G:C8	2.47	0.49
27:A:2364:C:H2'	27:A:2365:A:H8	1.78	0.49
21:3:28:LEU:HD23	21:3:35:VAL:HG22	1.94	0.49
27:A:270:U:C2'	27:A:271:A:H5'	2.42	0.49
27:A:362:A:H2'	27:A:363:A:C8	2.48	0.49
27:A:2288:C:H2'	27:A:2289:C:H6	1.78	0.49
1:E:141:VAL:HG13	1:E:162:SER:HB2	1.94	0.49
10:Q:8:PRO:HG2	27:A:1870:U:C5	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:V:72:ASP:OD1	15:V:74:SER:OG	2.27	0.49
23:6:39:LYS:HA	23:6:50:PRO:HA	1.95	0.49
25:8:3:LYS:HG3	27:A:242:G:C8	2.48	0.49
27:A:349:G:H2'	27:A:350:A:H8	1.78	0.49
27:A:1224:G:H2'	27:A:1225:G:H8	1.77	0.49
27:A:1610:C:H2'	27:A:1611:A:C8	2.48	0.49
27:A:1690:A:H2'	27:A:1691:A:H8	1.78	0.49
27:A:2255:A:N3	27:A:2679:G:H1'	2.28	0.49
27:A:2777:G:C2	27:A:2807:G:H1'	2.48	0.49
27:A:3023:G:H2'	27:A:3024:A:O4'	2.12	0.49
4:H:76:ARG:HH21	28:B:42:C:N4	2.10	0.48
27:A:1158:U:H2'	27:A:1159:C:C6	2.47	0.48
27:A:2088:C:H2'	27:A:2089:C:C5	2.47	0.48
27:A:2761:U:H2'	27:A:2762:C:O4'	2.13	0.48
29:C:20:U:H2'	29:C:20:U:OP2	2.13	0.48
27:A:61:G:H2'	27:A:62:G:H8	1.78	0.48
27:A:2759:G:H2'	27:A:2760:G:C8	2.46	0.48
12:S:13:ARG:NH1	12:S:80:ILE:O	2.44	0.48
27:A:282:A:C6	27:A:305:G:C6	3.02	0.48
27:A:1537:U:H2'	27:A:1538:G:C8	2.48	0.48
27:A:1622:G:C2	27:A:1623:U:C5	3.01	0.48
27:A:2294:A:H2'	27:A:2295:C:C6	2.48	0.48
27:A:2672:A:H5'	27:A:2673:U:H2'	1.94	0.48
27:A:2778:U:H2'	27:A:2779:U:C6	2.47	0.48
27:A:88:A:H1'	27:A:89:A:C8	2.47	0.48
27:A:1002:C:H2'	27:A:1003:A:H3'	1.96	0.48
27:A:2043:C:O2'	27:A:2195:U:OP2	2.32	0.48
2:F:83:GLU:OE2	27:A:2859:C:O2'	2.28	0.48
13:T:36:LYS:NZ	27:A:1367:G:N7	2.60	0.48
26:4:26:SER:OG	26:4:27:THR:N	2.46	0.48
27:A:801:U:H2'	27:A:903:A:N1	2.29	0.48
27:A:1398:G:N2	27:A:1401:A:OP2	2.46	0.48
10:Q:20:LEU:HD11	27:A:1392:G:H4'	1.95	0.48
27:A:89:A:O2'	27:A:90:C:OP1	2.28	0.48
27:A:539:C:N4	27:A:542:A:OP2	2.32	0.48
27:A:1165:G:HO2'	27:A:1228:A:N6	2.06	0.48
27:A:2336:U:N3	27:A:2337:A:N7	2.61	0.48
27:A:2387:U:H3'	27:A:2388:G:C8	2.49	0.48
27:A:2388:G:C2	27:A:2389:U:H1'	2.49	0.48
27:A:2682:G:H21	27:A:2683:A:N6	2.11	0.48
5:I:104:LEU:HD22	5:I:124:PHE:CD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:94:GLU:OE1	7:M:95:LYS:NZ	2.45	0.48
16:W:10:ILE:HD12	16:W:37:SER:HB3	1.94	0.48
27:A:1535:C:H2'	27:A:1536:A:O4'	2.13	0.48
5:I:104:LEU:HD21	5:I:132:PHE:CE2	2.40	0.48
27:A:1002:C:H2'	27:A:1003:A:H5''	1.95	0.48
27:A:1476:G:H2'	27:A:1477:C:H6	1.78	0.48
2:F:38:ARG:C	2:F:39:ILE:HD13	2.39	0.48
27:A:988:U:O2'	27:A:990:G:O4'	2.32	0.48
27:A:1150:A:H2	27:A:1240:G:H1	1.62	0.48
27:A:1500:A:C4	27:A:1518:A:C2	3.02	0.48
27:A:1528:G:H2'	27:A:1529:U:C6	2.49	0.48
27:A:1612:U:H2'	27:A:1613:G:C8	2.49	0.48
27:A:2361:U:H3	27:A:2376:G:H1	1.61	0.48
17:X:91:THR:OG1	17:X:93:LYS:HG2	2.14	0.48
27:A:294:G:O6	27:A:342:C:N4	2.43	0.48
27:A:990:G:H1	27:A:1018:U:H3	0.69	0.48
27:A:1332:G:C6	27:A:1347:G:C6	3.02	0.48
27:A:2075:G:HO2'	27:A:2107:G:H1	0.62	0.48
27:A:2703:U:OP1	27:A:2761:U:O2'	2.31	0.48
27:A:2738:U:H2'	27:A:2739:C:H6	1.79	0.48
29:C:58:A:O2'	29:C:60:U:OP2	2.30	0.48
2:F:151:ILE:HG12	27:A:2275:A:H4'	1.96	0.47
4:H:100:GLY:H	4:H:103:MET:HE2	1.79	0.47
27:A:188:G:O6	27:A:204:G:O2'	2.29	0.47
27:A:735:U:H2'	27:A:736:G:O4'	2.14	0.47
27:A:1015:A:H2'	27:A:1016:C:O4'	2.12	0.47
27:A:2265:U:H2'	27:A:2266:A:C8	2.49	0.47
27:A:2363:A:N6	27:A:2375:G:O6	2.47	0.47
28:B:107:A:H2'	28:B:108:C:C6	2.49	0.47
1:E:225:VAL:HG11	27:A:2005:C:H5''	1.95	0.47
2:F:130:HIS:HB3	2:F:165:ARG:NH1	2.29	0.47
27:A:563:U:H4'	27:A:597:C:H5'	1.95	0.47
27:A:678:A:N1	27:A:924:G:O2'	2.40	0.47
27:A:738:A:O2'	27:A:740:A:OP1	2.32	0.47
27:A:2107:G:H4'	27:A:2107:G:OP1	2.13	0.47
27:A:3117:U:H2'	27:A:3118:U:C6	2.49	0.47
11:R:98:GLU:OE2	11:R:98:GLU:HA	2.14	0.47
27:A:263:G:H2'	27:A:264:G:O4'	2.14	0.47
27:A:601:A:H2'	27:A:602:A:H8	1.78	0.47
27:A:671:G:C2	27:A:1377:A:C5	3.02	0.47
27:A:979:G:H2'	27:A:980:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:993:G:N2	27:A:1015:A:O5'	2.44	0.47
27:A:998:G:N2	27:A:1010:U:H3	2.11	0.47
27:A:1541:G:H1	27:A:1631:A:N6	2.11	0.47
27:A:1656:A:H2'	27:A:1657:G:H8	1.79	0.47
27:A:2170:U:H2'	27:A:2171:C:H6	1.78	0.47
27:A:2353:U:N3	27:A:2354:G:O6	2.46	0.47
4:H:136:THR:HG21	27:A:2527:G:H21	1.79	0.47
5:I:89:GLU:HA	5:I:131:LYS:HA	1.97	0.47
27:A:1377:A:C6	27:A:1378:U:C4	3.03	0.47
27:A:1541:G:H22	27:A:1631:A:N6	2.12	0.47
27:A:2351:A:N3	27:A:2396:A:O2'	2.47	0.47
27:A:2622:C:H2'	27:A:2623:A:H8	1.80	0.47
27:A:2968:G:N7	27:A:2979:C:H1'	2.29	0.47
7:M:49:ASP:OD1	7:M:49:ASP:N	2.37	0.47
20:2:23:ARG:O	20:2:27:GLU:HG3	2.15	0.47
27:A:376:G:C5	27:A:426:G:C2	3.02	0.47
27:A:502:C:H2'	27:A:503:A:C8	2.49	0.47
27:A:2752:U:H3'	27:A:2754:G:H8	1.79	0.47
2:F:148:PRO:O	27:A:2735:U:O2'	2.30	0.47
27:A:1229:A:C8	27:A:1230:G:H1'	2.48	0.47
27:A:1523:U:H2'	27:A:1524:G:C8	2.50	0.47
27:A:1533:U:O2	27:A:1803:A:O2'	2.23	0.47
27:A:2299:C:OP2	27:A:2462:G:N2	2.45	0.47
2:F:56:GLU:HA	2:F:56:GLU:OE2	2.15	0.47
3:G:210:LYS:HB2	3:G:210:LYS:HE2	1.74	0.47
5:I:153:ARG:HE	5:I:154:ARG:H	1.63	0.47
19:1:45:ASN:OD1	19:1:45:ASN:N	2.47	0.47
20:2:53:GLU:O	20:2:57:VAL:HG23	2.15	0.47
27:A:429:A:H2'	27:A:430:A:H8	1.79	0.47
27:A:2096:G:H2'	27:A:2097:G:C8	2.49	0.47
27:A:2351:A:H2'	27:A:2352:C:C6	2.49	0.47
27:A:2739:C:H2'	27:A:2740:G:H8	1.79	0.47
27:A:2750:G:H1	27:A:2761:U:H3	1.63	0.47
27:A:3057:U:H2'	27:A:3058:A:C8	2.50	0.47
29:C:34:C:H2'	29:C:35:A:C8	2.49	0.47
3:G:139:LYS:NZ	27:A:401:C:OP2	2.36	0.47
3:G:154:VAL:HG23	3:G:193:ASP:HB2	1.95	0.47
3:G:192:ASP:OD1	9:O:5:LYS:NZ	2.45	0.47
19:1:41:ARG:HG3	19:1:42:PRO:HD2	1.96	0.47
27:A:159:A:N3	27:A:2431:C:O2'	2.46	0.47
27:A:2070:A:H2'	27:A:2071:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:108:ALA:HB1	3:G:112:ARG:NH1	2.29	0.47
4:H:76:ARG:NH2	28:B:42:C:N3	2.62	0.47
27:A:279:U:H2'	27:A:280:G:H8	1.80	0.47
27:A:990:G:O2'	27:A:991:C:OP2	2.29	0.47
5:I:30:LYS:HA	5:I:30:LYS:HD2	1.58	0.47
11:R:36:PRO:HG2	11:R:51:LEU:HD12	1.97	0.47
11:R:43:SER:O	11:R:112:ARG:NH2	2.37	0.47
27:A:543:U:H3'	27:A:544:U:C5'	2.45	0.47
27:A:1337:G:N2	27:A:1340:A:OP2	2.44	0.47
27:A:3057:U:H2'	27:A:3058:A:H8	1.80	0.47
5:I:126:VAL:HG22	5:I:132:PHE:HB2	1.97	0.46
27:A:1146:A:N3	27:A:2710:G:O2'	2.41	0.46
27:A:1630:U:H2'	27:A:1631:A:C8	2.50	0.46
27:A:1630:U:H2'	27:A:1631:A:H8	1.80	0.46
27:A:1885:G:N2	27:A:2216:G:OP2	2.42	0.46
27:A:2363:A:C6	27:A:2375:G:C6	3.03	0.46
27:A:2673:U:O3'	27:A:2674:A:H8	1.98	0.46
7:M:91:GLU:HA	7:M:94:GLU:HG2	1.95	0.46
10:Q:87:TYR:OH	10:Q:116:VAL:O	2.33	0.46
11:R:42:ARG:HA	11:R:47:ILE:HG13	1.96	0.46
11:R:83:ARG:O	11:R:87:LEU:HD13	2.15	0.46
18:Z:15:ASP:OD1	18:Z:16:SER:N	2.45	0.46
27:A:1825:C:N4	27:A:1840:G:OP2	2.29	0.46
27:A:2330:U:H3'	27:A:2331:U:C5	2.51	0.46
27:A:2363:A:H2'	27:A:2364:C:H6	1.77	0.46
27:A:2552:A:H2'	27:A:2553:G:H8	1.77	0.46
18:Z:12:ASN:HD21	27:A:2501:G:H3'	1.80	0.46
19:1:7:ILE:HG21	19:1:60:LYS:HG3	1.97	0.46
27:A:277:U:H2'	27:A:278:A:H8	1.79	0.46
27:A:844:G:O2'	27:A:878:G:H4'	2.15	0.46
27:A:929:C:H1'	27:A:1339:G:N2	2.30	0.46
27:A:1119:A:H2'	27:A:1120:G:O4'	2.15	0.46
27:A:1806:A:H2'	27:A:1807:C:C6	2.50	0.46
27:A:2580:G:H2'	27:A:2581:G:O4'	2.15	0.46
7:M:45:THR:OG1	13:T:64:ARG:NH2	2.48	0.46
12:S:14:ASP:OD1	12:S:15:ASP:N	2.49	0.46
14:U:25:GLU:OE2	27:A:1111:G:N2	2.46	0.46
22:5:4:PRO:HA	27:A:2839:U:C2	2.51	0.46
27:A:487:U:H2'	27:A:488:G:O4'	2.15	0.46
27:A:977:G:H2'	27:A:978:A:O4'	2.15	0.46
27:A:1536:A:H2'	27:A:1537:U:C6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2329:G:H2'	27:A:2330:U:C6	2.51	0.46
28:B:63:U:H2'	28:B:64:G:H8	1.80	0.46
2:F:188:GLU:OE1	2:F:188:GLU:N	2.29	0.46
7:M:72:LYS:NZ	27:A:1257:G:H5''	2.31	0.46
27:A:1244:A:H4'	27:A:1245:U:O4'	2.15	0.46
27:A:1509:U:H2'	27:A:1510:A:O4'	2.15	0.46
27:A:1523:U:H2'	27:A:1524:G:H8	1.80	0.46
27:A:2019:A:H2'	27:A:2020:A:C8	2.50	0.46
12:S:82:HIS:CE1	12:S:84:ASP:HB2	2.50	0.46
27:A:278:A:H2'	27:A:279:U:O4'	2.16	0.46
27:A:587:G:N1	27:A:590:A:OP2	2.42	0.46
27:A:1167:C:H1'	27:A:1231:U:H4'	1.96	0.46
27:A:2901:G:H2'	27:A:2902:A:H8	1.80	0.46
27:A:3043:G:H2'	27:A:3044:A:H5''	1.96	0.46
2:F:170:MET:HG2	2:F:171:GLY:N	2.30	0.46
10:Q:33:ARG:NH1	22:5:51:LEU:HD21	2.29	0.46
27:A:220:A:H2	27:A:266:U:H5''	1.81	0.46
27:A:967:G:H2'	27:A:968:C:H6	1.81	0.46
27:A:1922:G:H2'	27:A:1923:G:C8	2.50	0.46
27:A:2085:C:O2'	27:A:2086:U:O4'	2.34	0.46
2:F:144:VAL:HA	2:F:147:ARG:HD3	1.97	0.46
4:H:80:SER:N	4:H:88:GLU:OE2	2.49	0.46
9:O:31:LYS:O	9:O:31:LYS:HG2	2.15	0.46
17:X:82:ARG:NH2	27:A:382:A:OP2	2.49	0.46
27:A:166:A:H2'	27:A:167:G:O4'	2.15	0.46
27:A:1659:U:H2'	27:A:1660:A:H8	1.81	0.46
27:A:1705:C:H2'	27:A:1706:A:C8	2.50	0.46
27:A:2417:C:H2'	27:A:2418:U:O4'	2.16	0.46
27:A:2538:A:H2'	27:A:2539:G:C8	2.49	0.46
27:A:2815:C:N4	27:A:2816:G:O6	2.48	0.46
28:B:24:G:H2'	28:B:25:G:C8	2.50	0.46
29:C:26:G:HO2'	29:C:27:U:P	2.39	0.46
10:Q:8:PRO:HG2	27:A:1870:U:C4	2.50	0.46
17:X:73:VAL:HG11	17:X:105:ILE:HD13	1.97	0.46
27:A:308:U:H2'	27:A:309:G:C8	2.46	0.46
27:A:844:G:H4'	27:A:878:G:H5'	1.96	0.46
27:A:2678:G:N3	27:A:2678:G:H2'	2.31	0.46
29:C:37:A:H4'	29:C:37:A:OP1	2.16	0.46
17:X:37:GLY:HA2	17:X:40:ARG:NH2	2.31	0.46
27:A:34:C:H2'	27:A:35:A:C8	2.51	0.46
27:A:995:U:H2'	27:A:996:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:998:G:H2'	27:A:999:C:C6	2.51	0.46
27:A:1100:C:H5''	27:A:1101:A:OP1	2.17	0.46
27:A:1284:A:H2'	27:A:1285:G:C8	2.50	0.46
27:A:2330:U:H3'	27:A:2331:U:C6	2.50	0.46
27:A:2888:G:O5'	27:A:2888:G:H8	1.99	0.46
2:F:27:THR:OG1	2:F:196:GLY:O	2.28	0.45
2:F:160:VAL:HG21	27:A:2842:G:N2	2.21	0.45
15:V:38:GLU:O	15:V:42:ILE:HG13	2.16	0.45
27:A:443:C:H2'	27:A:444:U:O4'	2.16	0.45
27:A:621:U:H2'	27:A:622:C:C6	2.50	0.45
27:A:3118:U:H2'	27:A:3119:A:C8	2.51	0.45
28:B:63:U:H2'	28:B:64:G:C8	2.52	0.45
1:E:243:GLY:HA3	27:A:2821:G:H5''	1.98	0.45
5:I:126:VAL:HA	5:I:132:PHE:HB2	1.98	0.45
22:5:14:ARG:HB3	27:A:13:G:H5''	1.97	0.45
27:A:264:G:H4'	27:A:516:G:H22	1.81	0.45
27:A:546:G:O2'	27:A:557:G:O6	2.34	0.45
27:A:947:U:H2'	27:A:948:G:C8	2.51	0.45
27:A:1529:U:H3'	27:A:1530:G:H8	1.81	0.45
27:A:1630:U:O4	27:A:1631:A:N6	2.49	0.45
27:A:2374:U:H2'	27:A:2375:G:C8	2.51	0.45
27:A:2758:A:H2'	27:A:2759:G:O4'	2.16	0.45
9:O:34:GLY:HA2	27:A:1305:G:H5''	1.97	0.45
11:R:76:ASP:OD1	11:R:77:LYS:N	2.42	0.45
27:A:655:G:H22	27:A:670:A:H2	1.63	0.45
27:A:665:G:O2'	27:A:666:A:O5'	2.29	0.45
27:A:1437:A:N1	27:A:1448:C:O2'	2.44	0.45
27:A:1611:A:H2'	27:A:1612:U:H6	1.81	0.45
27:A:1639:G:H5'	27:A:1640:A:OP1	2.16	0.45
27:A:2712:U:H2'	27:A:2713:G:C8	2.51	0.45
29:C:11:A:H2'	29:C:12:G:H8	1.81	0.45
11:R:55:LEU:HD12	11:R:55:LEU:H	1.82	0.45
12:S:48:ARG:HB2	12:S:95:LYS:HG2	1.99	0.45
19:1:48:ARG:HB2	19:1:48:ARG:HH11	1.80	0.45
27:A:5:U:C2	27:A:6:G:C8	3.04	0.45
27:A:929:C:H1'	27:A:1339:G:H21	1.82	0.45
27:A:1679:A:H4'	27:A:1679:A:OP1	2.16	0.45
27:A:2084:A:H2'	27:A:2085:C:O4'	2.16	0.45
27:A:2366:C:H3'	27:A:2367:G:H8	1.82	0.45
3:G:4:LYS:HZ3	3:G:17:SER:HB3	1.80	0.45
4:H:44:ASN:HD21	27:A:2536:U:H2'	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:27:ARG:HG2	6:J:28:ASN:OD1	2.17	0.45
11:R:41:ASN:ND2	28:B:7:G:O3'	2.45	0.45
13:T:12:LYS:O	13:T:16:THR:HG23	2.16	0.45
14:U:79:LYS:NZ	27:A:1108:A:N1	2.65	0.45
16:W:69:THR:N	16:W:72:GLY:O	2.45	0.45
27:A:307:G:H2'	27:A:308:U:C6	2.52	0.45
27:A:789:G:C4	27:A:919:A:N6	2.84	0.45
27:A:1008:G:C2	27:A:1009:U:C4	3.03	0.45
27:A:1468:A:H2'	27:A:1469:A:C8	2.52	0.45
27:A:1650:G:H2'	27:A:1651:C:C6	2.52	0.45
29:C:26:G:H1	29:C:45:G:H21	1.64	0.45
1:E:233:HIS:NE2	1:E:246:PRO:HA	2.32	0.45
4:H:111:ILE:HD13	4:H:115:LEU:HD12	1.98	0.45
17:X:37:GLY:HA2	17:X:40:ARG:HH21	1.81	0.45
19:1:33:ILE:CG2	19:1:50:ASN:HB3	2.46	0.45
27:A:388:U:H2'	27:A:389:G:O4'	2.17	0.45
27:A:690:G:C6	27:A:776:G:C6	3.05	0.45
27:A:2086:U:H2'	27:A:2087:C:H6	1.81	0.45
27:A:2510:A:H4'	27:A:2511:A:O4'	2.16	0.45
27:A:2545:G:H5'	27:A:2546:A:OP2	2.16	0.45
3:G:108:ALA:HB1	3:G:112:ARG:HH11	1.81	0.45
3:G:165:GLY:O	3:G:169:VAL:HG22	2.17	0.45
5:I:45:ARG:HA	5:I:51:ILE:HG22	1.98	0.45
7:M:7:LYS:H	7:M:10:ASP:CG	2.24	0.45
11:R:73:ILE:HG22	11:R:75:GLY:H	1.81	0.45
27:A:577:G:C5	27:A:1399:A:C2	3.05	0.45
27:A:818:U:H2'	27:A:819:G:O4'	2.17	0.45
27:A:1377:A:C4	27:A:1378:U:C5	3.04	0.45
27:A:1554:U:H2'	27:A:1555:A:H8	1.77	0.45
27:A:2729:G:H2'	27:A:2800:G:H1	1.82	0.45
1:E:206:TRP:HE3	1:E:211:ARG:HE	1.64	0.45
4:H:128:GLN:HB2	4:H:135:TYR:CE1	2.51	0.45
5:I:3:ARG:O	5:I:6:LYS:HG2	2.17	0.45
11:R:83:ARG:HA	11:R:86:GLN:OE1	2.16	0.45
16:W:12:LEU:HA	20:2:33:ARG:NH1	2.31	0.45
16:W:24:ILE:HD11	16:W:96:PHE:CD2	2.52	0.45
27:A:218:A:N3	27:A:234:U:O2'	2.38	0.45
27:A:290:C:N4	27:A:300:G:H21	2.15	0.45
27:A:672:C:H2'	27:A:673:C:C6	2.51	0.45
27:A:736:G:N2	27:A:738:A:H3'	2.32	0.45
27:A:1396:G:H2'	27:A:1397:U:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1854:U:H2'	27:A:1855:A:H8	1.81	0.45
27:A:2074:G:N2	27:A:2110:U:O4	2.50	0.45
27:A:2356:G:H21	27:A:2381:A:N6	2.14	0.45
27:A:3024:A:H2'	27:A:3025:G:H8	1.81	0.45
3:G:67:ARG:HH21	3:G:71:THR:HA	1.82	0.45
7:M:91:GLU:OE1	7:M:91:GLU:N	2.49	0.45
27:A:988:U:H4'	27:A:989:G:OP1	2.17	0.45
27:A:1250:U:H3'	27:A:1251:A:H5''	1.98	0.45
27:A:2857:A:H2'	27:A:2858:G:H8	1.82	0.45
27:A:3014:A:N6	27:A:3113:A:OP2	2.49	0.45
3:G:152:LYS:HE3	3:G:152:LYS:HB2	1.83	0.45
5:I:30:LYS:HG2	5:I:81:THR:O	2.17	0.45
10:Q:14:SER:OG	27:A:2913:U:O2'	2.17	0.45
18:Z:32:LYS:HB3	27:A:759:G:C6	2.52	0.45
27:A:356:G:H4'	27:A:358:G:C6	2.52	0.45
27:A:460:G:O2'	27:A:488:G:O6	2.29	0.45
27:A:740:A:O2'	27:A:741:G:OP2	2.27	0.45
27:A:1628:A:H2	27:A:1631:A:C2	2.35	0.44
27:A:2094:G:O2'	27:A:2095:G:H8	2.00	0.44
27:A:2563:G:H2'	27:A:2564:A:H8	1.82	0.44
27:A:2581:G:OP2	27:A:2581:G:H8	1.99	0.44
27:A:2693:A:C6	27:A:2706:A:C8	3.05	0.44
27:A:2771:U:H2'	27:A:2772:G:H8	1.82	0.44
4:H:132:THR:HG22	4:H:132:THR:O	2.18	0.44
27:A:1937:U:H2'	27:A:1938:G:O4'	2.17	0.44
27:A:2338:G:H4'	27:A:2388:G:H22	1.82	0.44
27:A:2548:U:H5''	27:A:2549:G:H5''	2.00	0.44
27:A:3045:C:H2'	27:A:3046:C:O4'	2.17	0.44
1:E:222:ARG:HD2	27:A:2044:U:OP2	2.18	0.44
3:G:156:VAL:HG12	3:G:158:ILE:HG23	1.99	0.44
5:I:97:VAL:O	5:I:129:PRO:HA	2.18	0.44
6:J:10:GLU:HG3	6:J:11:HIS:ND1	2.31	0.44
7:M:45:THR:HG22	7:M:47:ASN:H	1.82	0.44
13:T:119:GLU:H	13:T:119:GLU:CD	2.24	0.44
27:A:978:A:H2'	27:A:979:G:H8	1.81	0.44
27:A:1154:G:C6	27:A:1238:G:C6	3.06	0.44
27:A:1656:A:H2'	27:A:1657:G:C8	2.52	0.44
27:A:2681:U:C4	27:A:2718:G:O6	2.70	0.44
28:B:92:G:H2'	28:B:93:U:C6	2.52	0.44
2:F:104:GLU:OE1	2:F:104:GLU:N	2.35	0.44
5:I:84:TYR:N	5:I:136:GLY:O	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:O:89:GLN:H	9:O:89:GLN:CD	2.22	0.44
27:A:301:U:C2	27:A:338:C:H5'	2.53	0.44
27:A:636:U:H5''	27:A:637:G:N9	2.33	0.44
27:A:662:G:C5	27:A:2254:A:N6	2.85	0.44
27:A:934:A:OP2	27:A:1302:G:N2	2.38	0.44
27:A:935:A:H4'	27:A:951:G:H22	1.82	0.44
27:A:984:U:C2	27:A:985:G:C8	3.06	0.44
27:A:2288:C:H2'	27:A:2289:C:C6	2.53	0.44
27:A:2471:A:H2'	27:A:2472:C:H6	1.82	0.44
28:B:47:A:C5	28:B:48:C:C5	3.06	0.44
5:I:35:LEU:HD22	5:I:36:ASP:H	1.82	0.44
21:3:40:ASN:O	21:3:44:ARG:HG2	2.17	0.44
27:A:947:U:H2'	27:A:948:G:H8	1.81	0.44
27:A:967:G:H2'	27:A:968:C:C6	2.53	0.44
27:A:1016:C:H2'	27:A:1017:G:O4'	2.17	0.44
27:A:1074:A:H2	27:A:2682:G:H4'	1.82	0.44
27:A:1549:G:O2'	27:A:1550:G:O5'	2.35	0.44
27:A:1550:G:O6	27:A:1620:U:O4	2.36	0.44
29:C:63:G:H2'	29:C:64:G:H8	1.83	0.44
3:G:61:GLY:HA3	3:G:80:ARG:HG2	2.00	0.44
4:H:12:LYS:HE3	4:H:104:TRP:NE1	2.32	0.44
5:I:2:SER:N	27:A:2973:A:H5'	2.32	0.44
6:J:5:LEU:HD22	6:J:9:VAL:HG11	2.00	0.44
11:R:25:LEU:HD11	11:R:103:ASP:OD1	2.17	0.44
11:R:125:LEU:HD23	11:R:125:LEU:HA	1.71	0.44
27:A:248:G:H5'	27:A:250:G:N7	2.33	0.44
27:A:324:C:O2	27:A:452:G:N2	2.50	0.44
27:A:2844:C:C4	27:A:2845:G:N7	2.86	0.44
28:B:29:C:O2'	28:B:60:G:N2	2.50	0.44
28:B:45:G:N2	28:B:49:C:C2	2.86	0.44
4:H:130:ASP:HB3	27:A:2527:G:O4'	2.18	0.44
4:H:171:ALA:O	4:H:174:ARG:HG2	2.18	0.44
27:A:215:A:C8	27:A:520:A:N6	2.86	0.44
27:A:298:G:H22	27:A:338:C:H42	1.65	0.44
27:A:747:A:H2	27:A:768:G:H21	1.66	0.44
27:A:1018:U:H1'	27:A:1019:C:N4	2.29	0.44
27:A:1326:G:H1'	27:A:1352:A:N6	2.33	0.44
27:A:2443:U:H2'	27:A:2444:C:C6	2.53	0.44
27:A:2581:G:H2'	27:A:2583:C:OP2	2.18	0.44
2:F:157:PRO:HG2	2:F:159:ARG:HG2	1.99	0.44
3:G:6:ASP:OD1	3:G:6:ASP:N	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Q:45:ARG:HB2	10:Q:46:PRO:HD3	2.00	0.44
14:U:7:VAL:O	14:U:13:GLN:HA	2.18	0.44
18:Z:75:ARG:HD2	27:A:2558:C:N4	2.33	0.44
27:A:72:G:N3	27:A:72:G:H2'	2.32	0.44
27:A:996:G:H2'	27:A:997:G:H8	1.82	0.44
27:A:2344:G:H4'	27:A:2391:G:H22	1.82	0.44
27:A:2613:G:H5''	27:A:2614:U:O4'	2.18	0.44
27:A:2876:C:N3	27:A:2893:G:N1	2.65	0.44
2:F:132:PHE:HE1	2:F:165:ARG:CZ	2.31	0.44
12:S:51:GLY:HA2	12:S:56:GLU:CD	2.43	0.44
25:8:24:ARG:NH2	27:A:2585:U:OP1	2.50	0.44
27:A:1013:U:N3	27:A:1014:G:H1'	2.33	0.44
27:A:2249:G:H2'	27:A:2250:A:H8	1.80	0.44
27:A:2531:G:H5'	27:A:2532:G:C8	2.53	0.44
27:A:2569:G:N3	27:A:2605:C:H2'	2.32	0.44
27:A:2729:G:O2'	27:A:2730:U:O5'	2.35	0.44
27:A:2878:A:N1	27:A:2889:A:H5''	2.33	0.44
27:A:3036:C:C4	27:A:3037:C:C5	3.06	0.44
28:B:75:U:C2	28:B:76:G:C8	3.06	0.44
2:F:104:GLU:H	2:F:104:GLU:CD	2.25	0.43
2:F:113:ASP:OD1	2:F:178:GLN:HA	2.18	0.43
4:H:40:LYS:HD2	4:H:99:ARG:NH2	2.33	0.43
27:A:685:G:N3	27:A:685:G:H2'	2.33	0.43
27:A:1001:C:C6	27:A:1002:C:H1'	2.53	0.43
27:A:1295:U:H2'	27:A:1296:G:H8	1.82	0.43
27:A:1738:G:C2	27:A:1739:A:C8	3.06	0.43
27:A:2815:C:H2'	27:A:2816:G:C8	2.51	0.43
27:A:3053:U:O4	27:A:3104:A:H5''	2.18	0.43
27:A:3070:G:O2'	27:A:3087:G:N2	2.51	0.43
28:B:1:G:C6	28:B:117:A:N1	2.86	0.43
4:H:75:ARG:HH21	4:H:78:ARG:HH22	1.66	0.43
4:H:110:LEU:HD12	4:H:114:ALA:HB3	2.00	0.43
4:H:126:PRO:O	4:H:174:ARG:NH1	2.46	0.43
5:I:147:ALA:O	5:I:151:ARG:HG3	2.17	0.43
14:U:16:VAL:HB	14:U:99:VAL:HG21	2.00	0.43
17:X:88:ASP:OD1	17:X:93:LYS:N	2.51	0.43
27:A:150:C:H2'	27:A:151:A:H8	1.82	0.43
27:A:222:A:O2'	27:A:508:G:N3	2.41	0.43
27:A:751:A:H2'	27:A:752:C:C6	2.53	0.43
27:A:790:A:N3	27:A:2667:C:O2'	2.42	0.43
27:A:978:A:H2'	27:A:979:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2755:A:H2	27:A:2882:C:O2	2.01	0.43
29:C:2:G:C2	29:C:72:A:C2	3.06	0.43
5:I:127:GLU:OE1	5:I:127:GLU:N	2.47	0.43
13:T:18:LEU:HA	13:T:18:LEU:HD23	1.81	0.43
27:A:306:U:H2'	27:A:307:G:H8	1.83	0.43
27:A:356:G:H4'	27:A:358:G:C4	2.53	0.43
27:A:580:G:H2'	27:A:581:G:O4'	2.19	0.43
27:A:1645:G:H2'	27:A:1646:U:C6	2.53	0.43
27:A:2777:G:N3	27:A:2807:G:H1'	2.33	0.43
1:E:37:LEU:HD13	1:E:62:TYR:HB2	2.00	0.43
8:N:63:VAL:HG23	8:N:64:ARG:HG3	2.00	0.43
11:R:9:ASN:OD1	11:R:10:ILE:N	2.51	0.43
11:R:85:GLY:O	11:R:88:ILE:HG22	2.19	0.43
24:7:18:VAL:O	24:7:23:LEU:HD22	2.18	0.43
27:A:583:G:C5	27:A:584:A:C8	3.06	0.43
27:A:666:A:N6	27:A:2257:A:H4'	2.34	0.43
27:A:844:G:H5'	27:A:845:C:H5''	2.00	0.43
27:A:1025:A:H2'	27:A:1026:A:C8	2.53	0.43
27:A:1528:G:H2'	27:A:1529:U:H6	1.83	0.43
27:A:1640:A:O2'	27:A:1641:U:OP1	2.36	0.43
27:A:2964:A:H2'	27:A:2965:A:C8	2.53	0.43
1:E:273:ARG:HB3	1:E:273:ARG:NH1	2.32	0.43
2:F:157:PRO:HB3	27:A:1248:U:H3	1.84	0.43
4:H:158:GLY:C	4:H:159:MET:HG3	2.42	0.43
5:I:39:GLU:CD	5:I:40:PRO:HD3	2.43	0.43
24:7:21:PHE:HB2	24:7:46:THR:HG21	2.01	0.43
27:A:270:U:H1'	27:A:512:G:N2	2.33	0.43
27:A:273:A:H62	27:A:313:G:H21	1.66	0.43
27:A:813:C:O2'	27:A:849:A:N6	2.49	0.43
27:A:1556:A:C2	27:A:1615:G:N1	2.86	0.43
27:A:1706:A:H2'	27:A:1707:G:C8	2.52	0.43
27:A:1733:C:H2'	27:A:1734:C:H6	1.83	0.43
27:A:2357:A:H2	27:A:2382:G:O4'	2.01	0.43
27:A:2759:G:N3	27:A:2760:G:C8	2.87	0.43
28:B:4:A:H4'	28:B:63:U:H4'	2.01	0.43
28:B:50:C:H2'	28:B:51:G:C8	2.53	0.43
5:I:91:PHE:CE1	5:I:164:ARG:HB2	2.54	0.43
27:A:6:G:H2'	27:A:2853:C:H42	1.83	0.43
27:A:356:G:N2	27:A:357:U:O4	2.51	0.43
27:A:668:U:H2'	27:A:669:G:C8	2.52	0.43
27:A:2093:G:HO2'	27:A:2094:G:H8	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2254:A:H4'	27:A:2255:A:N7	2.33	0.43
27:A:2394:A:H5'	27:A:2396:A:N7	2.34	0.43
27:A:2692:A:P	27:A:2700:A:H61	2.42	0.43
2:F:113:ASP:N	2:F:209:ARG:O	2.48	0.43
5:I:88:MET:HB3	5:I:132:PHE:CE1	2.54	0.43
27:A:347:U:H2'	27:A:348:G:C8	2.53	0.43
27:A:639:C:O2'	27:A:640:G:O5'	2.34	0.43
27:A:663:A:C6	27:A:2254:A:C6	3.07	0.43
27:A:1939:U:H3	27:A:1955:A:H62	1.66	0.43
27:A:2471:A:H2'	27:A:2472:C:C6	2.54	0.43
29:C:72:A:H3'	29:C:73:A:H5''	2.01	0.43
5:I:9:VAL:HG11	5:I:74:ALA:HB2	2.00	0.43
11:R:47:ILE:HD13	11:R:116:LEU:HD23	2.01	0.43
17:X:8:THR:O	17:X:74:VAL:HG12	2.17	0.43
27:A:161:U:H4'	27:A:162:A:OP1	2.18	0.43
27:A:361:A:N1	27:A:440:U:O2'	2.49	0.43
27:A:1378:U:C4	27:A:1379:G:C6	3.06	0.43
27:A:1471:G:H2'	27:A:1472:C:C6	2.53	0.43
27:A:1485:C:H2'	27:A:1486:G:O4'	2.19	0.43
27:A:1896:A:C4	27:A:1897:A:C8	3.07	0.43
27:A:2074:G:H21	27:A:2109:A:H62	1.65	0.43
27:A:2338:G:H4'	27:A:2388:G:N2	2.33	0.43
27:A:2385:G:O2'	27:A:2387:U:O4'	2.34	0.43
27:A:2971:G:O6	27:A:2979:C:H5''	2.19	0.43
1:E:158:SER:HB3	1:E:161:VAL:HG21	2.01	0.43
27:A:764:U:H2'	27:A:765:G:C8	2.54	0.43
27:A:1302:G:O5'	27:A:1302:G:H8	2.00	0.43
27:A:1703:G:H2'	27:A:1704:U:H6	1.83	0.43
27:A:2328:G:C6	27:A:2408:G:N1	2.86	0.43
27:A:2425:U:O2'	27:A:2427:G:OP1	2.29	0.43
27:A:2716:U:H2'	27:A:2717:U:C6	2.54	0.43
27:A:3115:A:C2	27:A:3116:C:C2	3.07	0.43
6:J:25:TYR:HE2	6:J:30:LEU:HD21	1.84	0.43
6:J:31:LEU:N	6:J:32:PRO:HD2	2.33	0.43
7:M:36:LEU:O	7:M:51:GLY:HA3	2.19	0.43
27:A:89:A:HO2'	27:A:90:C:P	2.40	0.43
27:A:1223:U:H2'	27:A:1224:G:C8	2.49	0.43
27:A:1900:C:OP2	27:A:1917:G:N2	2.41	0.43
27:A:2003:A:H1'	27:A:2162:A:N6	2.34	0.43
27:A:2968:G:OP2	27:A:2979:C:N4	2.52	0.43
27:A:3052:A:O2'	27:A:3105:C:OP1	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:8:LEU:HB3	4:H:13:GLN:HE21	1.83	0.42
11:R:73:ILE:HD12	11:R:73:ILE:N	2.33	0.42
14:U:67:HIS:ND1	14:U:95:THR:HG22	2.34	0.42
27:A:1906:U:O2'	27:A:1918:A:N7	2.46	0.42
27:A:2373:G:H2'	27:A:2374:U:C6	2.53	0.42
27:A:2622:C:H2'	27:A:2623:A:C8	2.54	0.42
29:C:72:A:H2'	29:C:73:A:O4'	2.19	0.42
4:H:182:PHE:HA	4:H:183:PRO:HD3	1.83	0.42
7:M:113:LYS:HE2	27:A:616:A:OP1	2.19	0.42
13:T:77:ASN:OD1	13:T:78:ARG:N	2.52	0.42
27:A:453:U:H2'	27:A:454:U:C6	2.54	0.42
27:A:660:U:N3	27:A:663:A:OP2	2.33	0.42
27:A:1118:A:H2'	27:A:1119:A:C8	2.54	0.42
27:A:2851:G:O2'	27:A:3005:A:N1	2.37	0.42
27:A:2873:U:H2'	27:A:2874:C:H6	1.83	0.42
4:H:74:VAL:O	28:B:42:C:N4	2.52	0.42
5:I:75:ASN:HD21	27:A:2971:G:P	2.40	0.42
8:N:24:VAL:HG12	8:N:30:ARG:HD3	2.00	0.42
8:N:110:LYS:HA	8:N:110:LYS:HD2	1.75	0.42
16:W:48:LYS:HE2	16:W:48:LYS:HB2	1.74	0.42
21:3:15:ALA:O	21:3:20:ARG:NH1	2.53	0.42
22:5:31:SER:HB2	22:5:36:GLN:OE1	2.19	0.42
27:A:21:G:H2'	27:A:22:U:C6	2.55	0.42
27:A:27:G:H2'	27:A:28:C:H6	1.84	0.42
27:A:1233:A:H2'	27:A:1234:U:O4'	2.18	0.42
27:A:2188:G:O2'	27:A:2191:C:OP2	2.20	0.42
27:A:2394:A:H3'	27:A:2396:A:C8	2.53	0.42
13:T:89:GLU:OE2	13:T:89:GLU:HA	2.20	0.42
27:A:692:C:H2'	27:A:693:G:H8	1.84	0.42
27:A:2401:U:H2'	27:A:2402:C:C6	2.55	0.42
3:G:13:LYS:C	3:G:13:LYS:HD2	2.45	0.42
5:I:77:VAL:HA	5:I:80:VAL:HG22	2.02	0.42
27:A:639:C:HO2'	27:A:640:G:C5'	2.31	0.42
27:A:646:U:H2'	27:A:647:G:O4'	2.19	0.42
27:A:680:U:H2'	27:A:681:C:C6	2.55	0.42
27:A:2211:C:H2'	27:A:2212:A:C8	2.52	0.42
27:A:2562:G:C2	27:A:2563:G:C8	3.07	0.42
4:H:92:ILE:HD13	4:H:92:ILE:HA	1.92	0.42
5:I:120:GLU:H	5:I:120:GLU:CD	2.22	0.42
9:O:55:MET:HE2	9:O:55:MET:HB2	1.93	0.42
11:R:67:GLU:OE2	11:R:67:GLU:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:X:1:MET:SD	17:X:28:PRO:HA	2.60	0.42
23:6:11:ILE:HD12	23:6:11:ILE:O	2.20	0.42
23:6:15:CYS:SG	23:6:16:GLU:N	2.93	0.42
25:8:34:GLU:HB2	27:A:2644:C:OP1	2.20	0.42
27:A:175:G:H3'	27:A:176:G:N2	2.34	0.42
27:A:618:C:OP1	27:A:653:G:N1	2.51	0.42
27:A:828:G:H2'	27:A:829:U:C6	2.54	0.42
27:A:911:U:H2'	27:A:912:C:C6	2.55	0.42
27:A:1158:U:H2'	27:A:1159:C:H6	1.84	0.42
27:A:1296:G:H2'	27:A:1297:G:C8	2.54	0.42
27:A:1437:A:C2	27:A:1438:G:C8	3.08	0.42
27:A:1501:C:H2'	27:A:1502:G:C8	2.54	0.42
27:A:1791:A:H2'	27:A:1792:A:H8	1.84	0.42
27:A:2098:U:H2'	27:A:2099:G:O4'	2.20	0.42
27:A:2238:A:H2'	27:A:2239:A:C8	2.54	0.42
27:A:2359:G:N1	27:A:2379:G:H1'	2.34	0.42
27:A:2901:G:H2'	27:A:2902:A:C8	2.54	0.42
28:B:110:G:H2'	28:B:111:C:C6	2.55	0.42
5:I:140:GLN:HE21	27:A:2983:G:H22	1.67	0.42
8:N:108:GLU:CD	8:N:108:GLU:N	2.76	0.42
11:R:4:LYS:HA	11:R:4:LYS:HD3	1.83	0.42
12:S:51:GLY:HA2	12:S:56:GLU:HG2	2.02	0.42
15:V:104:ARG:HH11	27:A:2237:A:H5'	1.85	0.42
27:A:216:A:H2'	27:A:217:G:C8	2.54	0.42
27:A:1077:A:O5'	27:A:1077:A:H8	2.02	0.42
27:A:1311:C:H2'	27:A:1312:G:H8	1.85	0.42
27:A:1538:G:H2'	27:A:1539:A:C8	2.55	0.42
27:A:1614:G:H2'	27:A:1615:G:C8	2.53	0.42
27:A:2152:A:H2'	27:A:2153:G:O4'	2.18	0.42
27:A:2351:A:H1'	27:A:2396:A:O2'	2.20	0.42
27:A:3083:A:H2'	27:A:3084:G:H8	1.83	0.42
1:E:147:LEU:HD23	1:E:147:LEU:HA	1.84	0.42
1:E:217:LYS:HB3	1:E:217:LYS:HE3	1.69	0.42
3:G:201:LEU:O	3:G:205:ILE:HG12	2.19	0.42
4:H:57:ILE:O	4:H:61:ILE:HG12	2.19	0.42
5:I:81:THR:HG1	5:I:82:GLU:CD	2.21	0.42
16:W:40:THR:OG1	27:A:141:U:H4'	2.19	0.42
26:4:12:THR:HG21	26:4:26:SER:HB3	2.02	0.42
26:4:15:GLN:HA	26:4:20:HIS:O	2.20	0.42
27:A:249:C:OP2	27:A:2618:C:O2'	2.28	0.42
27:A:1132:U:N3	27:A:1133:G:N7	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1157:G:H1	27:A:1234:U:H3	1.68	0.42
28:B:91:G:H2'	28:B:92:G:H8	1.84	0.42
4:H:31:ASN:OD1	4:H:33:MET:HG3	2.20	0.42
23:6:10:LYS:HE2	23:6:10:LYS:HB2	1.79	0.42
23:6:37:GLU:OE2	23:6:50:PRO:HB3	2.20	0.42
27:A:290:C:N4	27:A:299:G:H22	2.18	0.42
27:A:479:A:H1'	27:A:499:G:O4'	2.20	0.42
27:A:601:A:H2'	27:A:602:A:C8	2.54	0.42
27:A:1407:G:H2'	27:A:1408:C:C6	2.55	0.42
27:A:2318:U:C4	27:A:2319:G:N7	2.88	0.42
27:A:2325:U:H2'	27:A:2326:A:H8	1.83	0.42
27:A:2443:U:H2'	27:A:2444:C:H6	1.85	0.42
27:A:2717:U:C4	27:A:2718:G:C8	3.08	0.42
27:A:2885:G:H2'	27:A:2886:A:C8	2.54	0.42
27:A:2961:G:H2'	27:A:2962:A:C8	2.54	0.42
2:F:129:ARG:NH2	2:F:169:ARG:O	2.52	0.42
4:H:64:LEU:HD23	4:H:64:LEU:HA	1.87	0.42
11:R:67:GLU:CD	11:R:67:GLU:H	2.26	0.42
27:A:990:G:O2'	27:A:991:C:H5	2.02	0.42
27:A:1234:U:H2'	27:A:1235:U:H6	1.85	0.42
27:A:1859:A:H2'	27:A:1860:G:O4'	2.20	0.42
27:A:1927:C:O2'	27:A:3080:A:N3	2.47	0.42
27:A:2261:U:H2'	27:A:2262:C:C6	2.55	0.42
27:A:2324:A:N1	27:A:2412:U:C2	2.87	0.42
27:A:2326:A:C6	27:A:2410:A:C5	3.08	0.42
27:A:2642:G:H2'	27:A:2643:U:O4'	2.19	0.42
29:C:26:G:O2'	29:C:27:U:O5'	2.32	0.42
4:H:16:ARG:HE	4:H:16:ARG:HB2	1.61	0.41
6:J:10:GLU:HG3	6:J:11:HIS:CE1	2.55	0.41
27:A:1992:U:O4	27:A:2006:A:H2	2.02	0.41
27:A:2421:A:O2'	27:A:2422:A:H8	2.03	0.41
3:G:106:MET:HE2	27:A:773:G:H21	1.84	0.41
4:H:130:ASP:O	4:H:132:THR:N	2.45	0.41
8:N:2:ILE:HD13	8:N:2:ILE:HA	1.85	0.41
12:S:12:LEU:HA	12:S:12:LEU:HD12	1.78	0.41
27:A:9:U:O2	27:A:2850:C:H4'	2.21	0.41
27:A:33:G:C6	27:A:34:C:C4	3.08	0.41
27:A:81:A:C2	27:A:100:A:C5	3.08	0.41
27:A:1035:G:H21	27:A:2493:A:H8	1.67	0.41
27:A:1378:U:H2'	27:A:1379:G:C8	2.55	0.41
27:A:2882:C:H2'	27:A:2883:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B:88:C:H3'	28:B:89:C:C6	2.55	0.41
28:B:110:G:H2'	28:B:111:C:H6	1.84	0.41
4:H:36:PRO:HB3	4:H:167:ALA:HA	2.02	0.41
27:A:41:A:H2'	27:A:42:G:O4'	2.20	0.41
27:A:1533:U:H5''	27:A:1535:C:H42	1.85	0.41
27:A:1547:G:N2	27:A:1623:U:O2	2.35	0.41
27:A:1733:C:H2'	27:A:1734:C:C6	2.55	0.41
9:O:22:VAL:HG12	9:O:29:LYS:HD2	2.02	0.41
20:2:12:GLU:OE1	20:2:12:GLU:HA	2.20	0.41
23:6:7:VAL:O	23:6:8:ARG:C	2.64	0.41
27:A:296:A:C6	27:A:340:A:N6	2.87	0.41
27:A:307:G:C2	27:A:308:U:C2	3.08	0.41
27:A:737:A:N1	27:A:2593:A:O2'	2.49	0.41
27:A:1152:G:H2'	27:A:1153:U:C6	2.56	0.41
27:A:1487:U:O2'	27:A:2436:A:N3	2.49	0.41
27:A:1529:U:H2'	27:A:1530:G:O4'	2.21	0.41
27:A:1728:U:H4'	27:A:1729:A:O4'	2.21	0.41
27:A:2394:A:H3'	27:A:2396:A:N7	2.36	0.41
27:A:2676:C:H42	27:A:2728:U:H3	1.68	0.41
27:A:2876:C:N4	27:A:2893:G:O6	2.51	0.41
27:A:2887:G:H2'	27:A:2888:G:O4'	2.19	0.41
27:A:3021:A:H4'	27:A:3022:G:N7	2.36	0.41
27:A:3058:A:H2'	27:A:3059:G:H8	1.85	0.41
28:B:37:C:N3	28:B:50:C:O2'	2.47	0.41
4:H:101:ASP:OD1	4:H:102:ARG:N	2.54	0.41
23:6:37:GLU:C	23:6:37:GLU:OE1	2.64	0.41
27:A:4:G:H2'	27:A:5:U:H6	1.85	0.41
27:A:419:G:C5	27:A:420:G:H1'	2.56	0.41
27:A:673:C:H2'	27:A:674:U:C6	2.55	0.41
27:A:694:C:H2'	27:A:695:G:O4'	2.20	0.41
27:A:851:C:H2'	27:A:852:C:H6	1.85	0.41
27:A:994:A:N7	27:A:1014:G:O2'	2.52	0.41
27:A:1074:A:N1	27:A:2683:A:C8	2.88	0.41
27:A:1137:U:O2'	27:A:1139:A:N7	2.40	0.41
27:A:2376:G:H2'	27:A:2377:G:C8	2.54	0.41
27:A:2553:G:H2'	27:A:2554:U:C6	2.55	0.41
28:B:88:C:H2'	28:B:89:C:O4'	2.21	0.41
28:B:89:C:H2'	28:B:90:G:O4'	2.21	0.41
7:M:108:MET:O	27:A:1124:C:O2'	2.31	0.41
10:Q:70:ILE:O	10:Q:71:ARG:HB3	2.21	0.41
11:R:89:ALA:O	11:R:93:LYS:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:T:119:GLU:N	13:T:119:GLU:CD	2.79	0.41
14:U:26:LYS:HB3	14:U:26:LYS:HE2	1.77	0.41
26:4:28:LYS:HB2	26:4:33:ILE:HD11	2.03	0.41
27:A:98:U:H3'	27:A:99:G:H5'	2.03	0.41
27:A:739:U:O3'	27:A:740:A:H2'	2.20	0.41
27:A:750:C:H2'	27:A:751:A:C8	2.56	0.41
27:A:979:G:H2'	27:A:980:C:H6	1.84	0.41
27:A:2685:C:H2'	27:A:2686:U:C6	2.56	0.41
1:E:20:ASP:O	1:E:22:ALA:N	2.53	0.41
2:F:104:GLU:N	2:F:104:GLU:CD	2.79	0.41
4:H:59:GLY:HA3	4:H:157:ARG:HH12	1.85	0.41
6:J:25:TYR:HD2	6:J:30:LEU:HD11	1.84	0.41
6:J:37:ILE:HD13	6:J:37:ILE:HA	1.86	0.41
9:O:111:LYS:NZ	27:A:730:G:N7	2.56	0.41
27:A:362:A:O2'	27:A:363:A:O4'	2.27	0.41
27:A:736:G:H1'	27:A:740:A:N6	2.36	0.41
27:A:1633:U:H2'	27:A:1634:C:C6	2.56	0.41
27:A:1677:G:H2'	27:A:1678:U:O4'	2.21	0.41
27:A:2056:G:N3	27:A:2056:G:H2'	2.36	0.41
27:A:2074:G:N2	27:A:2109:A:H62	2.18	0.41
27:A:2253:A:C2'	27:A:2254:A:H5'	2.50	0.41
27:A:2350:G:H4'	27:A:2351:A:OP1	2.20	0.41
27:A:2758:A:C6	27:A:2759:G:C5	3.08	0.41
4:H:44:ASN:OD1	4:H:45:MET:N	2.53	0.41
12:S:61:ARG:NH1	12:S:70:GLU:OE1	2.54	0.41
13:T:49:ASP:OD2	27:A:621:U:O2'	2.28	0.41
27:A:311:G:C4	27:A:312:G:C8	3.08	0.41
27:A:1288:A:H2'	27:A:1289:A:C8	2.55	0.41
27:A:2884:A:H3'	27:A:2885:G:C8	2.56	0.41
1:E:21:PHE:HB3	1:E:24:ILE:HG12	2.03	0.41
3:G:117:ASP:CG	9:O:4:ILE:HG12	2.45	0.41
3:G:169:VAL:HB	3:G:175:VAL:HG11	2.03	0.41
4:H:57:ILE:HD13	4:H:57:ILE:HA	1.97	0.41
5:I:82:GLU:OE2	5:I:82:GLU:N	2.54	0.41
5:I:138:ASP:OD1	5:I:140:GLN:N	2.54	0.41
6:J:25:TYR:CE2	6:J:30:LEU:HD21	2.55	0.41
7:M:98:THR:HB	7:M:124:VAL:CG2	2.51	0.41
9:O:65:LYS:HB2	27:A:2640:G:H5''	2.01	0.41
26:4:38:CYS:SG	26:4:39:SER:N	2.93	0.41
27:A:662:G:C5	27:A:2254:A:C6	3.09	0.41
27:A:780:U:H2'	27:A:781:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:986:G:N3	27:A:987:A:H1'	2.36	0.41
27:A:1234:U:H2'	27:A:1235:U:C6	2.55	0.41
27:A:1533:U:H3'	27:A:1534:C:H5''	2.03	0.41
27:A:2061:U:C2	27:A:2062:G:C8	3.09	0.41
27:A:2071:A:H2	27:A:2311:G:O4'	2.04	0.41
27:A:2113:A:H2'	27:A:2114:A:C8	2.55	0.41
27:A:2142:A:O2'	27:A:2144:C:N4	2.53	0.41
27:A:2147:U:H2'	27:A:2148:C:C6	2.55	0.41
27:A:2265:U:H2'	27:A:2266:A:H8	1.86	0.41
27:A:2515:U:H2'	27:A:2516:U:H6	1.84	0.41
27:A:2673:U:O2'	27:A:2725:C:N4	2.54	0.41
28:B:59:A:C5	28:B:60:G:C8	3.08	0.41
28:B:74:A:C8	28:B:102:A:C6	3.09	0.41
3:G:13:LYS:HD2	3:G:13:LYS:O	2.21	0.41
4:H:8:LEU:HD12	4:H:8:LEU:HA	1.91	0.41
5:I:22:GLN:HE21	5:I:39:GLU:HA	1.86	0.41
5:I:82:GLU:CD	5:I:82:GLU:N	2.79	0.41
17:X:103:LYS:NZ	17:X:103:LYS:HB3	2.36	0.41
27:A:919:A:H5'	27:A:920:G:P	2.61	0.41
27:A:1007:G:C2	27:A:1008:G:C5	3.08	0.41
27:A:1756:G:H1'	27:A:1758:G:N1	2.36	0.41
27:A:1876:A:O2'	27:A:1877:U:H5'	2.21	0.41
27:A:2329:G:O6	27:A:2406:U:C4	2.74	0.41
27:A:2341:U:H5'	27:A:2342:A:OP1	2.20	0.41
27:A:3055:G:H2'	27:A:3100:A:N6	2.35	0.41
1:E:21:PHE:HB3	1:E:24:ILE:CG1	2.51	0.40
2:F:129:ARG:HD3	2:F:130:HIS:NE2	2.36	0.40
4:H:36:PRO:HA	4:H:166:THR:HB	2.02	0.40
5:I:111:SER:HB3	27:A:2890:C:H42	1.86	0.40
7:M:72:LYS:HZ1	27:A:1257:G:H5''	1.86	0.40
11:R:18:ARG:HD2	11:R:107:TYR:CZ	2.56	0.40
21:3:13:ILE:HG21	27:A:1106:A:N7	2.36	0.40
22:5:38:LYS:HA	22:5:38:LYS:HD3	1.81	0.40
27:A:814:A:H2'	27:A:815:G:O4'	2.22	0.40
27:A:1431:U:C2	27:A:1452:G:N2	2.88	0.40
27:A:1501:C:H2'	27:A:1502:G:H8	1.85	0.40
27:A:1725:G:H2'	27:A:1726:C:O4'	2.20	0.40
29:C:18:G:C6	29:C:58:A:C6	3.08	0.40
2:F:54:TYR:CG	2:F:55:GLY:N	2.89	0.40
3:G:27:VAL:HG22	3:G:116:SER:OG	2.21	0.40
4:H:80:SER:HB2	4:H:87:ARG:NH1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:111:SER:OG	27:A:2891:C:N3	2.51	0.40
7:M:55:ILE:HA	7:M:123:LYS:O	2.21	0.40
7:M:56:VAL:HB	7:M:124:VAL:HG12	2.02	0.40
8:N:122:LEU:HD13	12:S:69:VAL:HG11	2.02	0.40
13:T:109:LEU:HD23	13:T:109:LEU:HA	1.90	0.40
24:7:7:THR:O	27:A:801:U:O2'	2.36	0.40
27:A:7:U:H3'	27:A:8:U:C6	2.56	0.40
27:A:1000:C:H3'	27:A:1001:C:H5''	2.03	0.40
27:A:1560:U:H2'	27:A:1561:C:C6	2.56	0.40
27:A:1900:C:H2'	27:A:1901:C:C6	2.56	0.40
27:A:2375:G:H2'	27:A:2376:G:C8	2.56	0.40
27:A:2573:G:C6	27:A:2593:A:C6	3.09	0.40
3:G:34:MET:HE1	9:O:4:ILE:CD1	2.43	0.40
4:H:40:LYS:HG2	4:H:164:VAL:CG1	2.52	0.40
4:H:100:GLY:N	4:H:103:MET:HE2	2.36	0.40
11:R:65:SER:HA	11:R:70:VAL:HG11	2.04	0.40
27:A:24:G:O2'	27:A:25:A:OP2	2.36	0.40
27:A:289:A:C5	27:A:290:C:H5	2.40	0.40
27:A:632:G:C6	27:A:640:G:C6	3.09	0.40
27:A:1259:U:H1'	27:A:1261:A:C6	2.56	0.40
27:A:2541:U:H2'	27:A:2542:G:O4'	2.21	0.40
27:A:3034:C:H2'	27:A:3035:C:C6	2.55	0.40
4:H:142:GLN:HG3	4:H:148:ILE:HD13	2.02	0.40
5:I:12:PRO:HB2	5:I:15:VAL:HG12	2.02	0.40
5:I:86:GLN:OE1	5:I:86:GLN:HA	2.22	0.40
11:R:87:LEU:HA	11:R:90:GLU:OE2	2.22	0.40
17:X:40:ARG:H	17:X:40:ARG:HG2	1.71	0.40
27:A:227:A:N1	27:A:505:C:O2'	2.50	0.40
27:A:618:C:OP1	27:A:653:G:N2	2.54	0.40
27:A:1348:G:C6	27:A:1349:U:C4	3.09	0.40
27:A:1756:G:O2'	27:A:1757:U:O5'	2.32	0.40
27:A:2088:C:N3	27:A:2095:G:C6	2.89	0.40
27:A:2342:A:N6	27:A:2390:U:H1'	2.36	0.40
27:A:2378:U:H2'	27:A:2379:G:C8	2.55	0.40
27:A:3020:U:O2'	27:A:3021:A:N3	2.55	0.40
29:C:30:G:C4	29:C:31:G:C8	3.10	0.40
2:F:130:HIS:ND1	2:F:165:ARG:HD2	2.36	0.40
4:H:158:GLY:O	27:A:2529:A:N6	2.55	0.40
10:Q:63:ARG:O	10:Q:67:MET:HG3	2.22	0.40
19:1:3:ALA:HB1	19:1:12:PRO:HD3	2.04	0.40
20:2:20:ASP:O	20:2:24:GLU:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:6:44:ASN:OD1	23:6:44:ASN:N	2.54	0.40
27:A:384:G:H2'	27:A:385:G:H8	1.86	0.40
27:A:993:G:H22	27:A:1015:A:P	2.44	0.40
27:A:1074:A:C6	27:A:2683:A:C8	3.09	0.40
27:A:1704:U:H2'	27:A:1705:C:H6	1.84	0.40
27:A:2551:A:H2'	27:A:2552:A:C8	2.56	0.40
27:A:2563:G:C2	27:A:2564:A:C5	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	273/278 (98%)	267 (98%)	6 (2%)	0	100	100
2	F	205/217 (94%)	200 (98%)	5 (2%)	0	100	100
3	G	206/215 (96%)	199 (97%)	7 (3%)	0	100	100
4	H	178/187 (95%)	173 (97%)	5 (3%)	0	100	100
5	I	163/179 (91%)	159 (98%)	4 (2%)	0	100	100
6	J	39/151 (26%)	37 (95%)	2 (5%)	0	100	100
7	M	144/147 (98%)	143 (99%)	1 (1%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
10	Q	115/199 (58%)	112 (97%)	3 (3%)	0	100	100
11	R	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
12	S	110/113 (97%)	104 (94%)	6 (6%)	0	100	100
13	T	121/129 (94%)	120 (99%)	1 (1%)	0	100	100
14	U	98/103 (95%)	96 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	V	111/153 (72%)	109 (98%)	2 (2%)	0	100	100
16	W	94/100 (94%)	93 (99%)	1 (1%)	0	100	100
17	X	88/105 (84%)	86 (98%)	2 (2%)	0	100	100
18	Z	75/88 (85%)	71 (95%)	4 (5%)	0	100	100
19	1	60/64 (94%)	56 (93%)	4 (7%)	0	100	100
20	2	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
21	3	56/61 (92%)	54 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	52 (100%)	0	0	100	100
23	6	46/55 (84%)	43 (94%)	3 (6%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
26	4	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
All	All	2832/3260 (87%)	2754 (97%)	78 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	215/218 (99%)	215 (100%)	0	100	100
2	F	159/163 (98%)	155 (98%)	4 (2%)	42	63
3	G	168/173 (97%)	168 (100%)	0	100	100
4	H	149/156 (96%)	148 (99%)	1 (1%)	76	78
5	I	139/150 (93%)	137 (99%)	2 (1%)	59	71
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	117 (98%)	2 (2%)	53	70
8	N	100/100 (100%)	99 (99%)	1 (1%)	68	75
9	O	112/114 (98%)	111 (99%)	1 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Q	96/158 (61%)	95 (99%)	1 (1%)	68	75
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	99/100 (99%)	99 (100%)	0	100	100
13	T	96/99 (97%)	95 (99%)	1 (1%)	68	75
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	89/117 (76%)	89 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	77 (98%)	2 (2%)	42	63
18	Z	56/63 (89%)	56 (100%)	0	100	100
19	1	50/51 (98%)	48 (96%)	2 (4%)	28	54
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	51 (98%)	1 (2%)	50	68
22	5	43/46 (94%)	42 (98%)	1 (2%)	44	64
23	6	46/52 (88%)	46 (100%)	0	100	100
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	43/63 (68%)	43 (100%)	0	100	100
All	All	2344/2617 (90%)	2325 (99%)	19 (1%)	70	77

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

Mol	Chain	Res	Type
2	F	156	THR
2	F	161	PHE
2	F	162	LYS
2	F	164	THR
4	H	81	ILE
5	I	103	ASN
5	I	117	GLU
7	M	94	GLU
7	M	138	ILE
8	N	94	ARG
9	O	137	ILE
10	Q	54	HIS
13	T	59	LYS
17	X	20	LYS

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Mol	Chain	Res	Type
17	X	24	LEU
19	1	60	LYS
19	1	61	VAL
21	3	28	LEU
22	5	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
2	F	183	HIS
3	G	41	GLN
3	G	91	HIS
3	G	151	ASN
3	G	184	ASN
3	G	202	ASN
4	H	142	GLN
8	N	3	GLN
10	Q	54	HIS
10	Q	62	ASN
11	R	53	ASN
13	T	27	GLN
16	W	61	ASN
20	2	44	ASN
22	5	12	ASN
23	6	28	ASN
23	6	31	ASN
25	8	25	GLN
26	4	42	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3018/3119 (96%)	553 (18%)	15 (0%)
28	B	116/118 (98%)	17 (14%)	1 (0%)
29	C	75/76 (98%)	29 (38%)	3 (4%)
All	All	3209/3313 (96%)	599 (18%)	19 (0%)

All (599) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	9	U
27	A	12	G
27	A	20	G
27	A	29	C
27	A	32	G
27	A	33	G
27	A	55	G
27	A	60	A
27	A	68	A
27	A	71	A
27	A	72	G
27	A	82	G
27	A	89	A
27	A	90	C
27	A	94	G
27	A	98	U
27	A	99	G
27	A	115	A
27	A	117	U
27	A	125	C
27	A	148	A
27	A	164	A
27	A	195	A
27	A	198	A
27	A	212	A
27	A	214	G
27	A	215	A
27	A	221	A
27	A	227	A
27	A	229	U
27	A	230	G
27	A	231	U
27	A	248	G
27	A	265	A
27	A	271	A
27	A	272	A
27	A	275	C
27	A	279	U
27	A	283	U
27	A	285	U
27	A	286	G
27	A	290	C

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Mol	Chain	Res	Type
27	A	292	G
27	A	297	G
27	A	298	G
27	A	299	G
27	A	300	G
27	A	301	U
27	A	302	U
27	A	303	G
27	A	305	G
27	A	313	G
27	A	314	G
27	A	315	U
27	A	317	G
27	A	318	U
27	A	319	G
27	A	324	C
27	A	330	U
27	A	331	U
27	A	332	C
27	A	336	C
27	A	337	U
27	A	338	C
27	A	344	G
27	A	346	C
27	A	350	A
27	A	351	G
27	A	352	G
27	A	353	G
27	A	357	U
27	A	358	G
27	A	361	A
27	A	364	A
27	A	370	U
27	A	371	G
27	A	384	G
27	A	393	U
27	A	399	G
27	A	412	A
27	A	413	G
27	A	424	G
27	A	434	G
27	A	437	G

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Mol	Chain	Res	Type
27	A	444	U
27	A	445	U
27	A	446	G
27	A	447	A
27	A	450	G
27	A	452	G
27	A	454	U
27	A	460	G
27	A	474	G
27	A	489	A
27	A	493	U
27	A	494	G
27	A	505	C
27	A	509	U
27	A	512	G
27	A	523	U
27	A	543	U
27	A	544	U
27	A	555	G
27	A	566	A
27	A	568	A
27	A	569	G
27	A	578	G
27	A	589	A
27	A	591	G
27	A	592	A
27	A	594	U
27	A	595	A
27	A	596	C
27	A	597	C
27	A	617	U
27	A	618	C
27	A	619	C
27	A	620	G
27	A	635	G
27	A	636	U
27	A	637	G
27	A	638	U
27	A	639	C
27	A	640	G
27	A	642	G
27	A	644	G

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Mol	Chain	Res	Type
27	A	655	G
27	A	664	A
27	A	667	A
27	A	679	G
27	A	684	G
27	A	685	G
27	A	696	A
27	A	706	G
27	A	707	G
27	A	708	G
27	A	721	A
27	A	728	G
27	A	731	A
27	A	738	A
27	A	740	A
27	A	747	A
27	A	754	C
27	A	756	A
27	A	758	A
27	A	759	G
27	A	760	U
27	A	764	U
27	A	765	G
27	A	766	G
27	A	768	G
27	A	784	G
27	A	785	A
27	A	794	G
27	A	801	U
27	A	832	G
27	A	839	U
27	A	845	C
27	A	862	U
27	A	863	G
27	A	868	C
27	A	872	G
27	A	878	G
27	A	879	A
27	A	880	G
27	A	890	G
27	A	891	G
27	A	897	A

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Mol	Chain	Res	Type
27	A	899	G
27	A	920	G
27	A	927	C
27	A	942	U
27	A	944	A
27	A	960	G
27	A	961	U
27	A	972	A
27	A	975	U
27	A	981	U
27	A	982	A
27	A	987	A
27	A	988	U
27	A	989	G
27	A	990	G
27	A	991	C
27	A	994	A
27	A	995	U
27	A	1001	C
27	A	1002	C
27	A	1003	A
27	A	1004	C
27	A	1005	A
27	A	1007	G
27	A	1008	G
27	A	1009	U
27	A	1010	U
27	A	1012	C
27	A	1013	U
27	A	1014	G
27	A	1015	A
27	A	1018	U
27	A	1019	C
27	A	1022	C
27	A	1025	A
27	A	1030	C
27	A	1047	A
27	A	1048	A
27	A	1049	G
27	A	1058	A
27	A	1063	G
27	A	1069	G

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Mol	Chain	Res	Type
27	A	1076	A
27	A	1078	G
27	A	1085	G
27	A	1092	G
27	A	1101	A
27	A	1114	G
27	A	1130	C
27	A	1131	G
27	A	1144	A
27	A	1151	U
27	A	1158	U
27	A	1164	A
27	A	1230	G
27	A	1232	G
27	A	1235	U
27	A	1238	G
27	A	1240	G
27	A	1242	C
27	A	1244	A
27	A	1245	U
27	A	1248	U
27	A	1250	U
27	A	1251	A
27	A	1252	G
27	A	1253	C
27	A	1254	G
27	A	1260	C
27	A	1261	A
27	A	1292	U
27	A	1293	G
27	A	1298	C
27	A	1335	G
27	A	1344	A
27	A	1353	G
27	A	1359	G
27	A	1371	G
27	A	1386	G
27	A	1387	A
27	A	1389	U
27	A	1415	A
27	A	1416	A
27	A	1436	C

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Mol	Chain	Res	Type
27	A	1456	G
27	A	1465	C
27	A	1467	U
27	A	1480	A
27	A	1493	A
27	A	1494	U
27	A	1499	A
27	A	1507	G
27	A	1508	A
27	A	1510	A
27	A	1511	U
27	A	1522	G
27	A	1531	C
27	A	1533	U
27	A	1534	C
27	A	1539	A
27	A	1540	U
27	A	1543	A
27	A	1550	G
27	A	1551	U
27	A	1552	A
27	A	1553	C
27	A	1554	U
27	A	1625	G
27	A	1627	U
27	A	1628	A
27	A	1629	G
27	A	1630	U
27	A	1632	G
27	A	1633	U
27	A	1639	G
27	A	1640	A
27	A	1641	U
27	A	1648	A
27	A	1649	C
27	A	1670	G
27	A	1676	G
27	A	1679	A
27	A	1680	A
27	A	1681	U
27	A	1703	G
27	A	1710	A

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Mol	Chain	Res	Type
27	A	1711	G
27	A	1714	A
27	A	1716	A
27	A	1717	U
27	A	1724	G
27	A	1728	U
27	A	1731	A
27	A	1737	A
27	A	1754	G
27	A	1755	A
27	A	1756	G
27	A	1757	U
27	A	1758	G
27	A	1767	U
27	A	1786	G
27	A	1789	A
27	A	1798	U
27	A	1803	A
27	A	1826	A
27	A	1864	U
27	A	1866	C
27	A	1871	G
27	A	1872	A
27	A	1892	G
27	A	1895	A
27	A	1933	G
27	A	1946	U
27	A	1947	U
27	A	1949	C
27	A	1950	G
27	A	1973	C
27	A	1975	A
27	A	1981	U
27	A	1990	A
27	A	2003	A
27	A	2004	A
27	A	2008	A
27	A	2017	C
27	A	2018	G
27	A	2026	A
27	A	2033	U
27	A	2046	A

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Mol	Chain	Res	Type
27	A	2064	A
27	A	2065	A
27	A	2074	G
27	A	2075	G
27	A	2085	C
27	A	2086	U
27	A	2087	C
27	A	2088	C
27	A	2089	C
27	A	2090	U
27	A	2091	U
27	A	2092	U
27	A	2093	G
27	A	2094	G
27	A	2095	G
27	A	2096	G
27	A	2107	G
27	A	2130	G
27	A	2137	A
27	A	2141	U
27	A	2153	G
27	A	2154	G
27	A	2160	A
27	A	2161	A
27	A	2162	A
27	A	2163	U
27	A	2179	U
27	A	2188	G
27	A	2191	C
27	A	2194	A
27	A	2195	U
27	A	2196	G
27	A	2215	U
27	A	2217	U
27	A	2221	A
27	A	2244	A
27	A	2247	A
27	A	2251	G
27	A	2254	A
27	A	2255	A
27	A	2256	G
27	A	2257	A

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Mol	Chain	Res	Type
27	A	2263	G
27	A	2267	C
27	A	2279	C
27	A	2280	G
27	A	2284	A
27	A	2285	G
27	A	2286	A
27	A	2287	C
27	A	2316	G
27	A	2320	C
27	A	2322	C
27	A	2324	A
27	A	2325	U
27	A	2328	G
27	A	2329	G
27	A	2330	U
27	A	2331	U
27	A	2333	G
27	A	2334	U
27	A	2335	G
27	A	2338	G
27	A	2339	G
27	A	2340	A
27	A	2341	U
27	A	2342	A
27	A	2343	G
27	A	2351	A
27	A	2353	U
27	A	2354	G
27	A	2355	U
27	A	2356	G
27	A	2357	A
27	A	2368	C
27	A	2370	A
27	A	2371	G
27	A	2372	U
27	A	2382	G
27	A	2384	C
27	A	2386	U
27	A	2387	U
27	A	2388	G
27	A	2389	U

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Mol	Chain	Res	Type
27	A	2390	U
27	A	2393	A
27	A	2394	A
27	A	2395	U
27	A	2396	A
27	A	2399	A
27	A	2401	U
27	A	2402	C
27	A	2403	U
27	A	2404	G
27	A	2405	A
27	A	2407	C
27	A	2408	G
27	A	2410	A
27	A	2413	G
27	A	2421	A
27	A	2422	A
27	A	2427	G
27	A	2434	A
27	A	2436	A
27	A	2447	G
27	A	2449	A
27	A	2462	G
27	A	2463	G
27	A	2467	U
27	A	2503	G
27	A	2504	G
27	A	2507	C
27	A	2511	A
27	A	2512	A
27	A	2529	A
27	A	2532	G
27	A	2544	U
27	A	2545	G
27	A	2548	U
27	A	2549	G
27	A	2558	C
27	A	2559	A
27	A	2560	A
27	A	2567	U
27	A	2571	C
27	A	2574	C

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Mol	Chain	Res	Type
27	A	2582	A
27	A	2585	U
27	A	2607	G
27	A	2609	A
27	A	2626	U
27	A	2627	C
27	A	2647	U
27	A	2649	A
27	A	2653	G
27	A	2654	A
27	A	2655	U
27	A	2659	A
27	A	2665	C
27	A	2672	A
27	A	2673	U
27	A	2677	A
27	A	2678	G
27	A	2679	G
27	A	2688	C
27	A	2693	A
27	A	2694	G
27	A	2705	G
27	A	2714	G
27	A	2715	U
27	A	2718	G
27	A	2722	C
27	A	2726	G
27	A	2727	A
27	A	2729	G
27	A	2730	U
27	A	2731	C
27	A	2742	A
27	A	2744	C
27	A	2749	G
27	A	2753	G
27	A	2754	G
27	A	2759	G
27	A	2763	C
27	A	2766	A
27	A	2778	U
27	A	2786	U
27	A	2790	A

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Mol	Chain	Res	Type
27	A	2791	G
27	A	2796	A
27	A	2797	C
27	A	2800	G
27	A	2826	A
27	A	2827	G
27	A	2833	U
27	A	2837	U
27	A	2853	C
27	A	2854	A
27	A	2862	G
27	A	2865	G
27	A	2876	C
27	A	2913	U
27	A	2915	C
27	A	2926	A
27	A	2936	C
27	A	2938	G
27	A	2948	C
27	A	2950	C
27	A	2957	A
27	A	2968	G
27	A	2974	A
27	A	2980	U
27	A	2981	A
27	A	2982	A
27	A	2985	G
27	A	2989	A
27	A	3002	A
27	A	3009	U
27	A	3013	C
27	A	3014	A
27	A	3015	C
27	A	3021	A
27	A	3022	G
27	A	3029	U
27	A	3039	C
27	A	3042	A
27	A	3056	A
27	A	3082	U
27	A	3088	C
27	A	3093	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	A	3104	A
27	A	3105	C
27	A	3106	C
27	A	3107	G
27	A	3114	A
27	A	3115	A
28	B	3	U
28	B	4	A
28	B	9	G
28	B	11	U
28	B	12	C
28	B	13	C
28	B	30	G
28	B	36	U
28	B	42	C
28	B	53	A
28	B	54	A
28	B	57	U
28	B	68	G
28	B	87	U
28	B	89	C
28	B	107	A
28	B	115	A
29	C	7	G
29	C	8	U
29	C	9	G
29	C	13	C
29	C	16	C
29	C	17	C
29	C	18	G
29	C	20	U
29	C	21	A
29	C	22	G
29	C	24	U
29	C	26	G
29	C	27	U
29	C	28	C
29	C	37	A
29	C	38	A
29	C	46	A
29	C	47	U
29	C	48	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	C	49	G
29	C	52	G
29	C	53	G
29	C	54	U
29	C	56	C
29	C	63	G
29	C	73	A
29	C	74	C
29	C	75	C
29	C	76	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	89	A
27	A	97	U
27	A	316	U
27	A	335	G
27	A	357	U
27	A	445	U
27	A	643	G
27	A	974	G
27	A	1002	C
27	A	1004	C
27	A	1084	U
27	A	2094	G
27	A	2350	G
27	A	2381	A
27	A	2729	G
28	B	10	G
29	C	17	C
29	C	20	U
29	C	53	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.

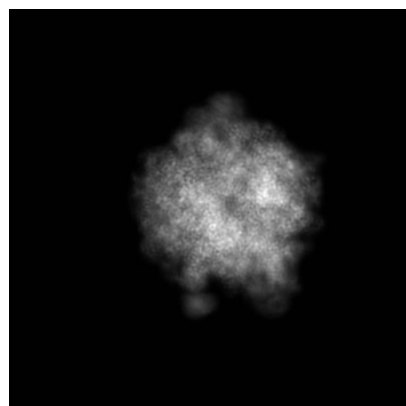
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37563. These allow visual inspection of the internal detail of the map and identification of artifacts.

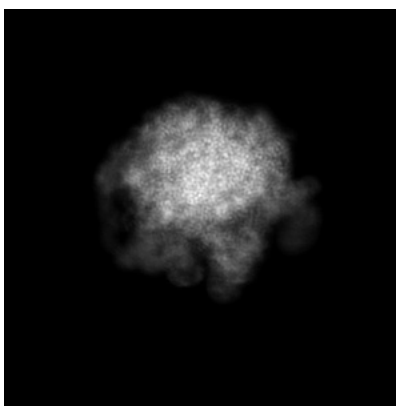
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

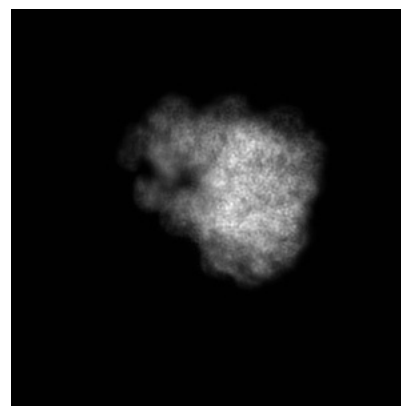
6.1.1 Primary map



X

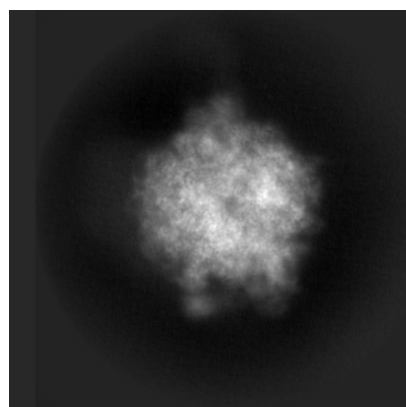


Y

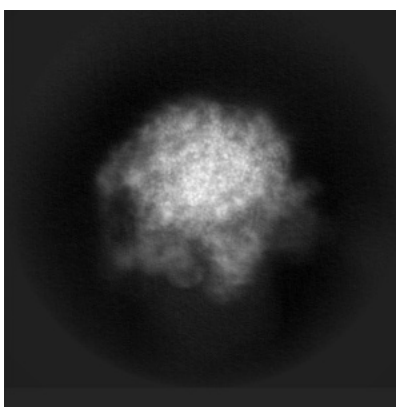


Z

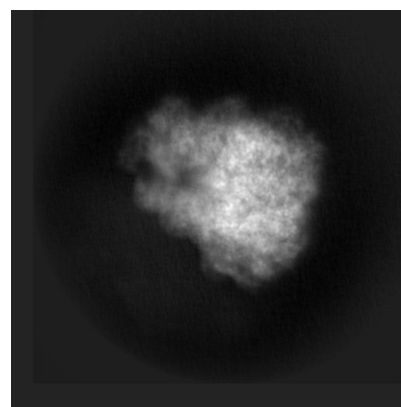
6.1.2 Raw map



X



Y

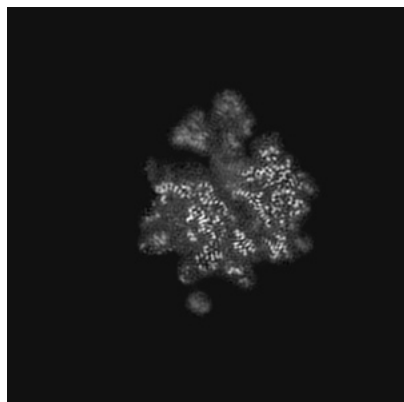


Z

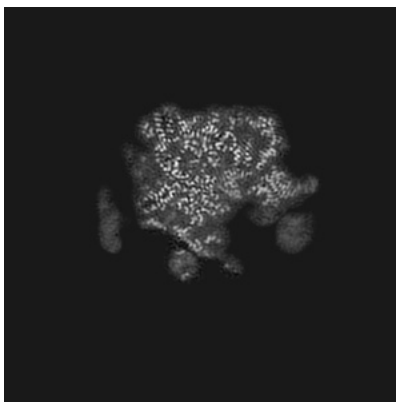
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

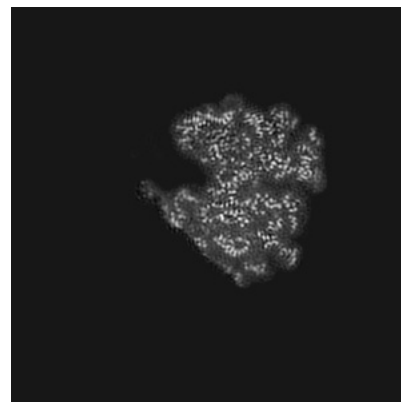
6.2.1 Primary map



X Index: 190

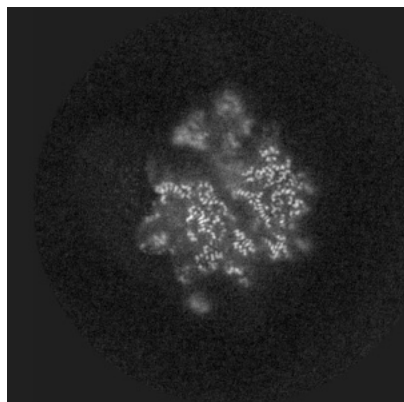


Y Index: 190

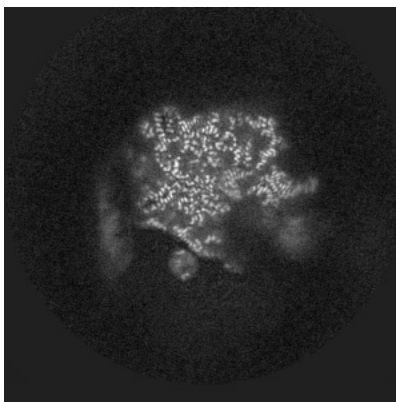


Z Index: 190

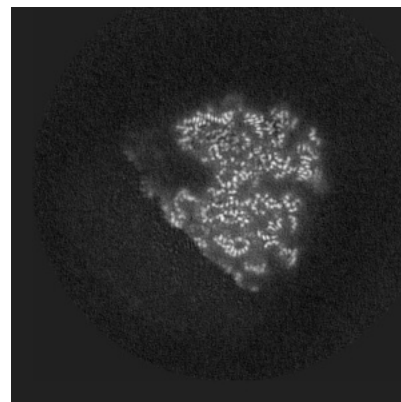
6.2.2 Raw map



X Index: 190



Y Index: 190

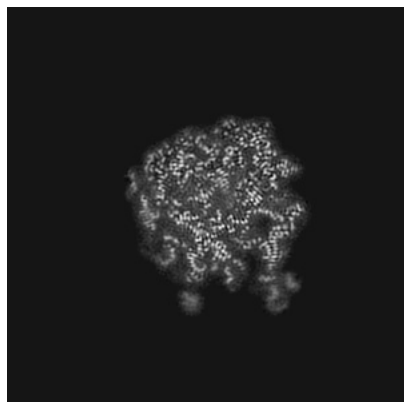


Z Index: 190

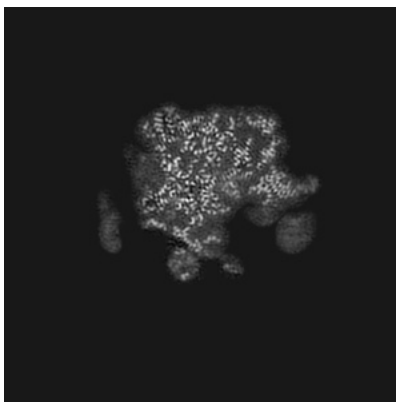
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

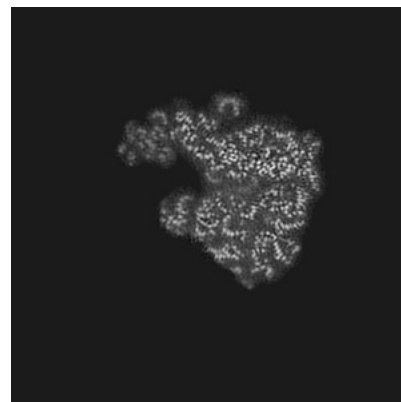
6.3.1 Primary map



X Index: 230

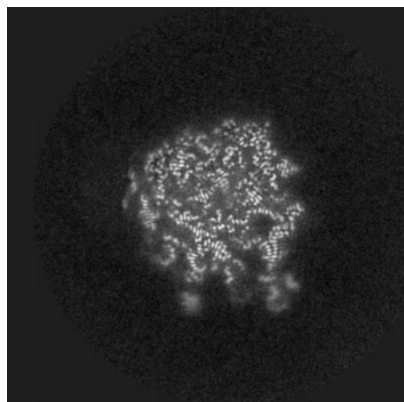


Y Index: 191

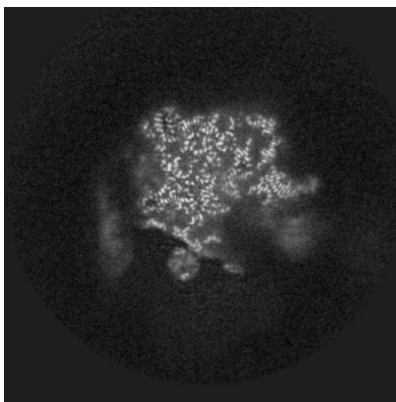


Z Index: 200

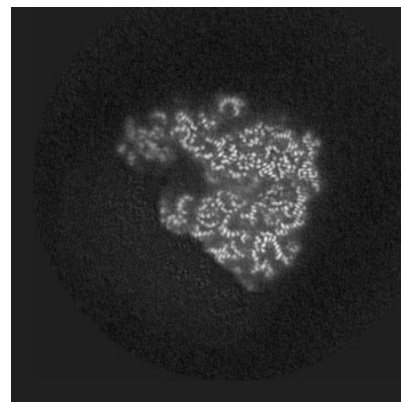
6.3.2 Raw map



X Index: 230



Y Index: 191

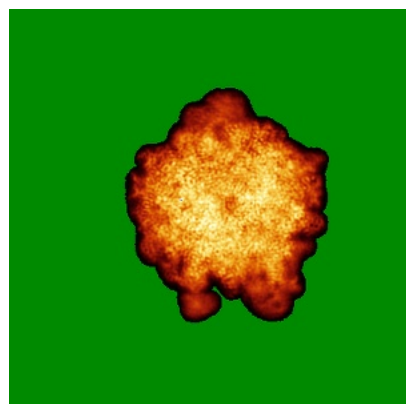


Z Index: 199

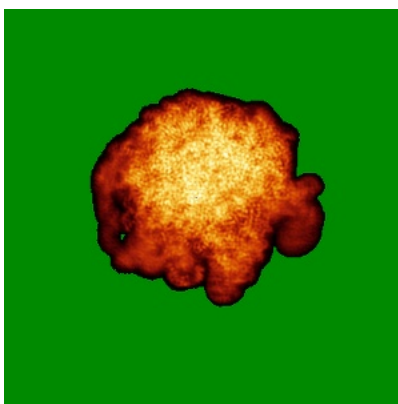
The images above show the largest variance slices of the map in three orthogonal directions.

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

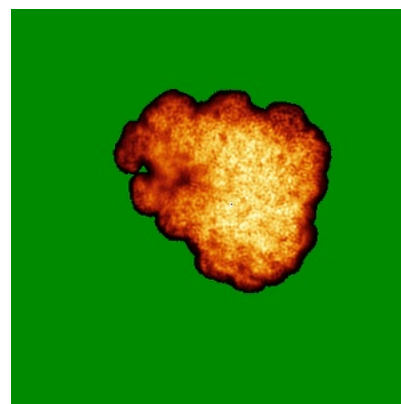
6.4.1 Primary map



X

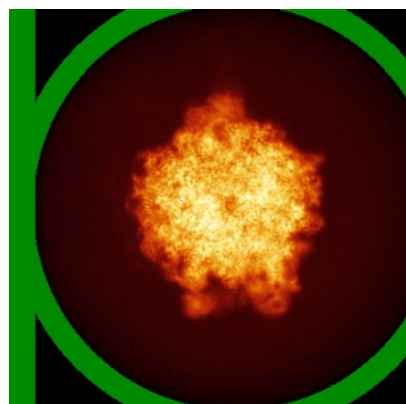


Y



Z

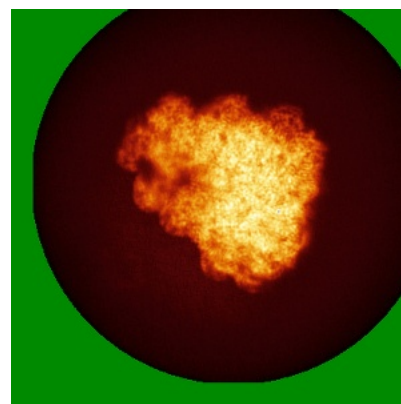
6.4.2 Raw map



X



Y

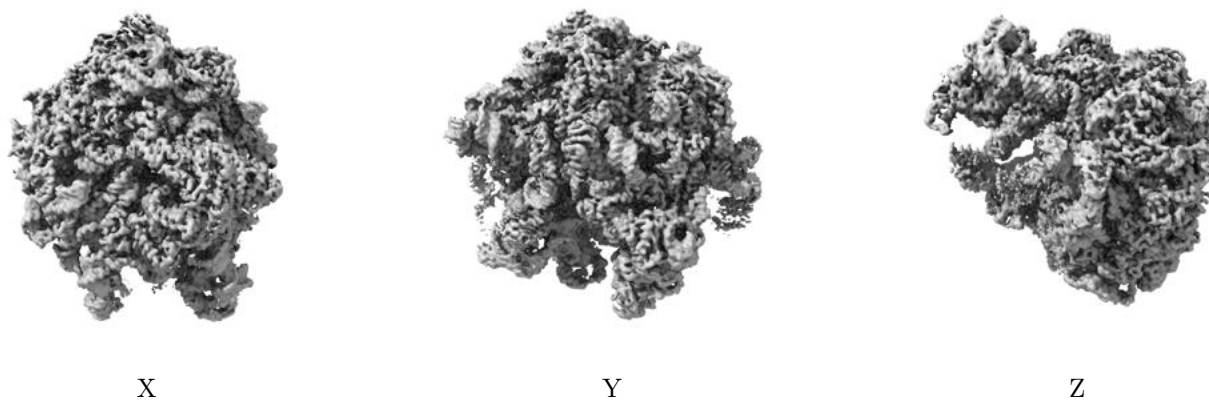


Z

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

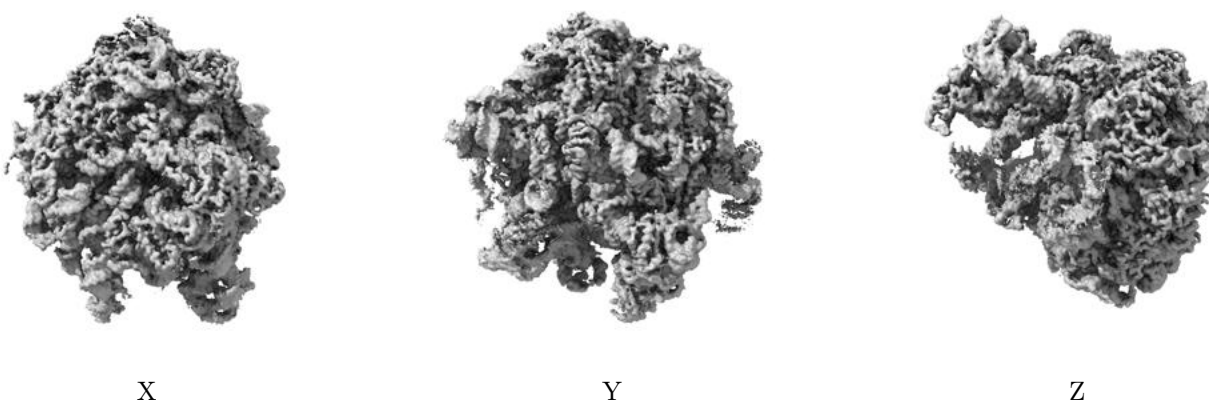
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

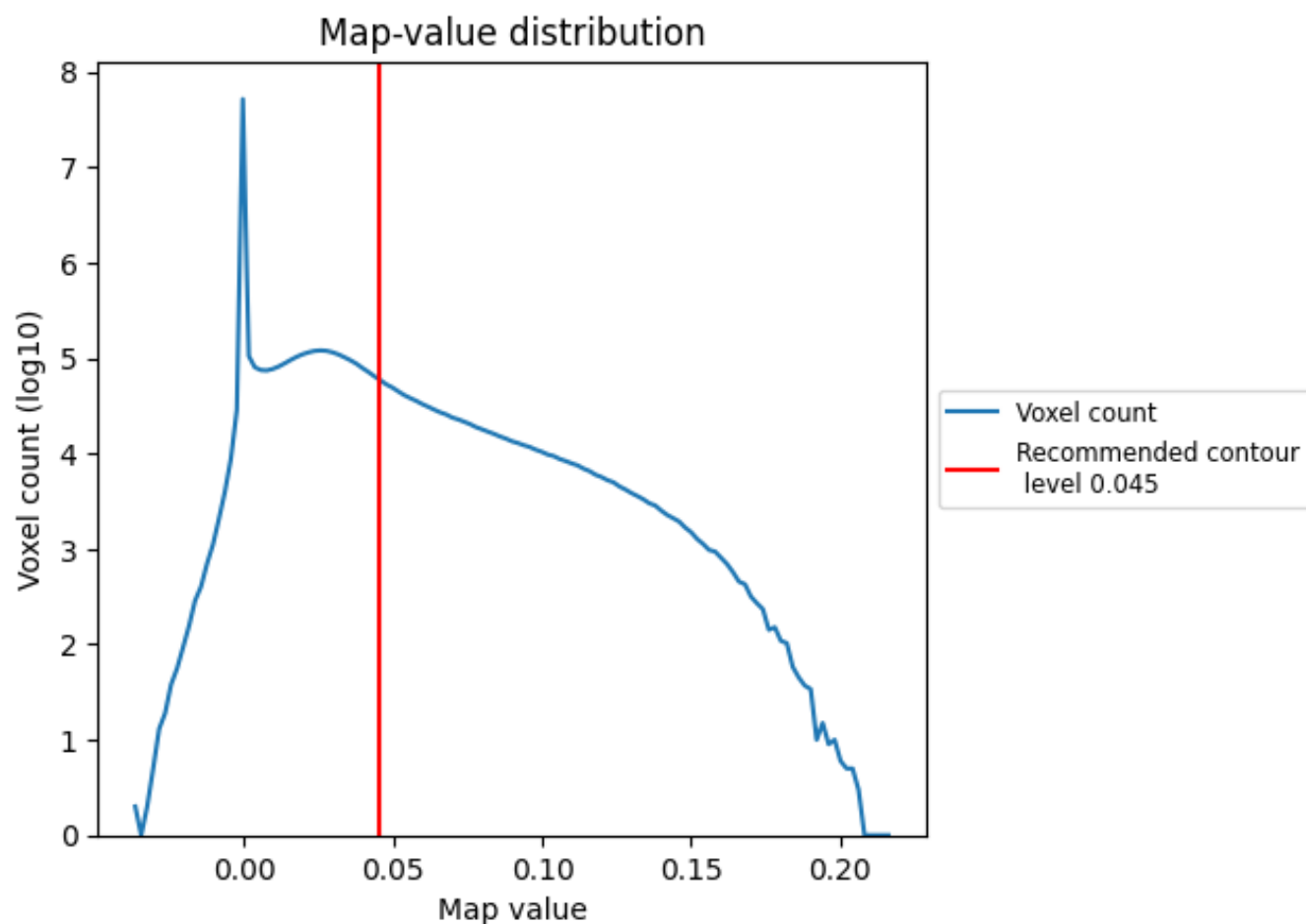
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

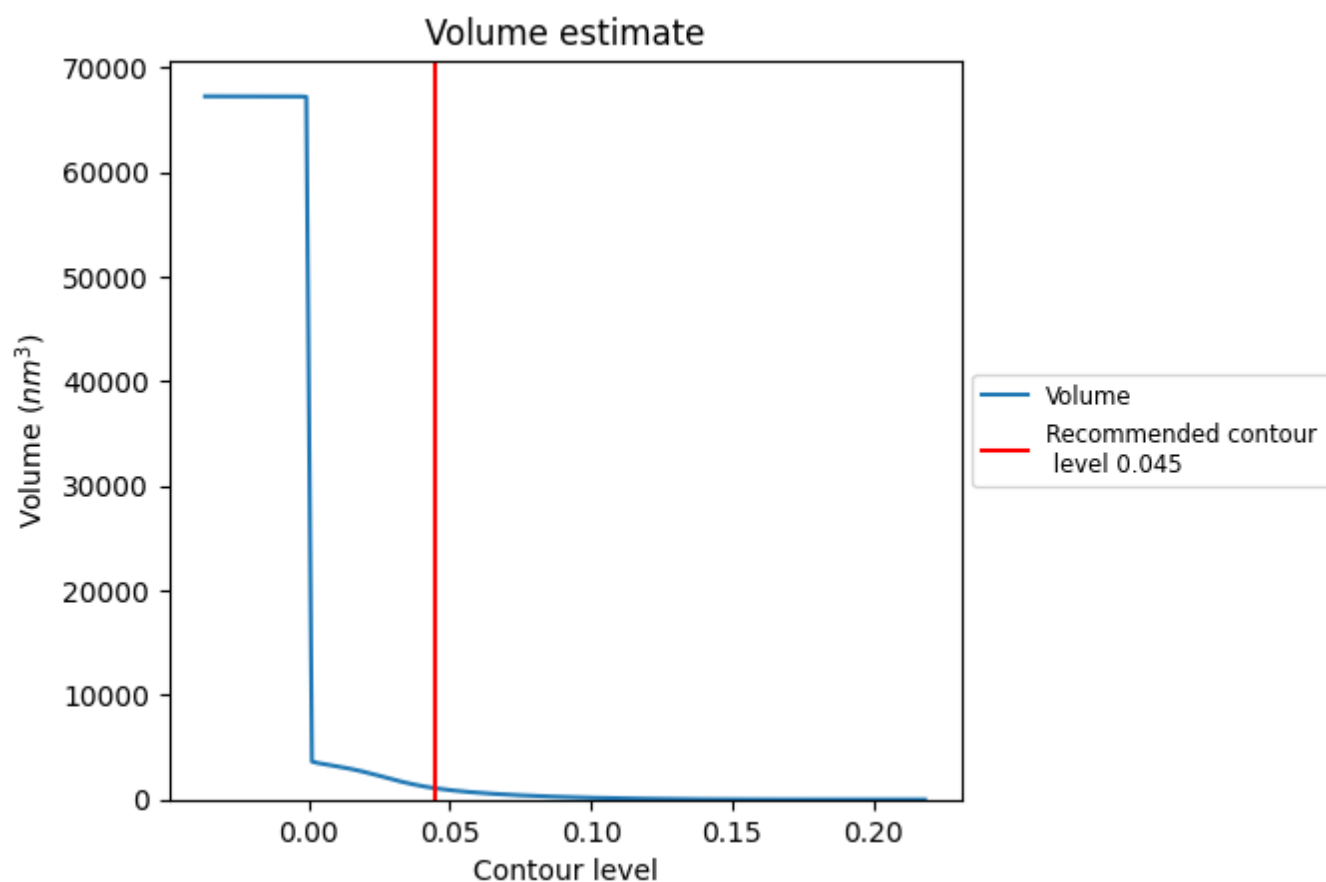
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

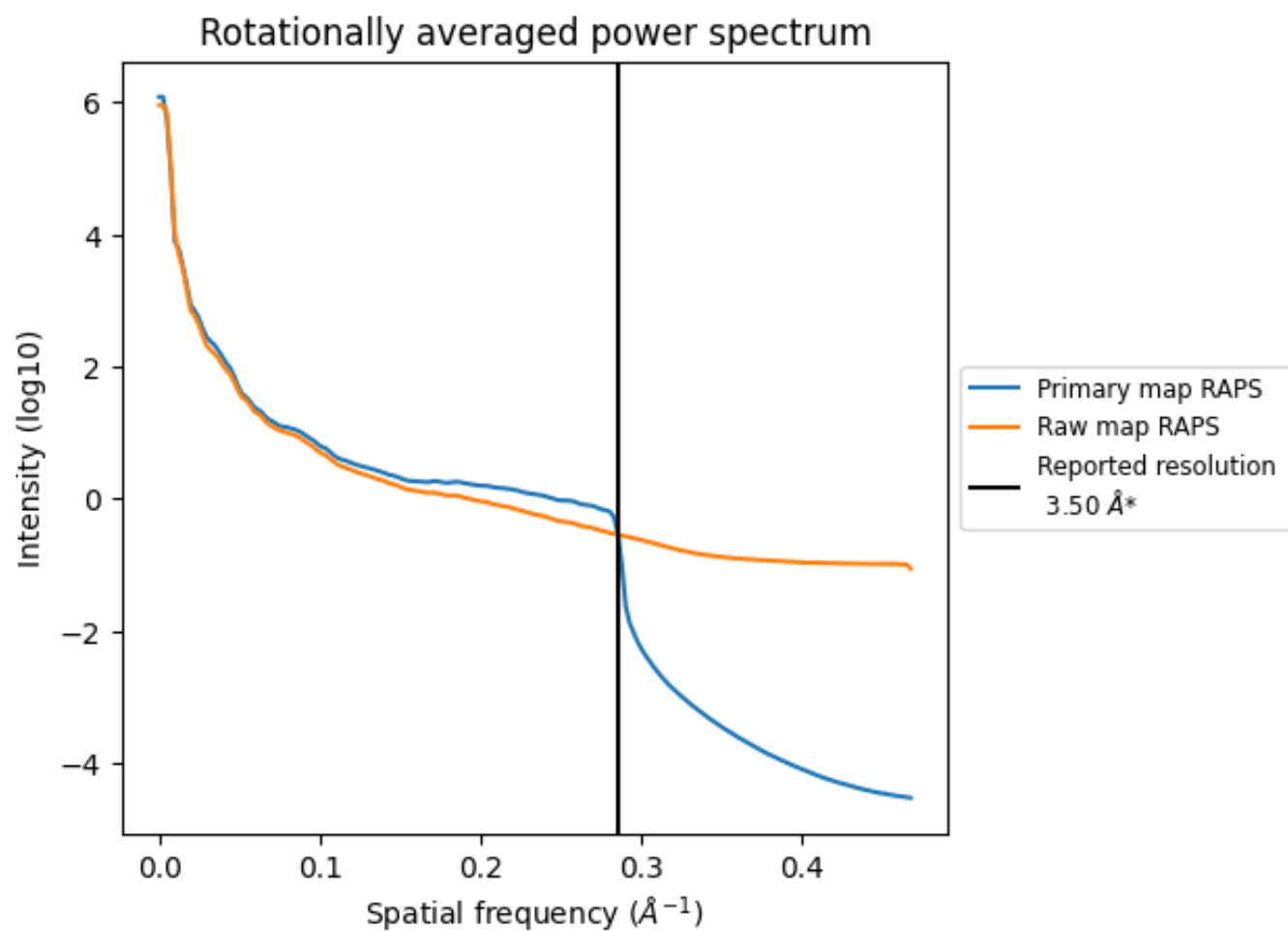
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1077 nm^3 ; this corresponds to an approximate mass of 973 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 ⓘ

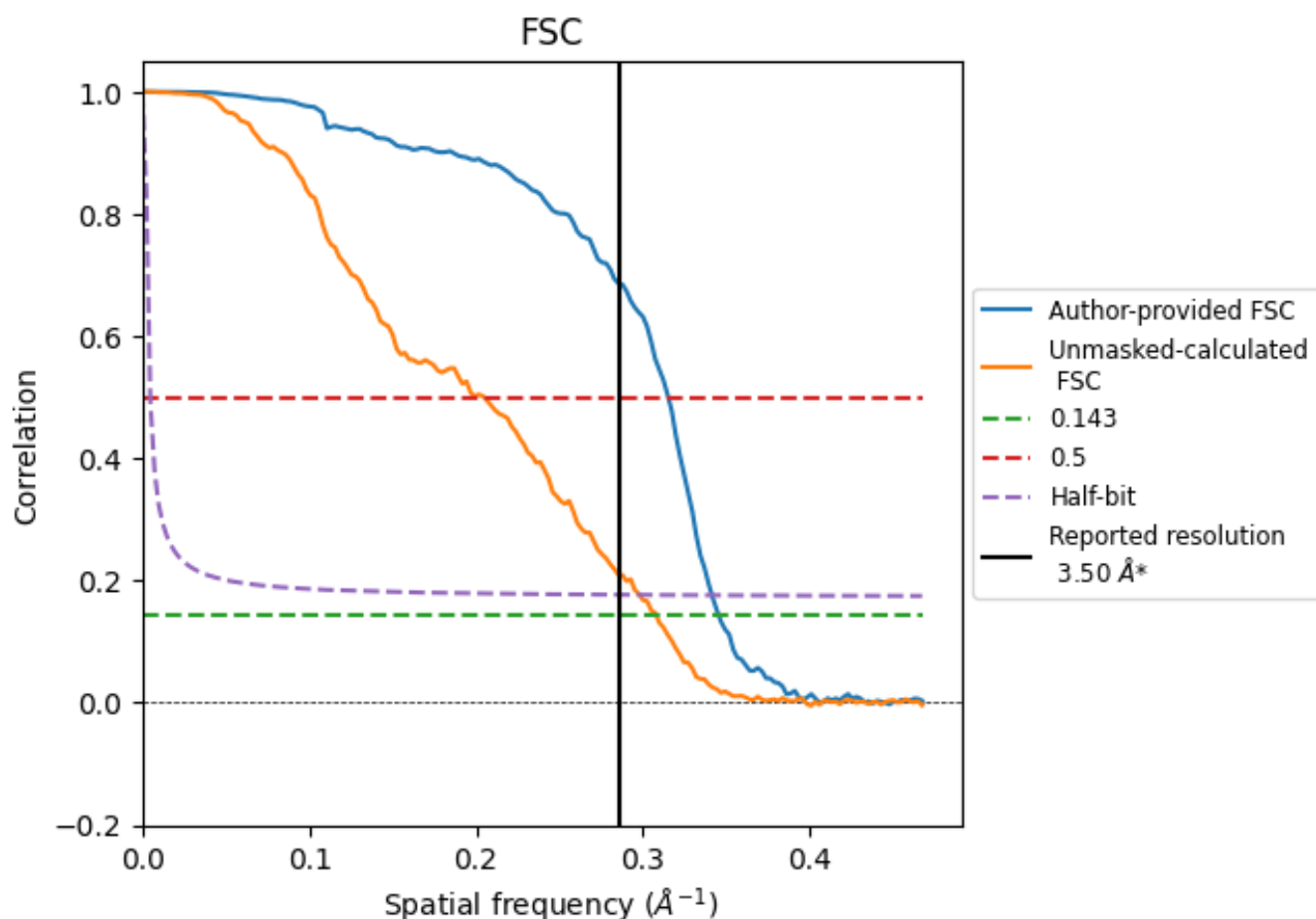


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

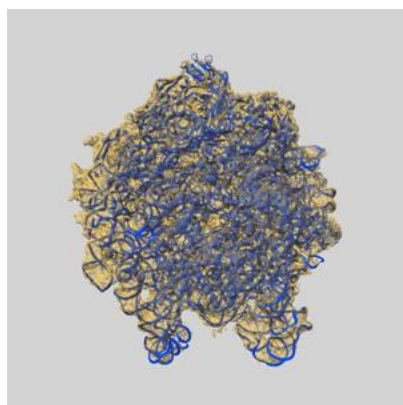
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.50
Author-provided FSC curve	2.90	3.17	2.93	-
Unmasked-calculated*	3.25	4.89	3.36	-

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

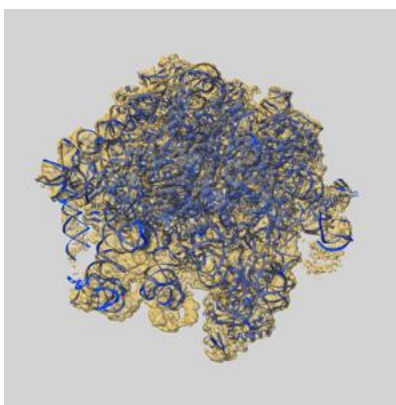
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37563 and PDB model 8WIC. Per-residue inclusion information can be found in section 3 on page 10.

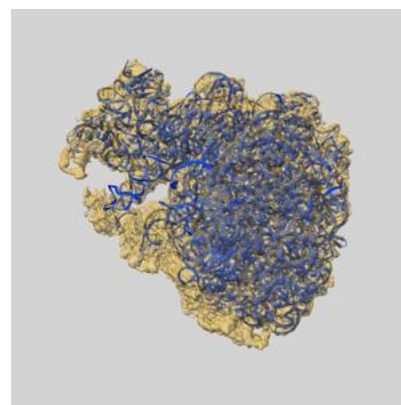
9.1 Map-model overlay [i](#)



X



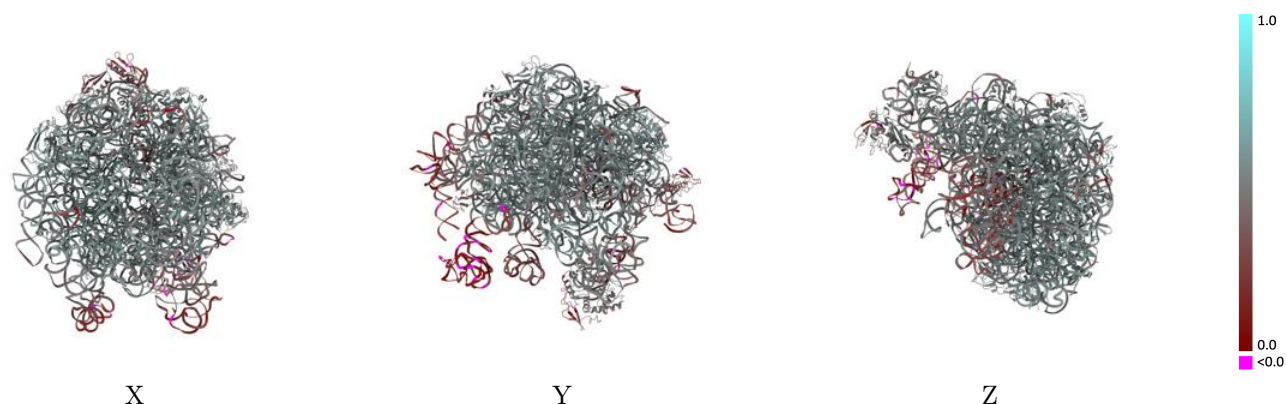
Y



Z

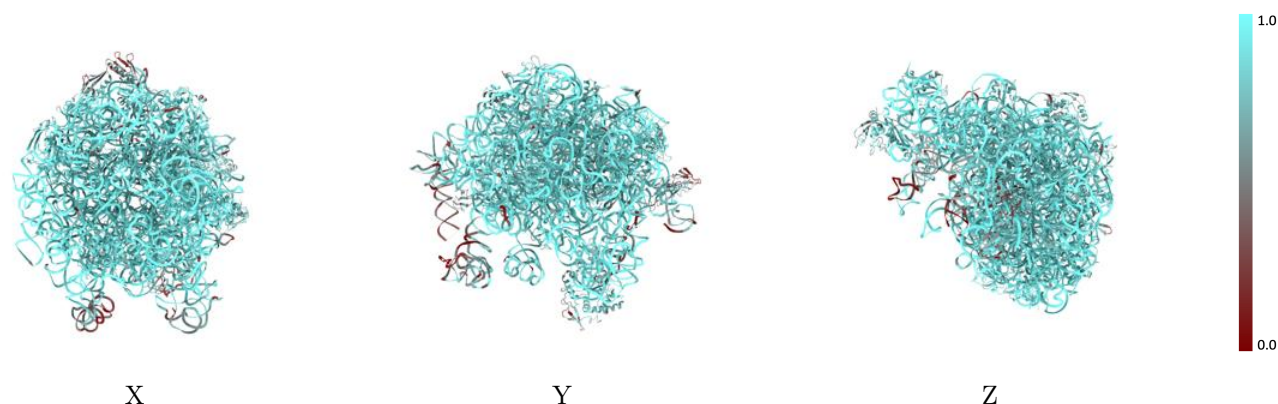
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



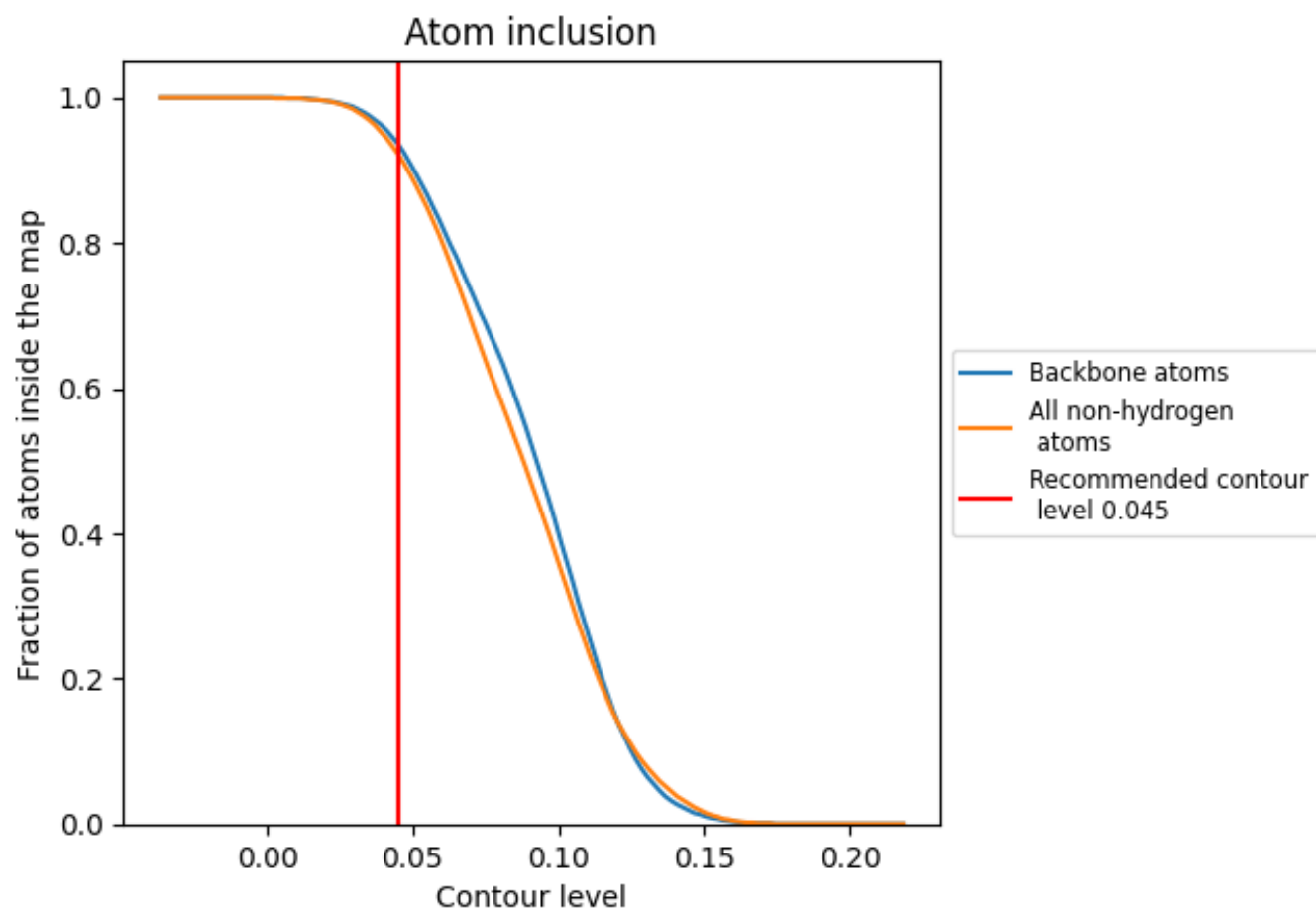
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9220	 0.4790
1	 0.9330	 0.5030
2	 0.8750	 0.5020
3	 0.9080	 0.5350
4	 0.5750	 0.2580
5	 0.8580	 0.5330
6	 0.8320	 0.4410
7	 0.9940	 0.5520
8	 0.9540	 0.5470
A	 0.9350	 0.4760
B	 0.9700	 0.4650
C	 0.8740	 0.2920
E	 0.9700	 0.5510
F	 0.9260	 0.5370
G	 0.8770	 0.5180
H	 0.8110	 0.4510
I	 0.5250	 0.2920
J	 0.6430	 0.3650
M	 0.9310	 0.5380
N	 0.9420	 0.5390
O	 0.9030	 0.5340
Q	 0.9620	 0.5480
R	 0.8480	 0.4800
S	 0.9210	 0.5280
T	 0.9510	 0.5440
U	 0.8850	 0.5530
V	 0.9540	 0.5450
W	 0.9060	 0.5270
X	 0.8140	 0.4930
Z	 0.9370	 0.5390

