



Full wwPDB EM Validation Report ⓘ

Sep 6, 2026 – 06:20 PM EDT

PDB ID : 11HE / pdb_000011he
EMDB ID : EMD-75687
Title : Rabbit 60S ribosomal subunit with eEF2 domain IV closed
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-24
Resolution : 2.86 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

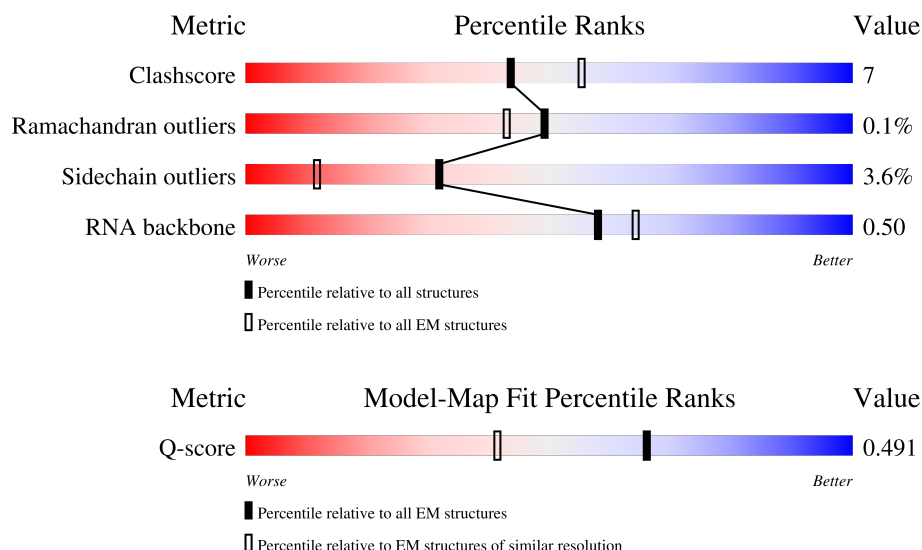
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.86 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.



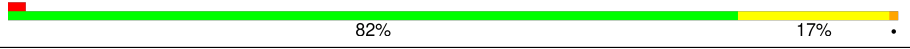
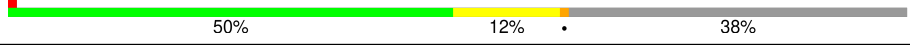
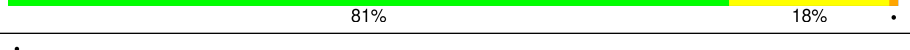
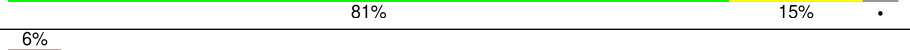
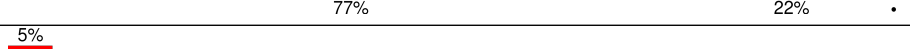
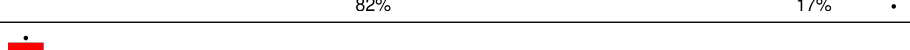
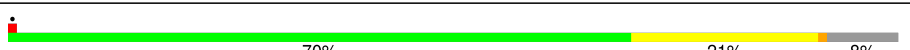
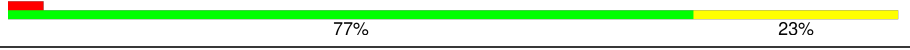
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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	58	156	
2	5	120	
3	L8	345	

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Mol	Chain	Length	Quality of chain
4	L3	394	
5	L4	362	
6	L5	293	
7	L6	347	
8	L7	225	
9	aa	240	
10	L9	190	
11	10	213	
12	11	170	
13	13	210	
14	14	138	
15	15	203	
16	bb	199	
17	17	153	
18	19	180	
19	20	192	
20	21	159	
21	22	99	
22	23	131	
23	24	63	
24	cc	118	
25	26	134	
26	27	135	
27	dd	147	
28	29	245	

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Mol	Chain	Length	Quality of chain
29	30	98	
30	31	107	
31	32	128	
32	ee	109	
33	34	114	
34	35	122	
35	36	102	
36	37	86	
37	38	69	
38	39	50	
39	40	52	
40	42	104	
41	ff	91	
42	gg	124	
43	s	196	
44	t	153	
45	EB	375	
46	u	206	
47	Q	188	
48	ES	5070	
49	28	4807	
50	v	857	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 147611 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	394	Total	C	N	O	S	0	0
			3173	2020	597	543	13		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	362	Total	C	N	O	S	0	0
			2884	1812	577	481	14		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	293	Total	C	N	O	S	0	0
			2392	1512	438	428	14		

- Molecule 7 is a protein called large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	216	Total	C	N	O	S	0	0
			1728	1115	329	281	3		

- Molecule 8 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 9 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	aa	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	190	Total	C	N	O	S	0	0
			1517	954	284	273	6		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	11	170	Total	C	N	O	S	0	0
			1363	861	254	242	6		

- Molecule 13 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	14	138	Total	C	N	O	S	0	0
			1138	727	221	183	7		

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 16 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	bb	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	17	153	Total	C	N	O	S	0	0
			1243	777	241	216	9		

- Molecule 18 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	19	159	Total	C	N	O	S	0	0
			1325	825	283	208	9		

- Molecule 19 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	20	176	Total	C	N	O	S	0	0
			1461	930	285	235	11		

- Molecule 20 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 21 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	22	99	Total	C	N	O	S	0	0
			810	519	141	148	2		

- Molecule 22 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	23	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 23 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	24	63	Total	C	N	O	S	0	0
			529	337	103	86	3		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	cc	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	26	134	Total	C	N	O	S	0	0
			1116	700	226	187	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	dd	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 28 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	30	98	Total	C	N	O	S	0	0
			762	481	134	141	6		

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	31	107	Total	C	N	O	S	0	0
			889	560	171	156	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	32	128	Total	C	N	O	S	0	0
			1054	667	216	166	5		

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ee	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 33 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	34	114	Total	C	N	O	S	0	0
			907	566	187	148	6		

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 35 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	36	102	Total	C	N	O	S	0	0
			831	520	176	130	5		

- Molecule 36 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	37	86	Total	C	N	O	S	0	0
			706	434	155	112	5		

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	42	104	Total	C	N	O	S	0	0
			852	533	174	139	6		

- Molecule 41 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	ff	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	gg	124	Total	C	N	O	S	0	0
			991	615	202	168	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1508	959	263	277	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1161	722	218	218	3		

- Molecule 45 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	EB	375	Total	C	N	O	S	0	0
			2932	1844	509	562	17		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	206	Total	C	N	O	S	0	0
			1655	1058	297	292	8		

- Molecule 47 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 48 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ES	67	Total	C	N	O	P	0	0
			1444	639	266	472	67		

- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	28	3486	Total	C	N	O	P	0	0
			74767	33297	13700	24284	3486		

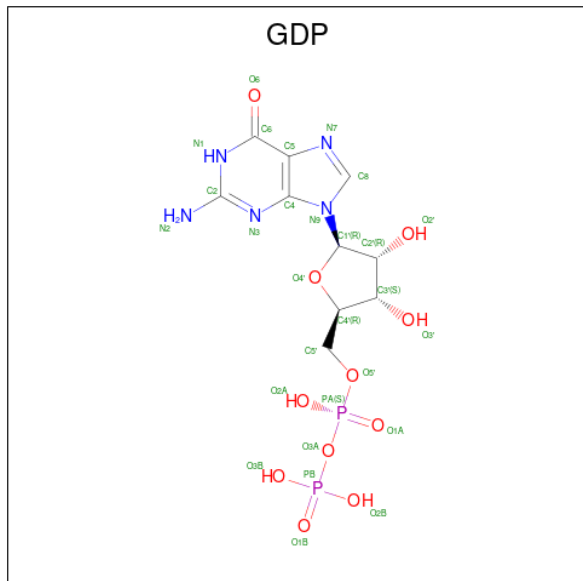
- Molecule 50 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	822	Total	C	N	O	S	0	0
			6409	4073	1097	1195	44		

- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	34	1	Total	Zn	0
			1	1	
51	37	1	Total	Zn	0
			1	1	
51	ff	1	Total	Zn	0
			1	1	

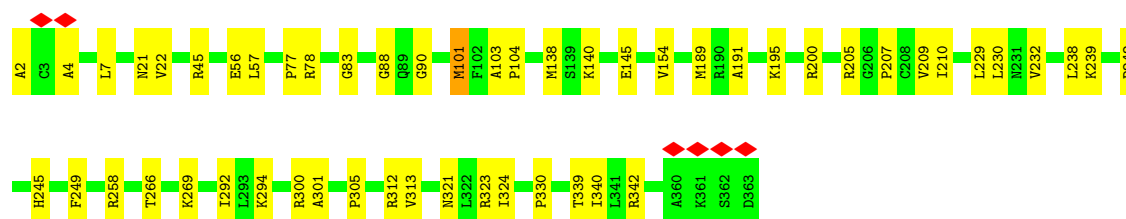
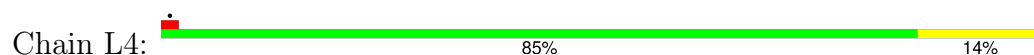
- Molecule 52 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



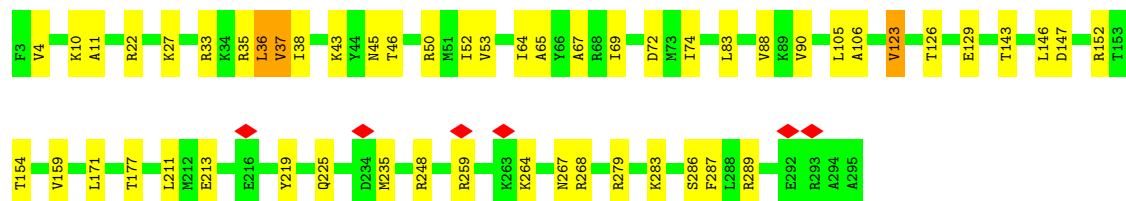
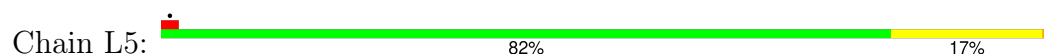
Mol	Chain	Residues	Atoms					AltConf
52	v	1	Total	C	N	O	P	0
			28	10	5	11	2	



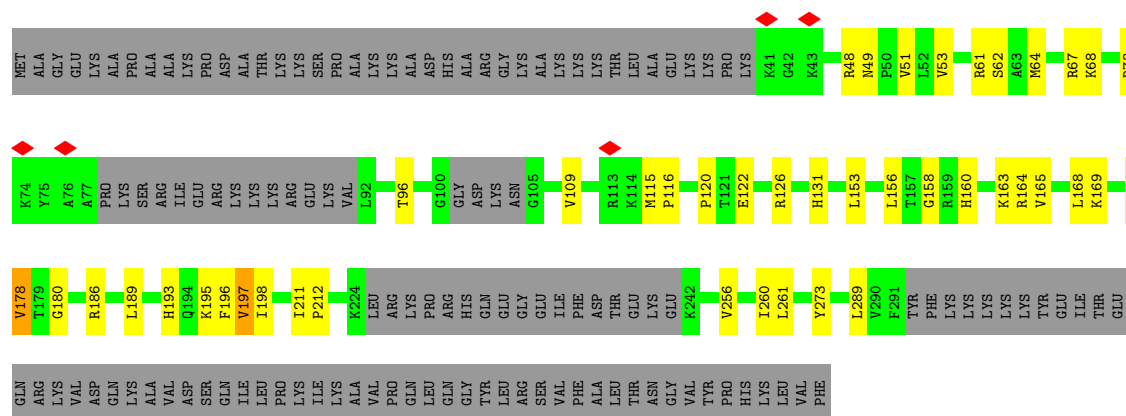
- Molecule 5: 60S ribosomal protein L4



- Molecule 6: 60S ribosomal protein L5

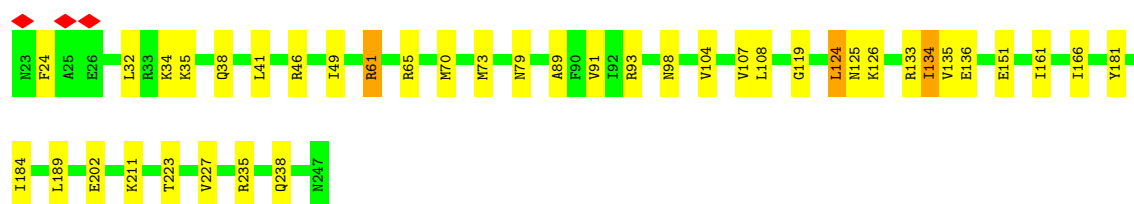


- Molecule 7: large ribosomal subunit protein eL6



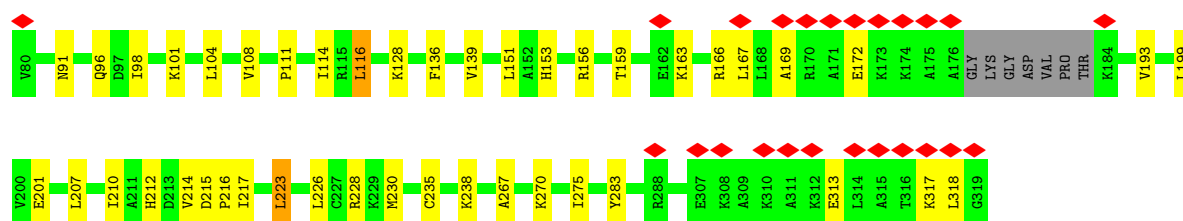
- Molecule 8: 60S ribosomal protein L7

Chain L7: 



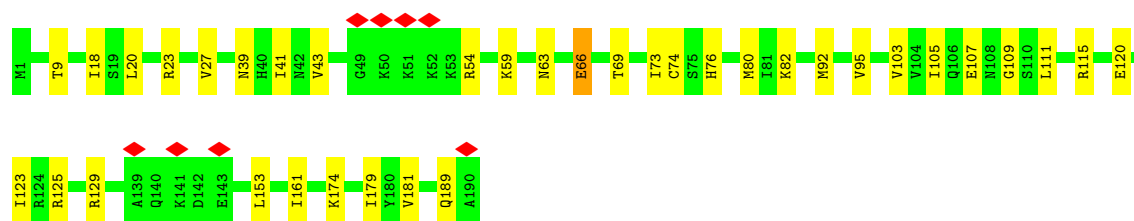
- Molecule 9: Large ribosomal subunit protein eL8

Chain aa: 



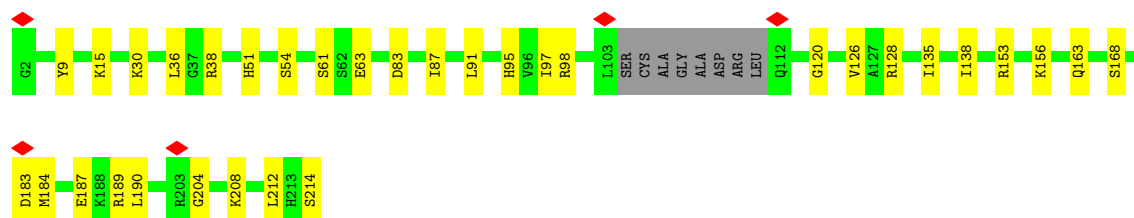
- Molecule 10: 60S ribosomal protein L9

Chain L9: 



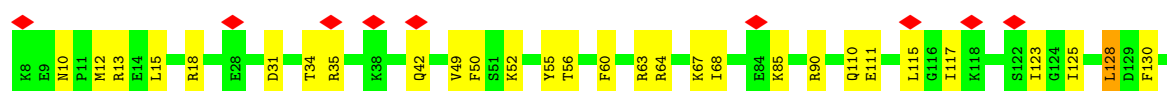
- Molecule 11: Ribosomal protein L10

Chain 10: 



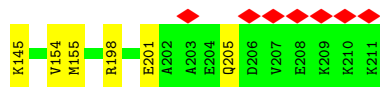
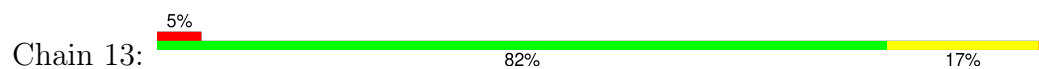
- Molecule 12: 60S ribosomal protein L11

Chain 11: 

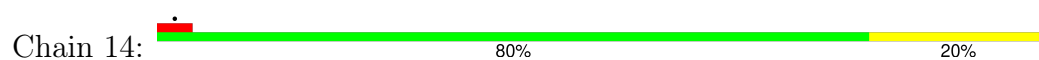




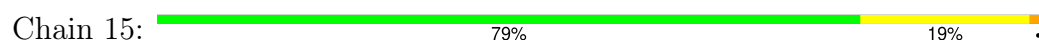
- Molecule 13: Large ribosomal subunit protein eL13



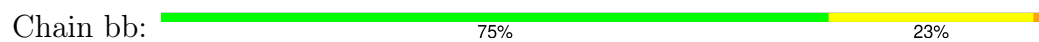
- Molecule 14: 60S ribosomal protein L14



- Molecule 15: 60S ribosomal protein L15



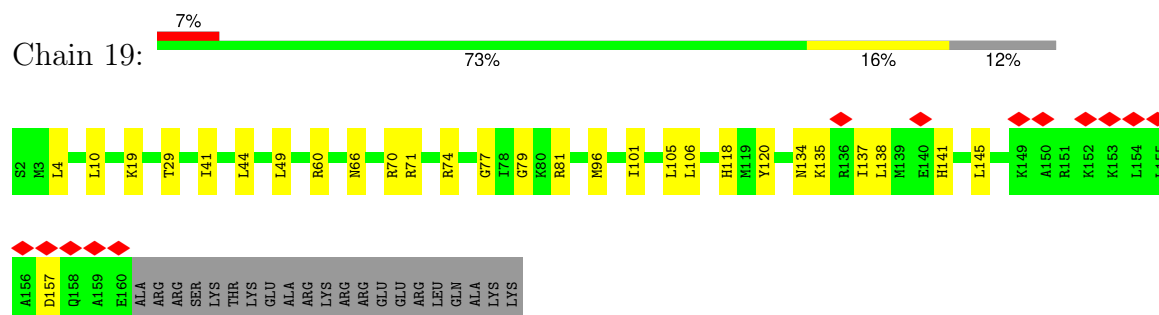
- Molecule 16: Large ribosomal subunit protein uL13



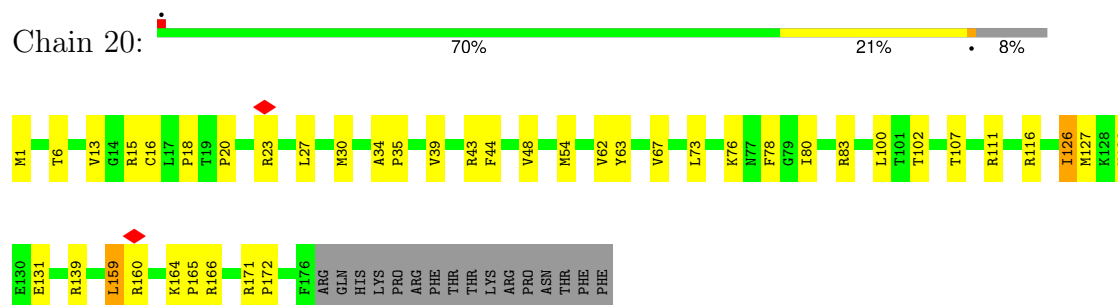
- Molecule 17: 60S ribosomal protein L17



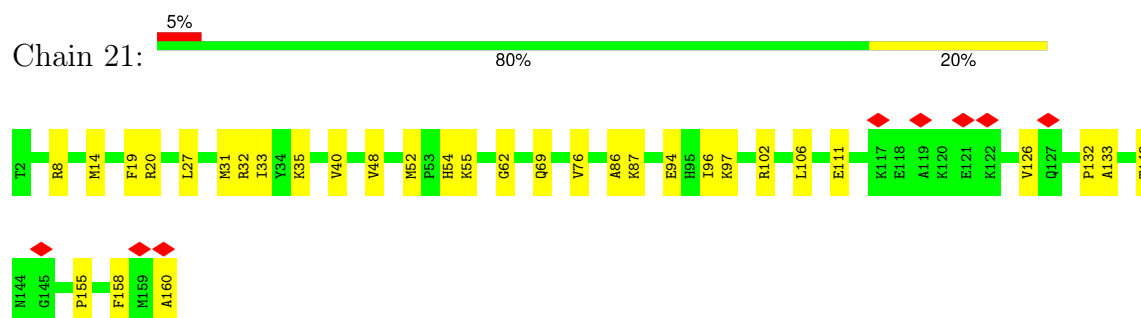
- Molecule 18: 60S ribosomal protein L19



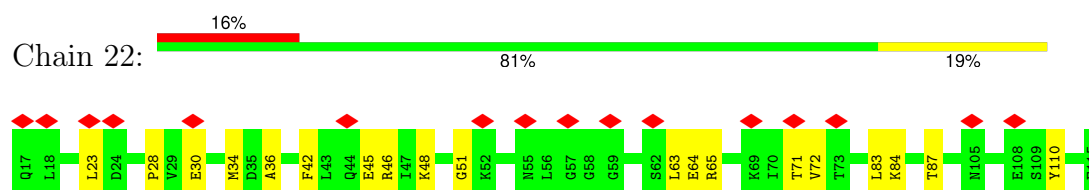
- Molecule 19: Large ribosomal subunit protein eL20



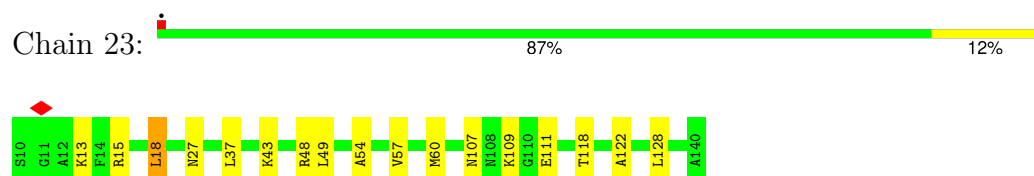
- Molecule 20: 60S ribosomal protein L21



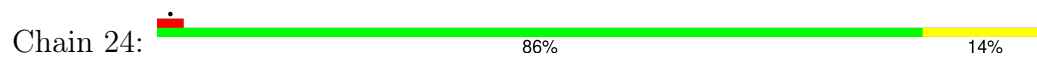
- Molecule 21: Large ribosomal subunit protein eL22



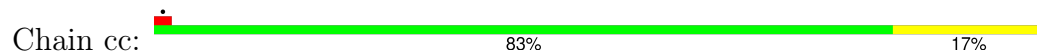
- Molecule 22: 60S ribosomal protein L23



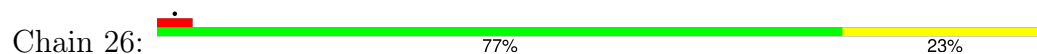
- Molecule 23: Ribosomal protein L24



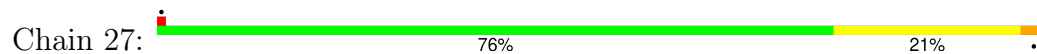
- Molecule 24: Large ribosomal subunit protein uL23



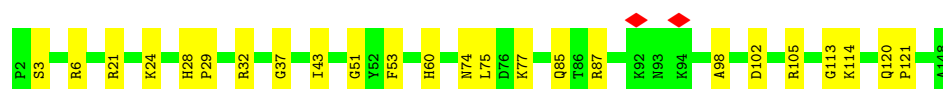
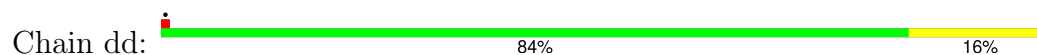
- Molecule 25: 60S ribosomal protein L26



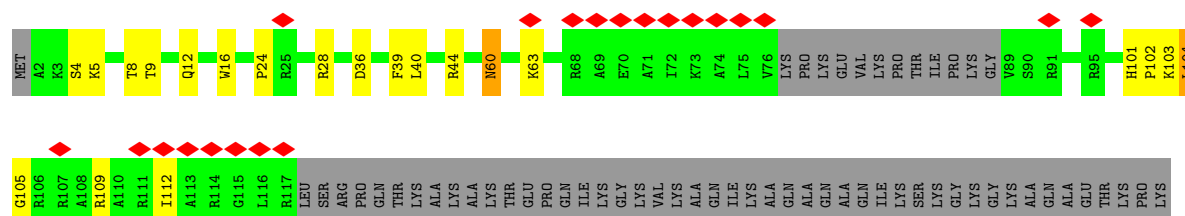
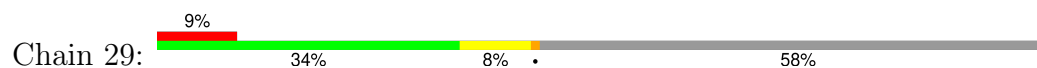
- Molecule 26: 60S ribosomal protein L27



- Molecule 27: 60S ribosomal protein L27a

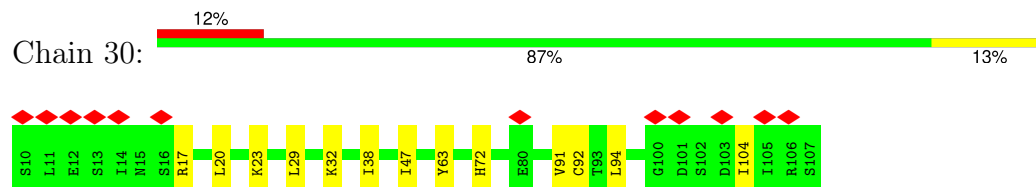


- Molecule 28: Large ribosomal subunit protein eL29

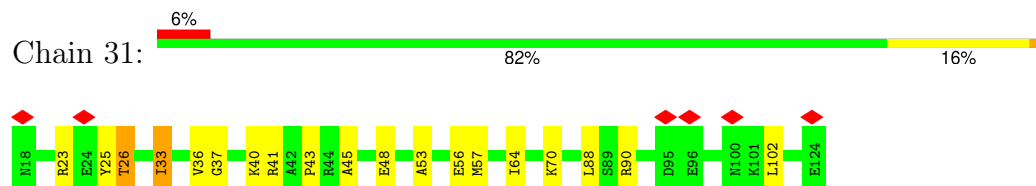


[illegible]

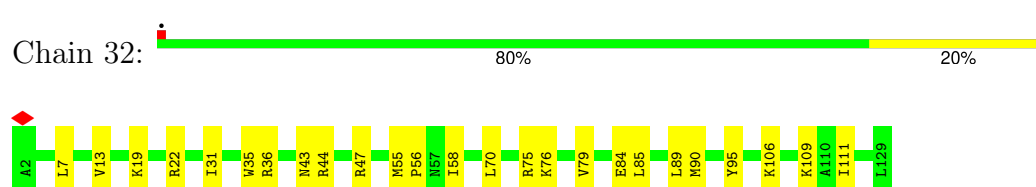
- Molecule 29: 60S ribosomal protein L30



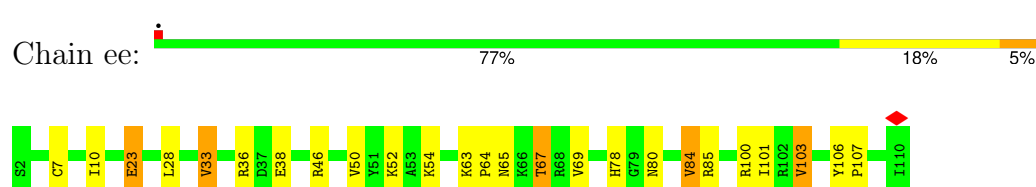
- Molecule 30: 60S ribosomal protein L31



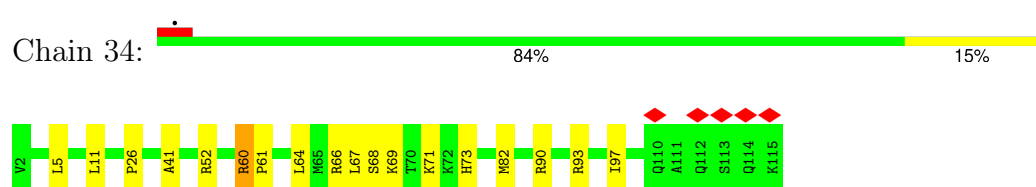
- Molecule 31: Large ribosomal subunit protein eL32



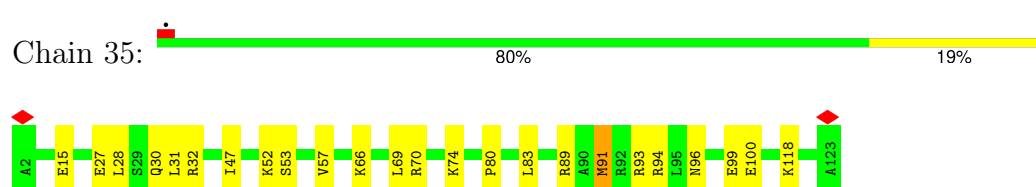
- Molecule 32: Large ribosomal subunit protein eL33



- Molecule 33: 60S ribosomal protein L34

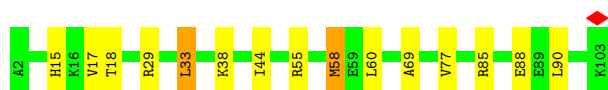


- Molecule 34: 60S ribosomal protein L35



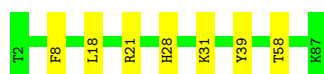
- Molecule 35: 60S ribosomal protein L36

Chain 36:  85% 13%



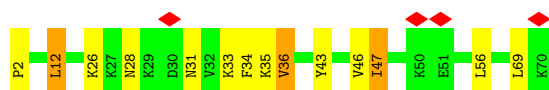
- Molecule 36: 60S ribosomal protein L37

Chain 37:  92% 8%



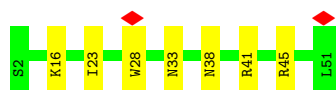
- Molecule 37: Large ribosomal subunit protein eL38

Chain 38:  6% 80% 16%



- Molecule 38: 60S ribosomal protein L39

Chain 39:  86% 14%



- Molecule 39: Large ribosomal subunit protein eL40

Chain 40:  6% 81% 17%



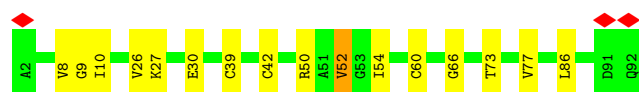
- Molecule 40: eL42

Chain 42:  82% 17%

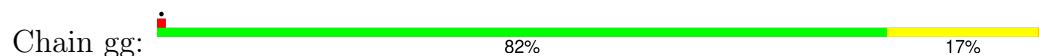


- Molecule 41: 60S ribosomal protein L37a

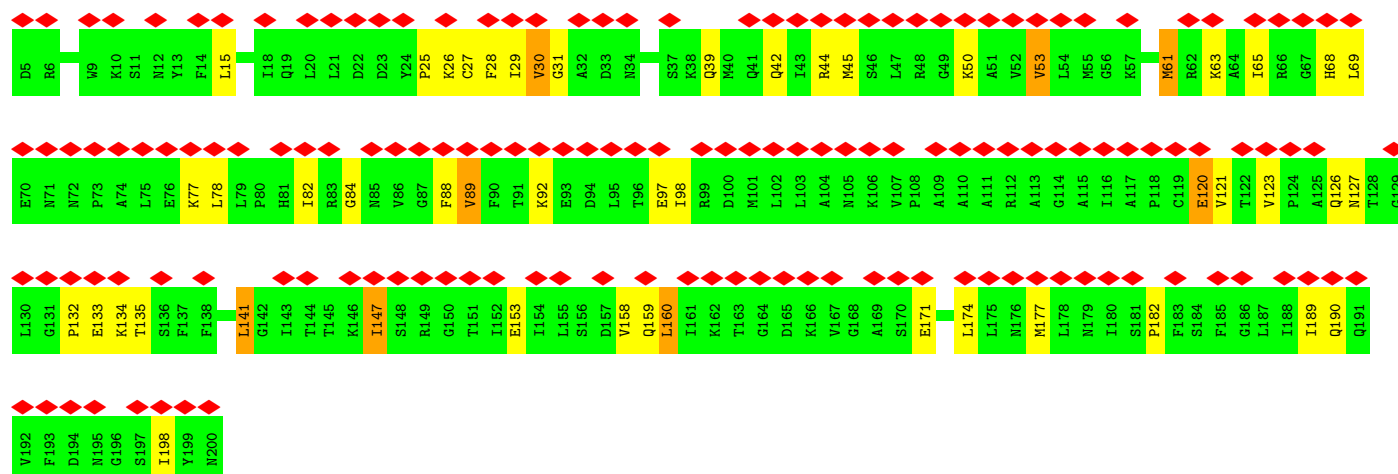
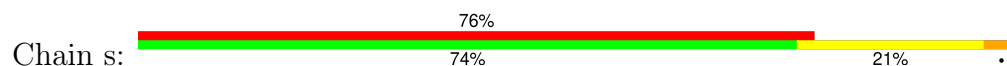
Chain ff:  82% 16%



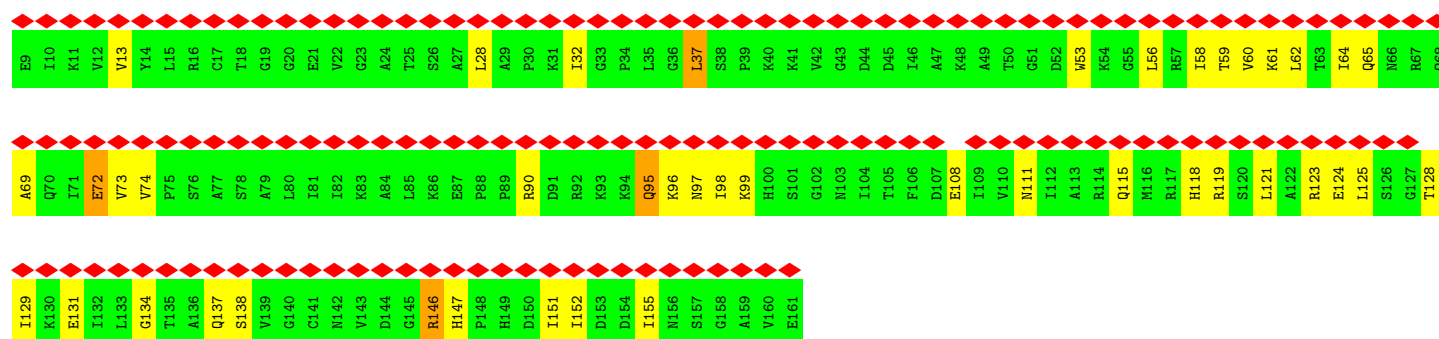
- Molecule 42: 60S ribosomal protein L28



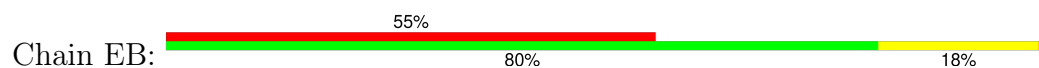
- Molecule 43: 60S acidic ribosomal protein P0

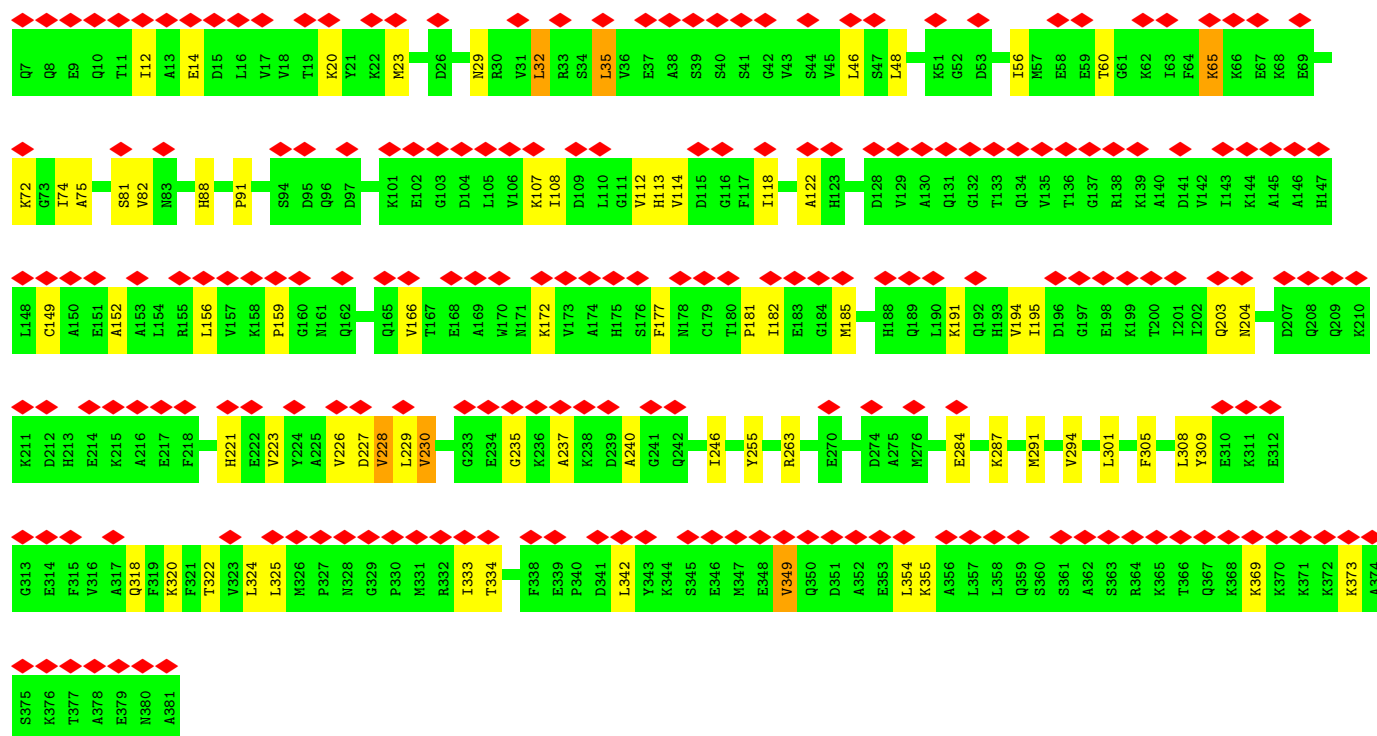


- Molecule 44: uL11

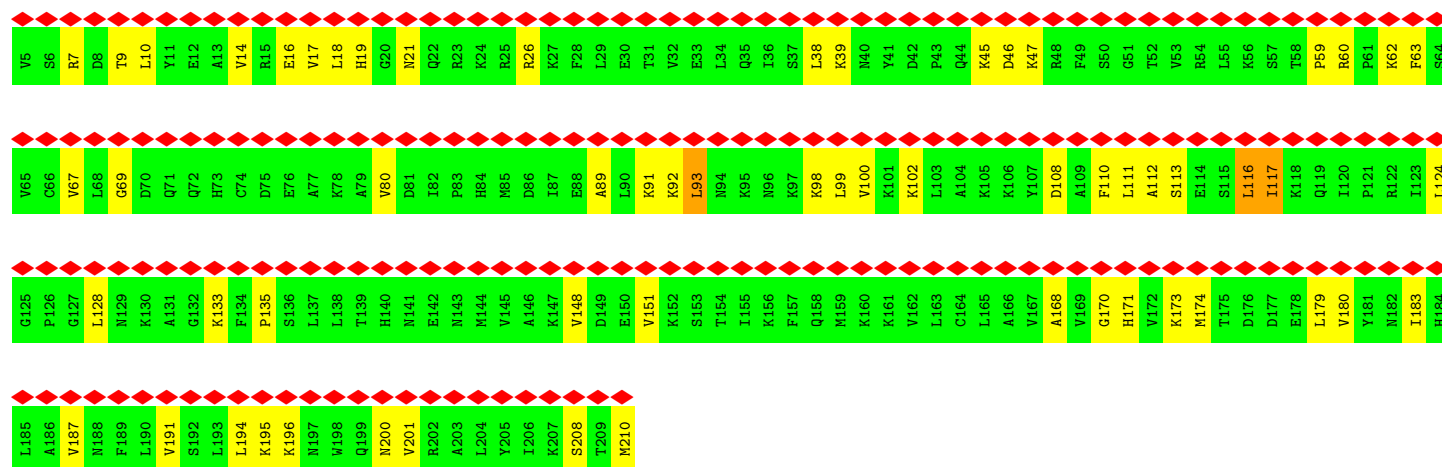
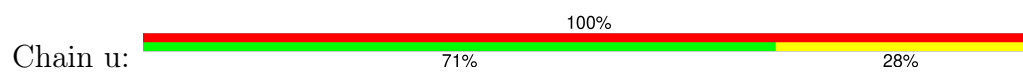


- Molecule 45: Proliferation-associated protein 2G4

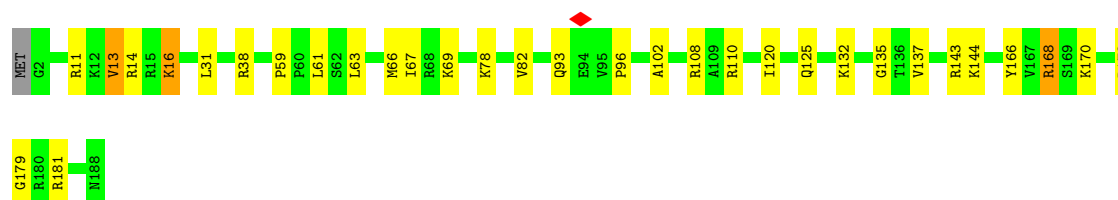
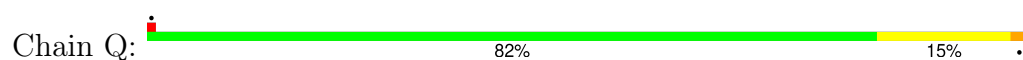




• Molecule 46: 60S ribosomal protein L10a



• Molecule 47: Large ribosomal subunit protein eL18

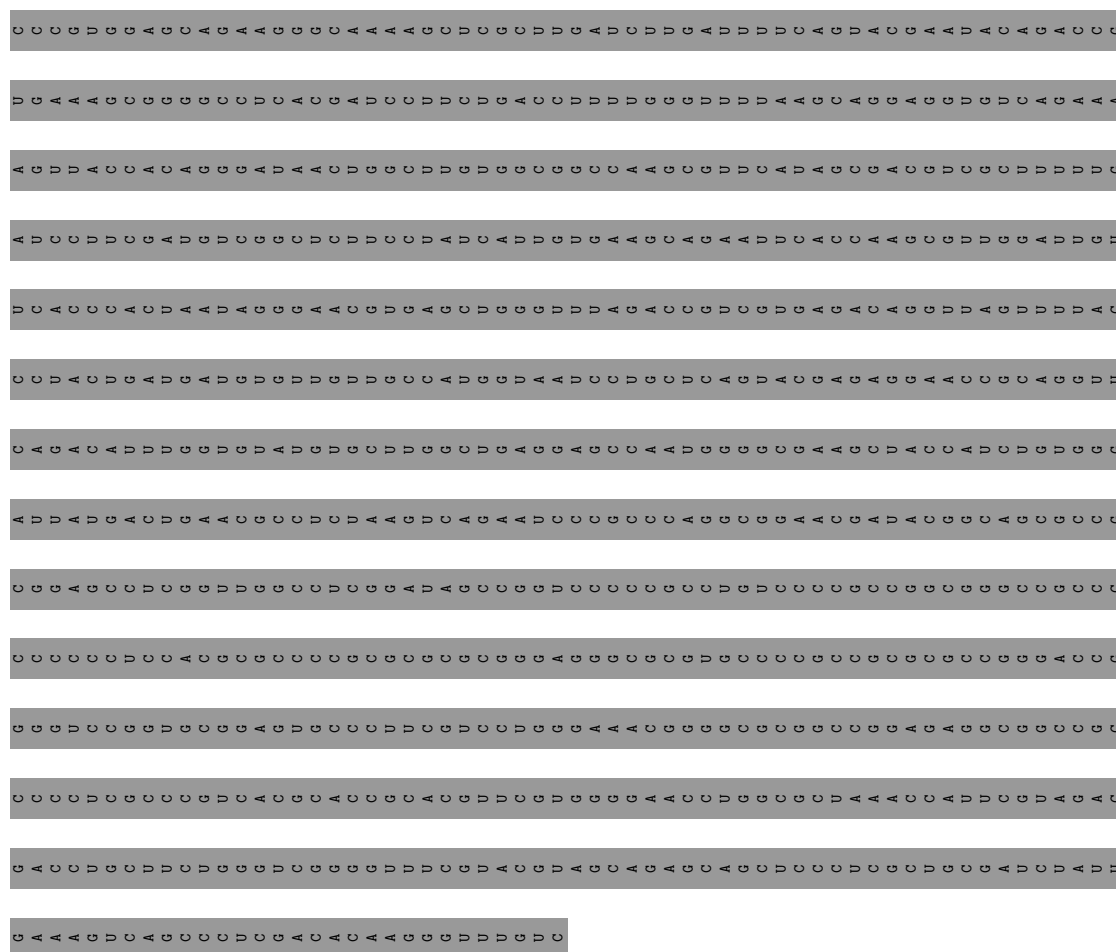


Chain ES: 99%



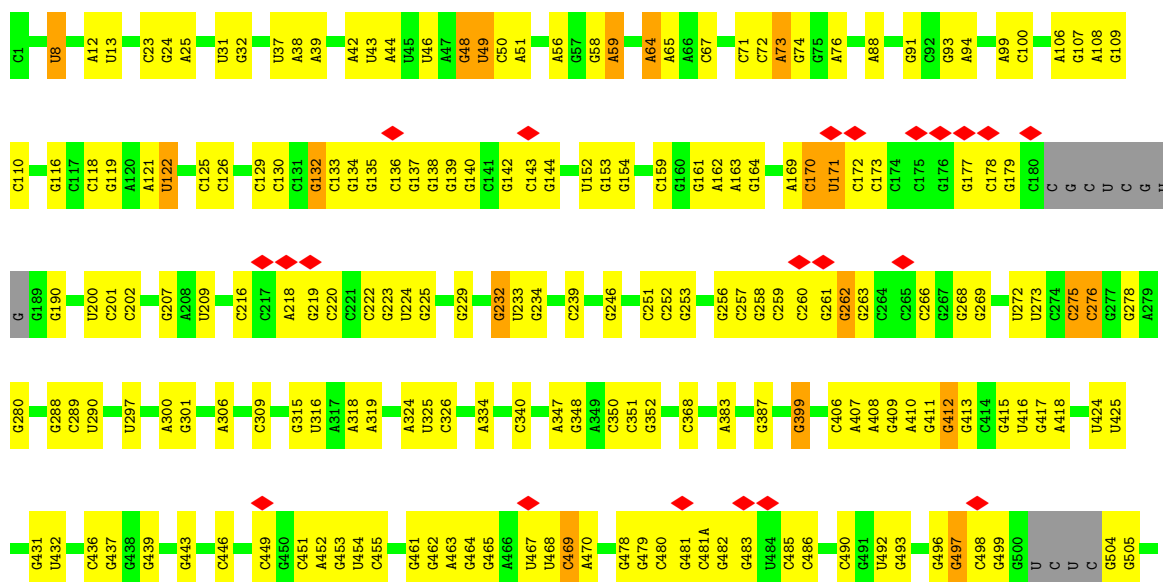






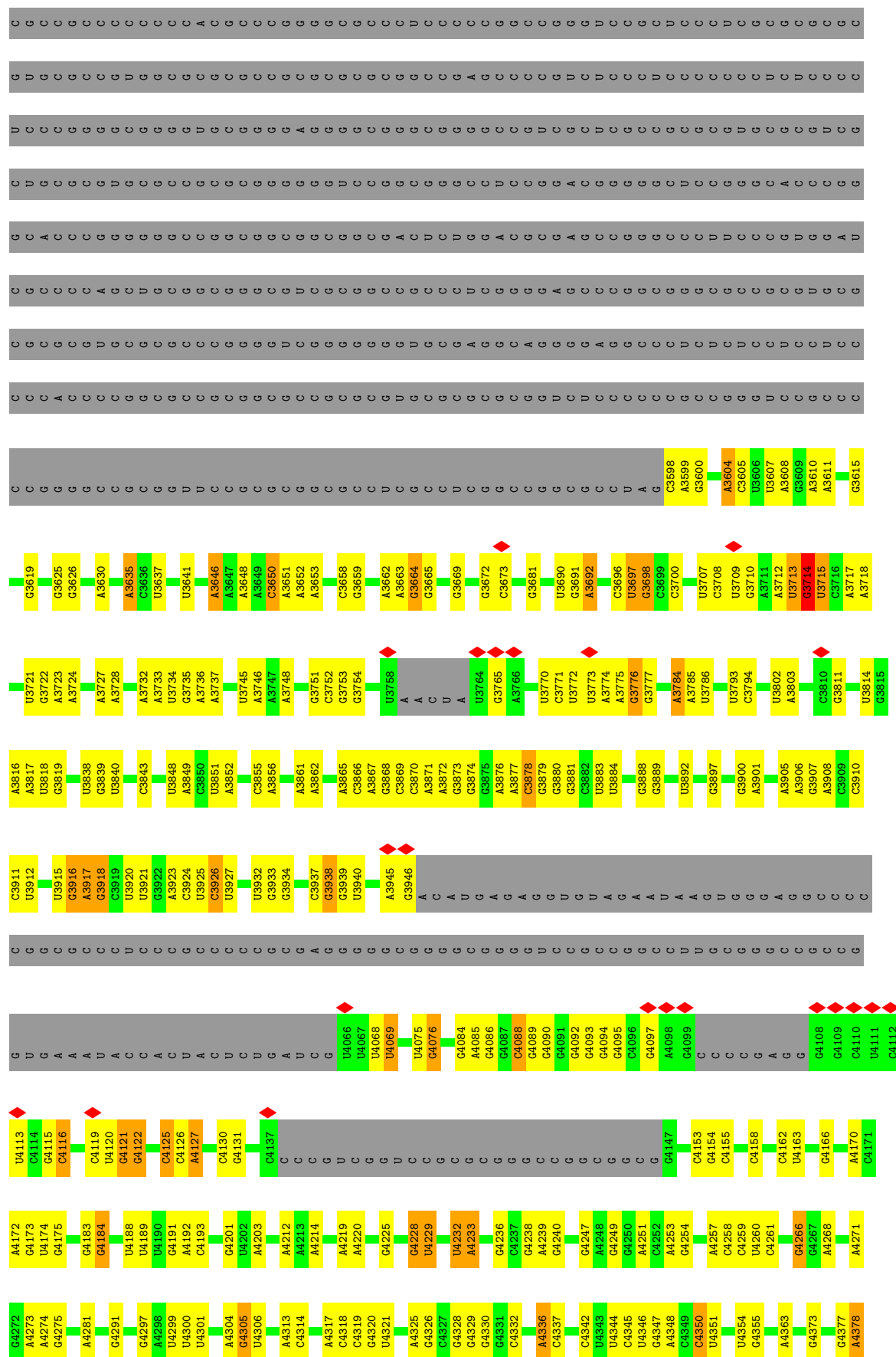
• Molecule 49: 28S rRNA

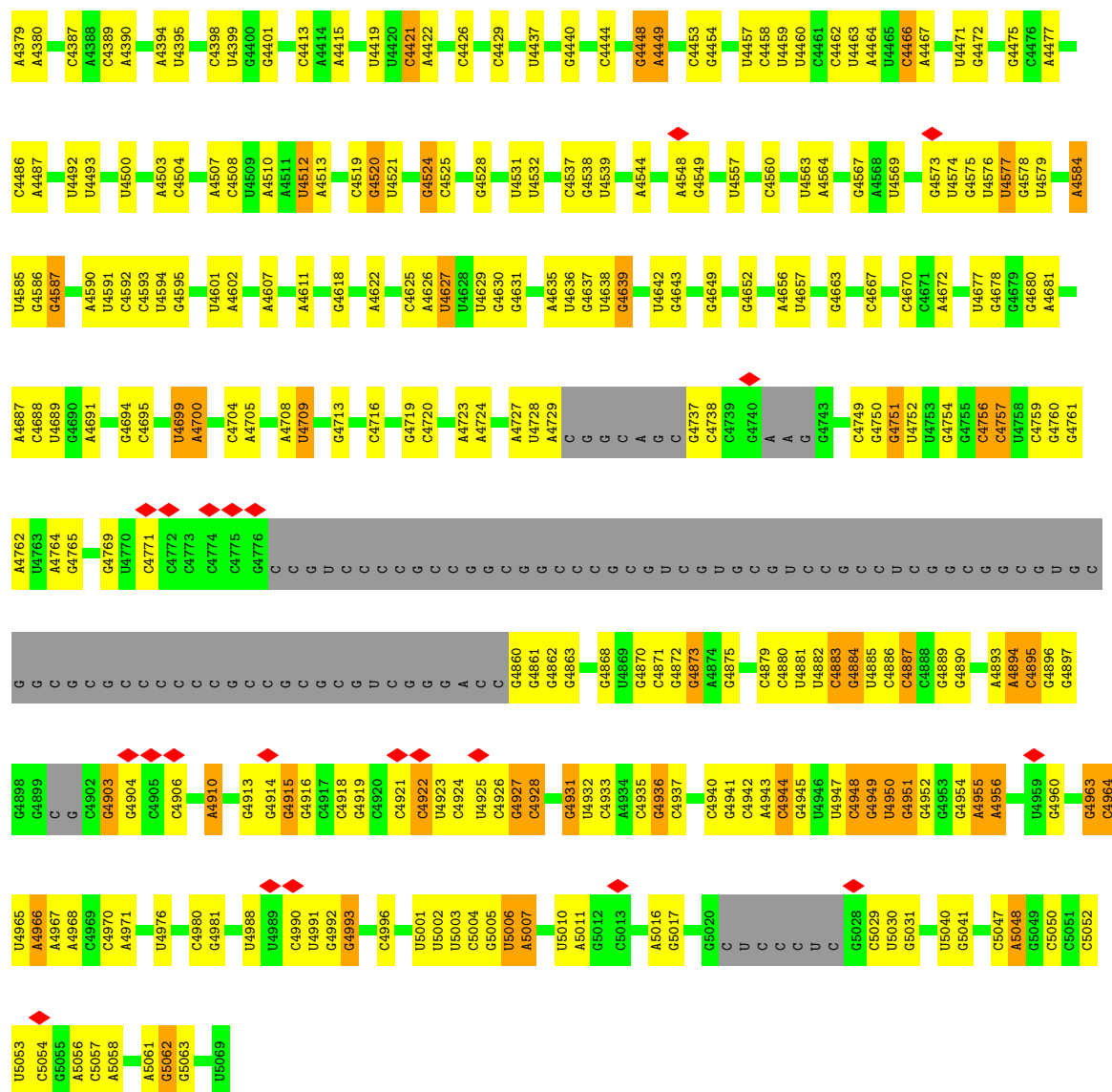
Chain 28: 41% 27% 27%



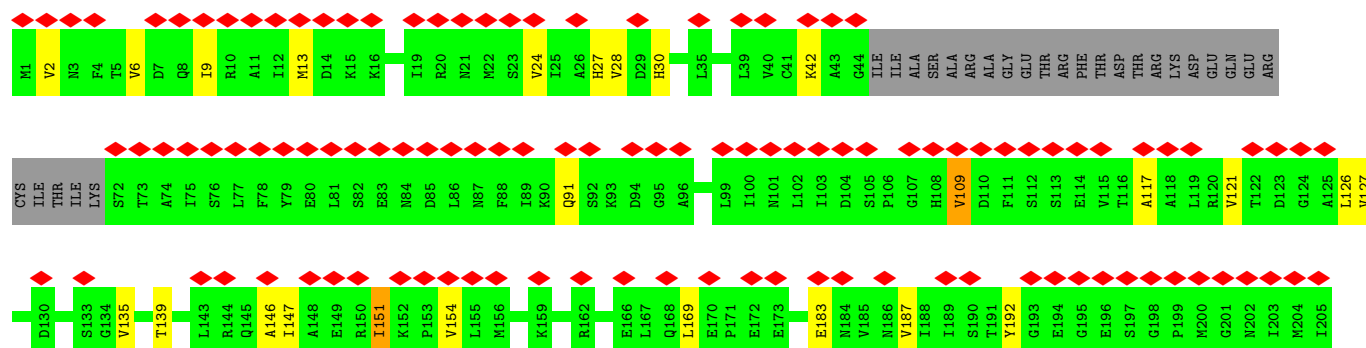
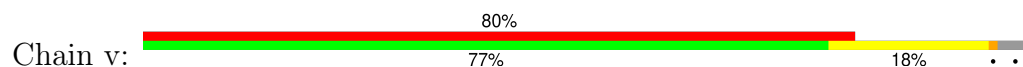


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C	A2787	U2708	G	A2507	G	G	G	G1975	G1884	U1781	G1676	G1559
C	U2788	C2709	G	A2513	G2421	G2297	G2055	G1976	G1885	A1787	U1677	A1560
G	A2789	C2710	A2623	G2519	C2422	U2300	A2056	G1977	C1893	A1788	A1682	G1561
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C	G2712	C2712	G	G2521	U2428	G2306	C2058	U1979	G1980	U1790	U1684	A1563
U	G2713	G2713	G	G2522	G	G	C	U1980	G1981	A1794	G1685	A1564
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G	U2716	U2716	G	U2530	U2439	A2313	A2069	A1984	C1914	G	G1574	G1574
G	U2717	U2717	G	A2537	G2440	A2314	U2070	G1985	A1802	A1802	C1696	G1577
G	U2718	U2718	G	U2538	C2441	G2315	G2075	U1986	G1803	G	G	U1578
C	U2719	U2719	G	U2539	G2448	G2316	G2076	G1987	A1804	A1804	C	G
G	G2720	U2720	G	U2540	G2450	G2317	U2079	G1988	A1805	A1805	A	G
G	G2721	U2721	G	C2541	G2453	G2318	G2080	G1989	G1806	G1806	A	G
G	G2722	U2722	G	G2542	G2457	G2330	G2081	U1990	G1807	G1807	C	G
G	U2723	U2723	G	A2543	G2461	G2331	G2082	A1991	C1808	C1808	C	U1591
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C	G2900	U2776	G	U2609	G2522	A2404	G2139	U2044	U1989	U1989	U1795	C1662





• Molecule 50: Elongation factor 2



Q818	I819	L820	P821	G822	D823	P824	M824	F825	D826	M827	S828	S829	P831	S832	Q833	V834	V835	A836	E837	T838	R839	K840	L841	LYS	GLY	LEU	LYS	GLU	ILE	A725	R726	L788	P789	V790	M791	E792	S793	F794	G795	F796	T797	A798	D799	L800	R801	S802	T804	G805	G806	Q807	A808	F809	P810	Q811	C812	V813	F814	D815	H816	W817
M697	R698	G699	V700	R701	F702	D703	V704	H705	D706	V707	T708	L709	H710	A711	D712	A713	L714	H715	R716	G717	G718	G719	Q720	I721	I722	P723	T724	A725	R726	K727	C728	L729	V730	A731	S732	V733	L734	T735	A736	Q737	P738	R739	L740	M741	P743	G744	V745	L746	V747	E748	I749	Q750	C751	P752	E753	Q754	V755	V756		
E637	K638	V639	E640	M641	D642	V643	A644	E645	A646	R647	K648	I649	V650	C651	F652	G653	P654	D655	G656	T657	G658	P659	M660	L661	L662	T663	D664	T665	T666	K667	G668	V669	Q670	D611	G612	L613	A614	E615	D616	L617	D618	K619	G620	E621	V622	S623	A624	R625	Q626	E627	L628	K629	Q630	R631	A632	R633	Y634	L635	A636	
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L517	P518	K519	V520	V521	E522	G523	L524	K525	R526	L527	A528	K529	S530	D531	P532	M533	V534	Q535	C536	I537	I538	E539	E540	S541	G542	E543	H544	I545	I546	A547	G548	A549	G550	E551	L552	H553	L554	E555	I556	C557	L558	K559	D560	L561	E562	E563	D564	H565	A566	C567	I568	P569	I570	K571	K572	S573	D574	P575	V576	
Y457	V458	E459	P460	T461	E462	D463	V464	P465	C466	G467	R468	I469	V470	G471	L472	V473	G474	V475	D476	Q477	F478	L479	V480	K481	T482	G483	T484	L485	T486	T487	F488	E489	H490	G491	H492	M493	M494	R495	V496	M497	K498	F499	S500	V501	S502	P503	V504	V505	R506	V507	A508	V509	E510	A511	N512	P513	P514	A515	D516	
Y397	I398	S399	K400	M401	V402	P403	T404	S405	D406	K407	G408	R409	F410	Y411	A412	F413	G414	R415	V416	F417	S418	G419	L420	V421	S422	T423	G424	L425	K426	V427	R428	I429	M430	G431	P432	N433	Y434	T435	P436	D437	K438	D439	E440	A441	L442	V443	L444	K445	C388	D389	P390	K391	G392	P393	L394	M395	M396			
K333	P334	L335	L336	A337	A338	R342	M343	A346	G347	D348	A349	L350	M353	I354	T355	I356	H357	L358	P359	S360	P361	V362	T363	A364	Q365	K366	Y367	R368	C369	E370	L371	L372	Y373	E374	G375	P376	P377	D378	D379	E380	A381	A382	M383	G384	I385	K386	S387	C388	D389	P390	K391	G392	P393	L394	M395	M396				
N270	G271	K272	F273	S274	K275	S276	A277	P280	E281	G282	K283	K284	L285	P286	R287	C290	Q291	L292	I293	L294	D295	I296	I297	F298	K299	V300	F301	D302	A303	I304	G242	Q243	L244	G245	P246	A247	E248	R249	A250	K251	K252	V253	E254	D255	M256	M257	K258	K259	L260	V261	G262	D263	R264	D267	P268	A269				
D206	P207	V208	T211	V212	G213	F214	G215	L218	H219	G220	V221	A222	F223	T224	L225	K226	A229	E230	M231	Y232	V233	A234	K235	F236	A237	A238	K239	G240	E241	G242	Q243	L244	G245	P246	A247	E248	R249	A250	K251	K252	V253	E254	D255	M256	M257	K258	K259	L260	V261	G262	D263	R264	D267	P268	A269					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22323	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	31.991	Depositor
Minimum map value	-14.192	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.049	Depositor
Recommended contour level	3.8	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

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

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	58	0.19	0/3581	0.29	0/5577
2	5	0.17	0/2858	0.25	0/4455
3	L8	0.20	0/1936	0.36	0/2596
4	L3	0.20	0/3241	0.33	0/4339
5	L4	0.19	0/2938	0.31	0/3946
6	L5	0.17	0/2438	0.33	0/3264
7	L6	0.17	0/1761	0.31	0/2362
8	L7	0.20	0/1911	0.31	0/2549
9	aa	0.19	0/1910	0.34	0/2569
10	L9	0.19	0/1536	0.36	0/2063
11	10	0.19	0/1702	0.31	0/2272
12	11	0.20	0/1386	0.37	0/1852
13	13	0.18	0/1733	0.34	0/2316
14	14	0.17	0/1159	0.32	0/1547
15	15	0.22	0/1746	0.37	0/2338
16	bb	0.21	0/1662	0.35	0/2222
17	17	0.19	0/1269	0.35	0/1700
18	19	0.16	0/1341	0.29	0/1776
19	20	0.19	0/1500	0.33	0/2012
20	21	0.19	0/1326	0.30	0/1770
21	22	0.15	0/824	0.34	0/1104
22	23	0.19	0/993	0.32	0/1332
23	24	0.18	0/542	0.30	0/720
24	cc	0.18	0/984	0.30	0/1323
25	26	0.18	0/1133	0.34	0/1504
26	27	0.16	0/1130	0.29	0/1507
27	dd	0.20	0/1191	0.31	0/1590
28	29	0.16	0/861	0.28	0/1138
29	30	0.15	0/772	0.29	0/1034
30	31	0.19	0/904	0.33	0/1216
31	32	0.20	0/1072	0.34	0/1429
32	ee	0.22	0/895	0.37	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	34	0.18	0/917	0.33	0/1220
34	35	0.16	0/1021	0.32	0/1348
35	36	0.17	0/842	0.30	0/1112
36	37	0.20	0/721	0.31	0/952
37	38	0.18	0/575	0.35	0/761
38	39	0.21	0/459	0.34	0/608
39	40	0.17	0/435	0.33	0/575
40	42	0.18	0/865	0.31	0/1140
41	ff	0.18	0/718	0.35	0/953
42	gg	0.19	0/1007	0.33	0/1349
43	s	0.15	0/1531	0.36	0/2064
44	t	0.15	0/1175	0.40	0/1582
45	EB	0.14	0/2979	0.30	0/4000
46	u	0.15	0/1681	0.38	0/2255
47	Q	0.21	0/1539	0.36	0/2054
48	ES	0.17	0/1609	0.38	0/2502
49	28	0.20	1/83633 (0.0%)	0.32	5/130425 (0.0%)
50	v	0.21	0/6536	0.41	0/8828
All	All	0.19	1/158478 (0.0%)	0.32	5/232348 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
50	v	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	28	3715	U	O3'-P	-12.54	1.42	1.61

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	28	3715	U	P-O3'-C3'	14.39	141.79	120.20
49	28	3714	G	O3'-P-O5'	-14.35	82.48	104.00
49	28	3715	U	OP2-P-O3'	-9.77	78.69	108.00
49	28	3715	U	O3'-P-O5'	8.50	116.75	104.00
49	28	3714	G	P-O3'-C3'	-5.79	111.51	120.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	v	500	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	58	3208	0	1629	39	0
2	5	2558	0	1296	21	0
3	L8	1898	0	1993	38	0
4	L3	3173	0	3310	53	0
5	L4	2884	0	3053	35	0
6	L5	2392	0	2424	36	0
7	L6	1728	0	1887	31	0
8	L7	1875	0	1995	26	0
9	aa	1879	0	2027	25	0
10	L9	1517	0	1597	22	0
11	10	1664	0	1712	19	0
12	11	1363	0	1399	23	0
13	13	1702	0	1820	23	0
14	14	1138	0	1211	16	0
15	15	1701	0	1749	33	0
16	bb	1630	0	1778	33	0
17	17	1243	0	1274	10	0
18	19	1325	0	1457	20	0
19	20	1461	0	1508	32	0
20	21	1298	0	1366	26	0
21	22	810	0	833	9	0
22	23	979	0	1039	10	0
23	24	529	0	541	5	0
24	cc	967	0	1040	12	0
25	26	1116	0	1205	17	0
26	27	1107	0	1182	15	0
27	dd	1162	0	1209	24	0
28	29	848	0	920	14	0
29	30	762	0	794	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	31	889	0	930	15	0
31	32	1054	0	1147	16	0
32	ee	876	0	912	19	0
33	34	907	0	998	11	0
34	35	1013	0	1147	19	0
35	36	831	0	916	7	0
36	37	706	0	737	3	0
37	38	569	0	637	10	0
38	39	447	0	480	6	0
39	40	429	0	469	6	0
40	42	852	0	924	13	0
41	ff	708	0	756	10	0
42	gg	991	0	1044	13	0
43	s	1508	0	1564	27	0
44	t	1161	0	1218	32	0
45	EB	2932	0	2967	40	0
46	u	1655	0	1760	37	0
47	Q	1515	0	1634	25	0
48	ES	1444	0	735	35	0
49	28	74767	0	37771	800	0
50	v	6409	0	6476	83	0
51	34	1	0	0	0	0
51	37	1	0	0	0	0
51	ff	1	0	0	0	0
52	v	28	0	12	0	0
All	All	147611	0	110482	1677	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (1677) 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)
41:ff:42:CYS:HB3	41:ff:60:CYS:SG	1.85	1.17
49:28:2007:G:H21	49:28:2012:A:N6	1.47	1.13
49:28:2007:G:N2	49:28:2012:A:H62	1.48	1.10
49:28:4421:C:H42	49:28:4475:G:N2	1.59	0.99
49:28:4421:C:N4	49:28:4475:G:H22	1.64	0.95
49:28:2638:G:H1	49:28:2697:A:H61	0.94	0.92
49:28:2557:G:H1	49:28:2570:U:H3	0.95	0.90
49:28:4887:C:H42	49:28:4932:U:H3	1.19	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:ES:2912:G:H1	48:ES:3282:U:H3	1.20	0.88
30:31:57:MET:HG3	30:31:90:ARG:HE	1.40	0.87
49:28:4421:C:H42	49:28:4475:G:H22	1.14	0.87
49:28:2638:G:H1	49:28:2697:A:N6	1.74	0.86
49:28:2638:G:N2	49:28:2697:A:N1	2.25	0.83
8:L7:61:ARG:HH22	8:L7:65:ARG:HH21	1.28	0.82
49:28:2492:C:H2'	49:28:2493:G:H8	1.43	0.81
3:L8:137:ILE:HD11	3:L8:149:LYS:HB3	1.62	0.81
16:bb:176:ARG:HD3	49:28:4769:G:H5'	1.62	0.81
10:L9:41:ILE:HG21	10:L9:73:ILE:HD11	1.61	0.81
20:21:87:LYS:HZ2	49:28:4305:G:H1	1.29	0.80
49:28:2845:A:H61	49:28:3843:C:H42	1.30	0.79
40:42:69:ARG:HG2	40:42:82:MET:HE1	1.65	0.78
49:28:138:G:H2'	49:28:139:G:C8	2.19	0.77
5:L4:323:ARG:HG3	49:28:1280:C:H2'	1.66	0.77
49:28:4886:C:H42	49:28:4933:C:H42	1.29	0.77
7:L6:96:THR:HG22	7:L6:109:VAL:HG22	1.67	0.76
8:L7:93:ARG:HE	8:L7:108:LEU:HD13	1.50	0.76
27:dd:85:GLN:HE22	49:28:508:G:H21	1.34	0.76
37:38:33:LYS:HG2	37:38:46:VAL:HG22	1.67	0.74
49:28:966:A:H62	49:28:2096:G:H2'	1.53	0.74
50:v:304:ILE:HG21	50:v:336:LEU:HB2	1.70	0.74
3:L8:82:ILE:HD11	3:L8:99:GLY:HA3	1.69	0.74
49:28:4949:G:H4'	49:28:4950:U:H5'	1.67	0.73
9:aa:139:VAL:HG21	9:aa:238:LYS:HG3	1.71	0.73
8:L7:227:VAL:HA	19:20:39:VAL:HG12	1.71	0.72
15:15:44:ARG:HH11	15:15:47:LYS:HB2	1.55	0.72
48:ES:2947:G:H1	48:ES:3247:A:H2	1.34	0.71
49:28:1332:C:H2'	49:28:1333:A:H8	1.52	0.71
49:28:2647:A:H62	49:28:2686:G:H8	1.38	0.71
15:15:125:SER:HB3	49:28:3937:C:H1'	1.72	0.71
48:ES:2955:A:H2	48:ES:3239:G:H1	1.39	0.71
3:L8:183:GLY:HA2	49:28:1613:A:H5''	1.72	0.70
3:L8:117:GLU:HB2	3:L8:162:ASN:HB2	1.73	0.70
7:L6:48:ARG:HB3	7:L6:67:ARG:HD3	1.71	0.70
42:gg:103:HIS:HD2	42:gg:106:LEU:HD22	1.55	0.70
49:28:137:G:H2'	49:28:138:G:C8	2.27	0.70
6:L5:83:LEU:HB3	6:L5:88:VAL:HB	1.73	0.70
12:11:111:GLU:HB2	12:11:125:ILE:HD11	1.72	0.70
17:17:126:ARG:HD3	17:17:140:MET:HE1	1.74	0.69
9:aa:111:PRO:HD2	9:aa:114:ILE:HD12	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4421:C:N4	49:28:4475:G:N2	2.30	0.69
49:28:1857:C:H2'	49:28:1858:A:H8	1.57	0.69
26:27:46:ILE:HD11	26:27:49:TYR:HA	1.75	0.69
5:L4:78:ARG:HB3	5:L4:88:GLY:HA2	1.74	0.69
32:ee:78:HIS:HB2	32:ee:85:ARG:HG3	1.74	0.69
46:u:148:VAL:HA	46:u:151:VAL:HG12	1.74	0.69
19:20:139:ARG:HH21	49:28:1952:G:H5'	1.58	0.68
15:15:50:ARG:HH11	49:28:278:G:H4'	1.58	0.68
24:cc:81:LEU:HD13	24:cc:97:VAL:HG12	1.75	0.68
49:28:4967:A:H2'	49:28:4968:A:H8	1.58	0.68
4:L3:95:THR:HG22	49:28:4910:A:H4'	1.74	0.68
50:v:327:ASP:HA	50:v:330:LYS:HE3	1.74	0.68
49:28:1199:G:H2'	49:28:1200:G:H8	1.59	0.68
46:u:39:LYS:HE2	46:u:200:ASN:HA	1.76	0.68
48:ES:3284:C:H2'	48:ES:3285:G:H8	1.58	0.67
49:28:1970:A:H5''	49:28:1971:U:H5'	1.77	0.67
46:u:26:ARG:HH21	46:u:210:MET:H	1.41	0.67
19:20:34:ALA:HB1	19:20:39:VAL:HG23	1.76	0.67
44:t:59:THR:HG23	44:t:74:VAL:HB	1.76	0.67
43:s:25:PRO:HD2	43:s:92:LYS:HD2	1.76	0.67
49:28:1503:A:H4'	49:28:1504:G:H5'	1.76	0.67
45:EB:191:LYS:HB2	45:EB:194:VAL:HB	1.77	0.67
47:Q:108:ARG:HH21	49:28:1354:A:H5'	1.59	0.67
48:ES:2945:C:H2'	48:ES:2946:G:H8	1.60	0.67
50:v:594:LYS:HG2	50:v:595:SER:O	1.94	0.67
4:L3:261:ARG:HB2	16:bb:64:THR:HG21	1.75	0.67
16:bb:27:VAL:HG13	16:bb:98:ALA:HB1	1.76	0.67
12:11:35:ARG:HB3	12:11:123:ILE:HG23	1.77	0.66
49:28:4915:G:H2'	49:28:4916:G:H8	1.59	0.66
4:L3:53:MET:HG2	4:L3:77:THR:HG22	1.76	0.66
18:19:60:ARG:HH12	49:28:2615:C:H5''	1.59	0.66
49:28:4897:G:N2	49:28:4923:U:O2	2.27	0.66
49:28:1954:U:H2'	49:28:1955:G:H8	1.60	0.66
2:5:92:C:H2'	2:5:93:G:H8	1.60	0.66
6:L5:90:VAL:HG11	6:L5:225:GLN:HB3	1.76	0.66
49:28:651:C:H2'	49:28:652:G:H8	1.61	0.66
42:gg:90:LEU:HG	42:gg:111:ILE:HG23	1.78	0.66
49:28:4115:G:H5''	49:28:4116:C:H5'	1.78	0.65
50:v:507:VAL:HG23	50:v:554:LEU:HD13	1.78	0.65
49:28:93:G:H2'	49:28:94:A:C8	2.32	0.65
10:L9:174:LYS:HG3	49:28:4477:A:H4'	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:137:GLN:HB3	44:t:146:ARG:HE	1.60	0.65
49:28:2335:C:H2'	49:28:2336:G:H8	1.60	0.65
49:28:2486:G:H2'	49:28:2487:G:C8	2.32	0.65
7:L6:49:ASN:H	7:L6:64:MET:HE1	1.62	0.65
9:aa:116:LEU:HD11	15:15:29:GLN:HG3	1.78	0.65
2:5:6:C:H4'	6:L5:52:ILE:HD13	1.79	0.64
45:EB:255:TYR:HB3	45:EB:301:LEU:HD21	1.78	0.64
46:u:112:ALA:HB1	46:u:116:LEU:HD21	1.78	0.64
49:28:4232:U:H4'	49:28:4233:A:O5'	1.97	0.64
49:28:3848:U:H2'	49:28:3849:A:H8	1.61	0.64
50:v:654:PRO:HD2	50:v:658:GLY:HA3	1.79	0.64
1:58:67:U:H2'	1:58:68:G:H8	1.62	0.64
4:L3:240:LEU:HB3	4:L3:244:THR:HG21	1.80	0.64
50:v:42:LYS:HG3	50:v:347:GLY:HA3	1.79	0.64
5:L4:140:LYS:HE2	5:L4:245:HIS:HB2	1.79	0.64
49:28:1066:G:H2'	49:28:1067:G:C8	2.31	0.64
50:v:653:GLY:HA2	50:v:683:PHE:CE2	2.32	0.64
16:bb:60:LYS:HE2	49:28:2046:G:H5'	1.79	0.64
15:15:64:ILE:HD11	15:15:102:ALA:HA	1.80	0.64
29:30:29:LEU:HD23	29:30:94:LEU:HD13	1.80	0.64
9:aa:163:LYS:HD2	9:aa:166:ARG:HH12	1.62	0.63
48:ES:3239:G:H2'	48:ES:3240:A:H8	1.63	0.63
7:L6:160:HIS:HB3	7:L6:163:LYS:HD2	1.80	0.63
48:ES:2945:C:H2'	48:ES:2946:G:C8	2.32	0.63
48:ES:2946:G:H2'	48:ES:2947:G:C8	2.34	0.63
49:28:1954:U:H2'	49:28:1955:G:C8	2.34	0.63
33:34:93:ARG:O	33:34:97:ILE:HG12	1.99	0.63
42:gg:32:LEU:HD23	42:gg:32:LEU:H	1.63	0.63
7:L6:196:PHE:HD1	32:ee:106:TYR:HB2	1.64	0.63
12:11:35:ARG:HD2	12:11:123:ILE:HA	1.80	0.63
21:22:63:LEU:HD12	21:22:72:VAL:HG22	1.79	0.63
33:34:68:SER:HB3	33:34:71:LYS:HD3	1.81	0.63
3:L8:179:ILE:HG23	3:L8:184:ARG:HB2	1.80	0.63
11:10:187:GLU:HG3	11:10:189:ARG:HG2	1.81	0.63
49:28:4887:C:N4	49:28:4932:U:H3	1.96	0.63
8:L7:126:LYS:HB2	20:21:133:ALA:HB3	1.81	0.63
25:26:30:MET:HB3	25:26:101:PRO:HG2	1.81	0.63
30:31:64:ILE:HD11	49:28:2373:C:H4'	1.79	0.63
14:14:40:GLY:HA3	14:14:45:VAL:HB	1.80	0.62
50:v:746:LEU:HB2	50:v:815:ASP:HB2	1.81	0.62
45:EB:181:PRO:HA	45:EB:230:VAL:HA	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1942:A:H2'	49:28:1943:A:C8	2.34	0.62
49:28:1802:A:H5''	49:28:1803:G:H5'	1.81	0.62
49:28:4174:U:H2'	49:28:4175:G:H8	1.64	0.62
49:28:300:A:H2'	49:28:301:G:H8	1.64	0.62
49:28:4238:G:H2'	49:28:4239:A:H8	1.64	0.62
50:v:653:GLY:HA3	50:v:660:ASN:HB2	1.80	0.62
22:23:15:ARG:HB3	49:28:4618:G:H5''	1.80	0.62
30:31:23:ARG:HH22	49:28:5058:A:H5'	1.65	0.62
12:11:146:ARG:HG2	12:11:147:ARG:HG2	1.82	0.62
49:28:1965:G:H4'	49:28:4695:C:H1'	1.81	0.62
49:28:2015:U:H2'	49:28:2016:C:H6	1.65	0.62
49:28:5057:C:H2'	49:28:5058:A:C8	2.35	0.62
14:14:57:LEU:HD23	14:14:57:LEU:H	1.65	0.62
49:28:1306:C:H2'	49:28:1307:A:H8	1.65	0.62
6:L5:33:ARG:HH11	20:21:27:LEU:HD12	1.65	0.62
18:19:44:LEU:HD22	18:19:49:LEU:HD12	1.82	0.62
40:42:24:THR:HG23	40:42:69:ARG:HB3	1.80	0.61
49:28:2467:U:H4'	49:28:2468:U:H5'	1.81	0.61
47:Q:67:ILE:HD12	47:Q:96:PRO:HD2	1.82	0.61
49:28:1332:C:H2'	49:28:1333:A:C8	2.34	0.61
49:28:4635:A:H2	49:28:4663:G:H21	1.46	0.61
49:28:1333:A:H2'	49:28:1334:A:C8	2.35	0.61
49:28:4594:U:H2'	49:28:4595:G:H8	1.65	0.61
46:u:93:LEU:HD11	46:u:99:LEU:HB2	1.83	0.61
49:28:979:C:H42	49:28:1276:C:H42	1.48	0.61
49:28:2520:C:H2'	49:28:2521:G:H8	1.65	0.61
2:5:59:G:H4'	6:L5:267:ASN:HD21	1.64	0.61
10:L9:43:VAL:HG12	10:L9:59:LYS:HD3	1.83	0.61
49:28:976:G:H22	49:28:1279:A:H2	1.48	0.61
49:28:1333:A:H2'	49:28:1334:A:H8	1.66	0.61
12:11:18:ARG:HG3	12:11:135:GLY:HA3	1.81	0.61
49:28:3910:C:H2'	49:28:3911:C:H6	1.66	0.61
37:38:35:LYS:HE2	49:28:2696:A:H62	1.66	0.60
49:28:2075:G:H2'	49:28:2076:G:H8	1.66	0.60
49:28:2745:A:H2'	49:28:2746:A:H8	1.66	0.60
49:28:4537:C:H2'	49:28:4538:G:H8	1.65	0.60
2:5:28:C:H1'	2:5:54:A:H61	1.65	0.60
22:23:13:LYS:HB2	22:23:128:LEU:HD21	1.82	0.60
31:32:85:LEU:HD11	31:32:111:ILE:HG23	1.83	0.60
49:28:64:A:H1'	49:28:76:A:H1'	1.83	0.60
49:28:3664:G:H2'	49:28:3665:G:H8	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L6:122:GLU:HG3	31:32:7:LEU:HD22	1.82	0.60
49:28:4095:G:H1	49:28:4113:U:H3	1.50	0.60
26:27:51:ARG:HD2	26:27:65:ARG:HD2	1.83	0.60
49:28:1818:G:O2'	49:28:1819:G:H5'	2.00	0.60
49:28:4459:U:H2'	49:28:4460:U:C6	2.37	0.60
49:28:4967:A:H2'	49:28:4968:A:C8	2.36	0.60
44:t:97:ASN:HB3	44:t:99:LYS:HE2	1.84	0.60
49:28:3599:A:H2'	49:28:3600:G:H8	1.67	0.60
49:28:3607:U:H2'	49:28:3608:A:H8	1.66	0.60
49:28:4915:G:H2'	49:28:4916:G:C8	2.37	0.60
10:L9:41:ILE:HD11	10:L9:69:THR:HB	1.83	0.60
19:20:35:PRO:HD2	19:20:39:VAL:HG21	1.83	0.60
25:26:27:ARG:HB2	25:26:75:ARG:CZ	2.32	0.60
30:31:26:THR:HG23	49:28:4996:C:H4'	1.84	0.60
37:38:69:LEU:HD21	49:28:2696:A:C5	2.37	0.60
49:28:3717:A:H2'	49:28:3718:A:H8	1.66	0.60
49:28:2844:A:O2'	49:28:4631:G:H4'	2.02	0.59
49:28:3717:A:H2'	49:28:3718:A:C8	2.36	0.59
3:L8:117:GLU:HG2	3:L8:124:GLY:H	1.67	0.59
49:28:137:G:H2'	49:28:138:G:H8	1.66	0.59
49:28:3648:A:H1'	49:28:3785:A:H61	1.66	0.59
19:20:83:ARG:HB2	19:20:127:MET:HE3	1.83	0.59
49:28:711:A:H2'	49:28:712:C:C6	2.38	0.59
3:L8:147:ARG:HG2	3:L8:157:VAL:HG22	1.84	0.59
15:15:40:PRO:HG3	49:28:8:U:H5''	1.83	0.59
32:ee:10:ILE:HD11	32:ee:100:ARG:HH21	1.68	0.59
49:28:1617:G:H1'	49:28:2513:A:N6	2.17	0.59
50:v:354:ILE:HG23	50:v:358:LEU:HD12	1.85	0.59
9:aa:139:VAL:HG11	9:aa:238:LYS:HE3	1.85	0.59
15:15:98:LEU:HD12	15:15:128:LYS:HD2	1.82	0.59
6:L5:287:PHE:HZ	11:10:214:SER:HB3	1.66	0.59
21:22:64:GLU:HG2	21:22:71:THR:HB	1.84	0.59
48:ES:2953:C:H2'	48:ES:2954:G:C8	2.37	0.59
49:28:252:C:H2'	49:28:253:G:C8	2.37	0.59
49:28:676:C:H2'	49:28:677:G:H8	1.66	0.59
49:28:1073:G:H1	49:28:1238:A:H2	1.51	0.59
11:10:98:ARG:HB3	11:10:120:GLY:HA3	1.85	0.59
27:dd:32:ARG:HD2	49:28:37:U:H4'	1.85	0.59
40:42:68:LEU:HD11	40:42:85:ILE:HD11	1.85	0.59
48:ES:3238:C:H2'	48:ES:3239:G:H8	1.67	0.59
49:28:1645:C:H2'	49:28:1646:A:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:3774:A:H2'	49:28:3775:A:N3	2.18	0.59
16:bb:125:LYS:HG3	16:bb:129:LEU:HD12	1.85	0.59
26:27:11:VAL:HG11	26:27:80:LEU:HD13	1.84	0.59
27:dd:21:ARG:HG3	49:28:2282:A:H4'	1.85	0.59
50:v:594:LYS:HB2	50:v:855:LEU:C	2.27	0.59
6:L5:22:ARG:HE	6:L5:27:LYS:HB2	1.68	0.59
49:28:1933:G:H2'	49:28:1934:A:C8	2.38	0.59
49:28:3873:G:H2'	49:28:3874:G:C8	2.38	0.59
49:28:4860:G:H2'	49:28:4861:G:H8	1.67	0.59
13:13:8:MET:HG3	47:Q:166:TYR:HB3	1.85	0.58
43:s:50:LYS:HZ1	43:s:98:ILE:HG13	1.68	0.58
49:28:2735:G:H2'	49:28:2736:G:H8	1.68	0.58
49:28:3916:G:H2'	49:28:3917:A:H8	1.68	0.58
49:28:3911:C:H2'	49:28:3912:U:H6	1.67	0.58
5:L4:45:ARG:HG3	5:L4:238:LEU:HD22	1.84	0.58
22:23:57:VAL:HG11	22:23:122:ALA:HB3	1.84	0.58
42:gg:46:ARG:HA	42:gg:70:GLN:HE22	1.67	0.58
49:28:1538:U:H2'	49:28:1539:G:H8	1.68	0.58
49:28:4601:U:H2'	49:28:4602:A:H8	1.67	0.58
50:v:432:PRO:HB3	50:v:496:VAL:HG21	1.84	0.58
49:28:4088:C:H2'	49:28:4089:G:H8	1.69	0.58
7:L6:158:GLY:HA2	49:28:4942:C:H5''	1.85	0.58
15:15:44:ARG:NH1	15:15:47:LYS:HB2	2.18	0.58
45:EB:56:ILE:HD11	45:EB:112:VAL:HB	1.86	0.58
49:28:3610:A:H2'	49:28:3611:A:H8	1.67	0.58
18:19:105:LEU:HD23	18:19:138:LEU:HD22	1.86	0.58
26:27:53:VAL:HG21	26:27:62:ILE:HG23	1.84	0.58
48:ES:2949:U:H3	48:ES:3245:G:H1	1.51	0.58
50:v:604:MET:HE1	50:v:729:LEU:HD23	1.86	0.58
1:58:141:C:H5'	15:15:113:LEU:HD11	1.84	0.58
16:bb:89:PRO:HD3	49:28:1914:C:H4'	1.86	0.58
44:t:137:GLN:HE21	49:28:1993:C:H1'	1.69	0.58
45:EB:223:VAL:HG22	45:EB:324:LEU:HG	1.84	0.58
47:Q:144:LYS:HG2	49:28:1460:C:H5''	1.86	0.58
21:22:23:LEU:HD11	21:22:83:LEU:HD21	1.85	0.58
38:39:28:TRP:HA	38:39:33:ASN:HD22	1.69	0.57
3:L8:87:PHE:CZ	49:28:4121:G:H5''	2.38	0.57
8:L7:24:PHE:HB3	49:28:966:A:H2'	1.86	0.57
8:L7:46:ARG:NH1	49:28:976:G:H5''	2.19	0.57
37:38:36:VAL:HG13	37:38:43:TYR:HB2	1.87	0.57
49:28:966:A:N6	49:28:2096:G:H2'	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:17:69:ARG:HD2	49:28:4981:G:H1'	1.85	0.57
49:28:4894:A:H5''	49:28:4895:C:C6	2.39	0.57
17:17:84:PRO:HB2	17:17:87:SER:HB3	1.86	0.57
31:32:79:VAL:HG13	31:32:84:GLU:HB2	1.85	0.57
37:38:26:LYS:HE2	49:28:2696:A:H5'	1.87	0.57
49:28:3861:A:H2'	49:28:3862:A:H8	1.69	0.57
49:28:4935:C:H2'	49:28:4936:G:H8	1.69	0.57
49:28:4940:C:H5''	49:28:4941:G:H5''	1.87	0.57
48:ES:2947:G:O6	48:ES:3247:A:N1	2.37	0.57
49:28:3652:A:H2'	49:28:3653:A:C8	2.40	0.57
49:28:4238:G:H2'	49:28:4239:A:C8	2.39	0.57
16:bb:18:ARG:HH22	16:bb:128:ARG:HH21	1.53	0.57
3:L8:181:LYS:HB2	49:28:1577:G:C5	2.40	0.57
33:34:69:LYS:HG3	33:34:73:HIS:CD2	2.39	0.57
34:35:80:PRO:HD2	34:35:83:LEU:HD12	1.87	0.57
49:28:162:A:H2'	49:28:163:A:H8	1.68	0.57
49:28:260:C:H2'	49:28:261:G:H8	1.69	0.57
49:28:647:G:H3'	49:28:648:G:H8	1.70	0.57
49:28:3910:C:H2'	49:28:3911:C:C6	2.40	0.57
49:28:4274:A:H2'	49:28:4275:G:H8	1.69	0.57
7:L6:115:MET:HE3	7:L6:116:PRO:HD2	1.86	0.57
38:39:23:ILE:HG23	38:39:38:ASN:HB2	1.85	0.57
49:28:2557:G:O6	49:28:2570:U:O4	2.23	0.57
8:L7:46:ARG:HH11	49:28:976:G:H5''	1.70	0.56
49:28:956:A:H1'	49:28:2076:G:H5''	1.86	0.56
49:28:1292:C:H3'	49:28:1293:G:H21	1.70	0.56
49:28:3916:G:H2'	49:28:3917:A:C8	2.40	0.56
3:L8:30:ARG:HH12	3:L8:33:ASP:CG	2.13	0.56
28:29:5:LYS:HE2	28:29:8:THR:HB	1.87	0.56
45:EB:32:LEU:HA	45:EB:35:LEU:HD23	1.87	0.56
48:ES:3580:G:H3'	48:ES:3581:C:H5''	1.87	0.56
49:28:178:C:H2'	49:28:179:G:C8	2.40	0.56
49:28:1857:C:H2'	49:28:1858:A:C8	2.39	0.56
50:v:609:PHE:HE1	50:v:701:ARG:HB3	1.70	0.56
6:L5:65:ALA:HB2	6:L5:74:ILE:HD13	1.87	0.56
18:19:66:ASN:O	18:19:70:ARG:HG2	2.05	0.56
43:s:31:GLY:HA3	43:s:190:GLN:HE22	1.71	0.56
43:s:132:PRO:HB3	43:s:147:ILE:HD11	1.86	0.56
44:t:128:THR:HA	44:t:131:GLU:HG2	1.88	0.56
45:EB:75:ALA:HB1	45:EB:118:ILE:HG23	1.88	0.56
46:u:180:VAL:HA	46:u:183:ILE:HG12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:978:G:N2	49:28:1277:G:H22	2.04	0.56
49:28:1942:A:H2'	49:28:1943:A:H8	1.70	0.56
49:28:3880:G:H2'	49:28:3881:G:C8	2.40	0.56
25:26:47:MET:HE2	25:26:115:ARG:HD2	1.86	0.56
26:27:54:THR:H	26:27:57:MET:HE2	1.70	0.56
36:37:21:ARG:HE	36:37:39:TYR:HA	1.69	0.56
45:EB:237:ALA:HB1	45:EB:308:LEU:HB3	1.87	0.56
49:28:132:G:C2	49:28:133:C:H1'	2.41	0.56
49:28:262:G:H2'	49:28:263:G:H8	1.70	0.56
49:28:2539:C:H2'	49:28:2540:C:H6	1.71	0.56
10:L9:111:LEU:HD21	10:L9:125:ARG:HG3	1.87	0.56
44:t:138:SER:HA	49:28:1976:G:H21	1.71	0.56
49:28:2770:C:H2'	49:28:2771:G:H8	1.70	0.56
50:v:669:VAL:HG11	50:v:707:VAL:HB	1.87	0.56
5:L4:312:ARG:HB3	49:28:2274:C:H5'	1.88	0.56
42:gg:108:MET:O	42:gg:112:ARG:HG2	2.05	0.56
47:Q:61:LEU:HD21	47:Q:66:MET:HB3	1.88	0.56
49:28:697:G:H2'	49:28:698:G:H8	1.71	0.56
50:v:527:LEU:HD21	50:v:557:CYS:HB3	1.87	0.56
50:v:594:LYS:HA	50:v:856:ASP:HB2	1.87	0.56
9:aa:98:ILE:HG21	49:28:4125:C:H4'	1.88	0.56
16:bb:168:TYR:CE2	16:bb:172:LYS:HD2	2.41	0.56
45:EB:35:LEU:HD11	45:EB:108:ILE:HD13	1.87	0.56
48:ES:3239:G:H2'	48:ES:3240:A:C8	2.40	0.56
49:28:2520:C:H2'	49:28:2521:G:C8	2.41	0.56
49:28:2539:C:H2'	49:28:2540:C:C6	2.41	0.56
1:58:148:A:H2'	1:58:149:G:C8	2.41	0.56
13:13:21:ARG:HB3	15:15:197:THR:HG22	1.88	0.56
49:28:1339:U:H2'	49:28:1340:C:C6	2.41	0.56
3:L8:14:SER:H	3:L8:17:ARG:HG3	1.71	0.55
8:L7:161:ILE:HB	8:L7:166:ILE:HD12	1.87	0.55
11:10:95:HIS:HD2	11:10:128:ARG:HD3	1.71	0.55
19:20:127:MET:HE1	20:21:155:PRO:HA	1.86	0.55
49:28:1066:G:H2'	49:28:1067:G:H8	1.71	0.55
18:19:105:LEU:HD13	18:19:135:LYS:HD2	1.87	0.55
20:21:35:LYS:HE2	49:28:1824:G:H5''	1.88	0.55
31:32:89:LEU:HD12	31:32:90:MET:HG2	1.87	0.55
49:28:3771:C:H2'	49:28:3772:U:C6	2.42	0.55
4:L3:47:LEU:HB2	4:L3:84:MET:HE3	1.89	0.55
16:bb:27:VAL:HG22	16:bb:101:ARG:HB2	1.88	0.55
18:19:105:LEU:HD22	18:19:135:LYS:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:137:GLN:NE2	49:28:1993:C:H1'	2.22	0.55
45:EB:159:PRO:HD3	45:EB:325:LEU:HD11	1.88	0.55
49:28:2793:G:H5'	49:28:2794:C:H5''	1.89	0.55
49:28:2845:A:H61	49:28:3843:C:N4	1.99	0.55
50:v:587:SER:HB2	50:v:605:LYS:HG3	1.87	0.55
5:L4:330:PRO:HD3	8:L7:46:ARG:HH21	1.71	0.55
6:L5:67:ALA:HA	6:L5:72:ASP:HB3	1.88	0.55
8:L7:104:VAL:HG13	8:L7:135:VAL:HG12	1.89	0.55
19:20:164:LYS:HB2	19:20:165:PRO:HD3	1.88	0.55
49:28:679:C:H2'	49:28:680:G:H8	1.72	0.55
49:28:2386:U:H2'	49:28:2387:G:H8	1.71	0.55
49:28:4635:A:H8	49:28:5048:A:H61	1.55	0.55
4:L3:89:ILE:HG22	4:L3:162:VAL:HG23	1.88	0.55
39:40:92:THR:HG22	39:40:94:ASN:H	1.72	0.55
49:28:129:C:H2'	49:28:130:C:C6	2.42	0.55
49:28:162:A:H2'	49:28:163:A:C8	2.42	0.55
49:28:1450:C:H2'	49:28:1451:G:C8	2.41	0.55
49:28:2495:U:H2'	49:28:2496:G:H8	1.72	0.55
49:28:3770:U:H2'	49:28:3771:C:H6	1.71	0.55
49:28:4889:G:H2'	49:28:4890:G:H8	1.72	0.55
8:L7:89:ALA:HB2	8:L7:124:LEU:HD21	1.88	0.55
11:10:95:HIS:CD2	11:10:128:ARG:HD3	2.41	0.55
43:s:120:GLU:HG3	43:s:159:GLN:HE22	1.71	0.55
49:28:3732:A:H2'	49:28:3733:A:C8	2.42	0.55
49:28:3945:A:H2'	49:28:3946:G:C8	2.42	0.55
50:v:501:VAL:HG11	50:v:813:VAL:HB	1.88	0.55
6:L5:35:ARG:HB2	49:28:4325:A:C2	2.41	0.55
7:L6:62:SER:HB2	49:28:1236:C:O2'	2.06	0.55
11:10:38:ARG:HD3	11:10:83:ASP:HB2	1.89	0.55
19:20:13:VAL:HG23	19:20:62:VAL:HB	1.89	0.55
49:28:325:U:H2'	49:28:326:C:C6	2.42	0.55
49:28:651:C:H2'	49:28:652:G:C8	2.40	0.55
49:28:3734:U:H2'	49:28:3735:G:O4'	2.07	0.55
7:L6:169:LYS:HG2	7:L6:177:LEU:HD23	1.89	0.55
49:28:1509:C:H2'	49:28:1510:G:H8	1.71	0.55
49:28:1867:A:H2'	49:28:1868:A:C8	2.42	0.55
49:28:2457:G:H21	49:28:3672:G:N2	2.05	0.55
49:28:3848:U:H2'	49:28:3849:A:C8	2.41	0.55
49:28:4274:A:H2'	49:28:4275:G:C8	2.41	0.55
12:11:42:GLN:HE22	12:11:117:ILE:HG12	1.70	0.54
27:dd:51:GLY:HA2	47:Q:178:ARG:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2634:C:H2'	49:28:2635:U:H6	1.72	0.54
49:28:3648:A:H1'	49:28:3785:A:N6	2.22	0.54
49:28:1346:C:H2'	49:28:1347:G:H8	1.70	0.54
49:28:1557:C:H2'	49:28:1558:A:H8	1.72	0.54
49:28:2745:A:H2'	49:28:2746:A:C8	2.42	0.54
49:28:3607:U:H2'	49:28:3608:A:C8	2.42	0.54
49:28:3713:U:O2	49:28:3715:U:H5	1.90	0.54
49:28:4378:A:O2'	49:28:4379:A:H2'	2.07	0.54
3:L8:146:THR:HG22	3:L8:148:VAL:HG23	1.89	0.54
11:10:87:ILE:HG12	11:10:138:ILE:HG12	1.89	0.54
49:28:962:C:H2'	49:28:963:G:C8	2.42	0.54
49:28:4951:G:H2'	49:28:4952:G:H8	1.73	0.54
50:v:504:VAL:HG23	50:v:505:VAL:HG23	1.88	0.54
9:aa:163:LYS:NZ	9:aa:166:ARG:HH22	2.05	0.54
32:ee:69:VAL:HG11	49:28:4944:C:H1'	1.89	0.54
49:28:469:C:H2'	49:28:470:A:H8	1.73	0.54
49:28:2448:G:H2'	49:28:2449:A:C8	2.43	0.54
49:28:3651:A:H2'	49:28:3652:A:C8	2.43	0.54
49:28:3651:A:H2'	49:28:3652:A:H8	1.71	0.54
49:28:648:G:H2'	49:28:649:A:H8	1.72	0.54
49:28:3732:A:H2'	49:28:3733:A:H8	1.72	0.54
49:28:3911:C:C2	49:28:3912:U:C5	2.95	0.54
4:L3:79:VAL:HB	4:L3:331:VAL:HG23	1.90	0.54
18:19:106:LEU:HB3	18:19:120:TYR:CE1	2.43	0.54
49:28:3770:U:H2'	49:28:3771:C:C6	2.43	0.54
49:28:4537:C:H2'	49:28:4538:G:C8	2.42	0.54
50:v:500:SER:H	50:v:501:VAL:HG13	1.71	0.54
50:v:742:GLU:HB3	50:v:820:LEU:HD12	1.89	0.54
19:20:13:VAL:HG22	19:20:63:TYR:HB3	1.90	0.54
34:35:74:LYS:HE2	49:28:133:C:C5	2.43	0.54
45:EB:118:ILE:HG13	45:EB:195:ILE:HG22	1.90	0.54
48:ES:2955:A:N1	48:ES:3239:G:O6	2.41	0.54
49:28:3855:C:H2'	49:28:3856:A:H8	1.73	0.54
4:L3:76:VAL:HG12	4:L3:334:LYS:HA	1.89	0.54
18:19:79:GLY:O	49:28:3619:G:H4'	2.08	0.54
19:20:1:MET:HB2	19:20:43:ARG:HH21	1.73	0.54
19:20:160:ARG:HB2	49:28:1921:C:H1'	1.90	0.54
33:34:60:ARG:HD3	33:34:61:PRO:HD2	1.90	0.54
46:u:59:PRO:HB2	46:u:170:GLY:H	1.73	0.54
48:ES:2943:C:H2'	48:ES:2944:G:H8	1.73	0.54
1:58:49:G:H5'	34:35:47:ILE:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:13:16:LYS:HG2	49:28:46:U:H5''	1.90	0.54
46:u:16:GLU:HA	46:u:19:HIS:CD2	2.44	0.54
49:28:1198:G:H2'	49:28:1199:G:C8	2.42	0.54
49:28:1732:C:H2'	49:28:1733:G:C8	2.43	0.54
5:L4:2:ALA:HB2	49:28:667:A:N7	2.23	0.53
18:19:4:LEU:HD11	18:19:29:THR:HG23	1.89	0.53
44:t:32:ILE:HG22	44:t:37:LEU:HB3	1.89	0.53
45:EB:29:ASN:HD21	45:EB:334:THR:HA	1.73	0.53
49:28:4948:C:H2'	49:28:4949:G:N2	2.23	0.53
7:L6:61:ARG:HD3	49:28:1237:C:C2	2.44	0.53
49:28:1199:G:H2'	49:28:1200:G:C8	2.42	0.53
49:28:4126:C:H5''	49:28:4127:A:H5''	1.90	0.53
48:ES:2943:C:H2'	48:ES:2944:G:C8	2.43	0.53
49:28:3697:U:H5''	49:28:3698:G:H5'	1.91	0.53
49:28:5006:U:H4'	49:28:5007:A:H5'	1.89	0.53
49:28:4708:A:N3	49:28:4709:U:H5'	2.24	0.53
2:5:110:G:H2'	2:5:111:C:C6	2.43	0.53
7:L6:73:ARG:HD3	49:28:983:C:C6	2.44	0.53
6:L5:64:ILE:HG13	6:L5:105:LEU:HD21	1.89	0.53
15:15:68:ARG:HE	15:15:128:LYS:HE2	1.73	0.53
29:30:29:LEU:HD22	29:30:91:VAL:HG11	1.89	0.53
30:31:37:GLY:O	30:31:41:ARG:HG3	2.09	0.53
40:42:17:LYS:HE2	40:42:19:GLN:HE21	1.74	0.53
44:t:90:ARG:HD3	44:t:95:GLN:H	1.74	0.53
49:28:3932:U:H2'	49:28:3933:G:H8	1.74	0.53
49:28:3610:A:H2'	49:28:3611:A:C8	2.44	0.53
49:28:4088:C:H2'	49:28:4089:G:C8	2.44	0.53
5:L4:305:PRO:HB3	47:Q:38:ARG:HH12	1.73	0.53
18:19:71:ARG:HH12	49:28:3604:A:H5''	1.74	0.53
44:t:61:LYS:HG2	44:t:72:GLU:HG2	1.91	0.53
49:28:496:G:O2'	49:28:497:G:H5'	2.08	0.53
49:28:2098:G:H2'	49:28:2099:C:C6	2.43	0.53
49:28:2723:U:H2'	49:28:2724:G:C8	2.43	0.53
4:L3:220:ILE:HG12	4:L3:278:THR:HG23	1.89	0.53
39:40:68:MET:HG2	39:40:79:PRO:HA	1.90	0.53
49:28:1893:C:H1'	49:28:1937:C:O2	2.09	0.53
49:28:163:A:H2'	49:28:164:G:H8	1.74	0.53
49:28:1804:A:H5''	49:28:1806:G:C8	2.44	0.53
49:28:2478:C:H2'	49:28:2479:G:H8	1.74	0.53
49:28:4756:C:H5'	49:28:4757:C:OP1	2.09	0.53
7:L6:165:VAL:HG11	7:L6:178:VAL:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L9:95:VAL:HG22	39:40:56:LEU:HB3	1.90	0.52
15:15:184:ILE:HD12	49:28:99:A:H5''	1.91	0.52
47:Q:181:ARG:HH22	49:28:1391:A:H5'	1.73	0.52
49:28:3784:A:O2'	49:28:3785:A:H3'	2.08	0.52
49:28:4935:C:H2'	49:28:4936:G:C8	2.44	0.52
50:v:91:GLN:HE22	50:v:359:PRO:HA	1.73	0.52
32:ee:7:CYS:HB2	32:ee:103:VAL:HG23	1.90	0.52
43:s:45:MET:HG2	44:t:123:ARG:NH1	2.25	0.52
4:L3:154:LYS:HD3	4:L3:191:ALA:HA	1.91	0.52
5:L4:77:PRO:O	5:L4:90:GLY:HA2	2.09	0.52
9:aa:201:GLU:HA	9:aa:230:MET:SD	2.49	0.52
22:23:107:ASN:HD21	22:23:111:GLU:HB2	1.74	0.52
49:28:1461:C:H2'	49:28:1462:A:H8	1.72	0.52
49:28:2477:A:H2'	49:28:2478:C:C6	2.44	0.52
49:28:3700:C:H2'	49:28:3746:A:H61	1.74	0.52
49:28:4172:A:H3'	49:28:4173:G:H8	1.74	0.52
49:28:4699:U:H1'	49:28:4700:A:H5''	1.91	0.52
49:28:4751:G:H1	49:28:4948:C:H5	1.56	0.52
1:58:67:U:H2'	1:58:68:G:C8	2.43	0.52
16:bb:54:TYR:HD2	16:bb:145:VAL:HG21	1.75	0.52
24:cc:81:LEU:HD11	24:cc:99:ILE:HG12	1.92	0.52
49:28:4219:A:H2'	49:28:4220:A:C8	2.45	0.52
12:11:56:THR:HG23	12:11:63:ARG:HA	1.91	0.52
44:t:146:ARG:NH1	44:t:146:ARG:HA	2.25	0.52
49:28:461:G:H2'	49:28:462:G:C8	2.45	0.52
49:28:1984:A:H2'	49:28:2011:C:H5'	1.91	0.52
2:5:92:C:H2'	2:5:93:G:C8	2.43	0.52
4:L3:57:VAL:HG22	4:L3:73:VAL:HG12	1.92	0.52
16:bb:54:TYR:CD2	16:bb:145:VAL:HG21	2.45	0.52
46:u:112:ALA:HB2	46:u:135:PRO:HB2	1.92	0.52
49:28:987:C:H2'	49:28:988:C:C6	2.45	0.52
5:L4:56:GLU:HG3	5:L4:57:LEU:HD22	1.91	0.52
7:L6:153:LEU:HB3	7:L6:197:VAL:HG13	1.92	0.52
49:28:138:G:H2'	49:28:139:G:H8	1.73	0.52
49:28:1557:C:H2'	49:28:1558:A:C8	2.45	0.52
49:28:4130:C:H2'	49:28:4131:G:H8	1.74	0.52
4:L3:116:ARG:HD3	4:L3:122:TRP:CD2	2.44	0.52
34:35:31:LEU:HB3	34:35:47:ILE:HG22	1.92	0.52
49:28:1346:C:H2'	49:28:1347:G:C8	2.45	0.52
49:28:2465:C:H1'	49:28:3672:G:H22	1.74	0.52
49:28:3641:U:H5	49:28:3646:A:N7	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:3775:A:H2'	49:28:3776:G:O4'	2.09	0.52
8:L7:73:MET:HE1	49:28:1088:C:O2	2.11	0.51
49:28:1559:G:H2'	49:28:1560:A:H8	1.75	0.51
49:28:2762:G:H2'	49:28:2764:A:H5''	1.91	0.51
49:28:4737:G:C6	49:28:4963:G:C6	2.98	0.51
50:v:682:GLY:HA2	50:v:722:ILE:HG23	1.91	0.51
19:20:15:ARG:HH12	19:20:18:PRO:HG3	1.75	0.51
32:ee:65:ASN:HB2	32:ee:67:THR:HG22	1.92	0.51
44:t:61:LYS:HD2	44:t:74:VAL:HG22	1.93	0.51
49:28:1472:C:H2'	49:28:1473:U:C6	2.45	0.51
1:58:124:U:H4'	1:58:125:C:O5'	2.09	0.51
19:20:107:THR:O	19:20:111:ARG:HD3	2.10	0.51
49:28:1884:C:H2'	49:28:1885:G:H8	1.74	0.51
19:20:126:ILE:HD11	19:20:129:VAL:HG23	1.92	0.51
32:ee:63:LYS:HG2	32:ee:64:PRO:HD2	1.92	0.51
49:28:1298:C:H2'	49:28:1299:G:H8	1.74	0.51
49:28:1804:A:H4'	49:28:1805:A:O5'	2.09	0.51
1:58:2:G:N3	1:58:2:G:H2'	2.25	0.51
16:bb:37:ARG:HD2	16:bb:108:ILE:HD11	1.93	0.51
15:15:45:PRO:O	15:15:49:ARG:HG3	2.10	0.51
27:dd:85:GLN:NE2	49:28:508:G:H21	2.07	0.51
44:t:56:LEU:HB2	44:t:58:ILE:HD11	1.91	0.51
2:5:55:A:H4'	12:11:155:HIS:HB2	1.92	0.51
12:11:85:LYS:HB3	12:11:115:LEU:HD12	1.92	0.51
49:28:153:G:H2'	49:28:154:G:H8	1.75	0.51
49:28:2607:C:H2'	49:28:2608:G:H8	1.75	0.51
49:28:4174:U:H2'	49:28:4175:G:C8	2.45	0.51
1:58:96:C:H5''	34:35:66:LYS:HG2	1.93	0.51
4:L3:206:PRO:HG2	4:L3:209:GLN:HG2	1.92	0.51
15:15:192:TRP:NE1	49:28:48:G:H5'	2.26	0.51
16:bb:8:VAL:HG12	16:bb:117:ARG:HG3	1.93	0.51
37:38:12:LEU:HD21	37:38:56:LEU:HD11	1.93	0.51
38:39:45:ARG:HH21	49:28:2796:G:H5'	1.75	0.51
43:s:134:LYS:HE3	43:s:177:MET:HE3	1.93	0.51
49:28:4680:G:H2'	49:28:4681:A:C8	2.46	0.51
49:28:5003:U:H2'	49:28:5004:C:C6	2.46	0.51
4:L3:41:VAL:HA	4:L3:187:GLY:HA3	1.93	0.51
12:11:55:TYR:HA	12:11:64:ARG:HE	1.76	0.51
24:cc:95:THR:HG22	24:cc:139:ARG:HA	1.92	0.51
42:gg:46:ARG:HA	42:gg:70:GLN:NE2	2.26	0.51
49:28:1476:C:H2'	49:28:1477:C:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1956:A:O2'	49:28:1957:U:H5'	2.11	0.51
49:28:4466:C:H2'	49:28:4467:A:H8	1.76	0.51
14:14:129:LYS:O	14:14:132:ARG:HG3	2.11	0.51
34:35:28:LEU:HD21	34:35:32:ARG:HE	1.76	0.51
45:EB:75:ALA:HB2	45:EB:113:HIS:HB3	1.92	0.51
49:28:1633:G:H2'	49:28:1641:G:N7	2.26	0.51
49:28:2722:G:H2'	49:28:2723:U:C6	2.46	0.51
49:28:3653:A:C2	49:28:3692:A:H4'	2.46	0.51
50:v:305:MET:HE3	50:v:336:LEU:HD22	1.93	0.51
50:v:722:ILE:HB	50:v:723:PRO:HD3	1.93	0.51
3:L8:117:GLU:HG2	3:L8:124:GLY:N	2.26	0.50
4:L3:317:LEU:HB2	4:L3:372:SER:HB2	1.93	0.50
49:28:1676:C:H41	49:28:4378:A:H5''	1.75	0.50
3:L8:234:LYS:HG2	3:L8:238:ILE:HD12	1.93	0.50
7:L6:120:PRO:O	42:gg:112:ARG:HD2	2.12	0.50
12:11:10:ASN:HB3	12:11:13:ARG:HG3	1.93	0.50
17:17:83:TRP:O	49:28:3856:A:H5''	2.11	0.50
1:58:4:C:H2'	1:58:5:U:H6	1.77	0.50
1:58:9:A:H2'	1:58:10:G:H8	1.76	0.50
1:58:19:C:H2'	1:58:20:A:H8	1.75	0.50
15:15:120:TRP:HE1	15:15:123:GLU:HB3	1.77	0.50
32:ee:28:LEU:HB2	32:ee:84:VAL:HG12	1.91	0.50
42:gg:103:HIS:CD2	42:gg:106:LEU:HD22	2.42	0.50
45:EB:227:ASP:HB3	45:EB:320:LYS:HG3	1.94	0.50
49:28:2824:C:H2'	49:28:2825:A:C8	2.46	0.50
49:28:3599:A:H2'	49:28:3600:G:C8	2.44	0.50
49:28:4459:U:H2'	49:28:4460:U:H6	1.74	0.50
5:L4:242:PRO:HB2	49:28:2297:G:H4'	1.92	0.50
32:ee:46:ARG:H	32:ee:107:PRO:HG2	1.77	0.50
49:28:4872:G:H4'	49:28:4873:G:H5'	1.92	0.50
7:L6:49:ASN:N	7:L6:64:MET:HE1	2.27	0.50
12:11:136:ARG:HD2	12:11:155:HIS:CE1	2.46	0.50
22:23:43:LYS:HA	49:28:4508:C:H4'	1.94	0.50
27:dd:102:ASP:HB3	27:dd:105:ARG:HB3	1.94	0.50
39:40:86:LYS:HB3	39:40:88:LYS:HG2	1.93	0.50
43:s:63:LYS:HE3	49:28:1960:A:C8	2.47	0.50
49:28:3611:A:H2	49:28:5016:A:H8	1.59	0.50
49:28:4992:G:H2'	49:28:4993:G:C8	2.46	0.50
1:58:37:A:OP2	34:35:89:ARG:HD2	2.11	0.50
2:5:57:C:H2'	2:5:58:A:H8	1.76	0.50
6:L5:37:VAL:HB	6:L5:50:ARG:HD3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:11:15:LEU:HD21	12:11:134:LEU:HB3	1.94	0.50
18:19:106:LEU:HB3	18:19:120:TYR:HE1	1.77	0.50
35:36:15:HIS:HD2	35:36:17:VAL:HG23	1.76	0.50
49:28:3868:G:H22	49:28:3900:G:H1'	1.75	0.50
50:v:594:LYS:HB3	50:v:854:PHE:HA	1.94	0.50
8:L7:133:ARG:HA	8:L7:136:GLU:HG3	1.92	0.50
20:21:87:LYS:NZ	49:28:4305:G:H1	2.06	0.50
48:ES:2947:G:N1	48:ES:3247:A:C2	2.69	0.50
49:28:1999:A:H2'	49:28:2000:G:C4	2.46	0.50
49:28:4956:A:H8	49:28:4956:A:OP2	1.95	0.50
30:31:33:ILE:O	30:31:36:VAL:HG22	2.12	0.50
3:L8:242:ARG:HG2	49:28:3745:U:H4'	1.94	0.50
4:L3:217:ILE:HD13	4:L3:284:ILE:HD11	1.94	0.50
4:L3:293:ILE:HA	4:L3:298:LEU:HA	1.94	0.50
13:13:14:PHE:HE1	15:15:198:LEU:HD11	1.76	0.50
21:22:42:PHE:CZ	21:22:46:ARG:HG3	2.47	0.50
49:28:2743:A:H2'	49:28:2744:A:C8	2.47	0.50
49:28:3707:U:H2'	49:28:3708:C:C6	2.47	0.50
49:28:4258:C:H2'	49:28:4259:C:H6	1.76	0.49
49:28:4538:G:H2'	49:28:4539:U:C6	2.47	0.49
50:v:27:HIS:O	50:v:30:HIS:HB2	2.13	0.49
14:14:49:ALA:HB2	19:20:100:LEU:HD11	1.94	0.49
49:28:451:C:O2'	49:28:1293:G:H2'	2.13	0.49
49:28:1472:C:H2'	49:28:1473:U:H6	1.76	0.49
50:v:402:VAL:HG13	50:v:411:TYR:HB2	1.94	0.49
50:v:505:VAL:O	50:v:547:ALA:HA	2.12	0.49
4:L3:60:VAL:HG12	4:L3:62:ARG:HG2	1.95	0.49
15:15:53:TYR:HB2	15:15:133:ILE:HD13	1.95	0.49
49:28:58:G:H4'	49:28:59:A:H4'	1.94	0.49
49:28:1598:C:H2'	49:28:1599:G:H8	1.76	0.49
49:28:3713:U:O2	49:28:3715:U:C5	2.64	0.49
6:L5:33:ARG:HA	6:L5:36:LEU:HB2	1.93	0.49
40:42:63:THR:HG23	40:42:87:ARG:HD3	1.95	0.49
45:EB:20:LYS:HA	45:EB:23:MET:HG2	1.94	0.49
49:28:1233:G:C2	49:28:1234:G:C5	3.01	0.49
49:28:1298:C:H2'	49:28:1299:G:C8	2.48	0.49
49:28:2306:G:H1'	49:28:2332:A:N6	2.27	0.49
49:28:3861:A:H2'	49:28:3862:A:C8	2.48	0.49
4:L3:160:ILE:HD13	4:L3:194:LEU:HD13	1.94	0.49
49:28:262:G:H2'	49:28:263:G:C8	2.46	0.49
49:28:4260:U:H2'	49:28:4261:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4260:U:H2'	49:28:4261:C:H6	1.77	0.49
19:20:76:LYS:HB3	19:20:131:GLU:OE1	2.12	0.49
49:28:1314:C:C2	49:28:1315:C:C5	3.00	0.49
49:28:1327:C:H2'	49:28:1328:G:C8	2.47	0.49
49:28:4413:C:H5	49:28:4429:C:H42	1.60	0.49
9:aa:101:LYS:HB3	24:cc:42:THR:HG23	1.95	0.49
13:13:142:GLU:HA	13:13:145:LYS:HE2	1.94	0.49
17:17:32:THR:HG23	17:17:91:LEU:HD21	1.94	0.49
37:38:34:PHE:CE1	37:38:47:ILE:HD11	2.47	0.49
45:EB:333:ILE:HG23	45:EB:334:THR:HG23	1.94	0.49
49:28:1292:C:H3'	49:28:1293:G:N2	2.26	0.49
49:28:2581:A:H1'	49:28:2654:C:O2'	2.12	0.49
50:v:224:THR:HG21	50:v:353:MET:HG2	1.95	0.49
4:L3:135:LYS:HA	4:L3:138:GLN:NE2	2.28	0.49
27:dd:51:GLY:HA2	47:Q:178:ARG:N	2.28	0.49
31:32:43:ASN:O	31:32:47:ARG:HG2	2.12	0.49
44:t:60:VAL:HG22	44:t:73:VAL:HG22	1.94	0.49
46:u:92:LYS:HE3	46:u:93:LEU:HD23	1.94	0.49
7:L6:131:HIS:HB2	49:28:1281:G:C6	2.48	0.49
9:aa:313:GLU:O	9:aa:317:LYS:HG2	2.12	0.49
11:10:61:SER:HA	11:10:126:VAL:HG23	1.95	0.49
10:L9:92:MET:HE2	10:L9:179:ILE:HG22	1.94	0.49
32:ee:50:VAL:HG22	32:ee:69:VAL:HG12	1.95	0.49
49:28:37:U:H2'	49:28:38:A:O4'	2.13	0.49
49:28:1939:A:H5'	49:28:1940:G:H4'	1.95	0.49
43:s:30:VAL:HB	43:s:189:ILE:HG22	1.94	0.48
31:32:70:LEU:HD11	31:32:76:LYS:HG2	1.95	0.48
34:35:91:MET:HA	34:35:94:ARG:HG3	1.95	0.48
45:EB:246:ILE:HB	45:EB:305:PHE:HB2	1.95	0.48
48:ES:3238:C:H2'	48:ES:3239:G:C8	2.48	0.48
48:ES:3587:C:H2'	48:ES:3588:C:C6	2.48	0.48
49:28:1461:C:H2'	49:28:1462:A:C8	2.48	0.48
49:28:1990:A:H3'	49:28:1991:A:H5''	1.95	0.48
49:28:4239:A:H2'	49:28:4240:G:H8	1.77	0.48
50:v:594:LYS:H	50:v:854:PHE:C	2.22	0.48
5:L4:7:LEU:HG	5:L4:21:ASN:HB3	1.94	0.48
8:L7:32:LEU:O	8:L7:35:LYS:HG3	2.13	0.48
10:L9:174:LYS:HG2	39:40:101:VAL:HG21	1.94	0.48
40:42:4:VAL:HG23	40:42:93:LEU:HD13	1.96	0.48
45:EB:12:ILE:HD11	45:EB:221:HIS:HA	1.94	0.48
45:EB:291:MET:O	45:EB:294:VAL:HG12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:676:C:H2'	49:28:677:G:C8	2.47	0.48
49:28:1955:G:H2'	49:28:1956:A:H8	1.78	0.48
50:v:727:ARG:HG2	50:v:854:PHE:HB2	1.95	0.48
2:5:3:C:H2'	2:5:4:U:C6	2.48	0.48
4:L3:285:TYR:CD1	4:L3:363:ILE:HD13	2.48	0.48
8:L7:61:ARG:NH2	8:L7:65:ARG:HH21	2.05	0.48
16:bb:58:LEU:HD21	16:bb:74:ARG:HH21	1.78	0.48
49:28:709:C:H1'	49:28:4942:C:H5	1.77	0.48
49:28:2607:C:H2'	49:28:2608:G:C8	2.49	0.48
11:10:204:GLY:HA3	11:10:208:LYS:HE2	1.95	0.48
15:15:50:ARG:NH1	49:28:278:G:H4'	2.26	0.48
42:gg:52:GLU:HB2	42:gg:61:VAL:HG23	1.95	0.48
49:28:643:C:H2'	49:28:644:G:H8	1.79	0.48
49:28:1338:G:H4'	49:28:1339:U:C6	2.49	0.48
49:28:4467:A:O2'	49:28:4510:A:H1'	2.11	0.48
5:L4:301:ALA:HB1	47:Q:132:LYS:HE3	1.95	0.48
13:13:19:GLN:HE22	49:28:1518:A:H61	1.60	0.48
20:21:87:LYS:HE3	49:28:4305:G:H22	1.78	0.48
44:t:64:ILE:HA	44:t:69:ALA:HA	1.94	0.48
45:EB:349:VAL:HG11	45:EB:355:LYS:HD3	1.95	0.48
46:u:99:LEU:HA	46:u:102:LYS:HE2	1.95	0.48
49:28:3911:C:H2'	49:28:3912:U:C6	2.47	0.48
49:28:4239:A:H2'	49:28:4240:G:C8	2.48	0.48
49:28:4563:U:C2	49:28:4564:A:C8	3.01	0.48
50:v:27:HIS:HB2	50:v:139:THR:HG23	1.95	0.48
1:58:19:C:H2'	1:58:20:A:C8	2.49	0.48
6:L5:211:LEU:HB3	6:L5:219:TYR:HB2	1.96	0.48
9:aa:128:LYS:HE2	49:28:3940:U:H5''	1.96	0.48
16:bb:18:ARG:NH2	16:bb:128:ARG:HH21	2.12	0.48
19:20:20:PRO:HA	19:20:23:ARG:HH22	1.79	0.48
23:24:9:SER:HB3	23:24:11:TYR:HD2	1.78	0.48
31:32:22:ARG:HE	31:32:36:ARG:HG3	1.79	0.48
33:34:90:ARG:HG3	49:28:4122:G:H4'	1.95	0.48
40:42:69:ARG:HD3	40:42:80:LYS:HD2	1.96	0.48
46:u:124:LEU:HD23	46:u:124:LEU:H	1.79	0.48
49:28:1338:G:H4'	49:28:1339:U:H6	1.77	0.48
49:28:2845:A:N6	49:28:3843:C:H42	2.04	0.48
1:58:141:C:H2'	1:58:142:U:C6	2.49	0.48
19:20:116:ARG:HE	49:28:1926:C:H5'	1.79	0.48
49:28:1340:C:H2'	49:28:1341:U:C6	2.49	0.48
49:28:2409:U:H4'	49:28:2428:A:H4'	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4508:C:N3	49:28:4512:U:H5	2.12	0.48
10:L9:92:MET:HE1	10:L9:161:ILE:HG13	1.95	0.48
20:21:8:ARG:HD2	20:21:52:MET:HE1	1.96	0.48
32:ee:54:LYS:HD3	49:28:443:G:H5''	1.95	0.48
43:s:26:LYS:HE3	43:s:92:LYS:HE3	1.96	0.48
49:28:1447:C:C2	49:28:1448:G:C8	3.02	0.48
49:28:2568:C:H2'	49:28:2569:G:C8	2.49	0.48
50:v:126:LEU:HD23	50:v:154:VAL:HG23	1.96	0.48
1:58:144:U:H2'	1:58:145:C:C6	2.49	0.48
6:L5:152:ARG:HG3	6:L5:154:THR:HG23	1.96	0.48
8:L7:235:ARG:HB2	8:L7:238:GLN:HB2	1.96	0.48
10:L9:41:ILE:HD13	10:L9:73:ILE:HD11	1.96	0.48
12:11:60:PHE:HB3	49:28:4257:A:C2	2.49	0.48
24:cc:65:ALA:HB2	34:35:69:LEU:HD11	1.95	0.48
40:42:61:LYS:NZ	40:42:87:ARG:HH12	2.12	0.48
45:EB:172:LYS:HB3	45:EB:354:LEU:HD11	1.95	0.48
49:28:1170:G:H2'	49:28:1171:G:H8	1.78	0.48
19:20:16:CYS:HB2	19:20:54:MET:SD	2.54	0.47
33:34:64:LEU:HD23	33:34:67:LEU:HD12	1.95	0.47
46:u:7:ARG:O	46:u:10:LEU:HG	2.14	0.47
49:28:1193:C:H2'	49:28:1194:G:C8	2.49	0.47
49:28:1911:C:H1'	49:28:1917:A:H2'	1.96	0.47
4:L3:14:LEU:HD22	4:L3:17:LEU:HD13	1.95	0.47
6:L5:53:VAL:HB	6:L5:159:VAL:HG13	1.96	0.47
15:15:187:SER:H	15:15:190:ALA:HB3	1.77	0.47
30:31:45:ALA:O	30:31:48:GLU:HG2	2.14	0.47
31:32:22:ARG:HD3	31:32:31:ILE:HG23	1.96	0.47
49:28:1645:C:H2'	49:28:1646:A:H8	1.79	0.47
49:28:3865:A:H2'	49:28:3866:C:C6	2.49	0.47
1:58:26:C:H2'	1:58:27:U:C6	2.49	0.47
1:58:144:U:H2'	1:58:145:C:H6	1.79	0.47
11:10:36:LEU:HD11	11:10:87:ILE:HD12	1.95	0.47
26:27:91:LEU:H	26:27:117:LYS:HZ3	1.60	0.47
49:28:1733:G:N3	49:28:4214:A:H2'	2.30	0.47
49:28:1806:G:H2'	49:28:1807:C:H6	1.78	0.47
49:28:2627:C:H41	49:28:4649:G:H1	1.62	0.47
49:28:2634:C:H2'	49:28:2635:U:C6	2.49	0.47
49:28:2764:A:H2'	49:28:2765:A:H8	1.79	0.47
49:28:4727:A:H2'	49:28:4728:U:O4'	2.15	0.47
4:L3:252:ALA:HB1	49:28:4524:G:N3	2.28	0.47
49:28:4130:C:H2'	49:28:4131:G:C8	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4927:G:H3'	49:28:4928:C:O2	2.14	0.47
4:L3:128:LYS:HG3	49:28:4966:A:H5'	1.96	0.47
15:15:6:TYR:HA	35:36:44:ILE:HD11	1.95	0.47
19:20:78:PHE:CE1	19:20:102:THR:HG22	2.50	0.47
21:22:36:ALA:HB3	21:22:65:ARG:HE	1.80	0.47
23:24:44:ARG:HD2	49:28:3615:G:H1'	1.97	0.47
42:gg:41:ASN:OD1	42:gg:44:ILE:HG12	2.14	0.47
45:EB:88:HIS:ND1	45:EB:305:PHE:HB3	2.29	0.47
46:u:14:VAL:HA	46:u:17:VAL:HG12	1.95	0.47
47:Q:11:ARG:HG3	49:28:2081:C:H5''	1.97	0.47
49:28:979:C:H2'	49:28:980:U:H6	1.79	0.47
49:28:1195:G:H2'	49:28:1196:G:H8	1.80	0.47
49:28:1884:C:H4'	49:28:2070:U:C4	2.50	0.47
49:28:2503:G:H2'	49:28:2504:C:C6	2.49	0.47
49:28:2521:G:H2'	49:28:2522:G:C8	2.49	0.47
49:28:3721:U:H2'	49:28:3722:G:H8	1.80	0.47
6:L5:129:GLU:HG3	6:L5:177:THR:HG21	1.95	0.47
16:bb:12:ARG:HE	19:20:171:ARG:HH22	1.62	0.47
20:21:14:MET:HE1	20:21:55:LYS:HB2	1.97	0.47
23:24:35:LYS:HE2	23:24:51:TRP:CZ2	2.49	0.47
32:ee:33:VAL:HG23	32:ee:38:GLU:HB2	1.96	0.47
49:28:923:C:H4'	49:28:923:C:OP1	2.14	0.47
49:28:2765:A:H2'	49:28:2766:A:H8	1.80	0.47
49:28:4903:G:H2'	49:28:4904:G:H8	1.80	0.47
49:28:5004:C:H2'	49:28:5005:G:O4'	2.13	0.47
50:v:253:VAL:O	50:v:257:MET:HG2	2.15	0.47
5:L4:101:MET:HE3	49:28:2343:G:C4	2.50	0.47
27:dd:28:HIS:CD2	27:dd:32:ARG:HG2	2.50	0.47
29:30:38:ILE:HG21	29:30:63:TYR:HB3	1.96	0.47
31:32:75:ARG:HB2	31:32:95:TYR:HD1	1.79	0.47
43:s:61:MET:O	43:s:65:ILE:HG12	2.14	0.47
45:EB:156:LEU:HD13	45:EB:166:VAL:HA	1.97	0.47
49:28:23:C:H2'	49:28:24:G:O4'	2.15	0.47
49:28:48:G:O6	49:28:290:U:H5'	2.15	0.47
49:28:1524:A:H61	49:28:1651:G:H22	1.63	0.47
49:28:2386:U:H2'	49:28:2387:G:C8	2.49	0.47
49:28:2478:C:H2'	49:28:2479:G:C8	2.50	0.47
49:28:3723:A:H2'	49:28:3724:A:H8	1.79	0.47
49:28:3933:G:H2'	49:28:3934:G:H8	1.78	0.47
50:v:365:GLN:HA	50:v:368:ARG:HB2	1.97	0.47
50:v:653:GLY:HA2	50:v:683:PHE:CZ	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:15:77:LYS:HD3	49:28:3669:G:OP2	2.15	0.47
25:26:52:ASP:O	25:26:110:LYS:HB2	2.14	0.47
28:29:112:ILE:H	28:29:112:ILE:HD12	1.79	0.47
49:28:922(B):C:H3'	49:28:923:C:H5''	1.97	0.47
49:28:1376:C:H5''	49:28:1377:G:OP2	2.14	0.47
49:28:3870:C:H2'	49:28:3871:A:H8	1.79	0.47
49:28:4896:G:H2'	49:28:4897:G:H8	1.80	0.47
3:L8:21:LYS:HG2	49:28:1541:C:H5''	1.96	0.47
7:L6:168:LEU:HD21	7:L6:260:ILE:HD11	1.96	0.47
8:L7:125:ASN:HB2	20:21:132:PRO:HB2	1.97	0.47
9:aa:163:LYS:HZ1	9:aa:166:ARG:HH22	1.62	0.47
12:11:50:PHE:CG	12:11:67:LYS:HD3	2.49	0.47
49:28:106:A:H2'	49:28:107:G:O4'	2.15	0.47
11:10:91:LEU:HD12	11:10:135:ILE:HG23	1.97	0.47
30:31:53:ALA:HA	30:31:88:LEU:HD21	1.96	0.47
43:s:77:LYS:HD2	43:s:198:ILE:HD11	1.96	0.47
48:ES:2950:G:O6	48:ES:3244:U:O4	2.33	0.47
49:28:1191:C:H2'	49:28:1192:C:C6	2.50	0.47
49:28:2639:U:H2'	49:28:2694:G:N1	2.30	0.47
49:28:4236:G:H4'	49:28:4328:G:O2'	2.15	0.47
49:28:4591:U:H2'	49:28:4592:C:C6	2.50	0.47
49:28:4941:G:O2'	49:28:4942:C:H5'	2.15	0.47
49:28:5056:A:H2'	49:28:5057:C:H6	1.80	0.47
23:24:8:PHE:CD1	23:24:46:PRO:HG3	2.50	0.46
40:42:9:ARG:HA	40:42:20:PRO:HA	1.96	0.46
46:u:14:VAL:HG21	46:u:179:LEU:HD12	1.97	0.46
49:28:325:U:H2'	49:28:326:C:H6	1.79	0.46
49:28:922:C:H2'	49:28:922(A):G:H8	1.79	0.46
49:28:978:G:H22	49:28:1277:G:H22	1.63	0.46
49:28:2786:C:H5''	49:28:2787:A:H5'	1.98	0.46
49:28:4749:C:H2'	49:28:4750:G:O4'	2.15	0.46
1:58:8:U:H2'	1:58:9:A:C8	2.50	0.46
2:5:15:C:H2'	2:5:16:A:H8	1.80	0.46
7:L6:64:MET:HG3	7:L6:68:LYS:HE2	1.97	0.46
15:15:49:ARG:HH12	49:28:152:U:P	2.37	0.46
16:bb:157:GLU:HA	16:bb:160:ARG:HG2	1.97	0.46
24:cc:83:THR:HG22	24:cc:85:SER:H	1.81	0.46
38:39:28:TRP:HA	38:39:33:ASN:ND2	2.30	0.46
43:s:28:PHE:HB2	43:s:89:VAL:HG13	1.98	0.46
43:s:121:VAL:HG22	43:s:182:PRO:HG2	1.95	0.46
49:28:223:G:H4'	49:28:225:G:N7	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:318:A:H2'	49:28:319:A:H8	1.80	0.46
49:28:2007:G:H21	49:28:2012:A:H62	0.66	0.46
49:28:2079:G:H2'	49:28:2080:U:C6	2.51	0.46
49:28:2540:C:H2'	49:28:2541:G:H8	1.81	0.46
14:14:15:VAL:HG22	14:14:50:MET:HE1	1.98	0.46
43:s:50:LYS:NZ	43:s:98:ILE:HG13	2.30	0.46
48:ES:3284:C:H2'	48:ES:3285:G:C8	2.45	0.46
49:28:2411:C:H2'	49:28:2412:A:H8	1.80	0.46
49:28:4507:A:H2'	49:28:4508:C:C6	2.48	0.46
4:L3:81:THR:OG1	4:L3:207:VAL:HG21	2.16	0.46
24:cc:77:ILE:HD12	24:cc:116:LEU:HD12	1.96	0.46
49:28:673:C:H2'	49:28:674:G:H8	1.81	0.46
49:28:1196:G:H2'	49:28:1197:C:C6	2.50	0.46
49:28:1350:C:H2'	49:28:1351:G:C8	2.51	0.46
49:28:3752:C:O2'	49:28:3776:G:H1'	2.15	0.46
49:28:4228:G:H5''	49:28:4229:U:O4'	2.16	0.46
49:28:4750:G:H2'	49:28:4751:G:C8	2.50	0.46
50:v:385:ILE:HD11	50:v:395:MET:HG2	1.96	0.46
50:v:502:SER:H	50:v:814:PHE:HB3	1.81	0.46
50:v:601:ARG:HH12	50:v:858:LEU:HD23	1.79	0.46
1:58:92:U:H2'	1:58:93:C:O4'	2.15	0.46
3:L8:136:VAL:HA	3:L8:148:VAL:HG22	1.98	0.46
3:L8:233:ARG:HB2	49:28:4184:G:H5'	1.98	0.46
14:14:89:THR:HG22	14:14:91:TRP:H	1.80	0.46
31:32:106:LYS:HA	31:32:109:LYS:HG2	1.97	0.46
46:u:69:GLY:HA2	46:u:113:SER:HB3	1.97	0.46
49:28:1188:C:H2'	49:28:1189:G:H8	1.80	0.46
49:28:1685:G:H2'	49:28:1686:C:H6	1.81	0.46
49:28:1732:C:O2'	49:28:1733:G:H5'	2.15	0.46
49:28:1870:C:H2'	49:28:1871:A:H8	1.81	0.46
49:28:3650:C:H2'	49:28:3651:A:H8	1.80	0.46
49:28:3802:U:O2'	49:28:3803:A:H5'	2.15	0.46
21:22:84:LYS:O	21:22:87:THR:HG22	2.15	0.46
35:36:85:ARG:O	35:36:88:GLU:HG2	2.15	0.46
48:ES:3245:G:H2'	48:ES:3246:G:H8	1.81	0.46
49:28:347:A:H2'	49:28:348:G:C8	2.50	0.46
49:28:3938:G:H4'	49:28:3939:G:O5'	2.15	0.46
49:28:4448:G:H5''	49:28:4449:A:H5'	1.98	0.46
49:28:4625:C:O2'	49:28:4626:A:H5'	2.16	0.46
49:28:4723:A:H2'	49:28:4724:A:C8	2.50	0.46
1:58:14:U:H5''	17:17:123:PRO:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L5:123:VAL:HG22	6:L5:248:ARG:NH2	2.30	0.46
11:10:30:LYS:HG3	11:10:63:GLU:HG2	1.98	0.46
12:11:68:ILE:HD11	49:28:4258:C:H5'	1.97	0.46
13:13:129:ARG:HH22	49:28:173:C:H5''	1.81	0.46
14:14:60:PHE:HE1	14:14:85:LYS:HE2	1.81	0.46
19:20:15:ARG:HB3	19:20:27:LEU:HD13	1.96	0.46
35:36:58:MET:SD	35:36:90:LEU:HD22	2.55	0.46
46:u:67:VAL:HG12	46:u:111:LEU:HB3	1.98	0.46
46:u:171:HIS:H	46:u:174:MET:HE3	1.81	0.46
49:28:48:G:H1'	49:28:49:U:OP2	2.16	0.46
49:28:121:A:H5'	49:28:122:U:OP2	2.15	0.46
49:28:2412:A:H2'	49:28:2413:U:C6	2.51	0.46
49:28:2765:A:H2'	49:28:2766:A:C8	2.51	0.46
49:28:3736:A:H2'	49:28:3737:A:C8	2.51	0.46
49:28:4678:G:N2	49:28:4713:G:H1'	2.31	0.46
49:28:5056:A:H2'	49:28:5057:C:C6	2.51	0.46
50:v:117:ALA:HB1	50:v:399:SER:HB2	1.98	0.46
2:5:49:A:OP1	6:L5:225:GLN:HB2	2.16	0.46
5:L4:4:ALA:HA	49:28:490:C:O2'	2.16	0.46
6:L5:4:VAL:HG11	49:28:4247:G:H5'	1.98	0.46
20:21:27:LEU:O	20:21:31:MET:HG2	2.16	0.46
26:27:50:PRO:HD3	26:27:68:ILE:HG12	1.98	0.46
49:28:424:U:H2'	49:28:425:U:C6	2.50	0.46
49:28:1340:C:H2'	49:28:1341:U:H6	1.81	0.46
49:28:1494:U:H2'	49:28:1495:G:C8	2.51	0.46
49:28:2810:U:H2'	49:28:2811:G:O4'	2.16	0.46
50:v:481:LYS:HE3	50:v:532:PRO:HG3	1.98	0.46
34:35:74:LYS:HE2	49:28:133:C:H5	1.80	0.46
43:s:44:ARG:HH11	49:28:1997:U:H4'	1.81	0.46
44:t:13:VAL:HG12	44:t:62:LEU:HB2	1.97	0.46
49:28:288:G:H2'	49:28:289:C:C6	2.51	0.46
49:28:1662:C:H2'	49:28:1663:C:C6	2.50	0.46
50:v:252:LYS:HA	50:v:255:ASP:OD2	2.16	0.46
1:58:5:U:H2'	1:58:6:C:H6	1.81	0.46
6:L5:43:LYS:HB3	6:L5:46:THR:HB	1.96	0.46
6:L5:268:ARG:NH2	49:28:1176:C:H5''	2.31	0.46
27:dd:87:ARG:HG2	27:dd:120:GLN:HE22	1.81	0.46
29:30:17:ARG:HB3	29:30:104:ILE:HB	1.98	0.46
43:s:27:CYS:SG	43:s:88:PHE:HB3	2.56	0.46
48:ES:2908:U:H3	48:ES:3586:G:H1	1.64	0.46
49:28:418:A:H4'	49:28:2311:C:H5'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1616:U:H2'	49:28:1617:G:H8	1.81	0.46
49:28:1771:U:H2'	49:28:1772:C:C6	2.51	0.46
4:L3:229:LYS:HA	49:28:2836:A:H4'	1.98	0.45
7:L6:126:ARG:HH22	49:28:971(A):G:N2	2.14	0.45
7:L6:164:ARG:HD3	7:L6:273:TYR:CZ	2.50	0.45
10:L9:18:ILE:HG22	10:L9:27:VAL:HG22	1.99	0.45
15:15:35:ALA:HA	15:15:65:ARG:HG2	1.98	0.45
15:15:182:HIS:HA	15:15:195:ARG:HH12	1.81	0.45
16:bb:80:PHE:O	16:bb:83:THR:HG22	2.16	0.45
20:21:62:GLY:HA3	20:21:76:VAL:HG12	1.99	0.45
43:s:39:GLN:O	43:s:42:GLN:HG3	2.16	0.45
49:28:170:C:H2'	49:28:171:U:H4'	1.98	0.45
49:28:1789:C:H2'	49:28:1790:U:C6	2.51	0.45
49:28:2485:U:H2'	49:28:2486:G:C8	2.50	0.45
49:28:4538:G:H2'	49:28:4539:U:H6	1.81	0.45
49:28:4576:U:H2'	49:28:4577:U:C6	2.51	0.45
49:28:4578:G:H2'	49:28:4579:U:C6	2.51	0.45
49:28:4594:U:H2'	49:28:4595:G:C8	2.48	0.45
2:5:52:C:H1'	12:11:12:MET:HE2	1.98	0.45
10:L9:129:ARG:HG2	10:L9:153:LEU:HD22	1.98	0.45
49:28:2465:C:H2'	49:28:2466:G:O4'	2.15	0.45
49:28:2491:C:H2'	49:28:2492:C:C6	2.51	0.45
49:28:2639:U:H2'	49:28:2694:G:H1	1.81	0.45
49:28:4068:U:H2'	49:28:4069:U:O4'	2.16	0.45
1:58:4:C:H2'	1:58:5:U:C6	2.51	0.45
10:L9:120:GLU:HG2	49:28:4611:A:H2	1.80	0.45
49:28:1794:A:H5''	49:28:4214:A:H61	1.81	0.45
49:28:2358:G:H2'	49:28:2359:U:O4'	2.16	0.45
49:28:4258:C:H2'	49:28:4259:C:C6	2.51	0.45
49:28:4761:G:H2'	49:28:4762:A:H8	1.80	0.45
1:58:7:U:H2'	1:58:8:U:C6	2.51	0.45
3:L8:194:ASN:HB2	49:28:1539:G:H4'	1.98	0.45
5:L4:103:ALA:HA	49:28:1517:G:H22	1.81	0.45
5:L4:200:ARG:HH22	25:26:11:ARG:CZ	2.29	0.45
49:28:2029:A:H2'	49:28:2030:A:C8	2.51	0.45
49:28:2421:G:OP2	49:28:2828:U:H1'	2.15	0.45
49:28:2521:G:H2'	49:28:2522:G:H8	1.81	0.45
3:L8:183:GLY:CA	49:28:1613:A:H5''	2.44	0.45
14:14:9:VAL:HG11	14:14:66:HIS:HA	1.98	0.45
16:bb:119:VAL:HG21	19:20:171:ARG:HE	1.81	0.45
22:23:18:LEU:HD13	22:23:54:ALA:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:26:44:VAL:HG21	25:26:119:LEU:HD13	1.98	0.45
49:28:275:C:H2'	49:28:276:C:C6	2.52	0.45
49:28:922(A):G:H2'	49:28:922(B):C:C6	2.52	0.45
1:58:16:G:N2	49:28:417:G:H1'	2.32	0.45
4:L3:94:GLU:HB2	4:L3:158:GLN:HG3	1.99	0.45
7:L6:189:LEU:HD21	7:L6:256:VAL:HG21	1.99	0.45
10:L9:9:THR:HG21	10:L9:54:ARG:HD2	1.99	0.45
22:23:48:ARG:NH1	22:23:49:LEU:HB3	2.32	0.45
37:38:34:PHE:HE1	37:38:47:ILE:HD11	1.80	0.45
45:EB:203:GLN:HE22	45:EB:229:LEU:H	1.64	0.45
49:28:1758:G:H2'	49:28:1759:G:H8	1.81	0.45
49:28:2546:G:H4'	49:28:2547:G:OP1	2.17	0.45
49:28:3871:A:H2'	49:28:3872:A:C8	2.52	0.45
49:28:4389:C:H2'	49:28:4390:A:C8	2.51	0.45
49:28:4760:G:H2'	49:28:4761:G:O4'	2.16	0.45
49:28:4954:G:H2'	49:28:4955:A:C8	2.51	0.45
50:v:593:SER:O	50:v:856:ASP:HB2	2.16	0.45
4:L3:107:ALA:HB1	4:L3:202:GLU:HG3	1.99	0.45
15:15:85:VAL:HG23	49:28:43:U:OP1	2.16	0.45
17:17:131:ARG:HG3	17:17:137:ASN:ND2	2.32	0.45
34:35:96:ASN:HB2	34:35:99:GLU:HG3	1.99	0.45
47:Q:82:VAL:O	47:Q:102:ALA:HA	2.15	0.45
49:28:648:G:H2'	49:28:649:A:C8	2.50	0.45
49:28:731:G:C6	49:28:932:A:C4	3.04	0.45
49:28:1317:U:H2'	49:28:1318:C:C6	2.51	0.45
49:28:1604:G:H2'	49:28:1605:G:C8	2.50	0.45
49:28:1794:A:H5''	49:28:4214:A:N6	2.32	0.45
50:v:594:LYS:HA	50:v:856:ASP:CB	2.46	0.45
1:58:64:U:C2	1:58:65:A:C8	3.05	0.45
2:5:120:U:H3'	6:L5:259:ARG:HE	1.82	0.45
3:L8:182:ALA:HB2	49:28:3652:A:O2'	2.16	0.45
4:L3:229:LYS:HG3	4:L3:272:LYS:HD3	1.99	0.45
5:L4:292:ILE:HG21	47:Q:31:LEU:HD11	1.99	0.45
7:L6:153:LEU:HD13	7:L6:197:VAL:HG11	1.99	0.45
8:L7:79:ASN:HA	20:21:143:THR:HG22	1.99	0.45
10:L9:82:LYS:HB3	10:L9:82:LYS:HE2	1.77	0.45
16:bb:10:ASP:OD1	16:bb:37:ARG:HD3	2.16	0.45
16:bb:36:VAL:HG22	16:bb:107:GLY:O	2.16	0.45
18:19:96:MET:HG2	49:28:2667:C:O4'	2.16	0.45
20:21:54:HIS:CD2	49:28:4301:U:H4'	2.51	0.45
27:dd:87:ARG:HE	47:Q:93:GLN:HG2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:u:100:VAL:HG11	46:u:128:LEU:HD13	1.99	0.45
49:28:139:G:H2'	49:28:140:G:H8	1.82	0.45
49:28:478:G:H2'	49:28:479:G:H8	1.82	0.45
49:28:1073:G:H2'	49:28:1074:G:H8	1.82	0.45
49:28:2373:C:H2'	49:28:2374:A:C8	2.52	0.45
49:28:2777:G:H5''	49:28:2778:G:H5'	1.98	0.45
49:28:4075:U:O3'	49:28:4076:G:H2'	2.17	0.45
50:v:154:VAL:HG22	50:v:358:LEU:HD21	1.98	0.45
4:L3:189:THR:HG22	4:L3:192:GLU:HG2	1.99	0.45
7:L6:165:VAL:HG13	7:L6:180:GLY:N	2.32	0.45
14:14:96:GLU:O	14:14:99:GLU:HG2	2.17	0.45
19:20:164:LYS:HA	19:20:164:LYS:HD3	1.79	0.45
44:t:53:TRP:HE3	44:t:56:LEU:HD12	1.82	0.45
49:28:436:C:H2'	49:28:437:G:H8	1.82	0.45
49:28:2080:U:H2'	49:28:2081:C:C6	2.51	0.45
49:28:2483:G:H1	49:28:2495:U:H3	1.65	0.45
49:28:2634:C:C2	49:28:2635:U:C5	3.04	0.45
49:28:2671:C:H2'	49:28:2672:C:C6	2.52	0.45
49:28:4458:C:H2'	49:28:4459:U:C6	2.51	0.45
49:28:4563:U:H2'	49:28:4564:A:H8	1.80	0.45
49:28:4601:U:H2'	49:28:4602:A:C8	2.50	0.45
49:28:4879:C:H2'	49:28:4880:C:O2	2.16	0.45
9:aa:215:ASP:HB2	9:aa:216:PRO:HD3	1.99	0.45
10:L9:115:ARG:HG2	10:L9:123:ILE:HG22	1.98	0.45
16:bb:117:ARG:HH22	16:bb:160:ARG:HH22	1.65	0.45
48:ES:3242:U:H2'	48:ES:3243:C:C6	2.52	0.45
49:28:3690:U:H2'	49:28:3691:G:O4'	2.17	0.45
49:28:3727:A:H2'	49:28:3728:A:C8	2.52	0.45
49:28:5062:G:C2	49:28:5063:G:C8	3.05	0.45
50:v:628:LEU:HD11	50:v:647:ARG:HA	1.99	0.45
5:L4:266:THR:HG22	5:L4:269:LYS:HB3	1.98	0.44
8:L7:107:VAL:HG21	8:L7:134:ILE:HG21	1.99	0.44
47:Q:110:ARG:HB2	47:Q:120:ILE:HD13	2.00	0.44
49:28:674:G:H2'	49:28:675:C:C6	2.51	0.44
49:28:1306:C:H2'	49:28:1307:A:C8	2.50	0.44
4:L3:167:GLN:HE21	4:L3:169:ARG:HH22	1.64	0.44
8:L7:34:LYS:HE3	8:L7:34:LYS:HB3	1.78	0.44
11:10:153:ARG:HA	11:10:156:LYS:HE2	1.99	0.44
16:bb:14:HIS:CE1	16:bb:119:VAL:HG13	2.53	0.44
16:bb:121:PRO:HD2	19:20:166:ARG:O	2.17	0.44
19:20:159:LEU:HD22	19:20:172:PRO:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:26:33:PRO:HD3	49:28:239:C:H5'	1.99	0.44
45:EB:240:ALA:HB3	45:EB:309:TYR:HD2	1.82	0.44
49:28:1318:C:H2'	49:28:1319:U:O4'	2.17	0.44
49:28:1356:U:H2'	49:28:1357:C:C6	2.53	0.44
49:28:4093:G:H2'	49:28:4094:G:H8	1.81	0.44
49:28:4903:G:H2'	49:28:4904:G:C8	2.52	0.44
1:58:154:G:H2'	1:58:155:C:C6	2.52	0.44
3:L8:118:GLU:O	3:L8:158:ILE:HD11	2.18	0.44
4:L3:154:LYS:HG2	4:L3:194:LEU:HD23	1.98	0.44
14:14:60:PHE:CE1	14:14:85:LYS:HE2	2.51	0.44
15:15:159:ARG:HB3	15:15:164:LEU:HB2	1.98	0.44
16:bb:66:PRO:HG2	49:28:4587:G:H5''	1.99	0.44
34:35:52:LYS:HD3	34:35:52:LYS:HA	1.79	0.44
41:ff:52:VAL:HG21	49:28:2739:C:H4'	2.00	0.44
49:28:922:C:H2'	49:28:922(A):G:C8	2.52	0.44
49:28:1186:U:H2'	49:28:1187:G:N3	2.32	0.44
49:28:4584:A:H2'	49:28:4585:U:O4'	2.17	0.44
50:v:733:VAL:O	50:v:738:PRO:HG3	2.17	0.44
50:v:788:LEU:HD12	50:v:789:PRO:HD2	1.99	0.44
1:58:26:C:H2'	1:58:27:U:H6	1.83	0.44
7:L6:193:HIS:HD2	7:L6:195:LYS:HB3	1.83	0.44
13:13:64:VAL:HG23	13:13:67:HIS:CD2	2.53	0.44
19:20:44:PHE:CZ	19:20:48:VAL:HG21	2.52	0.44
37:38:28:ASN:OD1	37:38:31:ASN:HB2	2.17	0.44
41:ff:39:CYS:HB3	41:ff:42:CYS:SG	2.57	0.44
49:28:50:C:C2	49:28:51:A:C8	3.05	0.44
49:28:318:A:H2'	49:28:319:A:C8	2.52	0.44
49:28:416:U:H4'	49:28:2330:G:H4'	1.99	0.44
49:28:956:A:N6	49:28:1283:G:H1'	2.32	0.44
49:28:1194:G:C6	49:28:1195:G:C8	3.05	0.44
49:28:2727:C:H2'	49:28:2728:U:C6	2.52	0.44
49:28:4336:A:H5'	49:28:4337:C:O4'	2.17	0.44
50:v:652:PHE:HA	50:v:660:ASN:O	2.17	0.44
9:aa:214:VAL:HG13	9:aa:217:ILE:HD12	1.98	0.44
12:11:31:ASP:HA	12:11:34:THR:HG22	1.99	0.44
43:s:78:LEU:O	43:s:82:ILE:HG13	2.18	0.44
49:28:670:G:H2'	49:28:671:G:H8	1.82	0.44
49:28:1094:G:H2'	49:28:1095:A:H8	1.83	0.44
49:28:4453:C:H2'	49:28:4454:G:O4'	2.17	0.44
49:28:4688:C:H2'	49:28:4689:U:C6	2.52	0.44
46:u:196:LYS:HG3	46:u:200:ASN:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:161:G:H2'	49:28:162:A:H8	1.83	0.44
49:28:1198:G:H2'	49:28:1199:G:H8	1.81	0.44
49:28:3713:U:H4'	49:28:3714:G:OP1	2.17	0.44
5:L4:207:PRO:HB3	5:L4:249:PHE:CD2	2.53	0.44
9:aa:104:LEU:O	9:aa:108:VAL:HG23	2.17	0.44
13:13:80:GLU:HG2	13:13:110:LEU:HD12	1.99	0.44
25:26:59:ARG:HG3	25:26:103:LYS:HD2	2.00	0.44
26:27:28:ASN:HB2	26:27:77:TYR:OH	2.18	0.44
26:27:73:LYS:HG2	26:27:75:TYR:CZ	2.52	0.44
30:31:33:ILE:HG12	30:31:48:GLU:OE2	2.18	0.44
32:ee:106:TYR:CD2	32:ee:107:PRO:HD3	2.52	0.44
43:s:135:THR:HG21	50:v:187:VAL:HG21	2.00	0.44
45:EB:122:ALA:HB3	45:EB:320:LYS:N	2.32	0.44
49:28:1308:C:H2'	49:28:1309:C:C6	2.53	0.44
49:28:2020:U:H2'	49:28:2021:G:H8	1.83	0.44
49:28:2032:U:H2'	49:28:2033:A:C8	2.53	0.44
49:28:2492:C:H2'	49:28:2493:G:C8	2.35	0.44
49:28:3650:C:C2	49:28:3651:A:C8	3.06	0.44
49:28:4188:U:H2'	49:28:4189:U:C6	2.53	0.44
49:28:4492:U:H5''	49:28:4493:U:H5'	2.00	0.44
49:28:4970:C:C2	49:28:4971:A:C8	3.05	0.44
50:v:531:ASP:HB3	50:v:534:VAL:HG22	2.00	0.44
1:58:124:U:H4'	1:58:125:C:C5'	2.48	0.44
3:L8:128:ARG:HG3	49:28:3681:G:H2'	1.99	0.44
4:L3:252:ALA:HB3	49:28:4457:U:O2	2.17	0.44
4:L3:261:ARG:HB3	49:28:4564:A:O2'	2.18	0.44
4:L3:262:VAL:HG21	4:L3:268:ARG:NH1	2.33	0.44
14:14:47:ARG:HG2	19:20:73:LEU:HD13	2.00	0.44
21:22:48:LYS:HD3	21:22:51:GLY:HA2	1.99	0.44
22:23:109:LYS:HG3	22:23:111:GLU:OE1	2.17	0.44
40:42:44:LYS:HE2	40:42:52:THR:HB	1.98	0.44
45:EB:185:MET:HG3	45:EB:229:LEU:HD13	1.99	0.44
49:28:163:A:H2'	49:28:164:G:C8	2.52	0.44
49:28:1195:G:H2'	49:28:1196:G:C8	2.53	0.44
49:28:2461:G:H2'	49:28:2462:C:C6	2.53	0.44
49:28:3722:G:H2'	49:28:3723:A:H8	1.82	0.44
49:28:3751:G:H21	49:28:3775:A:H8	1.65	0.44
49:28:3793:U:H2'	49:28:3794:C:H6	1.83	0.44
49:28:4094:G:H2'	49:28:4095:G:C8	2.53	0.44
50:v:331:GLU:O	50:v:334:PRO:HD2	2.18	0.44
50:v:364:ALA:O	50:v:368:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:v:428:ARG:NH2	50:v:489:GLU:HA	2.33	0.44
50:v:738:PRO:HB2	50:v:739:ARG:H	1.62	0.44
5:L4:230:LEU:HD21	5:L4:239:LYS:HD2	2.00	0.44
6:L5:36:LEU:HD23	6:L5:36:LEU:HA	1.90	0.44
6:L5:43:LYS:HE2	49:28:1817:U:H4'	2.00	0.44
32:ee:23:GLU:HG3	49:28:439:G:O2'	2.18	0.44
34:35:53:SER:O	34:35:57:VAL:HG23	2.18	0.44
44:t:152:ILE:HD12	44:t:155:ILE:HB	1.99	0.44
47:Q:59:PRO:HG3	47:Q:143:ARG:HA	2.00	0.44
49:28:222:C:H2'	49:28:223:G:O4'	2.18	0.44
49:28:258:G:H2'	49:28:259:C:C6	2.53	0.44
49:28:288:G:H2'	49:28:289:C:H6	1.82	0.44
49:28:1959:U:O4'	49:28:1961:G:H1'	2.18	0.44
49:28:4607:A:O5'	49:28:4607:A:H8	2.00	0.44
50:v:147:ILE:HG12	50:v:192:TYR:HB3	2.00	0.44
50:v:675:ILE:HD11	50:v:721:ILE:HG13	2.00	0.44
2:5:65:G:O3'	6:L5:10:LYS:HE2	2.18	0.43
9:aa:136:PHE:HB3	9:aa:212:HIS:HB2	2.00	0.43
9:aa:169:ALA:O	9:aa:172:GLU:HG3	2.18	0.43
18:19:60:ARG:NH1	49:28:2615:C:H5''	2.30	0.43
33:34:82:MET:HE1	33:34:90:ARG:HE	1.83	0.43
44:t:90:ARG:CZ	44:t:98:ILE:HD13	2.48	0.43
46:u:26:ARG:HH22	46:u:208:SER:HB2	1.82	0.43
49:28:1381:U:H5'	49:28:1382:G:OP2	2.18	0.43
49:28:2411:C:H2'	49:28:2412:A:C8	2.53	0.43
49:28:4980:C:H3'	49:28:4981:G:H21	1.82	0.43
3:L8:96:LEU:HD12	3:L8:166:VAL:HG21	2.00	0.43
5:L4:195:LYS:HE3	49:28:2333:G:H5''	1.99	0.43
6:L5:36:LEU:HB3	6:L5:37:VAL:H	1.60	0.43
13:13:42:ARG:O	13:13:46:ILE:HG12	2.17	0.43
15:15:178:HIS:HA	15:15:181:HIS:NE2	2.33	0.43
26:27:105:ALA:HA	26:27:108:ARG:HE	1.83	0.43
28:29:12:GLN:HB3	28:29:16:TRP:CZ2	2.54	0.43
40:42:36:GLN:HB2	49:28:4363:A:H5''	2.00	0.43
44:t:28:LEU:O	44:t:32:ILE:HG13	2.18	0.43
45:EB:65:LYS:N	45:EB:65:LYS:HD3	2.33	0.43
49:28:1933:G:O5'	49:28:1933:G:H8	2.00	0.43
49:28:4862:G:H2'	49:28:4863:G:H8	1.82	0.43
2:5:3:C:H2'	2:5:4:U:H6	1.83	0.43
4:L3:135:LYS:HD3	4:L3:138:GLN:HE21	1.84	0.43
5:L4:205:ARG:HG3	49:28:2297:G:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L9:59:LYS:HE3	10:L9:66:GLU:HB3	1.98	0.43
11:10:51:HIS:CD2	11:10:168:SER:HB2	2.53	0.43
12:11:128:LEU:HD11	12:11:130:PHE:CE1	2.54	0.43
13:13:120:TYR:HB2	13:13:155:MET:HE1	2.00	0.43
13:13:135:LYS:HD3	13:13:135:LYS:HA	1.87	0.43
18:19:101:ILE:HD13	49:28:2897:G:H4'	2.00	0.43
19:20:54:MET:HE3	19:20:54:MET:HB3	1.92	0.43
28:29:105:GLY:O	28:29:109:ARG:HG2	2.18	0.43
33:34:69:LYS:HD3	49:28:2769:U:N3	2.33	0.43
35:36:33:LEU:HD21	35:36:38:LYS:HB2	2.00	0.43
46:u:45:LYS:HD3	46:u:45:LYS:HA	1.92	0.43
48:ES:2947:G:C6	48:ES:3247:A:N1	2.86	0.43
49:28:177:G:H2'	49:28:178:C:C6	2.52	0.43
49:28:259:C:H2'	49:28:260:C:C6	2.54	0.43
49:28:691:C:H2'	49:28:692:A:C8	2.53	0.43
49:28:693:C:H2'	49:28:694:C:H6	1.83	0.43
49:28:2751:G:H2'	49:28:2752:G:H8	1.84	0.43
49:28:4893:A:H2'	49:28:4894:A:C4	2.54	0.43
49:28:4922:C:H2'	49:28:4923:U:C6	2.53	0.43
49:28:4991:U:H2'	49:28:4992:G:H8	1.83	0.43
50:v:6:VAL:O	50:v:9:ILE:HG13	2.19	0.43
4:L3:204:GLN:HE21	4:L3:204:GLN:HB3	1.61	0.43
4:L3:258:HIS:NE2	49:28:3878:C:N3	2.67	0.43
6:L5:11:ALA:HB1	49:28:1743:A:H5'	2.00	0.43
9:aa:153:HIS:CE1	9:aa:156:ARG:HH11	2.35	0.43
11:10:54:SER:HB2	11:10:135:ILE:HD11	2.00	0.43
16:bb:62:MET:HA	49:28:2045:G:C5	2.54	0.43
20:21:102:ARG:HG3	20:21:106:LEU:HD23	1.99	0.43
49:28:2710:C:H2'	49:28:2712:G:H5''	1.99	0.43
49:28:4266:G:H2'	49:28:4266:G:N3	2.33	0.43
49:28:4860:G:H2'	49:28:4861:G:C8	2.50	0.43
49:28:4862:G:H2'	49:28:4863:G:C8	2.54	0.43
4:L3:30:LYS:HG3	49:28:4716:C:OP2	2.18	0.43
4:L3:112:ASP:O	4:L3:116:ARG:HG2	2.19	0.43
5:L4:101:MET:SD	5:L4:104:PRO:HA	2.58	0.43
9:aa:235:CYS:HB3	9:aa:275:ILE:HD13	2.00	0.43
19:20:80:ILE:HG12	19:20:129:VAL:HG22	2.01	0.43
28:29:101:HIS:CE1	28:29:103:LYS:HB2	2.53	0.43
44:t:115:GLN:HA	44:t:118:HIS:ND1	2.33	0.43
48:ES:2949:U:H2'	48:ES:2950:G:C8	2.53	0.43
49:28:1065:G:H2'	49:28:1066:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1509:C:H2'	49:28:1510:G:C8	2.52	0.43
49:28:3932:U:H2'	49:28:3933:G:C8	2.54	0.43
50:v:9:ILE:O	50:v:13:MET:HG3	2.19	0.43
16:bb:135:PHE:HE2	16:bb:137:TYR:CZ	2.36	0.43
30:31:25:TYR:CZ	30:31:56:GLU:HG2	2.54	0.43
32:ee:46:ARG:HD2	32:ee:106:TYR:HE2	1.84	0.43
49:28:1239:C:O2'	49:28:1244:G:H5'	2.18	0.43
49:28:1964:A:H3'	49:28:1965:G:H8	1.83	0.43
49:28:4299:U:H2'	49:28:4300:U:H6	1.84	0.43
49:28:4897:G:C2	49:28:4923:U:O2	2.71	0.43
4:L3:122:TRP:CE2	4:L3:127:LYS:HE3	2.54	0.43
17:17:69:ARG:CD	49:28:4981:G:H1'	2.48	0.43
25:26:56:GLN:HB2	25:26:105:VAL:HG13	1.99	0.43
27:dd:43:ILE:HD12	49:28:1682:A:H2	1.83	0.43
39:40:71:ARG:HE	39:40:96:ARG:HB3	1.83	0.43
49:28:2373:C:H2'	49:28:2374:A:H8	1.84	0.43
50:v:650:TRP:CD1	50:v:676:LYS:HE3	2.54	0.43
1:58:27:U:H2'	1:58:28:C:C6	2.54	0.43
7:L6:73:ARG:HD3	49:28:983:C:C5	2.54	0.43
9:aa:267:ALA:O	9:aa:270:LYS:HG3	2.18	0.43
15:15:48:ALA:HB1	15:15:53:TYR:HB3	2.01	0.43
18:19:19:LYS:HG2	49:28:2823:G:OP1	2.19	0.43
28:29:28:ARG:HB3	49:28:1805:A:C4	2.54	0.43
44:t:99:LYS:HB2	44:t:99:LYS:HE3	1.80	0.43
45:EB:149:CYS:HB3	45:EB:228:VAL:HG11	2.00	0.43
49:28:979:C:H2'	49:28:980:U:C6	2.53	0.43
49:28:1662:C:H2'	49:28:1663:C:H6	1.83	0.43
49:28:2079:G:H2'	49:28:2080:U:H6	1.83	0.43
49:28:2453:A:H1'	49:28:2507:A:N1	2.33	0.43
49:28:3883:U:H2'	49:28:3884:U:C6	2.52	0.43
49:28:4642:U:H2'	49:28:4643:G:H8	1.83	0.43
50:v:146:ALA:HB1	50:v:151:ILE:HG23	2.01	0.43
50:v:512:LYS:HE3	50:v:569:PRO:HD2	2.01	0.43
2:5:112:U:H2'	2:5:113:G:H8	1.84	0.43
3:L8:209:HIS:CE1	3:L8:235:VAL:HG11	2.54	0.43
7:L6:156:LEU:HD11	7:L6:198:ILE:HG13	2.00	0.43
13:13:48:PRO:HG3	34:35:118:LYS:HE3	2.01	0.43
13:13:63:THR:O	13:13:65:ARG:N	2.52	0.43
25:26:10:ASP:HB3	25:26:13:LYS:HB2	2.00	0.43
26:27:74:VAL:HG23	26:27:101:PHE:CZ	2.54	0.43
34:35:89:ARG:O	34:35:93:ARG:HD3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:36:60:LEU:HB3	35:36:69:ALA:HB2	2.00	0.43
44:t:108:GLU:HA	44:t:111:ASN:ND2	2.34	0.43
49:28:251:C:H2'	49:28:252:C:C6	2.53	0.43
49:28:697:G:H2'	49:28:698:G:C8	2.51	0.43
49:28:1341:U:H2'	49:28:1342:A:C8	2.54	0.43
50:v:594:LYS:HB2	50:v:856:ASP:N	2.33	0.43
3:L8:213:GLY:HA3	49:28:4544:A:H5''	2.00	0.43
4:L3:56:ILE:HD12	4:L3:56:ILE:HA	1.80	0.43
11:10:183:ASP:O	11:10:187:GLU:HG2	2.18	0.43
12:11:52:LYS:H	12:11:52:LYS:HG2	1.72	0.43
13:13:58:ILE:HG23	13:13:70:VAL:HG11	2.00	0.43
28:29:101:HIS:HE1	28:29:103:LYS:HB2	1.84	0.43
32:ee:36:ARG:HG3	32:ee:80:ASN:HA	2.00	0.43
34:35:70:ARG:HB3	34:35:83:LEU:HD22	2.00	0.43
44:t:119:ARG:H	44:t:119:ARG:HD3	1.84	0.43
45:EB:152:ALA:O	45:EB:156:LEU:HB2	2.19	0.43
46:u:46:ASP:C	46:u:47:LYS:HG3	2.44	0.43
46:u:194:LEU:HB3	46:u:200:ASN:HD22	1.84	0.43
49:28:981:C:H2'	49:28:982:U:C6	2.54	0.43
49:28:1199:G:C2	49:28:1200:G:C5	3.07	0.43
49:28:2636:U:H2'	49:28:2637:U:C6	2.54	0.43
49:28:2861:C:H2'	49:28:2862:G:O4'	2.19	0.43
49:28:3650:C:H2'	49:28:3651:A:C8	2.53	0.43
49:28:4344:U:H2'	49:28:4345:C:H6	1.83	0.43
50:v:538:ILE:HG22	50:v:544:HIS:CD2	2.54	0.43
28:29:4:SER:HB2	49:28:1855:G:OP1	2.18	0.42
30:31:33:ILE:HD13	30:31:33:ILE:HA	1.77	0.42
41:ff:73:THR:O	41:ff:77:VAL:HG23	2.19	0.42
46:u:16:GLU:HA	46:u:19:HIS:HD2	1.84	0.42
46:u:62:LYS:HE3	46:u:62:LYS:HB3	1.90	0.42
46:u:98:LYS:HG2	46:u:102:LYS:NZ	2.32	0.42
49:28:272:U:H2'	49:28:273:U:C6	2.54	0.42
49:28:1073:G:H2'	49:28:1074:G:C8	2.53	0.42
49:28:2264:C:H2'	49:28:2265:G:O4'	2.18	0.42
49:28:2749:C:H2'	49:28:2750:G:C8	2.54	0.42
49:28:3635:A:N7	49:28:3692:A:H1'	2.34	0.42
49:28:3867:A:H2'	49:28:3868:G:C8	2.54	0.42
49:28:4708:A:C2	49:28:4709:U:H5'	2.54	0.42
4:L3:37:PRO:O	4:L3:188:GLY:HA2	2.19	0.42
6:L5:279:ARG:HD3	6:L5:283:LYS:HE3	2.01	0.42
25:26:50:ARG:HB2	25:26:115:ARG:HH21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:32:35:TRP:CZ2	31:32:56:PRO:HD2	2.54	0.42
41:ff:86:LEU:HD13	41:ff:86:LEU:HA	1.93	0.42
44:t:124:GLU:O	44:t:128:THR:HG23	2.19	0.42
49:28:1074:G:H2'	49:28:1075:G:C8	2.53	0.42
49:28:1468:C:H2'	49:28:1469:C:C6	2.53	0.42
49:28:1848:C:H2'	49:28:1849:U:O4'	2.19	0.42
49:28:2051:C:H2'	49:28:2052:G:O4'	2.19	0.42
49:28:2080:U:H2'	49:28:2081:C:H6	1.84	0.42
4:L3:252:ALA:HB1	49:28:4524:G:C2	2.54	0.42
4:L3:373:LYS:HE2	49:28:4627:U:H4'	2.01	0.42
5:L4:138:MET:HE1	5:L4:145:GLU:HG3	2.00	0.42
12:11:152:GLY:O	12:11:156:ARG:HG3	2.19	0.42
13:13:103:ARG:HH12	49:28:73:A:N6	2.17	0.42
32:ee:46:ARG:HD2	32:ee:106:TYR:CE2	2.55	0.42
43:s:84:GLY:C	49:28:2021:G:H4'	2.45	0.42
46:u:89:ALA:HA	46:u:92:LYS:HE2	2.00	0.42
48:ES:3245:G:H2'	48:ES:3246:G:C8	2.55	0.42
49:28:268:G:H2'	49:28:269:G:H8	1.84	0.42
49:28:1350:C:H2'	49:28:1351:G:H8	1.83	0.42
49:28:1504:G:H2'	49:28:1505:C:C6	2.54	0.42
49:28:3598:C:H2'	49:28:3599:A:C8	2.54	0.42
49:28:3920:U:H2'	49:28:3921:U:C6	2.54	0.42
1:58:6:C:H2'	1:58:7:U:C6	2.54	0.42
1:58:70:G:H5''	25:26:27:ARG:CZ	2.49	0.42
5:L4:83:GLY:H	49:28:368:C:H1'	1.83	0.42
8:L7:98:ASN:OD1	49:28:1897:A:H5''	2.19	0.42
12:11:90:ARG:HA	12:11:90:ARG:HD3	1.82	0.42
26:27:100:VAL:HG13	26:27:106:LEU:HB3	2.00	0.42
27:dd:77:LYS:HE2	49:28:1502:G:H22	1.84	0.42
28:29:60:ASN:O	28:29:63:LYS:HG3	2.19	0.42
29:30:20:LEU:HA	29:30:23:LYS:HG2	2.02	0.42
43:s:160:LEU:HD23	43:s:160:LEU:H	1.84	0.42
46:u:91:LYS:HD3	46:u:91:LYS:HA	1.85	0.42
47:Q:13:VAL:HG11	49:28:1690:C:C5	2.55	0.42
47:Q:14:ARG:HH12	47:Q:16:LYS:HE2	1.84	0.42
49:28:169:A:H2'	49:28:170:C:C2	2.54	0.42
49:28:951:G:H2'	49:28:952:G:H8	1.84	0.42
49:28:1558:A:H2'	49:28:1559:G:H8	1.84	0.42
49:28:2686:G:H5'	49:28:2687:U:OP1	2.19	0.42
49:28:4861:G:H2'	49:28:4862:G:H8	1.84	0.42
1:58:71:A:H4'	1:58:72:A:O5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L3:56:ILE:O	4:L3:73:VAL:HA	2.20	0.42
6:L5:264:LYS:HE3	6:L5:264:LYS:HB2	1.92	0.42
10:L9:92:MET:HG2	10:L9:181:VAL:HA	2.01	0.42
24:cc:146:ALA:HA	24:cc:149:VAL:HG22	2.02	0.42
29:30:47:ILE:HB	29:30:94:LEU:HB3	2.01	0.42
45:EB:81:SER:OG	45:EB:107:LYS:HE2	2.19	0.42
49:28:643:C:H2'	49:28:644:G:C8	2.53	0.42
49:28:1494:U:H2'	49:28:1495:G:H8	1.84	0.42
49:28:1957:U:O2'	49:28:1958:A:H8	2.03	0.42
49:28:2680:G:H2'	49:28:2681:G:O4'	2.20	0.42
49:28:2735:G:H2'	49:28:2736:G:C8	2.52	0.42
49:28:3698:G:C8	49:28:3698:G:OP2	2.72	0.42
49:28:4192:A:H2'	49:28:4193:C:H6	1.85	0.42
49:28:4520:G:H2'	49:28:4521:U:O4'	2.19	0.42
50:v:109:VAL:HG11	50:v:809:PHE:CE1	2.54	0.42
50:v:461:ILE:HD12	50:v:461:ILE:HA	1.95	0.42
2:5:58:A:H2'	2:5:59:G:H8	1.84	0.42
3:L8:142:GLU:C	3:L8:144:LYS:H	2.27	0.42
6:L5:106:ALA:HB1	6:L5:171:LEU:HD13	2.02	0.42
30:31:70:LYS:HE2	49:28:2389:A:H5'	2.02	0.42
32:ee:28:LEU:HD21	32:ee:101:ILE:HD11	2.01	0.42
40:42:37:GLY:HA3	49:28:4342:C:O3'	2.19	0.42
45:EB:60:THR:HG22	45:EB:72:LYS:HD2	2.01	0.42
49:28:2528:G:H4'	49:28:2783:A:H4'	2.02	0.42
49:28:4344:U:H2'	49:28:4345:C:C6	2.55	0.42
1:58:140:C:H2'	1:58:141:C:C6	2.54	0.42
3:L8:158:ILE:HD12	3:L8:158:ILE:HA	1.86	0.42
6:L5:146:LEU:HD23	6:L5:147:ASP:N	2.35	0.42
10:L9:23:ARG:NH1	10:L9:39:ASN:HA	2.34	0.42
13:13:8:MET:HE3	47:Q:168:ARG:HB3	2.01	0.42
16:bb:47:PHE:HA	16:bb:136:ALA:HB2	2.02	0.42
27:dd:77:LYS:H	27:dd:77:LYS:HG2	1.71	0.42
46:u:60:ARG:CZ	46:u:168:ALA:HB1	2.50	0.42
48:ES:2957:G:N7	48:ES:3237:G:C6	2.87	0.42
49:28:300:A:H2'	49:28:301:G:C8	2.49	0.42
49:28:950:G:H2'	49:28:951:G:H8	1.84	0.42
49:28:983:C:H42	49:28:1071:C:H42	1.66	0.42
49:28:3664:G:H2'	49:28:3665:G:C8	2.51	0.42
49:28:4462:C:O2'	49:28:4463:U:H5'	2.20	0.42
49:28:4578:G:H2'	49:28:4579:U:H6	1.85	0.42
49:28:4948:C:H3'	49:28:4949:G:H5''	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:v:27:HIS:HD2	50:v:28:VAL:H	1.68	0.42
50:v:630:GLN:O	50:v:633:ARG:HG2	2.19	0.42
4:L3:62:ARG:HG3	4:L3:65:SER:OG	2.19	0.42
7:L6:131:HIS:HE1	49:28:1282:G:OP2	2.02	0.42
8:L7:91:VAL:O	8:L7:119:GLY:HA2	2.19	0.42
14:14:93:LYS:O	14:14:96:GLU:HG3	2.20	0.42
20:21:86:ALA:HB2	28:29:24:PRO:HG3	2.01	0.42
21:22:28:PRO:HB2	21:22:34:MET:HG2	2.01	0.42
27:dd:29:PRO:HA	49:28:1654:G:H5'	2.01	0.42
30:31:90:ARG:HD3	30:31:102:LEU:HD13	2.01	0.42
45:EB:46:LEU:HB3	45:EB:91:PRO:HG2	2.01	0.42
49:28:1507:C:H2'	49:28:1508:A:H8	1.85	0.42
49:28:1789:C:H2'	49:28:1790:U:H6	1.85	0.42
49:28:1995:G:H2'	49:28:1996:C:C6	2.55	0.42
49:28:2015:U:H2'	49:28:2016:C:C6	2.51	0.42
49:28:2056:G:C8	49:28:2058:G:C8	3.07	0.42
50:v:775:GLN:HB2	50:v:782:PHE:CZ	2.54	0.42
50:v:776:VAL:HG21	50:v:781:MET:HE3	2.00	0.42
5:L4:191:ALA:HB2	49:28:2334:C:C5	2.55	0.42
22:23:43:LYS:HD3	22:23:60:MET:HE3	2.01	0.42
24:cc:100:VAL:HG21	24:cc:109:ILE:HD11	2.01	0.42
27:dd:3:SER:HA	27:dd:6:ARG:HH11	1.84	0.42
27:dd:37:GLY:HA3	27:dd:53:PHE:HZ	1.85	0.42
27:dd:51:GLY:HA2	47:Q:179:GLY:H	1.85	0.42
49:28:1468:C:H2'	49:28:1469:C:H6	1.84	0.42
49:28:1538:U:H2'	49:28:1539:G:C8	2.52	0.42
49:28:1551:C:H2'	49:28:1552:G:O4'	2.20	0.42
49:28:2749:C:H2'	49:28:2750:G:H8	1.83	0.42
49:28:3653:A:H8	49:28:3653:A:P	2.43	0.42
1:58:5:U:H2'	1:58:6:C:C6	2.54	0.42
1:58:77:A:C6	1:58:78:G:C6	3.08	0.42
1:58:140:C:H2'	1:58:141:C:H6	1.85	0.42
2:5:24:C:H2'	2:5:25:G:O4'	2.19	0.42
3:L8:28:ARG:HB2	3:L8:123:ARG:HH11	1.85	0.42
4:L3:248:LEU:H	4:L3:248:LEU:HG	1.78	0.42
8:L7:181:TYR:CZ	8:L7:202:GLU:HG2	2.55	0.42
9:aa:91:ASN:HB3	9:aa:96:GLN:HG2	2.02	0.42
14:14:24:LEU:HD11	14:14:86:TRP:CD2	2.55	0.42
16:bb:119:VAL:HG11	19:20:171:ARG:HD3	2.01	0.42
20:21:48:VAL:HG21	20:21:94:GLU:HG2	2.02	0.42
24:cc:64:SER:HB2	34:35:69:LEU:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:cc:76:ILE:HG23	24:cc:77:ILE:HG13	2.02	0.42
26:27:128:LYS:HE2	26:27:128:LYS:HB3	1.88	0.42
28:29:40:LEU:O	28:29:44:ARG:HG3	2.19	0.42
45:EB:322:THR:O	45:EB:333:ILE:HG22	2.19	0.42
48:ES:3244:U:H2'	48:ES:3245:G:H8	1.85	0.42
49:28:351:C:H2'	49:28:352:G:O4'	2.19	0.42
49:28:1078:A:C6	49:28:1233:G:C6	3.07	0.42
49:28:1197:C:H2'	49:28:1198:G:C8	2.55	0.42
49:28:1726:U:H2'	49:28:1727:U:H6	1.84	0.42
49:28:2009:A:N3	49:28:2009:A:H2'	2.35	0.42
49:28:4347:G:O2'	49:28:4348:A:H5'	2.20	0.42
49:28:4524:G:H4'	49:28:4524:G:OP2	2.20	0.42
49:28:4593:C:H2'	49:28:4594:U:H6	1.84	0.42
4:L3:287:ILE:HG12	4:L3:331:VAL:HG12	2.02	0.41
13:13:5:ARG:HH12	49:28:1849:U:H3'	1.85	0.41
15:15:192:TRP:CD1	49:28:48:G:H5'	2.55	0.41
26:27:23:ALA:HA	26:27:45:GLY:HA2	2.02	0.41
28:29:102:PRO:HA	28:29:109:ARG:HH22	1.85	0.41
44:t:137:GLN:HB3	44:t:146:ARG:NE	2.30	0.41
46:u:117:ILE:H	46:u:117:ILE:HG13	1.71	0.41
46:u:195:LYS:HG3	46:u:196:LYS:HG2	2.02	0.41
49:28:961:G:O6	49:28:971(A):G:C6	2.73	0.41
49:28:1168:G:H2'	49:28:1169:G:H8	1.84	0.41
49:28:2384:U:H2'	49:28:2385:U:H6	1.84	0.41
49:28:4883:C:H2'	49:28:4884:G:H8	1.84	0.41
5:L4:339:THR:HG22	5:L4:342:ARG:CZ	2.50	0.41
8:L7:70:MET:O	8:L7:73:MET:HG2	2.19	0.41
18:19:10:LEU:HB3	18:19:41:ILE:HG13	2.01	0.41
25:26:109:LEU:HD22	25:26:115:ARG:NH1	2.36	0.41
27:dd:98:ALA:HB2	27:dd:121:PRO:HB2	2.02	0.41
37:38:2:PRO:HD2	49:28:2642:A:C2	2.55	0.41
48:ES:2950:G:H1	48:ES:3244:U:H3	1.67	0.41
49:28:3723:A:H2'	49:28:3724:A:C8	2.55	0.41
49:28:3870:C:H2'	49:28:3871:A:C8	2.55	0.41
49:28:4503:A:H2'	49:28:4504:C:C6	2.55	0.41
7:L6:193:HIS:CD2	7:L6:195:LYS:HB3	2.56	0.41
13:13:55:ILE:O	13:13:56:ARG:HD3	2.20	0.41
13:13:198:ARG:HA	13:13:201:GLU:OE2	2.19	0.41
15:15:140:LYS:HD3	15:15:140:LYS:HA	1.74	0.41
20:21:87:LYS:CE	49:28:4305:G:H22	2.33	0.41
20:21:158:PHE:CE1	20:21:160:ALA:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:23:48:ARG:HH11	22:23:49:LEU:HB3	1.85	0.41
25:26:11:ARG:HG3	49:28:229:G:H5''	2.00	0.41
30:31:23:ARG:HG3	30:31:25:TYR:CE2	2.56	0.41
33:34:41:ALA:O	33:34:52:ARG:HD3	2.20	0.41
41:ff:50:ARG:HB3	41:ff:54:ILE:HG13	2.02	0.41
44:t:134:GLY:O	44:t:137:GLN:HG2	2.19	0.41
46:u:110:PHE:CD2	46:u:133:LYS:HD3	2.54	0.41
47:Q:63:LEU:O	47:Q:67:ILE:HG12	2.21	0.41
47:Q:69:LYS:HD2	49:28:1458:C:H5''	2.03	0.41
49:28:1742:A:H2'	49:28:1743:A:H8	1.85	0.41
49:28:2293:U:H2'	49:28:2294:G:C8	2.56	0.41
50:v:552:LEU:O	50:v:556:ILE:HG13	2.20	0.41
3:L8:201:GLY:HA3	3:L8:209:HIS:CE1	2.55	0.41
4:L3:46:PHE:CZ	4:L3:207:VAL:HG22	2.56	0.41
8:L7:49:ILE:HD11	8:L7:184:ILE:HG13	2.01	0.41
17:17:122:ALA:HB3	17:17:143:PRO:HG2	2.02	0.41
38:39:16:LYS:HD3	38:39:16:LYS:HA	1.92	0.41
45:EB:181:PRO:HG2	45:EB:204:ASN:CG	2.46	0.41
47:Q:78:LYS:HG2	47:Q:137:VAL:HG23	2.02	0.41
49:28:31:U:H2'	49:28:32:G:O4'	2.20	0.41
49:28:408:A:H4'	49:28:409:G:H3'	2.02	0.41
49:28:1341:U:H2'	49:28:1342:A:H8	1.85	0.41
49:28:2439:G:H5'	49:28:2778:G:OP2	2.20	0.41
49:28:2732:G:H2'	49:28:2733:C:C6	2.55	0.41
49:28:2764:A:H2'	49:28:2765:A:C8	2.56	0.41
49:28:3925:U:H2'	49:28:3926:C:O4'	2.20	0.41
49:28:4963:G:C5	49:28:4964:C:N4	2.89	0.41
50:v:718:GLY:O	50:v:722:ILE:HG13	2.20	0.41
3:L8:200:ARG:HG2	49:28:3651:A:OP1	2.20	0.41
5:L4:323:ARG:HB2	49:28:1281:G:H5'	2.02	0.41
14:14:137:LYS:HD3	14:14:137:LYS:HA	1.91	0.41
23:24:46:PRO:HB2	23:24:54:LEU:HD12	2.02	0.41
28:29:104:LEU:H	28:29:104:LEU:HG	1.69	0.41
29:30:47:ILE:HD13	29:30:72:HIS:HB3	2.02	0.41
41:ff:9:GLY:H	41:ff:27:LYS:HE2	1.85	0.41
42:gg:84:LYS:HE2	42:gg:88:ALA:HB1	2.02	0.41
43:s:133:GLU:HG2	43:s:134:LYS:HG3	2.03	0.41
44:t:98:ILE:HD12	44:t:98:ILE:HA	1.93	0.41
46:u:187:VAL:O	46:u:191:VAL:HG23	2.20	0.41
49:28:1207:C:H2'	49:28:1208:G:H8	1.86	0.41
49:28:2081:C:H2'	49:28:2082:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4094:G:C2	49:28:4095:G:C5	3.09	0.41
10:L9:63:ASN:H	10:L9:66:GLU:HG3	1.84	0.41
15:15:188:ARG:HE	15:15:188:ARG:HB2	1.56	0.41
16:bb:5:GLN:HE21	16:bb:6:VAL:HG23	1.85	0.41
45:EB:263:ARG:HH21	49:28:2709:C:H5''	1.84	0.41
45:EB:369:LYS:HD2	48:ES:3238:C:N4	2.35	0.41
49:28:49:U:H2'	49:28:50:C:H6	1.84	0.41
49:28:1756:U:H2'	49:28:1757:U:C6	2.55	0.41
49:28:2402:G:C2	49:28:2403:A:C8	3.09	0.41
49:28:2488:C:H3'	49:28:2490:U:O4	2.20	0.41
49:28:2611:A:O5'	49:28:2688:G:H4'	2.21	0.41
49:28:3816:A:OP1	49:28:3818:U:H5	2.04	0.41
49:28:3923:A:H2'	49:28:3924:C:C6	2.56	0.41
1:58:30:U:H2'	1:58:31:G:H8	1.86	0.41
2:5:19:C:H2'	2:5:20:U:C6	2.55	0.41
3:L8:23:ARG:HA	3:L8:52:PRO:HD2	2.02	0.41
5:L4:340:ILE:HD11	49:28:946:C:O2'	2.20	0.41
33:34:26:PRO:HD2	49:28:2521:G:H4'	2.03	0.41
41:ff:8:VAL:HG22	49:28:2876:G:OP1	2.21	0.41
48:ES:3587:C:H2'	48:ES:3588:C:H6	1.86	0.41
49:28:644:G:H2'	49:28:645:G:H8	1.85	0.41
49:28:1196:G:C6	49:28:1197:C:C4	3.09	0.41
49:28:1478:C:H2'	49:28:1479:G:C8	2.56	0.41
49:28:2519:U:H1'	49:28:2520:C:C6	2.55	0.41
49:28:2676:A:C5	49:28:2677:G:C8	3.09	0.41
49:28:2727:C:H2'	49:28:2728:U:H6	1.84	0.41
49:28:5030:U:H2'	49:28:5031:G:H8	1.84	0.41
50:v:296:PRO:O	50:v:300:VAL:HG23	2.20	0.41
50:v:445:LYS:HD2	50:v:446:PRO:HD2	2.03	0.41
50:v:729:LEU:O	50:v:733:VAL:HG13	2.21	0.41
3:L8:83:HIS:CD2	3:L8:86:GLN:HB2	2.56	0.41
3:L8:150:LEU:HB3	3:L8:151:PRO:HD2	2.03	0.41
4:L3:223:THR:HA	4:L3:338:VAL:HG22	2.03	0.41
9:aa:207:LEU:HD11	9:aa:275:ILE:HD12	2.03	0.41
16:bb:10:ASP:HB2	16:bb:117:ARG:HB3	2.02	0.41
18:19:77:GLY:O	18:19:81:ARG:HG3	2.21	0.41
20:21:97:LYS:HB2	20:21:97:LYS:HE3	1.86	0.41
24:cc:90:ILE:HG23	24:cc:146:ALA:HB1	2.03	0.41
25:26:22:PRO:O	25:26:26:ARG:HG2	2.20	0.41
27:dd:74:ASN:HB3	27:dd:114:LYS:HB3	2.03	0.41
28:29:36:ASP:OD1	28:29:39:PHE:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:31:40:LYS:C	30:31:43:PRO:HD2	2.45	0.41
44:t:146:ARG:HG3	44:t:147:HIS:H	1.85	0.41
45:EB:229:LEU:HG	45:EB:318:GLN:HG2	2.02	0.41
49:28:411:G:H4'	49:28:412:G:H5''	2.03	0.41
49:28:1955:G:H2'	49:28:1956:A:C8	2.55	0.41
49:28:2560:C:H2'	49:28:2561:C:C6	2.56	0.41
49:28:2870:A:H2'	49:28:2871:A:H8	1.85	0.41
49:28:3658:C:H2'	49:28:3659:G:H8	1.86	0.41
49:28:4486:C:H2'	49:28:4487:A:O4'	2.21	0.41
1:58:33:G:H5''	1:58:34:U:OP1	2.21	0.41
3:L8:70:LYS:HD3	3:L8:72:ARG:NH1	2.35	0.41
4:L3:13:SER:HB2	49:28:4622:A:H4'	2.02	0.41
5:L4:210:ILE:HA	5:L4:230:LEU:O	2.20	0.41
5:L4:321:ASN:OD1	5:L4:324:ILE:HG12	2.21	0.41
6:L5:45:ASN:OD1	20:21:33:ILE:HD13	2.21	0.41
6:L5:286:SER:HA	6:L5:289:ARG:HG2	2.02	0.41
9:aa:210:ILE:HD11	9:aa:223:LEU:HD22	2.02	0.41
9:aa:318:LEU:HD13	9:aa:318:LEU:HA	1.94	0.41
10:L9:76:HIS:O	10:L9:80:MET:HG3	2.21	0.41
11:10:9:TYR:CG	11:10:97:ILE:HG12	2.56	0.41
13:13:129:ARG:HH12	49:28:173:C:H5''	1.85	0.41
14:14:69:ARG:HH21	49:28:738(A):C:H4'	1.86	0.41
15:15:177:GLY:HA2	49:28:67:C:O3'	2.20	0.41
18:19:118:HIS:HA	49:28:2663:G:OP1	2.20	0.41
18:19:141:HIS:CE1	18:19:145:LEU:HD11	2.56	0.41
21:22:84:LYS:HD2	21:22:110:TYR:OH	2.20	0.41
25:26:89:LYS:HG2	25:26:90:ALA:H	1.85	0.41
27:dd:75:LEU:HG	27:dd:113:GLY:HA2	2.03	0.41
29:30:32:LYS:HB2	29:30:32:LYS:HE3	1.90	0.41
31:32:35:TRP:HH2	31:32:55:MET:HG2	1.86	0.41
31:32:58:ILE:HD12	31:32:58:ILE:HA	1.89	0.41
35:36:55:ARG:HA	35:36:58:MET:HE2	2.03	0.41
41:ff:10:ILE:HG21	41:ff:30:GLU:HB3	2.03	0.41
43:s:141:LEU:HD11	43:s:171:GLU:HG3	2.03	0.41
45:EB:65:LYS:HB2	48:ES:3247:A:OP1	2.21	0.41
46:u:18:LEU:HD23	46:u:18:LEU:HA	1.94	0.41
46:u:174:MET:SD	46:u:179:LEU:HD23	2.61	0.41
49:28:674:G:H2'	49:28:675:C:H6	1.86	0.41
49:28:693:C:H2'	49:28:694:C:C6	2.56	0.41
49:28:756:G:O2'	49:28:757:G:H5'	2.21	0.41
49:28:932:A:C2	49:28:939:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1245:C:H2'	49:28:1246:G:H8	1.85	0.41
49:28:1344:C:H2'	49:28:1345:A:C8	2.56	0.41
49:28:1962:A:N3	49:28:1962:A:H2'	2.36	0.41
49:28:2032:U:H2'	49:28:2033:A:H8	1.84	0.41
49:28:2540:C:H2'	49:28:2541:G:C8	2.56	0.41
49:28:4320:G:H2'	49:28:4321:U:C6	2.56	0.41
49:28:4737:G:C6	49:28:4738:C:C4	3.08	0.41
49:28:5010:U:H2'	49:28:5011:A:H8	1.85	0.41
50:v:604:MET:HG2	50:v:728:CYS:SG	2.60	0.41
5:L4:209:VAL:HB	5:L4:229:LEU:HD13	2.02	0.41
10:L9:105:ILE:HG21	10:L9:109:GLY:HA2	2.03	0.41
16:bb:61:ARG:HA	16:bb:70:PRO:HD2	2.03	0.41
26:27:122:TYR:HB2	26:27:131:PHE:CE1	2.56	0.41
31:32:22:ARG:HD3	31:32:31:ILE:CG2	2.50	0.41
32:ee:52:LYS:HE2	32:ee:52:LYS:HB3	1.87	0.41
34:35:27:GLU:O	34:35:30:GLN:HG2	2.21	0.41
36:37:8:PHE:HE2	49:28:1638:A:C6	2.39	0.41
40:42:61:LYS:HB3	40:42:61:LYS:HE2	1.64	0.41
48:ES:3236:G:O2'	48:ES:3237:G:H8	2.03	0.41
49:28:1757:U:H2'	49:28:1758:G:C8	2.56	0.41
49:28:2561:C:H2'	49:28:2562:G:C8	2.56	0.41
49:28:4153:C:H2'	49:28:4154:G:H8	1.86	0.41
49:28:4642:U:H2'	49:28:4643:G:C8	2.56	0.41
50:v:680:VAL:O	50:v:684:GLN:HG2	2.21	0.41
2:5:120:U:H3'	6:L5:259:ARG:HH21	1.85	0.40
3:L8:80:GLU:HG3	41:ff:66:GLY:HA2	2.02	0.40
13:13:91:ALA:HB1	13:13:96:ILE:HB	2.04	0.40
14:14:110:TYR:OH	14:14:114:LYS:HE3	2.21	0.40
20:21:87:LYS:NZ	49:28:4305:G:H22	2.19	0.40
20:21:96:ILE:HD13	20:21:96:ILE:HA	1.85	0.40
27:dd:21:ARG:HB3	49:28:1318:C:OP1	2.21	0.40
27:dd:77:LYS:HE3	27:dd:77:LYS:HB3	1.92	0.40
42:gg:122:LYS:HG2	42:gg:123:PRO:HD2	2.03	0.40
49:28:659:G:O2'	49:28:660:G:H5'	2.21	0.40
49:28:1620:U:H2'	49:28:1621:A:H8	1.86	0.40
49:28:2479:G:H2'	49:28:2480:G:H8	1.85	0.40
49:28:2542:G:H2'	49:28:2543:A:C8	2.56	0.40
49:28:2644:G:H2'	49:28:2645:G:C8	2.56	0.40
49:28:3651:A:C4	49:28:3652:A:C8	3.09	0.40
49:28:4089:G:H2'	49:28:4090:G:H8	1.86	0.40
49:28:4398:C:H2'	49:28:4399:U:H6	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4704:C:H2'	49:28:4705:A:H8	1.86	0.40
50:v:721:ILE:HD13	50:v:721:ILE:HA	1.85	0.40
9:aa:228:ARG:HG3	9:aa:283:TYR:CG	2.55	0.40
11:10:15:LYS:HG3	49:28:1863:U:OP1	2.21	0.40
16:bb:47:PHE:CE1	16:bb:140:ARG:HG2	2.56	0.40
18:19:134:ASN:OD1	18:19:137:ILE:HG22	2.20	0.40
19:20:30:MET:HE2	19:20:30:MET:HB3	1.96	0.40
20:21:19:PHE:CE2	20:21:20:ARG:HG3	2.56	0.40
27:dd:60:HIS:O	49:28:88:A:H5'	2.21	0.40
31:32:19:LYS:HE3	49:28:2318:G:O6	2.21	0.40
38:39:41:ARG:HD2	38:39:41:ARG:HA	1.94	0.40
43:s:44:ARG:HE	43:s:53:VAL:HG13	1.86	0.40
43:s:127:ASN:HB2	43:s:153:GLU:OE1	2.21	0.40
44:t:32:ILE:CG2	44:t:37:LEU:HB3	2.52	0.40
47:Q:78:LYS:HG3	47:Q:135:GLY:O	2.21	0.40
49:28:232:G:O4'	49:28:383:A:H1'	2.21	0.40
49:28:911:U:H2'	49:28:912:G:O4'	2.21	0.40
49:28:3714:G:H2'	49:28:3715:U:O4'	2.21	0.40
49:28:4629:U:C2	49:28:4630:G:C8	3.09	0.40
49:28:4915:G:C2	49:28:4916:G:C5	3.09	0.40
2:5:83:A:H4'	8:L7:223:THR:HB	2.02	0.40
3:L8:15:VAL:HG12	3:L8:194:ASN:HD22	1.86	0.40
5:L4:22:VAL:HG22	5:L4:258:ARG:HE	1.87	0.40
25:26:13:LYS:O	25:26:17:ARG:HG2	2.22	0.40
34:35:15:GLU:H	34:35:15:GLU:HG3	1.77	0.40
36:37:28:HIS:ND1	36:37:31:LYS:HE2	2.36	0.40
42:gg:93:ILE:HD11	42:gg:111:ILE:HA	2.03	0.40
44:t:119:ARG:NH1	44:t:121:LEU:H	2.20	0.40
45:EB:182:ILE:HD13	45:EB:235:GLY:HA2	2.02	0.40
49:28:99:A:H2'	49:28:100:C:O2	2.20	0.40
49:28:324:A:H2'	49:28:325:U:C6	2.56	0.40
49:28:1669:A:H4'	49:28:1685:G:N2	2.36	0.40
49:28:2864:A:H2'	49:28:2865:U:C6	2.56	0.40
50:v:596:PRO:HD2	50:v:720:GLN:HB3	2.03	0.40
3:L8:31:ALA:HB2	3:L8:123:ARG:HH21	1.86	0.40
4:L3:4:ARG:HH21	49:28:4459:U:H5	1.69	0.40
5:L4:294:LYS:HE2	5:L4:294:LYS:HB3	1.75	0.40
11:10:184:MET:HE2	11:10:190:LEU:HG	2.03	0.40
17:17:18:ARG:O	49:28:399:G:H4'	2.21	0.40
27:dd:53:PHE:O	47:Q:178:ARG:HB2	2.21	0.40
43:s:45:MET:HE3	43:s:45:MET:HB3	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:257:C:H2'	49:28:258:G:C8	2.56	0.40
49:28:469:C:H2'	49:28:470:A:C8	2.54	0.40
49:28:1201:U:H2'	49:28:1202:C:C6	2.56	0.40
49:28:3637:U:O4	49:28:3651:A:H2	2.05	0.40
49:28:3917:A:H2'	49:28:3918:G:H8	1.85	0.40
49:28:4889:G:C6	49:28:4931:G:C6	3.09	0.40
50:v:772:GLU:HB3	50:v:785:LYS:HB2	2.03	0.40
1:58:106:G:H4'	1:58:137:A:H5'	2.04	0.40
6:L5:69:ILE:HD11	20:21:32:ARG:NH2	2.36	0.40
7:L6:186:ARG:HD2	7:L6:186:ARG:HA	1.97	0.40
7:L6:211:ILE:HD12	7:L6:212:PRO:HD2	2.04	0.40
12:11:110:GLN:HG2	12:11:111:GLU:HG2	2.04	0.40
13:13:39:ARG:CZ	49:28:1362:G:H5'	2.51	0.40
15:15:39:ALA:HB3	15:15:61:ILE:HD12	2.03	0.40
20:21:126:VAL:O	49:28:1834:U:H5	2.05	0.40
31:32:90:MET:HE2	31:32:90:MET:HA	2.03	0.40
33:34:11:LEU:HG	49:28:2513:A:OP1	2.21	0.40
46:u:63:PHE:CE1	46:u:108:ASP:HB2	2.56	0.40
49:28:679:C:H2'	49:28:680:G:C8	2.55	0.40
49:28:980:U:H2'	49:28:981:C:H6	1.86	0.40
49:28:1846:G:H2'	49:28:1847:C:H6	1.87	0.40
49:28:1882:U:C4	49:28:2279:A:C2	3.09	0.40
49:28:2267:U:O2	49:28:2270:G:H4'	2.22	0.40
49:28:3851:U:H2'	49:28:3852:A:O4'	2.22	0.40
49:28:4345:C:H2'	49:28:4346:U:H6	1.86	0.40
49:28:4350:C:C2	49:28:4351:U:C5	3.09	0.40
49:28:4638:U:H2'	49:28:4639:G:N3	2.36	0.40
49:28:5001:U:H2'	49:28:5002:U:O4'	2.21	0.40
50:v:222:ALA:HB3	50:v:346:ALA:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	L8	246/345 (71%)	236 (96%)	10 (4%)	0	100	100
4	L3	392/394 (100%)	383 (98%)	9 (2%)	0	100	100
5	L4	360/362 (99%)	350 (97%)	10 (3%)	0	100	100
6	L5	291/293 (99%)	275 (94%)	14 (5%)	2 (1%)	18	35
7	L6	208/347 (60%)	200 (96%)	8 (4%)	0	100	100
8	L7	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
9	aa	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
10	L9	188/190 (99%)	184 (98%)	4 (2%)	0	100	100
11	10	201/213 (94%)	196 (98%)	5 (2%)	0	100	100
12	11	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
13	13	208/210 (99%)	199 (96%)	8 (4%)	1 (0%)	24	42
14	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
15	15	201/203 (99%)	192 (96%)	8 (4%)	1 (0%)	24	42
16	bb	197/199 (99%)	192 (98%)	5 (2%)	0	100	100
17	17	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
18	19	157/180 (87%)	155 (99%)	2 (1%)	0	100	100
19	20	174/192 (91%)	169 (97%)	5 (3%)	0	100	100
20	21	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
21	22	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
22	23	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
23	24	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
24	cc	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
25	26	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
26	27	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
27	dd	145/147 (99%)	135 (93%)	10 (7%)	0	100	100
28	29	100/245 (41%)	96 (96%)	4 (4%)	0	100	100
29	30	96/98 (98%)	96 (100%)	0	0	100	100
30	31	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
31	32	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
32	ee	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
33	34	112/114 (98%)	112 (100%)	0	0	100	100
34	35	120/122 (98%)	117 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	36	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
36	37	84/86 (98%)	84 (100%)	0	0	100	100
37	38	67/69 (97%)	67 (100%)	0	0	100	100
38	39	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
39	40	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
40	42	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
41	ff	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
42	gg	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
43	s	194/196 (99%)	183 (94%)	11 (6%)	0	100	100
44	t	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
45	EB	373/375 (100%)	364 (98%)	9 (2%)	0	100	100
46	u	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
47	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
50	v	816/857 (95%)	800 (98%)	14 (2%)	2 (0%)	43	62
All	All	8051/8616 (93%)	7800 (97%)	245 (3%)	6 (0%)	49	68

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	15	77	LYS
50	v	738	PRO
50	v	739	ARG
13	13	64	VAL
6	L5	36	LEU
6	L5	37	VAL

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	
3	L8	190/263 (72%)	182 (96%)	8 (4%)	26	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L3	342/342 (100%)	330 (96%)	12 (4%)	32	57
5	L4	302/302 (100%)	296 (98%)	6 (2%)	48	71
6	L5	247/247 (100%)	241 (98%)	6 (2%)	43	67
7	L6	190/302 (63%)	184 (97%)	6 (3%)	34	59
8	L7	196/196 (100%)	188 (96%)	8 (4%)	27	52
9	aa	200/205 (98%)	192 (96%)	8 (4%)	28	53
10	L9	169/169 (100%)	163 (96%)	6 (4%)	31	56
11	10	175/180 (97%)	173 (99%)	2 (1%)	65	81
12	11	143/143 (100%)	139 (97%)	4 (3%)	38	62
13	13	175/175 (100%)	168 (96%)	7 (4%)	28	53
14	14	117/117 (100%)	114 (97%)	3 (3%)	40	65
15	15	171/171 (100%)	164 (96%)	7 (4%)	27	52
16	bb	171/171 (100%)	162 (95%)	9 (5%)	20	42
17	17	134/134 (100%)	131 (98%)	3 (2%)	45	69
18	19	141/159 (89%)	139 (99%)	2 (1%)	59	78
19	20	157/173 (91%)	153 (98%)	4 (2%)	42	66
20	21	139/139 (100%)	136 (98%)	3 (2%)	45	69
21	22	89/89 (100%)	87 (98%)	2 (2%)	45	69
22	23	101/101 (100%)	97 (96%)	4 (4%)	28	53
23	24	55/55 (100%)	54 (98%)	1 (2%)	51	73
24	cc	106/106 (100%)	104 (98%)	2 (2%)	50	72
25	26	124/124 (100%)	118 (95%)	6 (5%)	23	46
26	27	117/117 (100%)	110 (94%)	7 (6%)	17	36
27	dd	119/119 (100%)	118 (99%)	1 (1%)	73	86
28	29	84/184 (46%)	81 (96%)	3 (4%)	31	56
29	30	84/84 (100%)	83 (99%)	1 (1%)	63	80
30	31	98/98 (100%)	96 (98%)	2 (2%)	48	71
31	32	114/114 (100%)	112 (98%)	2 (2%)	51	73
32	ee	88/88 (100%)	83 (94%)	5 (6%)	18	39
33	34	98/98 (100%)	95 (97%)	3 (3%)	35	60
34	35	109/109 (100%)	107 (98%)	2 (2%)	51	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	36	86/86 (100%)	81 (94%)	5 (6%)	18	38
36	37	73/73 (100%)	71 (97%)	2 (3%)	39	63
37	38	64/64 (100%)	61 (95%)	3 (5%)	23	47
38	39	47/47 (100%)	47 (100%)	0	100	100
39	40	48/48 (100%)	47 (98%)	1 (2%)	47	70
40	42	92/92 (100%)	91 (99%)	1 (1%)	65	81
41	ff	74/74 (100%)	72 (97%)	2 (3%)	39	63
42	gg	107/108 (99%)	102 (95%)	5 (5%)	23	47
43	s	164/164 (100%)	147 (90%)	17 (10%)	7	14
44	t	126/126 (100%)	117 (93%)	9 (7%)	13	28
45	EB	321/321 (100%)	304 (95%)	17 (5%)	20	42
46	u	186/186 (100%)	177 (95%)	9 (5%)	23	46
47	Q	164/165 (99%)	159 (97%)	5 (3%)	36	61
50	v	701/730 (96%)	667 (95%)	34 (5%)	22	45
All	All	6998/7358 (95%)	6743 (96%)	255 (4%)	32	56

All (255) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L8	32	VAL
3	L8	97	ASN
3	L8	101	VAL
3	L8	102	LEU
3	L8	135	THR
3	L8	165	VAL
3	L8	208	GLU
3	L8	243	THR
4	L3	43	LEU
4	L3	47	LEU
4	L3	56	ILE
4	L3	90	VAL
4	L3	94	GLU
4	L3	101	THR
4	L3	146	LEU
4	L3	207	VAL
4	L3	240	LEU
4	L3	248	LEU

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Mol	Chain	Res	Type
4	L3	254	ILE
4	L3	262	VAL
5	L4	101	MET
5	L4	154	VAL
5	L4	189	MET
5	L4	232	VAL
5	L4	300	ARG
5	L4	313	VAL
6	L5	38	ILE
6	L5	123	VAL
6	L5	126	THR
6	L5	143	THR
6	L5	213	GLU
6	L5	235	MET
7	L6	51	VAL
7	L6	53	VAL
7	L6	178	VAL
7	L6	197	VAL
7	L6	261	LEU
7	L6	289	LEU
8	L7	38	GLN
8	L7	41	LEU
8	L7	61	ARG
8	L7	124	LEU
8	L7	134	ILE
8	L7	151	GLU
8	L7	189	LEU
8	L7	211	LYS
9	aa	116	LEU
9	aa	151	LEU
9	aa	159	THR
9	aa	167	LEU
9	aa	193	VAL
9	aa	199	LEU
9	aa	223	LEU
9	aa	226	LEU
10	L9	20	LEU
10	L9	66	GLU
10	L9	74	CYS
10	L9	103	VAL
10	L9	107	GLU
10	L9	189	GLN

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Mol	Chain	Res	Type
11	10	163	GLN
11	10	212	LEU
12	11	49	VAL
12	11	128	LEU
12	11	148	THR
12	11	175	LEU
13	13	59	VAL
13	13	67	HIS
13	13	71	ARG
13	13	124	LEU
13	13	144	LEU
13	13	154	VAL
13	13	205	GLN
14	14	38	VAL
14	14	62	LEU
14	14	105	THR
15	15	44	ARG
15	15	50	ARG
15	15	61	ILE
15	15	64	ILE
15	15	75	VAL
15	15	77	LYS
15	15	89	VAL
16	bb	27	VAL
16	bb	36	VAL
16	bb	42	ASN
16	bb	52	LEU
16	bb	72	HIS
16	bb	144	GLU
16	bb	145	VAL
16	bb	182	GLU
16	bb	188	LYS
17	17	91	LEU
17	17	104	LEU
17	17	114	ILE
18	19	74	ARG
18	19	157	ASP
19	20	6	THR
19	20	67	VAL
19	20	126	ILE
19	20	159	LEU
20	21	40	VAL

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Mol	Chain	Res	Type
20	21	69	GLN
20	21	111	GLU
21	22	30	GLU
21	22	45	GLU
22	23	18	LEU
22	23	27	ASN
22	23	37	LEU
22	23	118	THR
23	24	30	GLN
24	cc	120	ASP
24	cc	133	GLU
25	26	8	THR
25	26	40	GLN
25	26	79	VAL
25	26	82	ILE
25	26	104	VAL
25	26	120	GLU
26	27	11	VAL
26	27	46	ILE
26	27	72	VAL
26	27	76	ASN
26	27	77	TYR
26	27	91	LEU
26	27	120	GLU
27	dd	24	LYS
28	29	9	THR
28	29	60	ASN
28	29	104	LEU
29	30	92	CYS
30	31	26	THR
30	31	33	ILE
31	32	13	VAL
31	32	44	ARG
32	ee	23	GLU
32	ee	33	VAL
32	ee	67	THR
32	ee	84	VAL
32	ee	103	VAL
33	34	5	LEU
33	34	60	ARG
33	34	66	ARG
34	35	91	MET

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Mol	Chain	Res	Type
34	35	100	GLU
35	36	18	THR
35	36	29	ARG
35	36	33	LEU
35	36	58	MET
35	36	77	VAL
36	37	18	LEU
36	37	58	THR
37	38	12	LEU
37	38	36	VAL
37	38	47	ILE
39	40	101	VAL
40	42	85	ILE
41	ff	26	VAL
41	ff	52	VAL
42	gg	18	ILE
42	gg	75	THR
42	gg	78	VAL
42	gg	103	HIS
42	gg	124	VAL
43	s	15	LEU
43	s	29	ILE
43	s	30	VAL
43	s	53	VAL
43	s	61	MET
43	s	68	HIS
43	s	69	LEU
43	s	89	VAL
43	s	97	GLU
43	s	120	GLU
43	s	123	VAL
43	s	126	GLN
43	s	141	LEU
43	s	147	ILE
43	s	158	VAL
43	s	160	LEU
43	s	174	LEU
44	t	37	LEU
44	t	65	GLN
44	t	72	GLU
44	t	95	GLN
44	t	96	LYS

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Mol	Chain	Res	Type
44	t	125	LEU
44	t	129	ILE
44	t	146	ARG
44	t	151	ILE
45	EB	14	GLU
45	EB	32	LEU
45	EB	35	LEU
45	EB	48	LEU
45	EB	65	LYS
45	EB	74	ILE
45	EB	82	VAL
45	EB	114	VAL
45	EB	177	PHE
45	EB	226	VAL
45	EB	228	VAL
45	EB	230	VAL
45	EB	284	GLU
45	EB	287	LYS
45	EB	342	LEU
45	EB	349	VAL
45	EB	373	LYS
46	u	9	THR
46	u	21	ASN
46	u	38	LEU
46	u	80	VAL
46	u	93	LEU
46	u	116	LEU
46	u	117	ILE
46	u	173	LYS
46	u	201	VAL
47	Q	13	VAL
47	Q	16	LYS
47	Q	125	GLN
47	Q	168	ARG
47	Q	170	LYS
50	v	2	VAL
50	v	24	VAL
50	v	109	VAL
50	v	121	VAL
50	v	127	VAL
50	v	135	VAL
50	v	151	ILE

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Mol	Chain	Res	Type
50	v	169	LEU
50	v	183	GLU
50	v	218	LEU
50	v	225	LEU
50	v	241	GLU
50	v	256	MET
50	v	396	MET
50	v	401	MET
50	v	402	VAL
50	v	416	VAL
50	v	449	ARG
50	v	462	GLU
50	v	473	VAL
50	v	477	GLN
50	v	479	LEU
50	v	480	VAL
50	v	487	THR
50	v	497	MET
50	v	499	PHE
50	v	524	LEU
50	v	580	ARG
50	v	692	LEU
50	v	728	CYS
50	v	741	MET
50	v	747	VAL
50	v	790	VAL
50	v	813	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (124) such sidechains are listed below:

Mol	Chain	Res	Type
3	L8	8	GLN
3	L8	97	ASN
3	L8	194	ASN
3	L8	215	ASN
3	L8	216	HIS
4	L3	109	HIS
4	L3	138	GLN
4	L3	167	GLN
4	L3	179	HIS
4	L3	184	GLN
4	L3	203	GLN

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Mol	Chain	Res	Type
4	L3	204	GLN
4	L3	209	GLN
4	L3	376	HIS
5	L4	61	GLN
5	L4	119	GLN
5	L4	329	ASN
5	L4	338	ASN
5	L4	346	ASN
6	L5	122	GLN
6	L5	138	GLN
6	L5	202	GLN
7	L6	131	HIS
7	L6	193	HIS
8	L7	115	GLN
8	L7	205	ASN
9	aa	119	GLN
9	aa	138	GLN
9	aa	165	GLN
9	aa	261	ASN
9	aa	278	ASN
10	L9	63	ASN
10	L9	79	ASN
10	L9	189	GLN
12	11	23	ASN
12	11	42	GLN
12	11	46	GLN
12	11	104	ASN
12	11	168	GLN
13	13	19	GLN
13	13	149	GLN
13	13	205	GLN
14	14	48	GLN
14	14	70	GLN
14	14	83	ASN
15	15	29	GLN
15	15	149	GLN
15	15	201	HIS
16	bb	50	ASN
16	bb	150	GLN
17	17	25	HIS
17	17	34	GLN
17	17	80	GLN

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Mol	Chain	Res	Type
17	17	116	HIS
17	17	137	ASN
18	19	118	HIS
18	19	141	HIS
19	20	156	HIS
20	21	3	ASN
20	21	69	GLN
20	21	90	ASN
20	21	112	ASN
20	21	127	GLN
20	21	131	GLN
21	22	38	ASN
22	23	36	ASN
23	24	30	GLN
24	cc	57	GLN
25	26	20	ASN
25	26	61	HIS
25	26	65	GLN
25	26	127	GLN
26	27	76	ASN
27	dd	17	HIS
27	dd	85	GLN
27	dd	120	GLN
28	29	6	ASN
28	29	17	HIS
28	29	61	ASN
31	32	34	ASN
31	32	63	ASN
31	32	107	ASN
32	ee	56	ASN
33	34	112	GLN
34	35	68	ASN
35	36	15	HIS
36	37	57	ASN
36	37	66	HIS
38	39	4	HIS
38	39	33	ASN
40	42	51	GLN
41	ff	92	GLN
42	gg	70	GLN
42	gg	103	HIS
43	s	58	ASN

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Mol	Chain	Res	Type
43	s	126	GLN
43	s	190	GLN
44	t	156	ASN
45	EB	113	HIS
45	EB	134	GLN
45	EB	147	HIS
45	EB	171	ASN
45	EB	193	HIS
45	EB	203	GLN
45	EB	221	HIS
45	EB	299	HIS
46	u	19	HIS
46	u	22	GLN
46	u	84	HIS
46	u	158	GLN
46	u	184	HIS
46	u	199	GLN
47	Q	57	ASN
47	Q	93	GLN
47	Q	160	HIS
50	v	27	HIS
50	v	101	ASN
50	v	184	ASN
50	v	291	GLN
50	v	544	HIS
50	v	660	ASN
50	v	715	HIS
50	v	803	ASN
50	v	816	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	58	149/156 (95%)	31 (20%)	1 (0%)
2	5	119/120 (99%)	12 (10%)	0
48	ES	63/5070 (1%)	14 (22%)	1 (1%)
49	28	3460/4807 (71%)	720 (20%)	45 (1%)
All	All	3791/10153 (37%)	777 (20%)	47 (1%)

All (777) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	58	2	G
1	58	16	G
1	58	23	C
1	58	34	U
1	58	35	C
1	58	38	U
1	58	51	U
1	58	52	A
1	58	59	A
1	58	62	A
1	58	63	U
1	58	75	G
1	58	77	A
1	58	94	G
1	58	95	A
1	58	103	A
1	58	105	C
1	58	109	C
1	58	110	U
1	58	111	U
1	58	113	C
1	58	114	G
1	58	122	G
1	58	125	C
1	58	126	C
1	58	127	U
1	58	128	C
1	58	147	G
1	58	151	G
1	58	153	C
1	58	156	U
2	5	21	G
2	5	22	A
2	5	33	U
2	5	53	U
2	5	54	A
2	5	63	C
2	5	64	G
2	5	97	G
2	5	100	A
2	5	110	G
2	5	111	C
2	5	120	U

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Mol	Chain	Res	Type
48	ES	2912	G
48	ES	2941	G
48	ES	2942	C
48	ES	2943	C
48	ES	2948	C
48	ES	2958	C
48	ES	3237	G
48	ES	3247	A
48	ES	3283	G
48	ES	3288	G
48	ES	3581	C
48	ES	3582	C
48	ES	3583	U
48	ES	3591	C
49	28	8	U
49	28	12	A
49	28	13	U
49	28	25	A
49	28	39	A
49	28	42	A
49	28	44	A
49	28	49	U
49	28	56	A
49	28	59	A
49	28	64	A
49	28	65	A
49	28	71	C
49	28	72	C
49	28	73	A
49	28	74	G
49	28	91	G
49	28	108	A
49	28	109	G
49	28	110	C
49	28	116	G
49	28	118	C
49	28	119	G
49	28	122	U
49	28	126	C
49	28	132	G
49	28	134	G
49	28	135	G

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Mol	Chain	Res	Type
49	28	136	C
49	28	142	G
49	28	143	C
49	28	144	G
49	28	159	C
49	28	170	C
49	28	171	U
49	28	172	C
49	28	190	G
49	28	200	U
49	28	201	C
49	28	202	C
49	28	207	G
49	28	209	U
49	28	216	C
49	28	218	A
49	28	219	G
49	28	220	C
49	28	224	U
49	28	232	G
49	28	233	U
49	28	234	G
49	28	246	G
49	28	256	G
49	28	262	G
49	28	266	C
49	28	275	C
49	28	276	C
49	28	280	G
49	28	297	U
49	28	306	A
49	28	309	C
49	28	315	G
49	28	316	U
49	28	334	A
49	28	340	C
49	28	350	C
49	28	387	G
49	28	399	G
49	28	407	A
49	28	410	A
49	28	412	G

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Mol	Chain	Res	Type
49	28	413	G
49	28	415	G
49	28	431	G
49	28	432	U
49	28	446	C
49	28	449	C
49	28	452	A
49	28	453	G
49	28	454	U
49	28	455	C
49	28	463	A
49	28	464	G
49	28	465	G
49	28	467	U
49	28	468	U
49	28	469	C
49	28	481	G
49	28	481(A)	C
49	28	482	G
49	28	483	G
49	28	485	C
49	28	486	C
49	28	492	U
49	28	493	G
49	28	497	G
49	28	498	C
49	28	499	G
49	28	505	G
49	28	510	U
49	28	517	C
49	28	520	U
49	28	657	C
49	28	659	G
49	28	660	G
49	28	662	C
49	28	666	G
49	28	667	A
49	28	668	C
49	28	669	C
49	28	672	C
49	28	683	C
49	28	685	C

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Mol	Chain	Res	Type
49	28	686	A
49	28	687	U
49	28	696	C
49	28	697	G
49	28	704	C
49	28	705	G
49	28	708	G
49	28	730	G
49	28	731	G
49	28	738	C
49	28	738(A)	C
49	28	739	G
49	28	744	G
49	28	747	A
49	28	749	G
49	28	758	G
49	28	759	G
49	28	905	C
49	28	914	U
49	28	915	A
49	28	917	A
49	28	918	G
49	28	923	C
49	28	925	C
49	28	926	G
49	28	929	A
49	28	931	C
49	28	932	A
49	28	933	G
49	28	934	C
49	28	935	A
49	28	935(A)	G
49	28	936	C
49	28	938	C
49	28	939	G
49	28	941	C
49	28	943	A
49	28	944	A
49	28	945	U
49	28	946	C
49	28	956	A
49	28	959	G

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Mol	Chain	Res	Type
49	28	960	A
49	28	961	G
49	28	962	C
49	28	965	G
49	28	966	A
49	28	967	C
49	28	969	C
49	28	972	C
49	28	979	C
49	28	983	C
49	28	1066	G
49	28	1068	G
49	28	1070	G
49	28	1072	C
49	28	1073	G
49	28	1179	U
49	28	1184	A
49	28	1187	G
49	28	1193	C
49	28	1195	G
49	28	1204	C
49	28	1210	C
49	28	1211	G
49	28	1212	G
49	28	1214	C
49	28	1215	C
49	28	1216	C
49	28	1234	G
49	28	1235	G
49	28	1236	C
49	28	1237	C
49	28	1238	A
49	28	1239	C
49	28	1275	G
49	28	1276	C
49	28	1277	G
49	28	1284	G
49	28	1285	U
49	28	1287	G
49	28	1292	C
49	28	1295	U
49	28	1296	G

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Mol	Chain	Res	Type
49	28	1301	C
49	28	1303	A
49	28	1304	C
49	28	1314	C
49	28	1326	A
49	28	1330	A
49	28	1354	A
49	28	1358	G
49	28	1359	G
49	28	1371	A
49	28	1377	G
49	28	1379	C
49	28	1380	G
49	28	1381	U
49	28	1387	A
49	28	1394	G
49	28	1397	A
49	28	1398	A
49	28	1414	C
49	28	1419	G
49	28	1420	A
49	28	1421	G
49	28	1433	A
49	28	1445	U
49	28	1446	C
49	28	1456	C
49	28	1457	G
49	28	1475	G
49	28	1481	C
49	28	1482	G
49	28	1483	C
49	28	1484	G
49	28	1487	G
49	28	1497	A
49	28	1498	G
49	28	1502	G
49	28	1504	G
49	28	1516	G
49	28	1523	A
49	28	1525	A
49	28	1534	A
49	28	1547	A

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Mol	Chain	Res	Type
49	28	1563	A
49	28	1566	C
49	28	1574	G
49	28	1578	U
49	28	1586	G
49	28	1591	U
49	28	1596	U
49	28	1612	G
49	28	1613	A
49	28	1624	G
49	28	1625	G
49	28	1631	A
49	28	1633	G
49	28	1634	A
49	28	1638	A
49	28	1640	C
49	28	1641	G
49	28	1654	G
49	28	1661	C
49	28	1676	C
49	28	1677	U
49	28	1684	A
49	28	1740	C
49	28	1742	A
49	28	1751	A
49	28	1752	G
49	28	1754	U
49	28	1755	C
49	28	1756	U
49	28	1757	U
49	28	1761	G
49	28	1764	G
49	28	1765	A
49	28	1768	C
49	28	1772	C
49	28	1773	U
49	28	1775	A
49	28	1776	A
49	28	1781	U
49	28	1787	A
49	28	1797	G
49	28	1803	G

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Mol	Chain	Res	Type
49	28	1804	A
49	28	1805	A
49	28	1806	G
49	28	1808	C
49	28	1812	C
49	28	1815	G
49	28	1818	G
49	28	1820	U
49	28	1821	G
49	28	1828	C
49	28	1836	G
49	28	1837	A
49	28	1842	G
49	28	1855	G
49	28	1869	G
49	28	1882	U
49	28	1897	A
49	28	1910	G
49	28	1918	U
49	28	1920	C
49	28	1921	C
49	28	1922	G
49	28	1931	C
49	28	1935	C
49	28	1940	G
49	28	1947	U
49	28	1948	G
49	28	1951	G
49	28	1957	U
49	28	1958	A
49	28	1961	G
49	28	1962	A
49	28	1964	A
49	28	1972	G
49	28	1974	U
49	28	1975	G
49	28	1976	G
49	28	1978	C
49	28	1980	U
49	28	1984	A
49	28	1985	G
49	28	1987	C

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Mol	Chain	Res	Type
49	28	1991	A
49	28	1992	U
49	28	1997	U
49	28	2001	G
49	28	2002	A
49	28	2003	G
49	28	2004	U
49	28	2007	G
49	28	2011	C
49	28	2021	G
49	28	2025	A
49	28	2026	A
49	28	2046	G
49	28	2047	A
49	28	2048	U
49	28	2052	G
49	28	2055	G
49	28	2056	G
49	28	2062	C
49	28	2064	G
49	28	2069	A
49	28	2070	U
49	28	2084	U
49	28	2090	U
49	28	2092	G
49	28	2093	G
49	28	2094	C
49	28	2095	A
49	28	2097	A
49	28	2098	G
49	28	2100	G
49	28	2102	G
49	28	2104	A
49	28	2105	A
49	28	2107	A
49	28	2108	G
49	28	2110	G
49	28	2267	U
49	28	2268	A
49	28	2275	G
49	28	2289	C
49	28	2300	A

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Mol	Chain	Res	Type
49	28	2301	G
49	28	2306	G
49	28	2313	A
49	28	2314	G
49	28	2316	G
49	28	2331	G
49	28	2333	G
49	28	2348	G
49	28	2351	C
49	28	2360	A
49	28	2395	A
49	28	2398	U
49	28	2402	G
49	28	2417	A
49	28	2422	C
49	28	2425	U
49	28	2433	G
49	28	2434	G
49	28	2441	C
49	28	2450	G
49	28	2475	G
49	28	2488	C
49	28	2489	C
49	28	2490	U
49	28	2491	C
49	28	2503	G
49	28	2504	C
49	28	2505	C
49	28	2506	G
49	28	2513	A
49	28	2520	C
49	28	2529	A
49	28	2530	U
49	28	2537	A
49	28	2544	G
49	28	2545	U
49	28	2546	G
49	28	2547	G
49	28	2549	G
49	28	2553	A
49	28	2554	U
49	28	2575	U

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Mol	Chain	Res	Type
49	28	2583	C
49	28	2586	G
49	28	2587	A
49	28	2589	C
49	28	2602	G
49	28	2623	A
49	28	2627	C
49	28	2638	G
49	28	2640	G
49	28	2647	A
49	28	2649	G
49	28	2653	C
49	28	2659	A
49	28	2661	U
49	28	2662	G
49	28	2669	C
49	28	2686	G
49	28	2687	U
49	28	2695	A
49	28	2696	A
49	28	2703	G
49	28	2704	C
49	28	2705	G
49	28	2707	U
49	28	2708	U
49	28	2710	C
49	28	2711	G
49	28	2712	G
49	28	2714	G
49	28	2717	G
49	28	2719	C
49	28	2721	G
49	28	2724	G
49	28	2725	A
49	28	2726	G
49	28	2740	U
49	28	2743	A
49	28	2744	A
49	28	2753	G
49	28	2754	G
49	28	2758	G
49	28	2759	G

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Mol	Chain	Res	Type
49	28	2760	G
49	28	2761	U
49	28	2763	U
49	28	2764	A
49	28	2769	U
49	28	2787	A
49	28	2788	U
49	28	2790	U
49	28	2796	G
49	28	2798	A
49	28	2806	A
49	28	2814	C
49	28	2826	U
49	28	2827	G
49	28	2837	U
49	28	2838	G
49	28	2842	G
49	28	2848	G
49	28	2855	G
49	28	2856	C
49	28	2875	C
49	28	2898	G
49	28	3604	A
49	28	3605	C
49	28	3625	G
49	28	3626	G
49	28	3630	A
49	28	3635	A
49	28	3646	A
49	28	3650	C
49	28	3662	A
49	28	3663	A
49	28	3664	G
49	28	3673	C
49	28	3692	A
49	28	3696	C
49	28	3698	G
49	28	3709	U
49	28	3710	G
49	28	3712	A
49	28	3713	U
49	28	3714	G

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Mol	Chain	Res	Type
49	28	3748	A
49	28	3753	G
49	28	3754	G
49	28	3765	G
49	28	3773	U
49	28	3776	G
49	28	3777	G
49	28	3784	A
49	28	3786	U
49	28	3811	G
49	28	3814	U
49	28	3817	A
49	28	3819	G
49	28	3838	U
49	28	3839	G
49	28	3840	U
49	28	3869	C
49	28	3876	A
49	28	3877	A
49	28	3878	C
49	28	3879	G
49	28	3889	G
49	28	3892	U
49	28	3897	G
49	28	3901	A
49	28	3905	A
49	28	3906	A
49	28	3907	G
49	28	3908	A
49	28	3915	U
49	28	3916	G
49	28	3917	A
49	28	3918	G
49	28	3926	C
49	28	3927	U
49	28	3938	G
49	28	4069	U
49	28	4076	G
49	28	4084	G
49	28	4085	A
49	28	4086	G
49	28	4088	C

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Mol	Chain	Res	Type
49	28	4092	G
49	28	4097	G
49	28	4116	C
49	28	4119	C
49	28	4120	U
49	28	4121	G
49	28	4122	G
49	28	4125	C
49	28	4127	A
49	28	4155	C
49	28	4158	C
49	28	4162	C
49	28	4163	U
49	28	4166	G
49	28	4170	A
49	28	4183	G
49	28	4184	G
49	28	4191	G
49	28	4201	G
49	28	4203	A
49	28	4212	A
49	28	4225	G
49	28	4228	G
49	28	4229	U
49	28	4233	A
49	28	4249	G
49	28	4251	A
49	28	4253	A
49	28	4254	G
49	28	4266	G
49	28	4268	A
49	28	4271	A
49	28	4273	A
49	28	4281	A
49	28	4291	G
49	28	4297	G
49	28	4304	A
49	28	4305	G
49	28	4306	U
49	28	4313	A
49	28	4314	C
49	28	4317	A

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Mol	Chain	Res	Type
49	28	4318	C
49	28	4319	C
49	28	4326	G
49	28	4329	G
49	28	4330	G
49	28	4332	C
49	28	4336	A
49	28	4350	C
49	28	4354	U
49	28	4355	G
49	28	4373	G
49	28	4377	G
49	28	4378	A
49	28	4380	A
49	28	4387	C
49	28	4394	A
49	28	4395	U
49	28	4401	G
49	28	4415	A
49	28	4419	U
49	28	4421	C
49	28	4422	A
49	28	4426	C
49	28	4437	U
49	28	4440	G
49	28	4444	C
49	28	4448	G
49	28	4449	A
49	28	4464	A
49	28	4466	C
49	28	4471	U
49	28	4472	G
49	28	4500	U
49	28	4512	U
49	28	4513	A
49	28	4519	C
49	28	4520	G
49	28	4524	G
49	28	4525	C
49	28	4528	G
49	28	4531	U
49	28	4532	U

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Mol	Chain	Res	Type
49	28	4548	A
49	28	4549	G
49	28	4557	U
49	28	4560	C
49	28	4567	G
49	28	4569	U
49	28	4573	G
49	28	4574	U
49	28	4575	G
49	28	4577	U
49	28	4584	A
49	28	4586	G
49	28	4587	G
49	28	4590	A
49	28	4627	U
49	28	4636	U
49	28	4637	G
49	28	4639	G
49	28	4652	G
49	28	4656	A
49	28	4657	U
49	28	4667	C
49	28	4670	C
49	28	4672	A
49	28	4677	U
49	28	4687	A
49	28	4691	A
49	28	4694	G
49	28	4700	A
49	28	4709	U
49	28	4719	G
49	28	4720	C
49	28	4729	A
49	28	4751	G
49	28	4752	U
49	28	4754	G
49	28	4756	C
49	28	4757	C
49	28	4759	C
49	28	4764	A
49	28	4765	G
49	28	4771	C

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Mol	Chain	Res	Type
49	28	4868	G
49	28	4870	G
49	28	4871	C
49	28	4873	G
49	28	4875	G
49	28	4881	U
49	28	4882	U
49	28	4883	C
49	28	4885	U
49	28	4887	C
49	28	4894	A
49	28	4895	C
49	28	4903	G
49	28	4906	C
49	28	4910	A
49	28	4913	G
49	28	4914	G
49	28	4915	G
49	28	4918	C
49	28	4919	G
49	28	4921	C
49	28	4922	C
49	28	4924	C
49	28	4925	U
49	28	4926	C
49	28	4927	G
49	28	4928	C
49	28	4931	G
49	28	4937	C
49	28	4943	A
49	28	4944	C
49	28	4945	G
49	28	4947	U
49	28	4948	C
49	28	4949	G
49	28	4950	U
49	28	4951	G
49	28	4955	A
49	28	4956	A
49	28	4960	G
49	28	4963	G
49	28	4964	C

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Mol	Chain	Res	Type
49	28	4965	U
49	28	4966	A
49	28	4976	U
49	28	4988	U
49	28	4990	C
49	28	4993	G
49	28	5006	U
49	28	5007	A
49	28	5017	G
49	28	5029	C
49	28	5040	U
49	28	5041	G
49	28	5047	C
49	28	5048	A
49	28	5050	C
49	28	5052	C
49	28	5053	U
49	28	5054	C
49	28	5061	A
49	28	5062	G

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	58	124	U
48	ES	3236	G
49	28	12	A
49	28	48	G
49	28	125	C
49	28	142	G
49	28	275	C
49	28	406	C
49	28	480	C
49	28	485	C
49	28	492	U
49	28	504	G
49	28	696	C
49	28	930	G
49	28	966	A
49	28	971(A)	G
49	28	1072	C
49	28	1211	G

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Mol	Chain	Res	Type
49	28	1238	A
49	28	1291	G
49	28	1329	G
49	28	1370	G
49	28	1445	U
49	28	1455	G
49	28	1804	A
49	28	1979	A
49	28	2046	G
49	28	2089	G
49	28	2266	C
49	28	2502	A
49	28	2546	G
49	28	2639	U
49	28	2661	U
49	28	2695	A
49	28	3625	G
49	28	3697	U
49	28	3876	A
49	28	3888	G
49	28	4119	C
49	28	4232	U
49	28	4448	G
49	28	4699	U
49	28	4719	G
49	28	4884	G
49	28	4925	U
49	28	4936	G
49	28	4947	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
52	GDP	v	900	-	29,30,30	3.59	13 (44%)	45,47,47	2.17	13 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	GDP	v	900	-	-	4/16/32/32	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	v	900	GDP	O6-C6	9.62	1.41	1.23
52	v	900	GDP	C2'-C3'	-8.47	1.30	1.53
52	v	900	GDP	O4'-C4'	-7.09	1.29	1.45
52	v	900	GDP	O4'-C1'	6.08	1.56	1.42
52	v	900	GDP	C2-N2	4.88	1.45	1.34
52	v	900	GDP	C1'-N9	-4.56	1.34	1.47
52	v	900	GDP	C3'-C4'	4.09	1.63	1.53
52	v	900	GDP	PA-O3A	3.61	1.63	1.59
52	v	900	GDP	O2'-C2'	3.41	1.51	1.43
52	v	900	GDP	C6-N1	-2.86	1.33	1.38
52	v	900	GDP	C5-N7	-2.54	1.34	1.39
52	v	900	GDP	C2-N1	-2.37	1.31	1.37
52	v	900	GDP	C8-N9	-2.32	1.32	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	v	900	GDP	C5-C4-N3	-6.93	117.36	128.39
52	v	900	GDP	C2-N3-C4	5.86	122.39	112.30
52	v	900	GDP	N9-C4-N3	4.90	135.74	125.95
52	v	900	GDP	C2'-C3'-C4'	4.31	110.93	102.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	v	900	GDP	C8-N7-C5	3.28	110.10	104.26
52	v	900	GDP	N9-C8-N7	-3.00	107.83	113.40
52	v	900	GDP	C4-C5-N7	-2.94	106.01	110.67
52	v	900	GDP	C2-N1-C6	-2.81	120.02	125.11
52	v	900	GDP	O6-C6-C5	-2.76	119.25	126.53
52	v	900	GDP	C6-C5-N7	2.49	134.82	130.29
52	v	900	GDP	C3'-C2'-C1'	2.46	106.12	101.46
52	v	900	GDP	C5-C6-N1	2.35	119.24	113.25
52	v	900	GDP	O3B-PB-O3A	2.00	111.36	104.64

There are no chirality outliers.

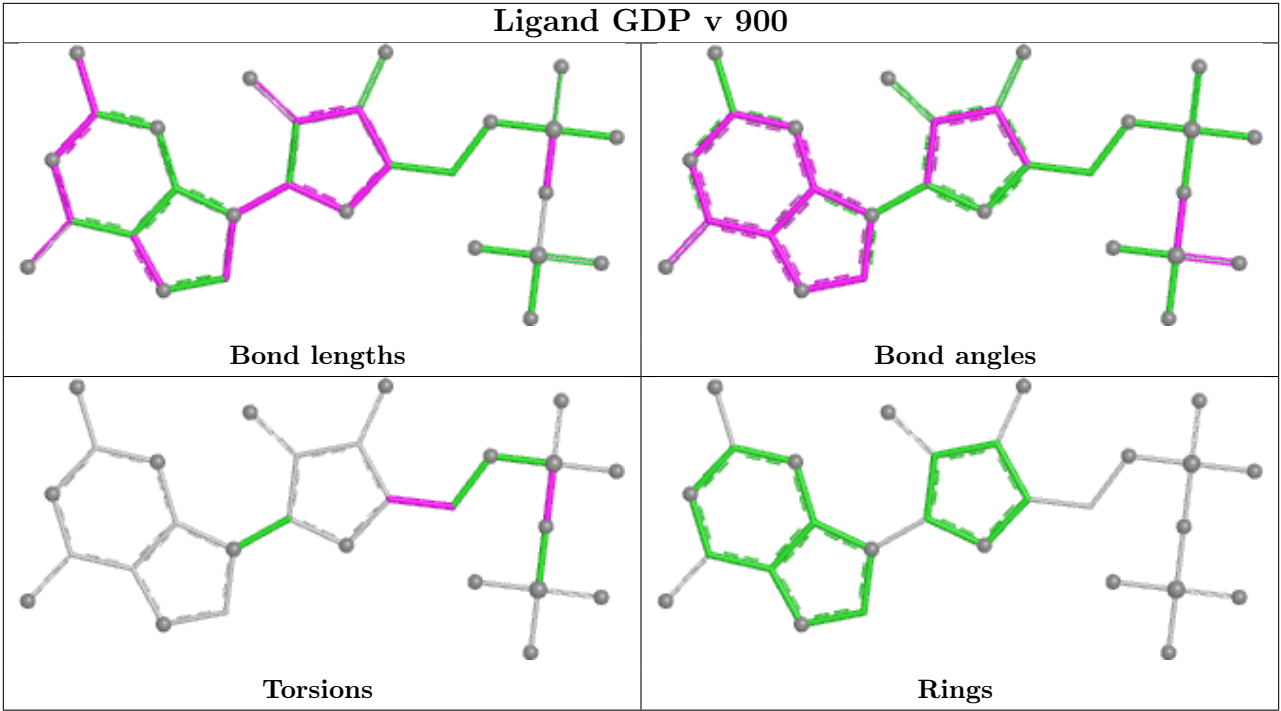
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
52	v	900	GDP	C3'-C4'-C5'-O5'
52	v	900	GDP	O4'-C4'-C5'-O5'
52	v	900	GDP	PB-O3A-PA-O2A
52	v	900	GDP	PB-O3A-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	28	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	28	3944:G	O3'	3945:A	P	4.51
1	28	2025:A	O3'	2026:A	P	3.18

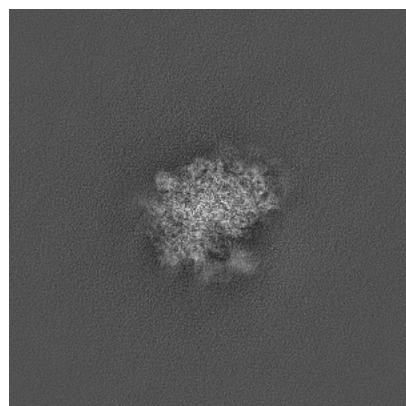
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75687. These allow visual inspection of the internal detail of the map and identification of artifacts.

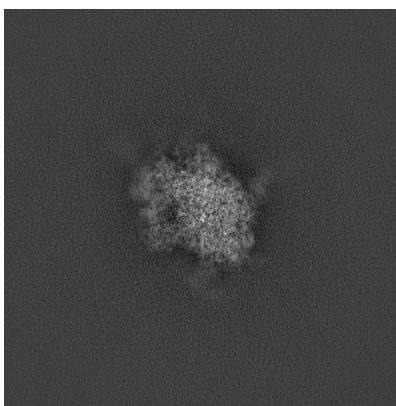
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

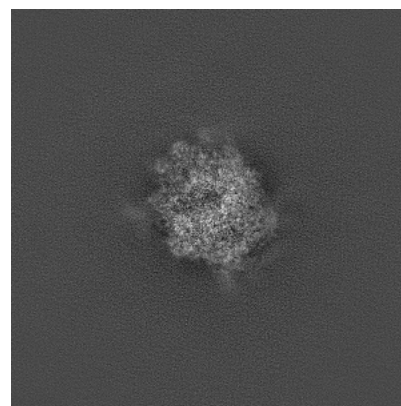
6.1.1 Primary map



X

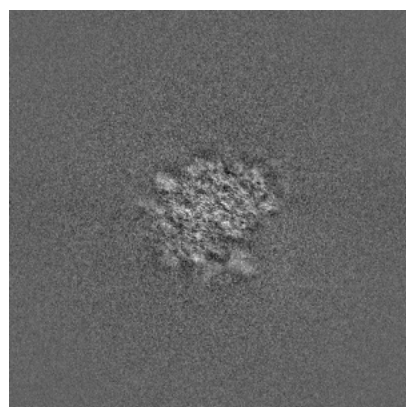


Y

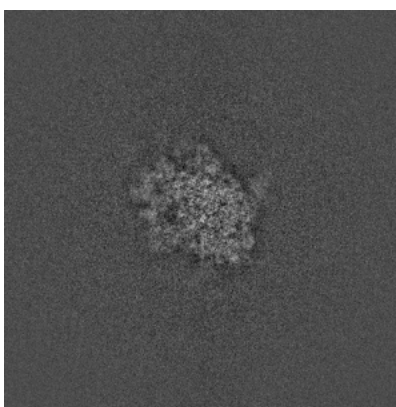


Z

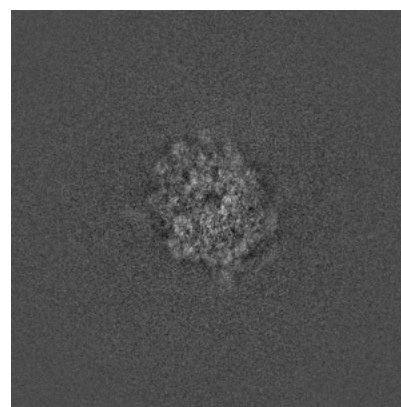
6.1.2 Raw map



X



Y

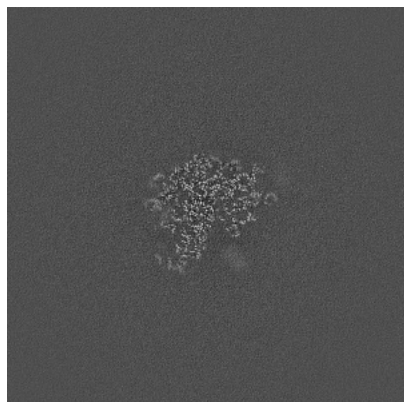


Z

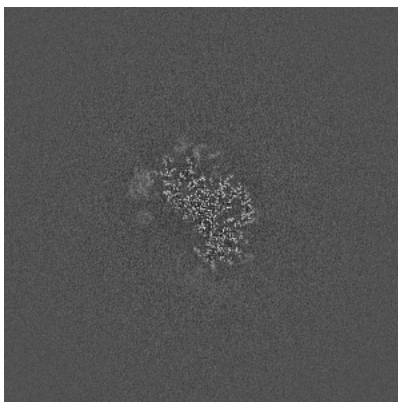
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

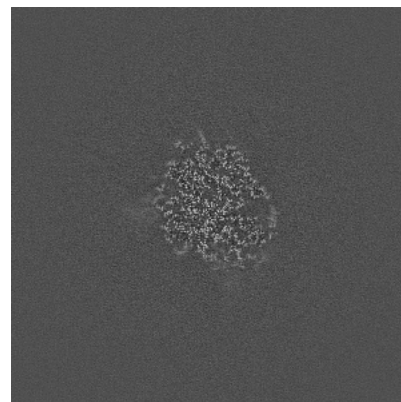
6.2.1 Primary map



X Index: 400

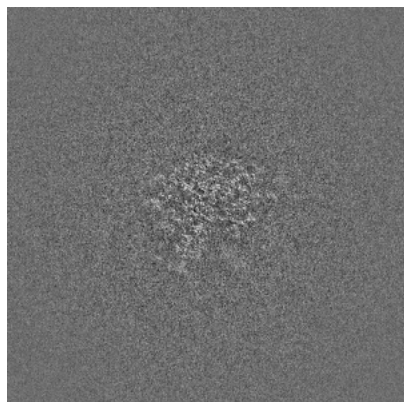


Y Index: 400

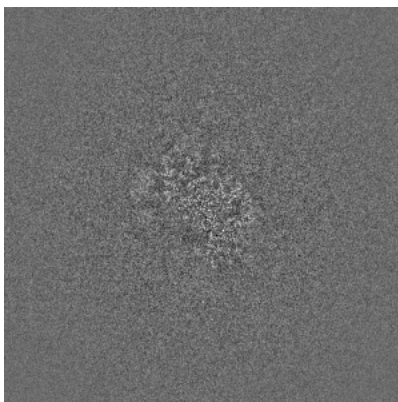


Z Index: 400

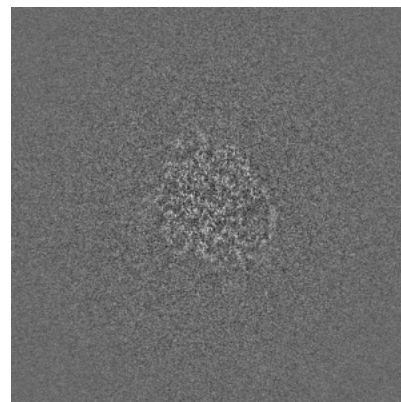
6.2.2 Raw map



X Index: 400



Y Index: 400

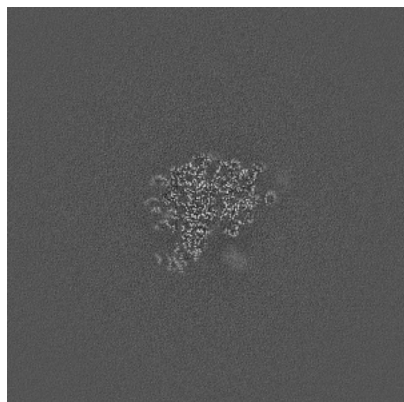


Z Index: 400

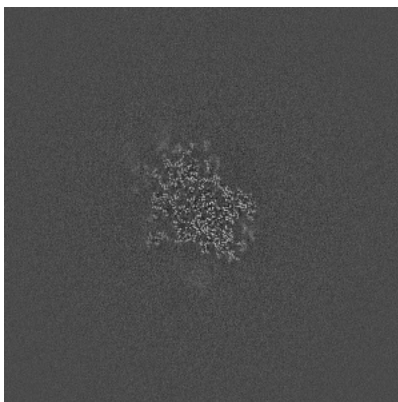
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

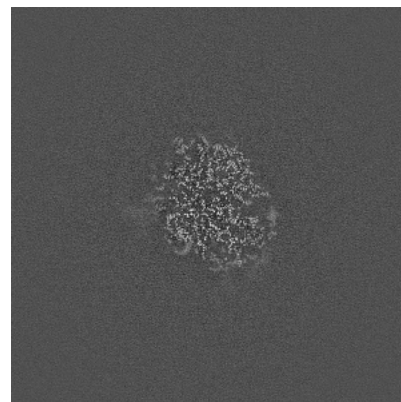
6.3.1 Primary map



X Index: 397

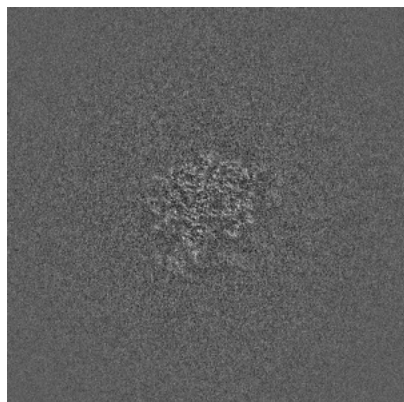


Y Index: 380

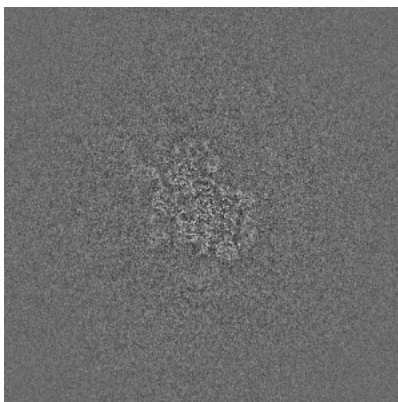


Z Index: 403

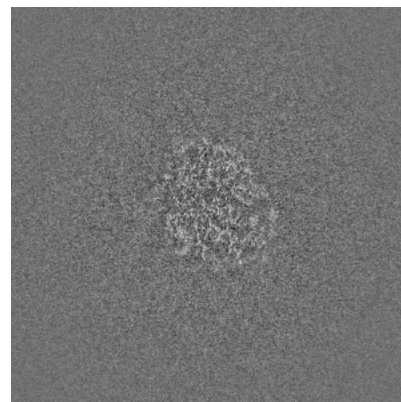
6.3.2 Raw map



X Index: 396



Y Index: 384

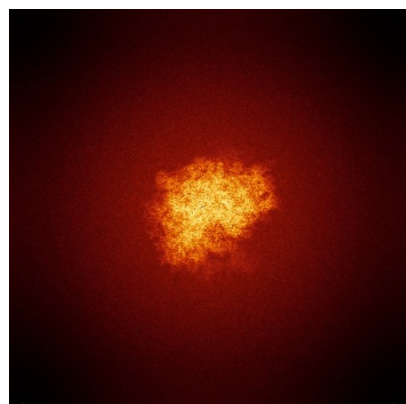


Z Index: 403

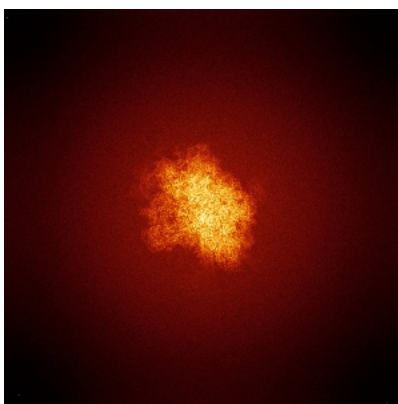
The images above show the largest variance slices of the map in three orthogonal directions.

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

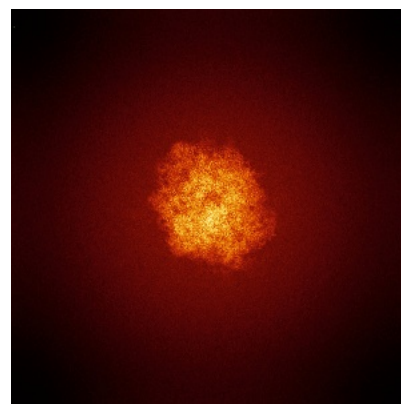
6.4.1 Primary map



X

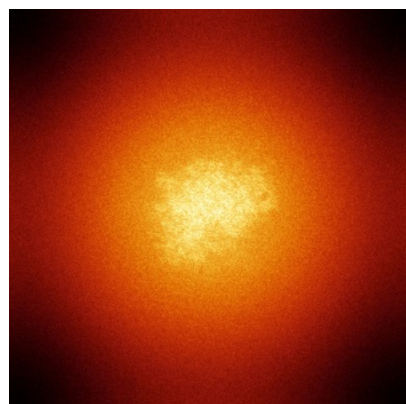


Y

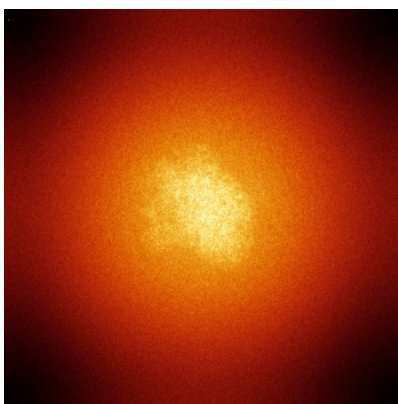


Z

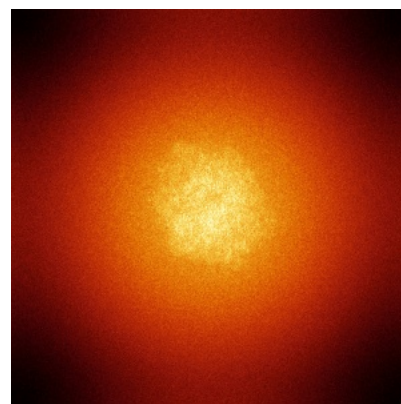
6.4.2 Raw map



X



Y

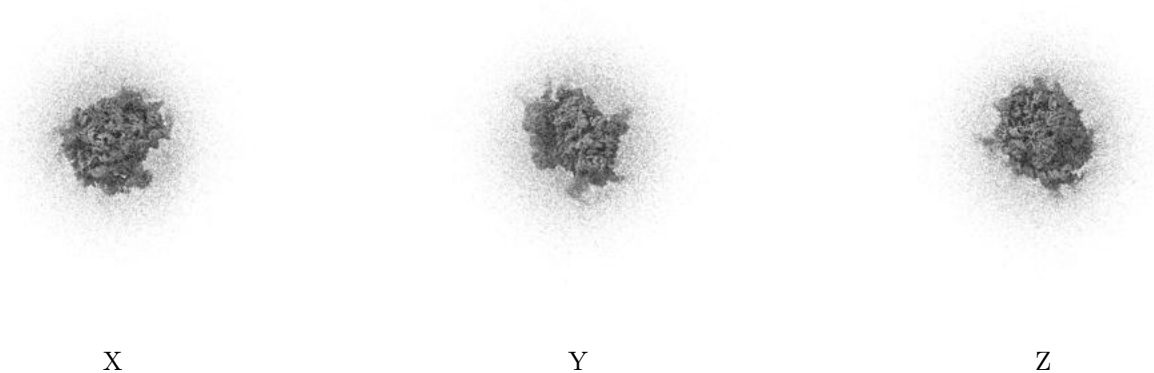


Z

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.

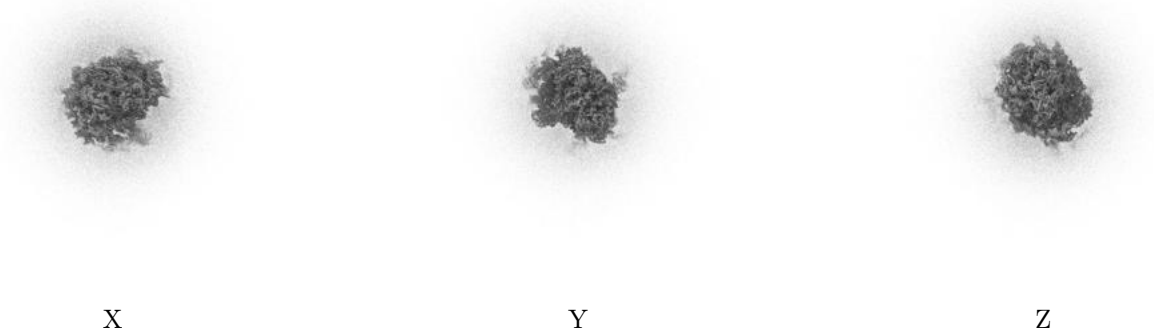
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.8. 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.

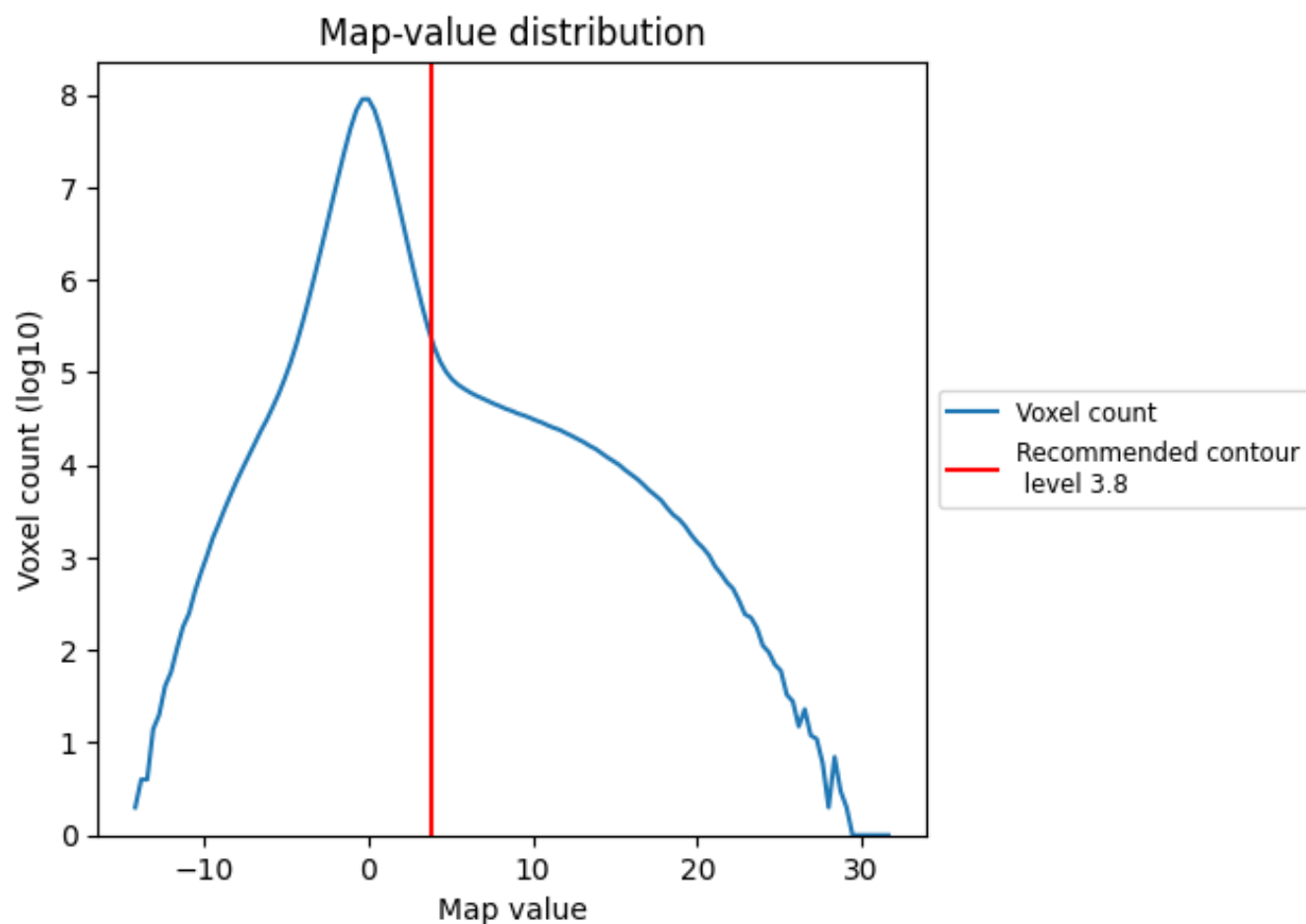
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

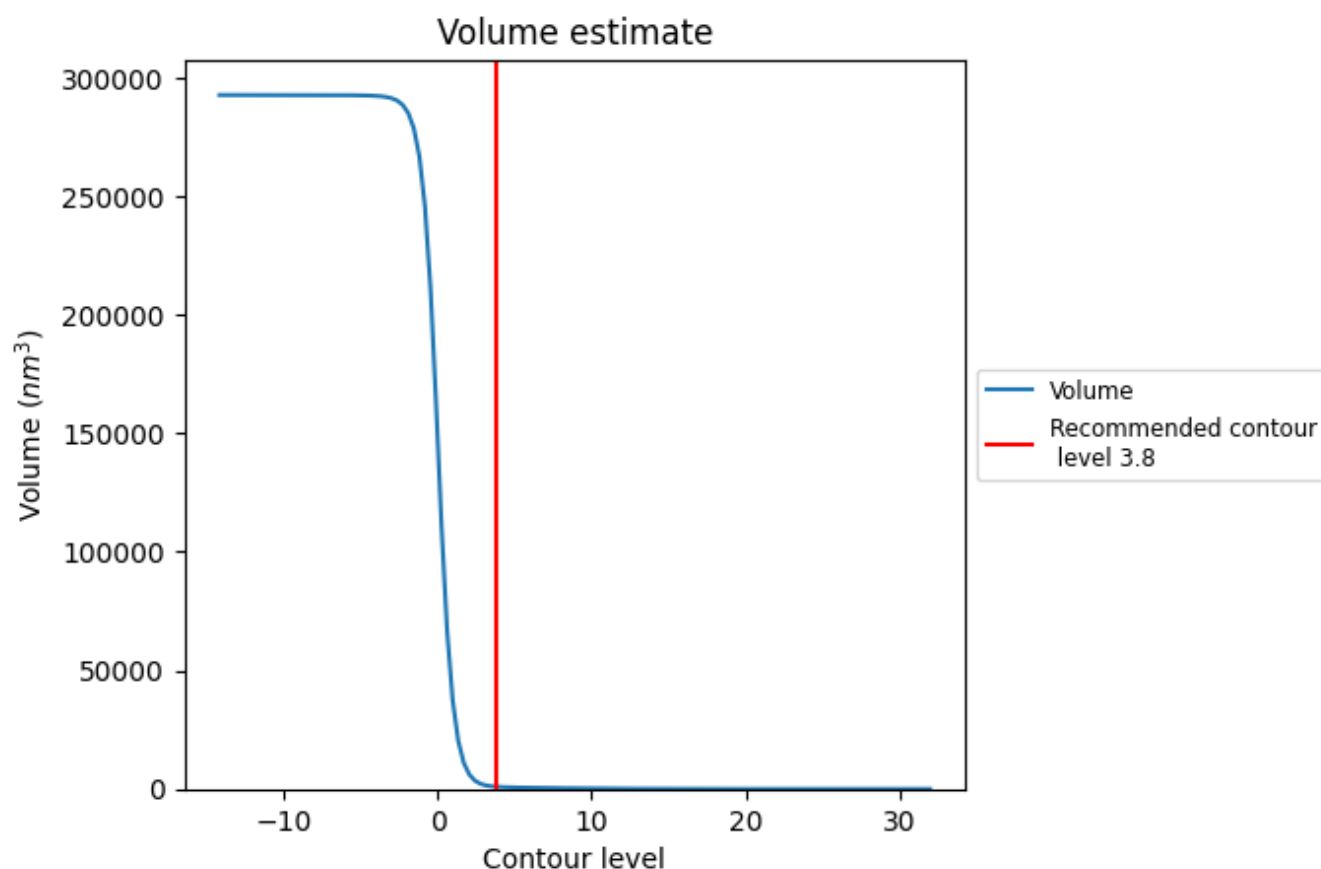
This section contains the results of statistical analysis of the map.

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.

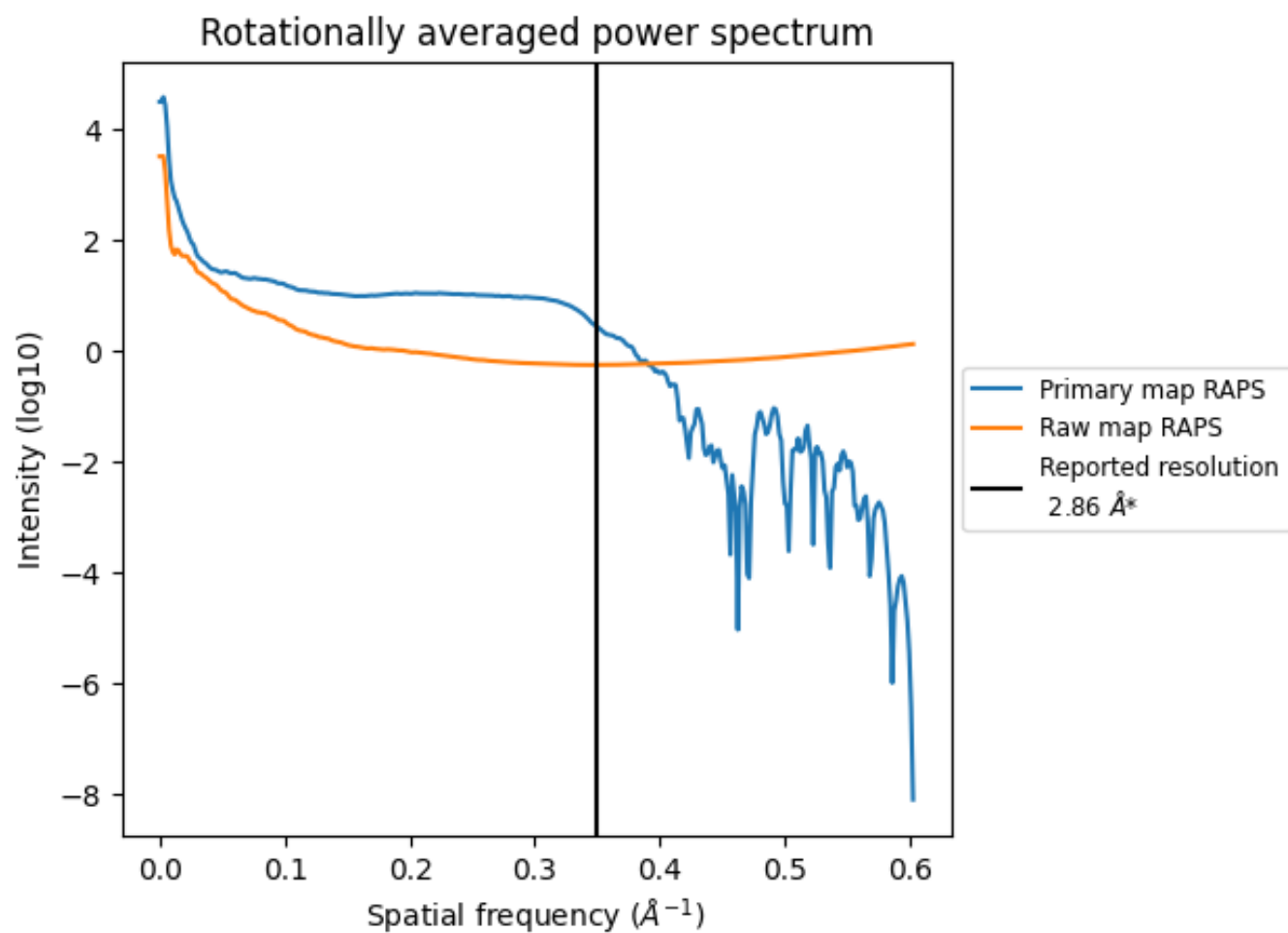
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 940 nm^3 ; this corresponds to an approximate mass of 849 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 ⓘ

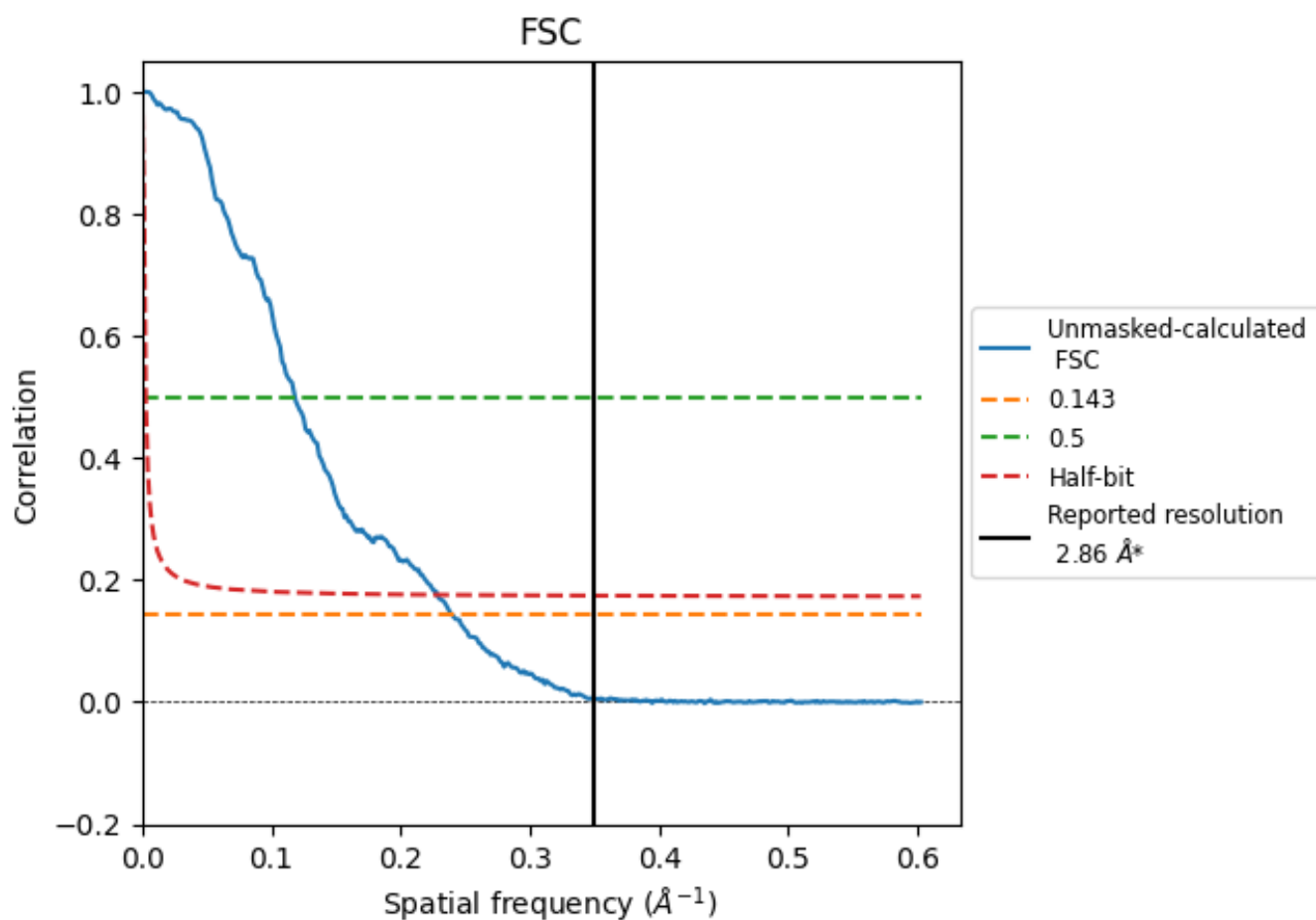


*Reported resolution corresponds to spatial frequency of $0.350 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

8.2 Resolution estimates [i](#)

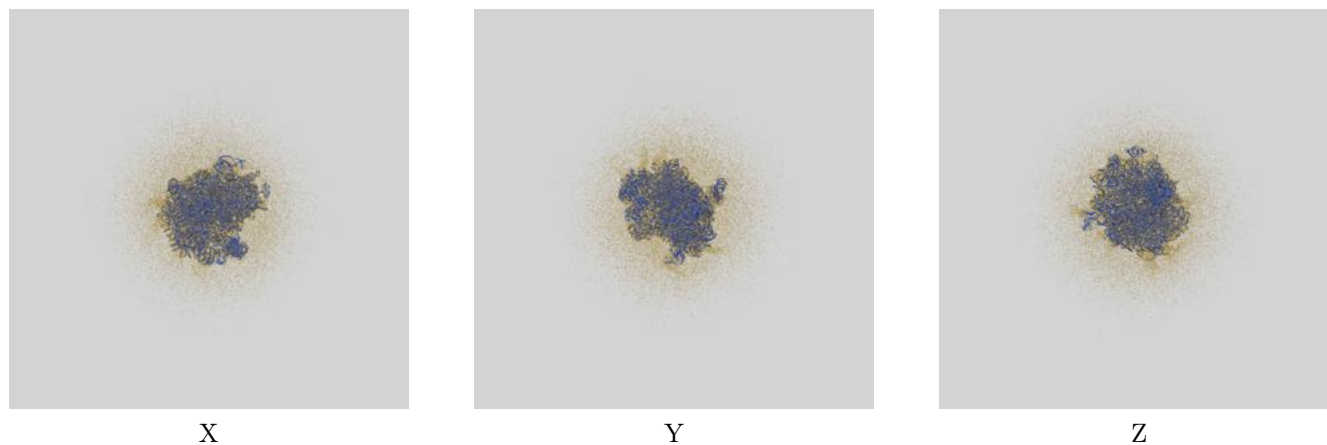
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.18	8.45	4.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.18 differs from the reported value 2.86 by more than 10 %

9 Map-model fit [i](#)

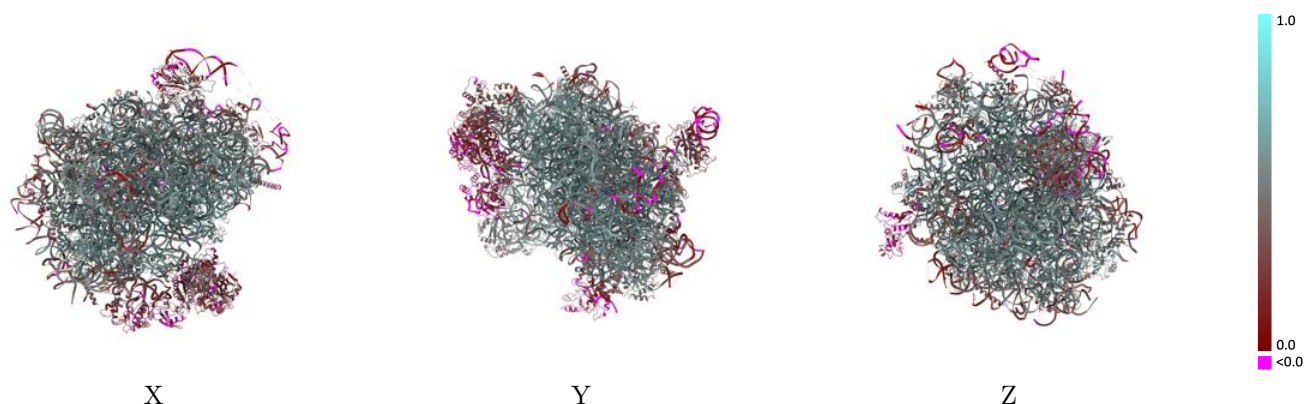
This section contains information regarding the fit between EMDB map EMD-75687 and PDB model 11HE. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



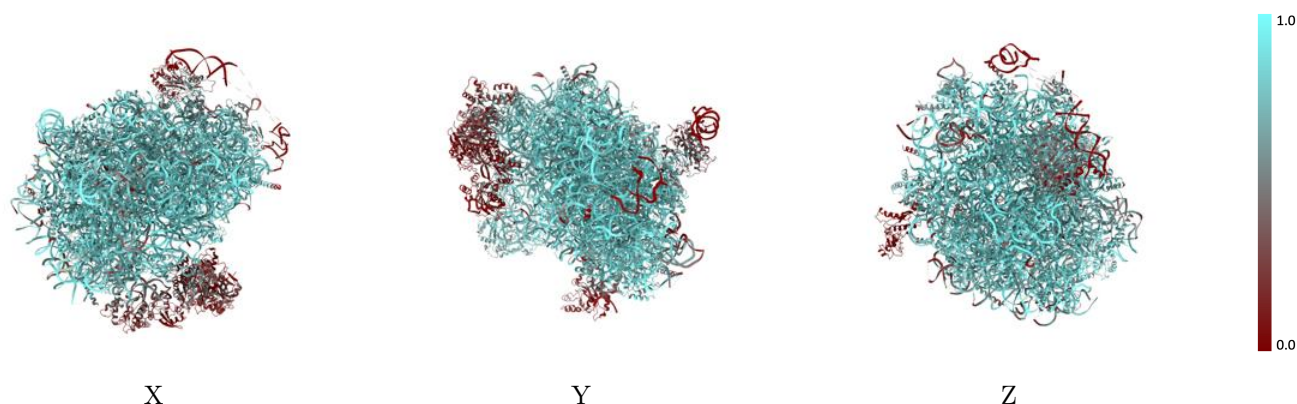
The images above show the 3D surface view of the map at the recommended contour level 3.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



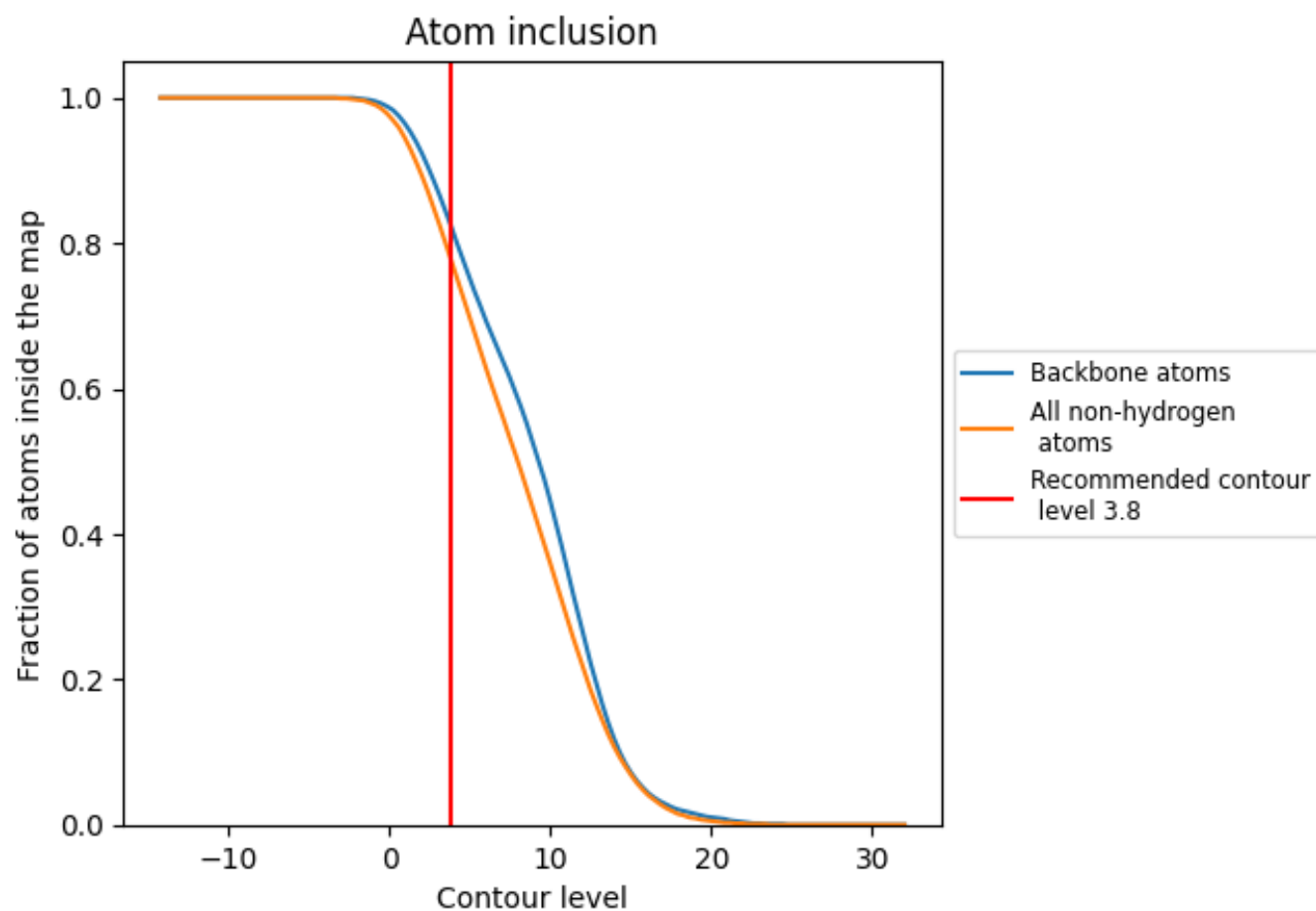
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (3.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.4910
10	 0.8120	 0.5290
11	 0.6750	 0.4140
13	 0.8000	 0.5200
14	 0.8330	 0.5300
15	 0.8860	 0.5860
17	 0.8530	 0.5620
19	 0.7660	 0.5020
20	 0.8570	 0.5590
21	 0.8020	 0.5310
22	 0.6170	 0.3860
23	 0.8190	 0.5540
24	 0.8080	 0.5360
26	 0.8250	 0.5310
27	 0.7880	 0.5120
28	 0.8670	 0.5200
29	 0.6660	 0.4380
30	 0.7030	 0.4640
31	 0.7870	 0.5160
32	 0.8570	 0.5760
34	 0.8040	 0.5470
35	 0.7810	 0.5200
36	 0.7950	 0.5090
37	 0.8740	 0.5750
38	 0.6710	 0.4450
39	 0.8240	 0.5500
40	 0.7810	 0.5100
42	 0.8090	 0.5250
5	 0.9250	 0.5650
58	 0.8840	 0.5410
EB	 0.3820	 0.2900
ES	 0.0310	 0.0430
L3	 0.8390	 0.5540
L4	 0.8440	 0.5550
L5	 0.7840	 0.5010



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Chain	Atom inclusion	Q-score
L6	 0.7990	 0.5120
L7	 0.8560	 0.5660
L8	 0.8540	 0.5700
L9	 0.7600	 0.5110
Q	 0.8690	 0.5710
aa	 0.7340	 0.4710
bb	 0.8540	 0.5640
cc	 0.8080	 0.5330
dd	 0.8720	 0.5770
ee	 0.8790	 0.5800
ff	 0.8100	 0.5390
gg	 0.8600	 0.5640
s	 0.2790	 0.2310
t	 0.0760	 0.0790
u	 0.0310	 0.0530
v	 0.2000	 0.2160