



Full wwPDB EM Validation Report ⓘ

Mar 4, 2026 – 09:00 PM UTC

PDB ID : 7QV3 / pdb_00007qv3
EMDB ID : EMD-14159
Title : Bacillus subtilis MutS2-collided disome complex (MutS2 conf.2; Leading 70S)
Authors : Filbeck, S.; Pfeffer, S.
Deposited on : 2022-01-19
Resolution : 5.14 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

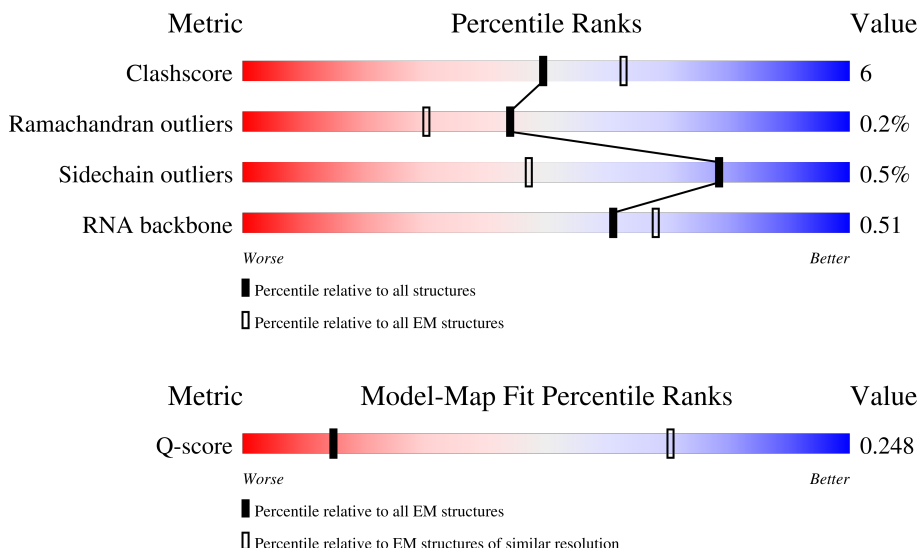
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 5.14 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.



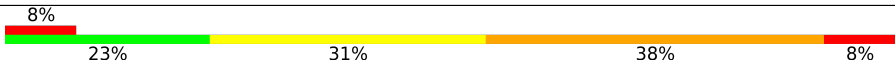
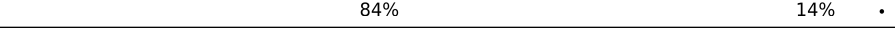
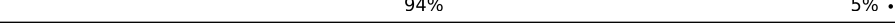
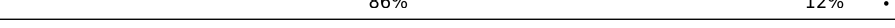
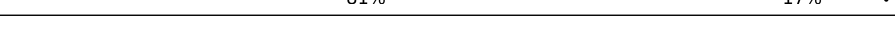
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	700 (4.64 - 5.64)

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	0	59	 81% 8% 8%
2	1	49	 78% 20%
3	2	44	 91% 9%

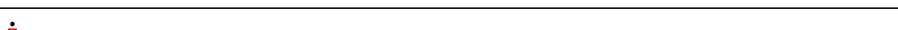
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Mol	Chain	Length	Quality of chain
4	3	66	
5	4	37	
6	6	66	
7	A	26	
8	B	112	
9	C	277	
10	D	209	
11	E	207	
12	F	179	
13	G	179	
14	H	77	
15	I	24	
16	J	145	
17	K	122	
18	L	146	
19	M	144	
20	N	120	
21	O	120	
22	P	115	
23	Q	119	
24	R	102	
25	S	113	
26	T	95	
27	U	103	
28	V	2928	

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Mol	Chain	Length	Quality of chain
29	W	94	
30	X	149	
31	Y	66	
32	Z	59	
33	a	1533	
34	b	57	
35	c	218	
36	d	200	
37	e	166	
38	f	95	
39	g	156	
40	h	132	
41	i	130	
42	j	102	
43	k	131	
44	l	138	
45	m	121	
46	n	61	
47	o	89	
48	p	90	
49	q	87	
50	r	79	
51	s	92	
52	t	88	
53	u	62	

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Mol	Chain	Length	Quality of chain
54	v	785	
54	w	785	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149707 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 2 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	63	Total	C	N	O	S	0	0
			499	312	91	91	5		

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	26	Total	C	N	O	P	0	0
			559	251	106	176	26		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 14 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 15 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	I	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	2887	Total	C	N	O	P	0	0
			61998	27661	11460	19993	2884		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	243	G	A	conflict	GB 1491848961
V	325	A	-	insertion	GB 1491848961
V	326	A	-	insertion	GB 1491848961
V	327	G	-	insertion	GB 1491848961
V	328	G	-	insertion	GB 1491848961
V	640	U	C	conflict	GB 1491848961
V	2232	A	G	conflict	GB 1491848961

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

Mol	Chain	Residues	Atoms				AltConf	Trace
29	W	82	Total	C	N	O	0	0
			630	390	123	117		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	149	Total	C	N	O	S	0	0
			1151	726	205	219	1		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 33 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 34 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	57	Total	C	N	O	S	0	0
			476	295	97	83	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	30	ALA	GLN	conflict	UNP P21478

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	151	Total	C	N	O	S	0	0
			1203	755	224	218	6		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	103	Total	C	N	O	S	0	0
			784	485	151	148			

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	118	Total	C	N	O	S	0	0
			871	537	171	161	2		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	92	Total	C	N	O	S	0	0
			740	459	145	136			

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	60	Total	C	N	O	S	0	0
			497	317	98	77	5		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	77	Total	C	N	O	S	0	0
			624	403	110	109	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 53 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 54 is a protein called Endonuclease MutS2.

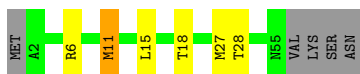
Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	548	Total	C	N	O	S	0	0
			4289	2680	743	850	16		
54	w	593	Total	C	N	O	S	0	0
			4644	2904	804	919	17		

3 Residue-property plots [i](#)

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

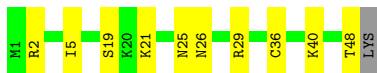
- Molecule 1: 50S ribosomal protein L32

Chain 0:  81% 8% 8%



- Molecule 2: 50S ribosomal protein L33 1

Chain 1:  78% 20% .



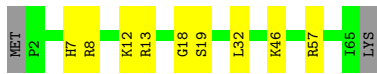
- Molecule 3: 50S ribosomal protein L34

Chain 2:  91% 9%



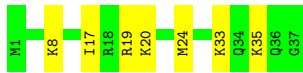
- Molecule 4: 50S ribosomal protein L35

Chain 3:  83% 14% .

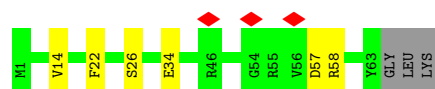
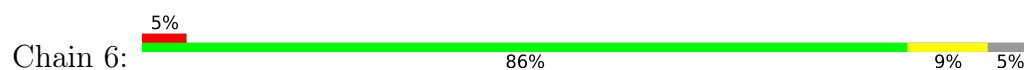


- Molecule 5: 50S ribosomal protein L36

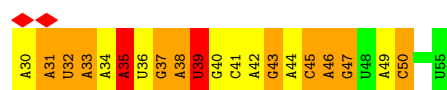
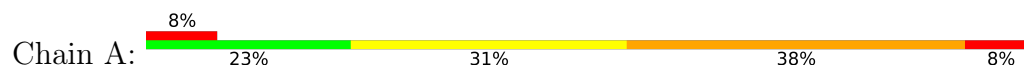
Chain 4:  81% 19%



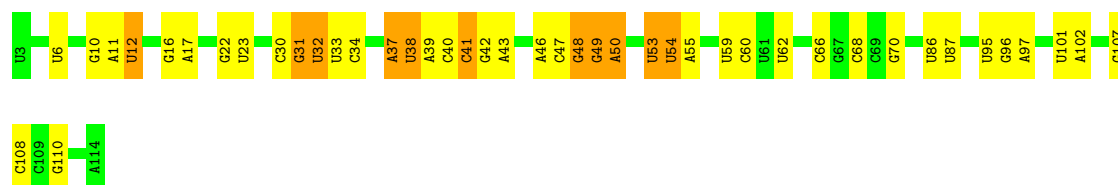
- Molecule 6: 50S ribosomal protein L31



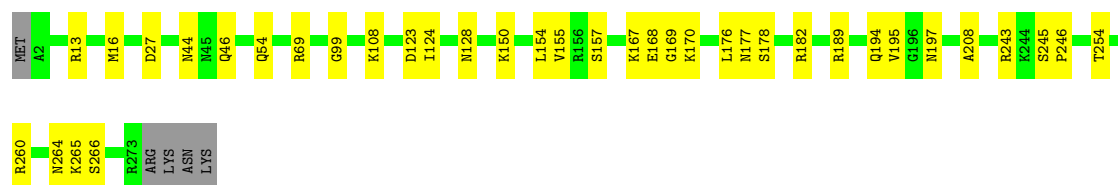
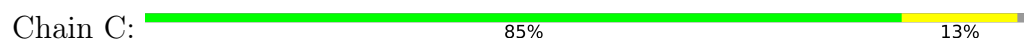
- Molecule 7: mRNA



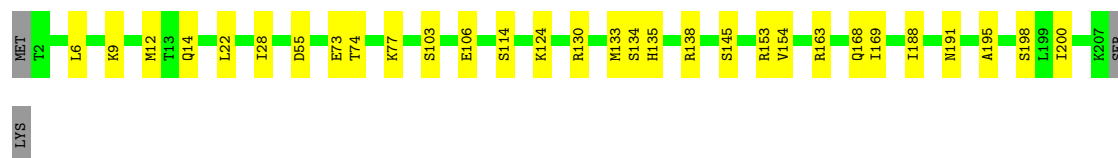
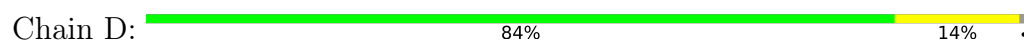
- Molecule 8: 5S ribosomal RNA



- Molecule 9: 50S ribosomal protein L2



- Molecule 10: 50S ribosomal protein L3



- Molecule 11: 50S ribosomal protein L4



- Molecule 12: 50S ribosomal protein L5

Chain F:  86% 12%



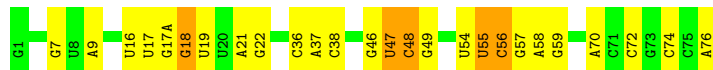
- Molecule 13: 50S ribosomal protein L6

Chain G:  81% 17%



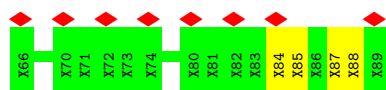
- Molecule 14: P-site tRNA

Chain H:  66% 27% 6%



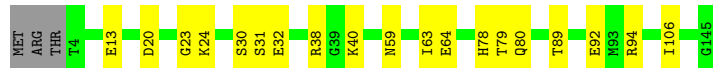
- Molecule 15: Nascent chain

Chain I:  33% 83% 17%



- Molecule 16: 50S ribosomal protein L13

Chain J:  85% 13%



- Molecule 17: 50S ribosomal protein L14

Chain K:  83% 17%



- Molecule 18: 50S ribosomal protein L15

Chain L:  86% 14%



- Molecule 19: 50S ribosomal protein L16

Chain M:  83% 10% 6%



- Molecule 20: 50S ribosomal protein L17

Chain N:  84% 15% .



- Molecule 21: 50S ribosomal protein L18

Chain O:  91% 9%



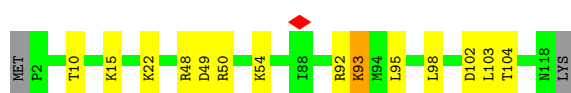
- Molecule 22: 50S ribosomal protein L19

Chain P:  90% 10%



- Molecule 23: 50S ribosomal protein L20

Chain Q:  87% 11% ..



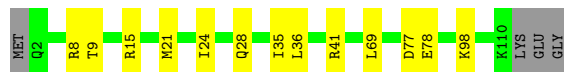
- Molecule 24: 50S ribosomal protein L21

Chain R:  82% 17% .



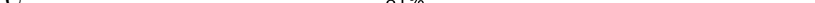
- Molecule 25: 50S ribosomal protein L22

Chain S:  85% 12% .



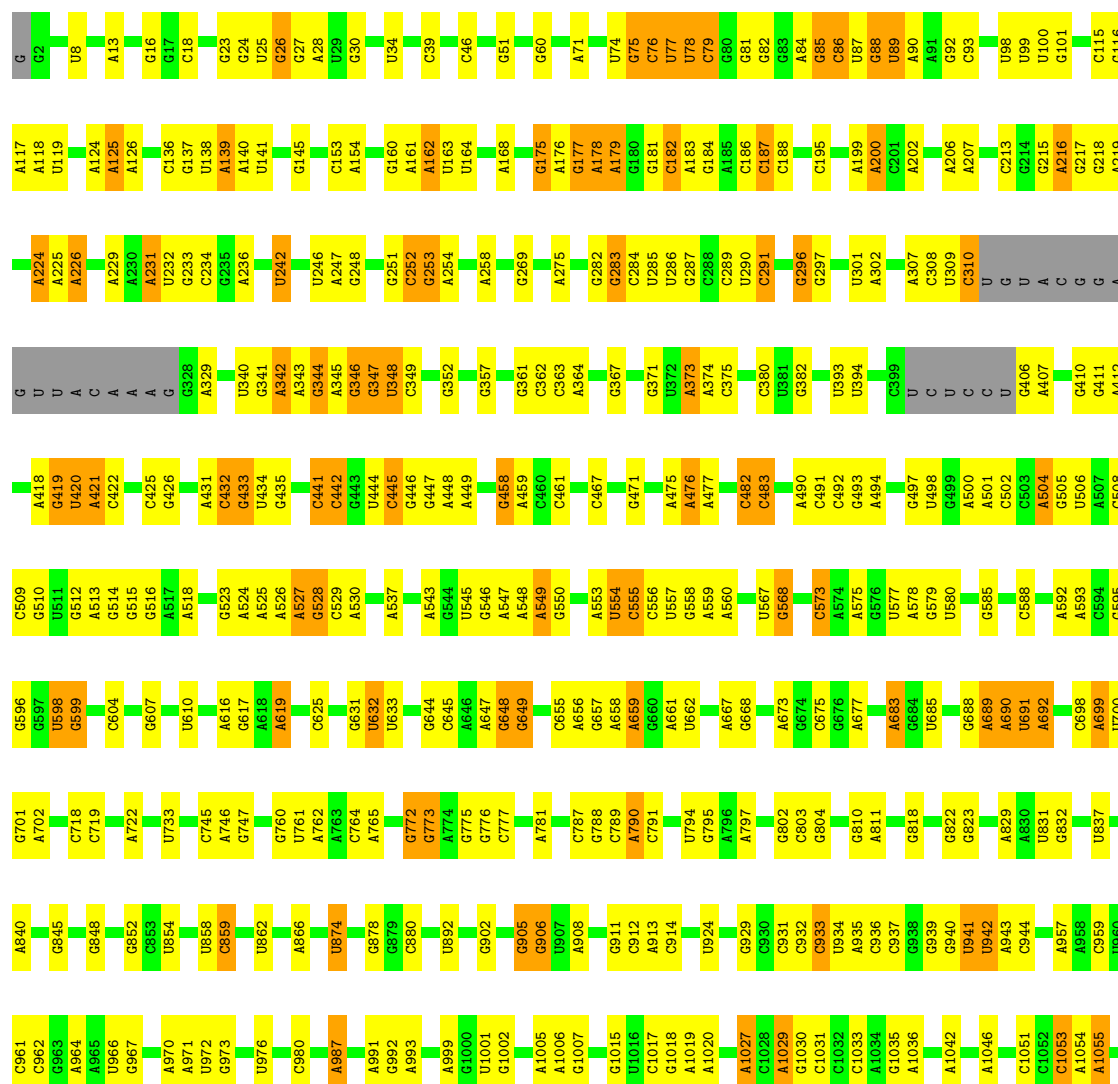
- Molecule 26: 50S ribosomal protein L23

Sequence logo for the 1000th iteration. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows amino acid positions from 1 to 15. The sequence is MET K2 R5 D31 V32 R33 A34 N35 K36 T37 E38 Y59 E91 ILE PHE GLU ALA. MET, K2, R5, and E91 are highlighted in red, indicating high conservation. D31, V32, R33, A34, N35, K36, T37, E38, Y59, and ILE are highlighted in green, indicating moderate conservation. PHE, GLU, and ALA are highlighted in grey, indicating low conservation.

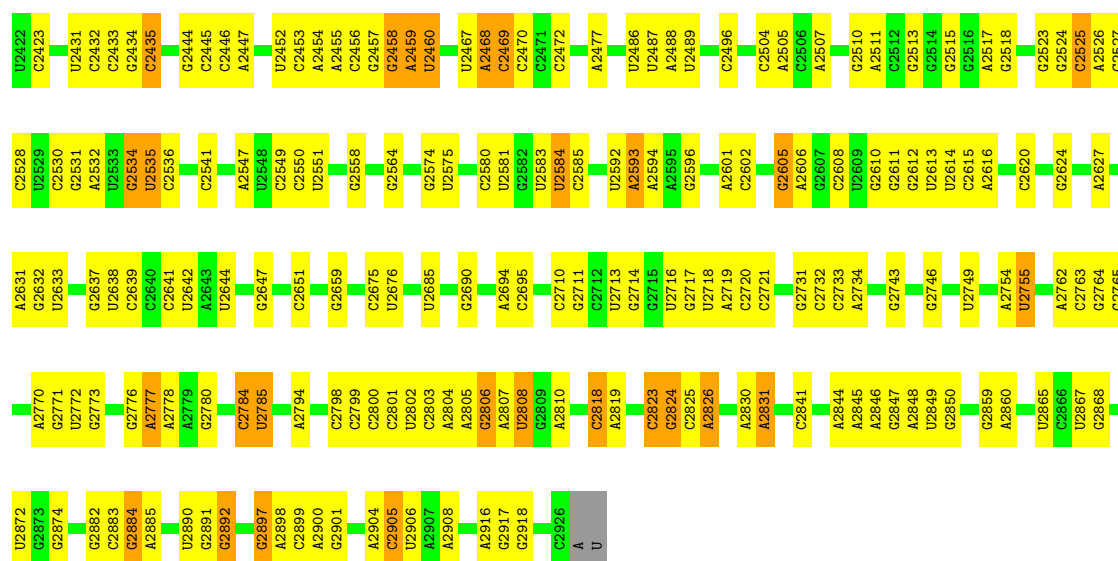
- Chain U:  81% 17%



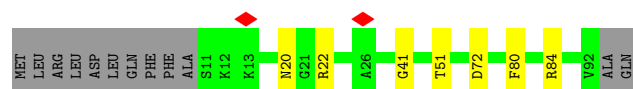
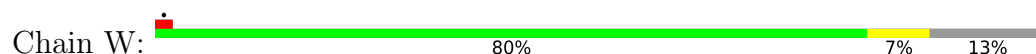
- Chain V: 59% 31% 9%



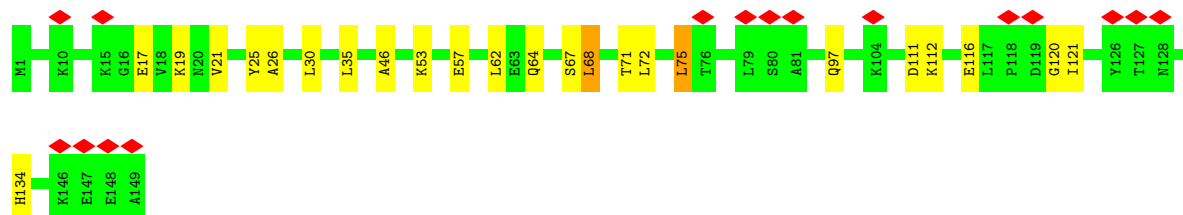
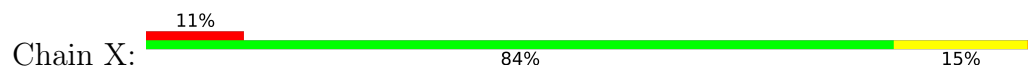
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G2245	G2246	A2247	A2248	A2249	A2250	A2251	A2252	A2253	A2254	A2255	A2256	A2257	A2258	A2259	A2260	A2261	A2262	A2263	A2264	A2265	A2266	A2267	A2268	A2269	A2270	A2271	A2272	A2273	A2274	A2275	A2276	A2277	A2278	A2279	A2280	A2281	A2282	A2283	A2284	A2285	A2286	A2287	A2288	A2289	A2290	A2291	A2292	A2293	A2294	A2295	A2296	A2297	A2298	A2299	A2300	A2301	A2302	A2303	A2304	A2305	A2306	A2307	A2308	A2309	A2310	A2311	A2312	A2313	A2314	A2315	A2316	A2317	A2318	A2319	A2320	A2321	A2322	A2323	A2324	A2325	A2326	A2327	A2328	A2329	A2330	A2331	A2332	A2333	A2334	A2335	A2336	A2337	A2338	A2339	A2340	A2341	A2342	A2343	A2344	A2345	A2346	A2347	A2348	A2349	A2350	A2351	A2352	A2353	A2354	A2355	A2356	A2357	A2358	A2359	A2360	A2361	A2362	A2363	A2364	A2365	A2366	A2367	A2368	A2369	A2370	A2371	A2372	A2373	A2374	A2375	A2376	A2377	A2378	A2379	A2380	A2381	A2382	A2383	A2384	A2385	A2386	A2387	A2388	A2389	A2390	A2391	A2392	A2393	A2394	A2395	A2396	A2397	A2398	A2399	A2400	A2401	A2402	A2403	A2404	A2405	A2406	A2407	A2408	A2409	A2410	A2411	A2412	A2413	A2414	A2415	A2416	A2417	A2418	A2419	A2420	A2421	A2422	A2423	A2424	A2425	A2426	A2427	A2428	A2429	A2430	A2431	A2432	A2433	A2434	A2435	A2436	A2437	A2438	A2439	A2440	A2441	A2442	A2443	A2444	A2445	A2446	A2447	A2448	A2449	A2450	A2451	A2452	A2453	A2454	A2455	A2456	A2457	A2458	A2459	A2460	A2461	A2462	A2463	A2464	A2465	A2466	A2467	A2468	A2469	A2470	A2471	A2472	A2473	A2474	A2475	A2476	A2477	A2478	A2479	A2480	A2481	A2482	A2483	A2484	A2485	A2486	A2487	A2488	A2489	A2490	A2491	A2492	A2493	A2494	A2495	A2496	A2497	A2498	A2499	A2500	A2501	A2502	A2503	A2504	A2505	A2506	A2507	A2508	A2509	A2510	A2511	A2512	A2513	A2514	A2515	A2516	A2517	A2518	A2519	A2520	A2521	A2522	A2523	A2524	A2525	A2526	A2527	A2528	A2529	A2530	A2531	A2532	A2533	A2534	A2535	A2536	A2537	A2538	A2539	A2540	A2541	A2542	A2543	A2544	A2545	A2546	A2547	A2548	A2549	A2550	A2551	A2552	A2553	A2554	A2555	A2556	A2557	A2558	A2559	A2560	A2561	A2562	A2563	A2564	A2565	A2566	A2567	A2568	A2569	A2570	A2571	A2572	A2573	A2574	A2575	A2576	A2577	A2578	A2579	A2580	A2581	A2582	A2583	A2584	A2585	A2586	A2587	A2588	A2589	A2590	A2591	A2592	A2593	A2594	A2595	A2596	A2597	A2598	A2599	A2600	A2601	A2602	A2603	A2604	A2605	A2606	A2607	A2608	A2609	A2610	A2611	A2612	A2613	A2614	A2615	A2616	A2617	A2618	A2619	A2620	A2621	A2622	A2623	A2624	A2625	A2626	A2627	A2628	A2629	A2630	A2631	A2632	A2633	A2634	A2635	A2636	A2637	A2638	A2639	A2640	A2641	A2642	A2643	A2644	A2645	A2646	A2647	A2648	A2649	A2650	A2651	A2652	A2653	A2654	A2655	A2656	A2657	A2658	A2659	A2660	A2661	A2662	A2663	A2664	A2665	A2666	A2667	A2668	A2669	A2670	A2671	A2672	A2673	A2674	A2675	A2676	A2677	A2678	A2679	A2680	A2681	A2682	A2683	A2684	A2685	A2686	A2687	A2688	A2689	A2690	A2691	A2692	A2693	A2694	A2695	A2696	A2697	A2698	A2699	A2700	A2701	A2702	A2703	A2704	A2705	A2706	A2707	A2708	A2709	A2710	A2711	A2712	A2713	A2714	A2715	A2716	A2717	A2718	A2719	A2720	A2721	A2722	A2723	A2724	A2725	A2726	A2727	A2728	A2729	A2730	A2731	A2732	A2733	A2734	A2735	A2736	A2737	A2738	A2739	A2740	A2741	A2742	A2743	A2744	A2745	A2746	A2747	A2748	A2749	A2750	A2751	A2752	A2753	A2754	A2755	A2756	A2757	A2758	A2759	A2760	A2761	A2762	A2763	A2764	A2765	A2766	A2767	A2768	A2769	A2770	A2771	A2772	A2773	A2774	A2775	A2776	A2777	A2778	A2779	A2780	A2781	A2782	A2783	A2784	A2785	A2786	A2787	A2788	A2789	A2790	A2791	A2792	A2793	A2794	A2795	A2796	A2797	A2798	A2799	A2800	A2801	A2802	A2803	A2804	A2805	A2806	A2807	A2808	A2809	A2810	A2811	A2812	A2813	A2814	A2815	A2816	A2817	A2818	A2819	A2820	A2821	A2822	A2823	A2824	A2825	A2826	A2827	A2828	A2829	A2830	A2831	A2832	A2833	A2834	A2835	A2836	A2837	A2838	A2839	A2840	A2841	A2842	A2843	A2844	A2845	A2846	A2847	A2848	A2849	A2850	A2851	A2852	A2853	A2854	A2855	A2856	A2857	A2858	A2859	A2860	A2861	A2862	A2863	A2864	A2865	A2866	A2867	A2868	A2869	A2870	A2871	A2872	A2873	A2874	A2875	A2876	A2877	A2878	A2879	A2880	A2881	A2882	A2883	A2884	A2885	A2886	A2887	A2888	A2889	A2890	A2891	A2892	A2893	A2894	A2895	A2896	A2897	A2898	A2899	A2900	A2901	A2902	A2903	A2904	A2905	A2906	A2907	A2908	A2909	A2910	A2911	A2912	A2913	A2914	A2915	A2916	A2917	A2918	A2919	A2920	A2921	A2922	A2923	A2924	A2925	A2926	A2927	A2928	A2929	A2930	A2931	A2932	A2933	A2934	A2935	A2936	A2937	A2938	A2939	A2940	A2941	A2942	A2943	A2944	A2945	A2946	A2947	A2948	A2949	A2950	A2951	A2952	A2953	A2954	A2955	A2956	A2957	A2958	A2959	A2960	A2961	A2962	A2963	A2964	A2965	A2966	A2967	A2968	A2969	A2970	A2971	A2972	A2973	A2974	A2975	A2976	A2977	A2978	A2979	A2980	A2981	A2982	A2983	A2984	A2985	A2986	A2987	A2988	A2989	A2990	A2991	A2992	A2993	A2994	A2995	A2996	A2997	A2998	A2999	A3000	A3001	A3002	A3003	A3004	A3005	A3006	A3007	A3008	A3009	A3010	A3011	A3012	A3013	A3014	A3015	A3016	A3017	A3018	A3019	A3020	A3021	A3022	A3023	A3024	A3025	A3026	A3027	A3028	A3029	A3030	A3031	A3032	A3033	A3034	A3035	A3036	A3037	A3038	A3039	A3040	A3041	A3042	A3043	A3044	A3045	A3046	A3047	A3048	A3049	A3050	A3051	A3052	A3053	A3054	A3055	A3056	A3057	A3058	A3059	A3060	A3061	A3062	A3063	A3064	A3065	A3066	A3067	A3068	A3069	A3070	A3071	A3072	A3073	A3074	A3075	A3076	A3077	A3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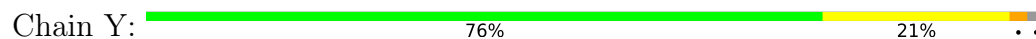
• Molecule 29: 50S ribosomal protein L27



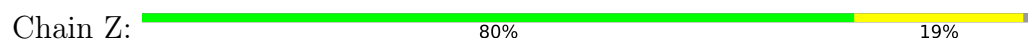
• Molecule 30: 50S ribosomal protein L9



• Molecule 31: 50S ribosomal protein L29

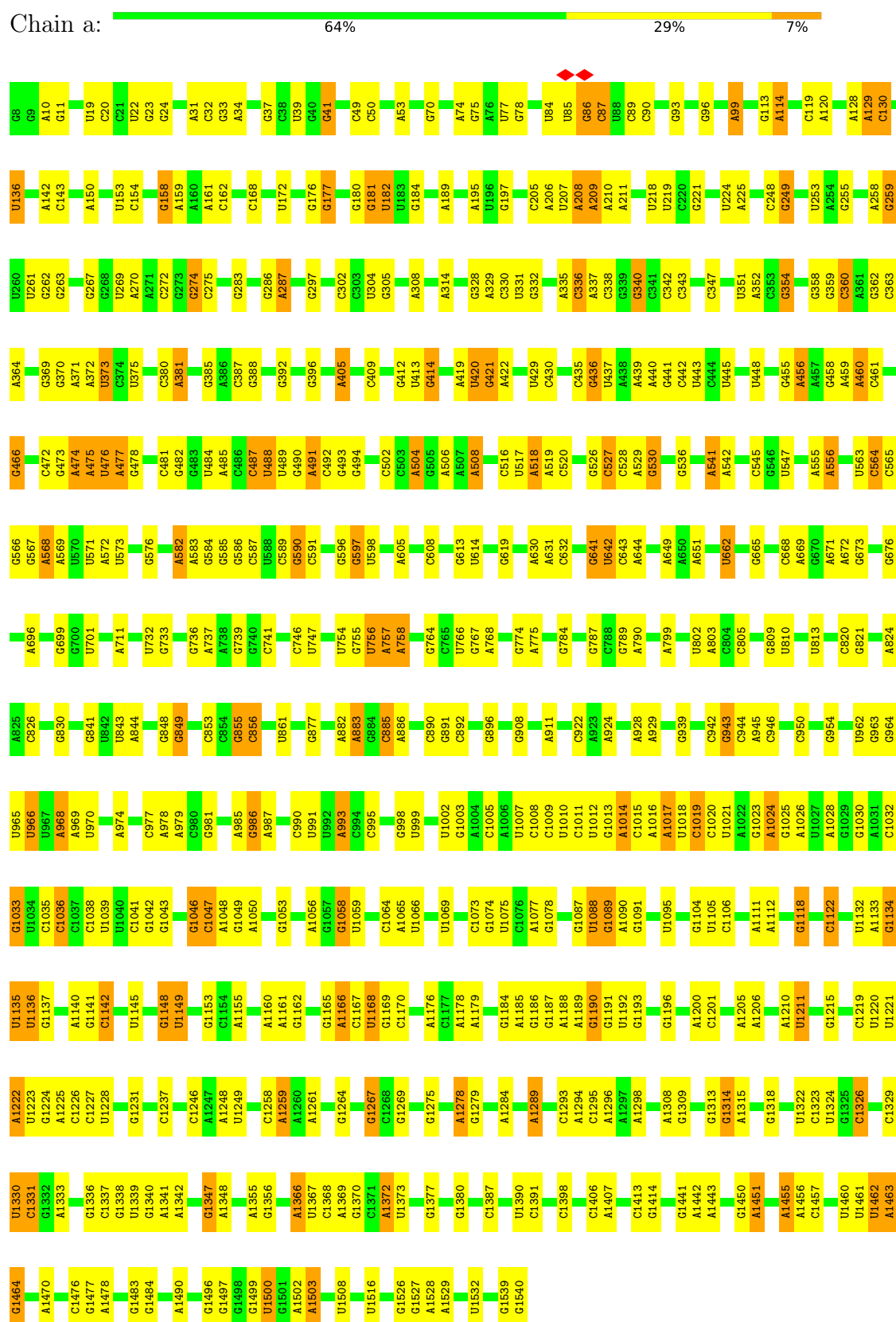


• Molecule 32: 50S ribosomal protein L30

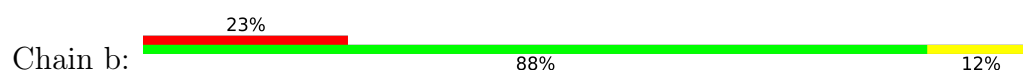


- Molecule 33: 16S ribosomal RNA

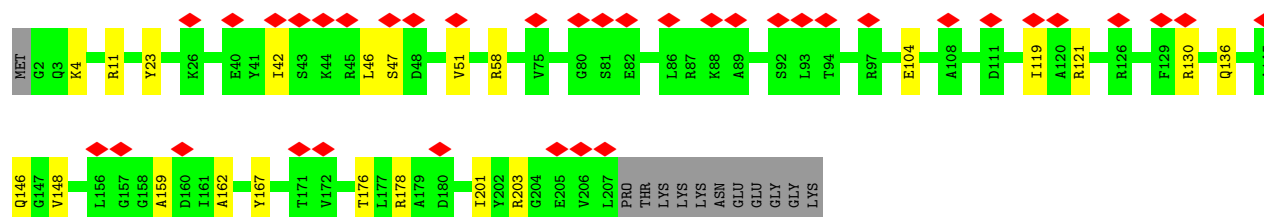
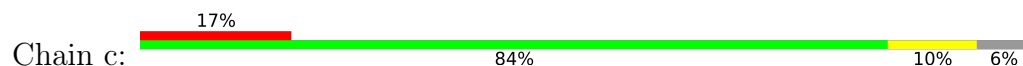
Chain a:



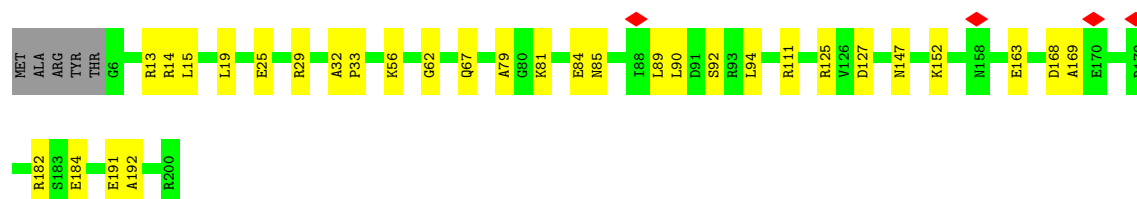
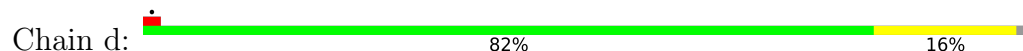
- Molecule 34: 30S ribosomal protein S21



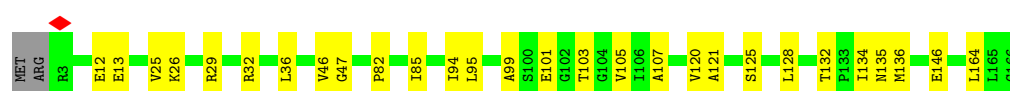
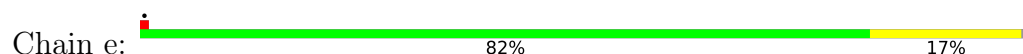
- Molecule 35: 30S ribosomal protein S3



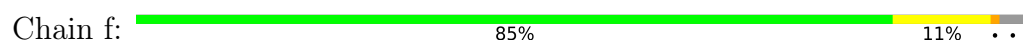
- Molecule 36: 30S ribosomal protein S4



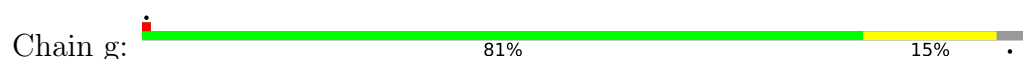
- Molecule 37: 30S ribosomal protein S5



- Molecule 38: 30S ribosomal protein S6

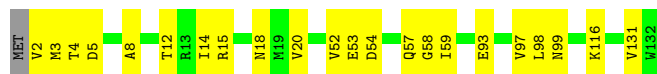


- Molecule 39: 30S ribosomal protein S7



- Molecule 40: 30S ribosomal protein S8

Chain h:  83% 17% .



- Molecule 41: 30S ribosomal protein S9

Chain i:  65% 15% 21%



- Molecule 42: 30S ribosomal protein S10

Chain j:  82% 11% 7%



- Molecule 43: 30S ribosomal protein S11

Chain k:  82% 8% 10%



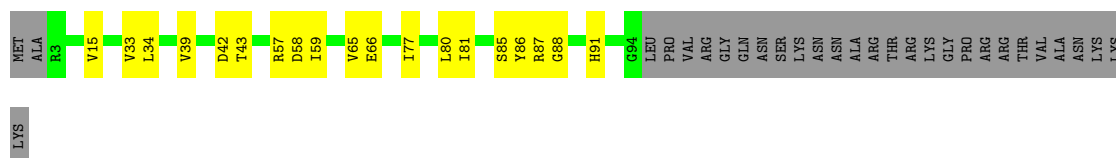
- Molecule 44: 30S ribosomal protein S12

Chain l:  86% 13% .



- Molecule 45: 30S ribosomal protein S13

Chain m:  60% 16% 24%



- Molecule 46: 30S ribosomal protein S14

Chain n:  84% 13%



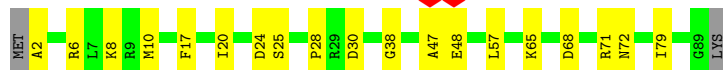
- Molecule 47: 30S ribosomal protein S15

Chain o:  70% 26%



- Molecule 48: 30S ribosomal protein S16

Chain p:  77% 21%



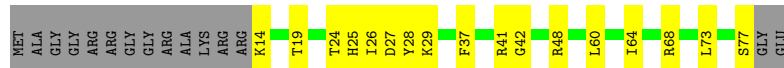
- Molecule 49: 30S ribosomal protein S17

Chain q:  80% 16%



- Molecule 50: 30S ribosomal protein S18

Chain r:  59% 22% 19%



- Molecule 51: 30S ribosomal protein S19

Chain s:  74% 10% 16%



- Molecule 52: 30S ribosomal protein S20

Chain t:  80% 15% 6%



-

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5078	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.5	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.341	Depositor
Minimum map value	-0.207	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0172	Depositor
Map size ($\text{\AA}$)	590.64, 590.64, 590.64	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.605, 1.605, 1.605	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.12	0/433	0.28	0/574
2	1	0.14	0/406	0.27	0/540
3	2	0.18	0/370	0.31	0/483
4	3	0.13	0/519	0.34	0/680
5	4	0.15	0/299	0.25	0/393
6	6	0.12	0/509	0.24	0/678
7	A	0.66	4/627 (0.6%)	0.85	5/975 (0.5%)
8	B	0.08	0/2675	0.21	0/4170
9	C	0.13	0/2120	0.30	0/2845
10	D	0.15	0/1591	0.34	0/2132
11	E	0.11	0/1580	0.28	0/2132
12	F	0.38	0/1405	0.79	5/1887 (0.3%)
13	G	0.10	0/1360	0.24	0/1832
14	H	0.07	0/1834	0.21	0/2858
16	J	0.13	0/1146	0.28	0/1542
17	K	0.15	0/927	0.29	0/1245
18	L	0.13	0/1093	0.28	0/1457
19	M	0.12	0/1099	0.25	0/1468
20	N	0.12	0/960	0.28	0/1284
21	O	0.23	0/921	0.42	0/1236
22	P	0.14	0/957	0.29	0/1279
23	Q	0.15	0/952	0.34	0/1266
24	R	0.11	0/797	0.29	0/1070
25	S	0.13	0/851	0.32	0/1146
26	T	0.12	0/731	0.24	0/974
27	U	0.13	0/772	0.27	0/1032
28	V	0.15	0/69444	0.32	23/108334 (0.0%)
29	W	0.13	0/638	0.31	0/847
30	X	0.12	0/1162	0.38	0/1551
31	Y	0.14	0/531	0.25	0/707
32	Z	0.11	0/457	0.29	0/613
33	a	0.09	0/36826	0.22	0/57450
34	b	0.16	0/480	0.33	0/628
35	c	0.13	0/1641	0.30	0/2208

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	d	0.13	0/1598	0.31	0/2147
37	e	0.12	0/1230	0.27	0/1655
38	f	0.12	0/766	0.28	0/1031
39	g	0.11	0/1220	0.29	0/1637
40	h	0.14	0/1048	0.33	0/1407
41	i	0.12	0/794	0.30	0/1074
42	j	0.11	0/773	0.28	0/1044
43	k	0.13	0/885	0.30	0/1196
44	l	0.14	0/1069	0.33	0/1435
45	m	0.14	0/744	0.35	0/994
46	n	0.12	0/507	0.32	0/672
47	o	0.12	0/718	0.30	0/960
48	p	0.13	0/708	0.32	0/950
49	q	0.12	0/699	0.30	0/933
50	r	0.13	0/526	0.34	0/705
51	s	0.11	0/640	0.27	0/861
52	t	0.12	0/639	0.34	0/852
53	u	0.13	0/448	0.30	0/596
54	v	0.64	0/4341	1.09	0/5847
54	w	0.64	0/4703	1.12	1/6337 (0.0%)
All	All	0.20	4/162169 (0.0%)	0.38	34/241849 (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
28	V	0	16
54	w	0	2
All	All	0	18

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	41	C	C1'-N1	5.46	1.56	1.48
7	A	42	A	C1'-N9	-5.36	1.40	1.48
7	A	39	U	C1'-N1	5.35	1.55	1.47
7	A	50	C	C1'-N1	5.22	1.56	1.48

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	V	138	U	OP1-P-O3'	-29.77	18.68	108.00
7	A	32	U	P-O3'-C3'	-7.69	108.67	120.20
28	V	2336	G	C4'-C3'-O3'	7.11	120.07	109.40
28	V	1449	C	P-O3'-C3'	-6.97	109.74	120.20
7	A	37	G	P-O3'-C3'	-6.92	109.82	120.20
28	V	1450	C	P-O3'-C3'	-6.87	109.89	120.20
7	A	38	A	P-O3'-C3'	-6.85	109.93	120.20
28	V	2349	A	C1'-O4'-C4'	-6.79	102.92	109.70
28	V	1447	C	P-O3'-C3'	-6.70	110.15	120.20
28	V	2342	C	C5'-C4'-C3'	-6.68	105.97	116.00
28	V	2123	A	P-O3'-C3'	-6.57	110.35	120.20
28	V	139	A	OP1-P-OP2	-6.37	100.50	119.60
28	V	2331	U	C5'-C4'-C3'	-6.37	106.45	116.00
28	V	2342	C	O3'-P-O5'	-6.33	94.51	104.00
12	F	119	LYS	CA-C-N	6.20	128.59	120.28
12	F	119	LYS	C-N-CA	6.20	128.59	120.28
12	F	163	ASP	CA-CB-CG	6.04	118.64	112.60
54	w	422	ASP	CA-CB-CG	5.76	118.36	112.60
12	F	84	PRO	O-C-N	-5.75	116.21	123.10
28	V	2333	G	C5'-C4'-C3'	-5.72	107.41	116.00
7	A	35	A	P-O3'-C3'	-5.72	111.62	120.20
28	V	2122	G	P-O3'-C3'	-5.50	111.95	120.20
28	V	2330	A	C5'-C4'-O4'	5.48	118.02	109.80
28	V	1448	U	C4'-C3'-O3'	5.45	117.58	109.40
28	V	2335	U	O4'-C4'-C3'	5.44	109.44	104.00
28	V	2350	G	C5'-C4'-C3'	-5.39	107.91	116.00
28	V	2347	G	C5'-C4'-C3'	-5.34	107.99	116.00
12	F	40	VAL	N-CA-C	5.32	115.95	109.30
28	V	2349	A	C5'-C4'-O4'	5.26	116.99	109.10
28	V	2226	U	P-O3'-C3'	-5.22	112.38	120.20
28	V	1452	C	P-O3'-C3'	-5.19	112.41	120.20
28	V	2060	A	C2'-C3'-O3'	5.19	117.28	109.50
7	A	31	A	P-O3'-C3'	-5.14	112.48	120.20
28	V	420	U	P-O3'-C3'	-5.12	112.53	120.20

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	V	2323	C	Sidechain
28	V	2326	C	Sidechain
28	V	2327	A	Sidechain
28	V	2329	A	Sidechain

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Mol	Chain	Res	Type	Group
28	V	2333	G	Sidechain
28	V	2334	U	Sidechain
28	V	2335	U	Sidechain
28	V	2337	G	Sidechain
28	V	2340	A	Sidechain
28	V	2342	C	Sidechain
28	V	2343	A	Sidechain
28	V	2344	U	Sidechain
28	V	2346	C	Sidechain
28	V	2362	A	Sidechain
28	V	2364	A	Sidechain
28	V	924	U	Sidechain
54	w	308	ARG	Sidechain
54	w	456	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	0	445	4	0
2	1	401	0	413	6	0
3	2	367	0	410	4	0
4	3	512	0	564	12	0
5	4	296	0	342	6	0
6	6	499	0	491	4	0
7	A	559	0	281	20	0
8	B	2392	0	1213	30	0
9	C	2083	0	2168	31	0
10	D	1569	0	1637	20	0
11	E	1561	0	1647	8	0
12	F	1386	0	1446	12	0
13	G	1342	0	1388	23	0
14	H	1643	0	831	14	0
15	I	120	0	28	3	0
16	J	1123	0	1162	17	0
17	K	920	0	977	18	0
18	L	1081	0	1132	17	0
19	M	1076	0	1145	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	N	953	0	983	13	0
21	O	912	0	947	7	0
22	P	944	0	1020	11	0
23	Q	940	0	1005	10	0
24	R	786	0	826	13	0
25	S	842	0	899	11	0
26	T	725	0	770	5	0
27	U	762	0	821	11	0
28	V	61998	0	31207	570	0
29	W	630	0	644	7	0
30	X	1151	0	1222	16	0
31	Y	530	0	568	10	0
32	Z	455	0	491	8	0
33	a	32891	0	16559	321	0
34	b	476	0	521	6	0
35	c	1619	0	1658	14	0
36	d	1568	0	1604	19	0
37	e	1218	0	1300	20	0
38	f	755	0	746	8	0
39	g	1203	0	1251	18	0
40	h	1036	0	1095	19	0
41	i	784	0	803	14	0
42	j	761	0	795	8	0
43	k	871	0	895	10	0
44	l	1052	0	1112	18	0
45	m	740	0	787	15	0
46	n	497	0	531	8	0
47	o	710	0	735	16	0
48	p	695	0	721	14	0
49	q	691	0	728	11	0
50	r	518	0	555	13	0
51	s	624	0	636	8	0
52	t	637	0	696	10	0
53	u	444	0	487	8	0
54	v	4289	0	4345	24	0
54	w	4644	0	4700	21	0
All	All	149707	0	102383	1366	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1366) 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)
28:V:310:C:O2	28:V:406:G:N2	1.93	1.01
33:a:890:C:H5'	44:l:9:ARG:NH1	1.74	1.00
7:A:50:C:N4	33:a:1406:C:O2'	1.95	1.00
28:V:28:A:N6	28:V:558:G:O2'	2.00	0.93
33:a:474:A:O2'	33:a:475:A:O5'	1.87	0.92
33:a:1461:U:O2'	33:a:1462:U:OP1	1.88	0.91
33:a:209:A:O2'	33:a:210:A:O4'	1.89	0.90
33:a:413:U:OP1	33:a:414:G:O2'	1.88	0.89
28:V:1216:C:O2	28:V:1220:G:N2	2.05	0.89
28:V:1866:C:O2'	28:V:1956:A:N3	2.06	0.89
33:a:1038:C:O2	33:a:1043:G:N2	2.05	0.88
33:a:1258:C:O2'	41:i:70:GLY:O	1.91	0.86
33:a:207:U:O2'	33:a:208:A:O5'	1.94	0.86
28:V:2287:C:O2'	28:V:2456:C:OP2	1.92	0.86
28:V:125:A:O2'	28:V:126:A:O4'	1.92	0.86
28:V:2610:G:OP2	28:V:2610:G:N2	2.08	0.85
28:V:2144:G:N2	28:V:2148:A:OP1	2.10	0.84
28:V:1808:U:OP2	28:V:1813:A:N6	2.09	0.84
48:p:6:ARG:NH2	48:p:28:PRO:O	2.11	0.84
18:L:21:ARG:NH1	28:V:1290:G:OP2	2.09	0.84
28:V:2135:G:N2	28:V:2212:C:O2	2.10	0.84
33:a:262:G:O3'	49:q:73:LYS:NZ	2.09	0.84
33:a:1414:G:O2'	33:a:1528:A:O2'	1.96	0.84
28:V:2386:U:O2	28:V:2390:A:N6	2.11	0.84
9:C:99:GLY:O	28:V:1546:G:O2'	1.96	0.83
28:V:1359:G:OP2	28:V:1359:G:N2	2.11	0.83
28:V:2294:U:OP2	28:V:2295:A:O2'	1.96	0.83
4:3:8:ARG:NH2	28:V:246:U:OP2	2.12	0.83
14:H:17(A):G:O2'	14:H:18:G:OP1	1.96	0.83
28:V:1968:U:OP1	28:V:2633:U:O2'	1.97	0.83
39:g:68:ASN:O	39:g:138:ARG:NH2	2.12	0.83
33:a:181:G:O2'	33:a:182:U:OP1	1.97	0.83
33:a:1135:U:O2'	33:a:1136:U:O5'	1.96	0.83
2:1:21:LYS:NZ	2:1:26:ASN:O	2.11	0.82
2:1:2:ARG:NH2	28:V:2314:C:OP2	2.11	0.82
33:a:699:G:O6	43:k:55:ARG:NH2	2.12	0.82
33:a:225:A:OP1	33:a:472:C:O2'	1.97	0.82
28:V:1364:C:OP1	28:V:1692:U:O2'	1.97	0.82
28:V:1742:G:OP2	28:V:1743:A:O2'	1.97	0.82
8:B:49:G:O2'	8:B:50:A:O5'	1.98	0.81
28:V:2361:C:OP1	29:W:84:ARG:NH1	2.13	0.81
33:a:986:G:OP2	33:a:1367:U:O2'	1.98	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:t:61:ALA:HB1	52:t:67:VAL:HG21	1.62	0.81
5:4:8:LYS:NZ	28:V:2496:C:OP1	2.14	0.81
33:a:516:C:OP2	33:a:517:U:O2'	1.99	0.81
28:V:1991:C:O2'	28:V:1992:C:O5'	1.98	0.81
45:m:85:SER:O	45:m:88:GLY:N	2.13	0.80
28:V:1243:A:O2'	28:V:1244:A:OP1	1.98	0.80
28:V:1726:G:O2'	28:V:1727:A:OP1	1.98	0.80
30:X:17:GLU:OE2	30:X:19:LYS:HD2	1.80	0.80
33:a:1132:U:O4	33:a:1133:A:N6	2.14	0.80
33:a:1170:C:O2	33:a:1184:G:N2	2.16	0.79
33:a:372:A:O2'	33:a:373:U:O5'	2.01	0.79
36:d:32:ALA:HB3	36:d:33:PRO:HD3	1.63	0.79
25:S:28:GLN:NE2	25:S:69:LEU:O	2.16	0.79
28:V:1509:C:HO2'	28:V:2731:G:HO2'	1.16	0.79
6:6:26:SER:OG	12:F:140:GLU:OE2	1.99	0.79
8:B:37:A:O2'	8:B:38:U:O5'	2.00	0.79
28:V:2890:U:OP2	28:V:2891:G:O2'	2.00	0.78
28:V:905:G:O2'	28:V:906:G:OP1	2.01	0.78
43:k:45:SER:OG	43:k:76:SER:OG	1.99	0.78
33:a:567:G:OP2	33:a:568:A:O2'	2.00	0.78
33:a:1318:G:OP1	45:m:91:HIS:NE2	2.16	0.78
28:V:2372:U:HO2'	28:V:2402:A:HO2'	1.32	0.78
33:a:582:A:O2'	33:a:583:A:O4'	1.99	0.78
28:V:698:C:O2'	28:V:699:A:O4'	2.02	0.78
28:V:2551:U:O2'	28:V:2676:U:OP1	2.02	0.78
33:a:466:G:O6	33:a:484:U:C2	2.36	0.78
33:a:1347:G:O2'	33:a:1348:A:O4'	2.00	0.78
33:a:150:A:OP2	33:a:168:C:N4	2.16	0.78
51:s:36:ARG:NH2	51:s:75:ALA:O	2.17	0.78
26:T:59:TYR:OH	28:V:1379:U:OP2	2.02	0.77
28:V:1139:G:O2'	28:V:1140:U:O4'	2.02	0.77
25:S:41:ARG:NH1	28:V:2038:G:OP1	2.18	0.77
20:N:94:ARG:NH1	28:V:2905:C:O2'	2.17	0.77
33:a:1275:G:N2	33:a:1278:A:OP2	2.16	0.77
33:a:269:U:OP2	52:t:74:ARG:NH2	2.18	0.77
28:V:458:G:OP2	28:V:2435:C:O2'	2.01	0.77
28:V:2135:G:N1	28:V:2212:C:N3	2.33	0.77
28:V:1509:C:O2'	28:V:2731:G:O2'	1.94	0.77
28:V:1695:A:HO2'	28:V:1696:G:P	2.08	0.77
16:J:31:SER:OG	16:J:32:GLU:OE2	2.02	0.77
4:3:7:HIS:NE2	28:V:254:A:OP1	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1056:A:N6	33:a:1220:U:O2	2.18	0.77
28:V:645:C:O2'	28:V:649:G:OP1	2.02	0.76
28:V:1964:G:O2'	28:V:1966:A:N1	2.17	0.76
33:a:977:C:OP2	33:a:978:A:O2'	2.02	0.76
33:a:1337:C:N4	33:a:1338:G:O6	2.19	0.76
28:V:77:U:O2'	28:V:78:U:O5'	2.04	0.76
33:a:1390:U:O2'	39:g:78:ARG:NH1	2.18	0.76
17:K:97:ARG:NE	33:a:347:C:OP2	2.19	0.76
26:T:34:ALA:HA	26:T:38:GLU:OE1	1.85	0.76
16:J:38:ARG:NH1	28:V:1053:C:OP1	2.18	0.76
28:V:619:A:OP2	28:V:2528:C:O2'	2.03	0.76
28:V:1118:C:O2'	28:V:1143:U:OP1	2.04	0.76
28:V:1033:C:O2'	28:V:1046:A:N3	2.18	0.75
28:V:1116:A:O2'	28:V:1117:G:OP1	2.04	0.75
33:a:1089:G:O2'	33:a:1090:A:O4'	2.01	0.75
11:E:41:ARG:NH2	28:V:1242:U:O2'	2.18	0.75
22:P:114:ARG:NH2	33:a:1451:A:O2'	2.20	0.75
16:J:38:ARG:NH1	28:V:1053:C:H5'	2.02	0.75
28:V:2844:A:O2'	28:V:2846:A:N7	2.17	0.75
33:a:1069:U:O3'	46:n:45:ARG:NH2	2.20	0.75
14:H:38:C:O2'	33:a:799:A:OP1	2.04	0.75
17:K:6:THR:HG22	28:V:1711:G:O2'	1.87	0.75
33:a:890:C:H5''	44:l:9:ARG:HH12	1.50	0.75
28:V:116:G:OP2	28:V:118:A:O2'	2.05	0.74
14:H:16:U:O4'	14:H:59:G:N2	2.20	0.74
47:o:34:ASP:OD1	47:o:35:SER:N	2.20	0.74
33:a:1024:A:O2'	33:a:1025:G:O4'	2.00	0.74
41:i:27:ARG:NH1	41:i:28:ILE:O	2.21	0.74
33:a:954:G:N2	33:a:1348:A:OP2	2.21	0.74
33:a:1269:G:OP1	33:a:1293:C:O2'	2.05	0.74
7:A:43:G:O2'	33:a:1508:U:OP2	2.05	0.73
28:V:745:C:O2'	28:V:781:A:N6	2.21	0.73
4:3:13:ARG:NH1	18:L:61:LEU:O	2.22	0.73
33:a:805:C:O3'	43:k:129:ARG:NH1	2.21	0.73
33:a:458:G:OP2	33:a:459:A:O2'	2.06	0.73
28:V:790:A:O2'	28:V:1704:U:OP1	2.07	0.73
12:F:75:ALA:N	14:H:56:C:O2'	2.21	0.73
33:a:343:C:O2'	33:a:1442:A:N3	2.21	0.73
28:V:160:G:O2'	28:V:168:A:N6	2.20	0.73
28:V:1087:U:O2	28:V:1160:G:O6	2.07	0.73
28:V:425:C:N4	28:V:426:G:O6	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:1090:U:O2'	28:V:1157:A:N1	2.22	0.72
28:V:1695:A:O2'	28:V:1696:G:O5'	2.07	0.72
33:a:890:C:H5''	44:l:9:ARG:HH11	1.53	0.72
28:V:1542:A:O2'	28:V:1544:C:N4	2.21	0.72
10:D:130:ARG:NH1	10:D:133:MET:SD	2.62	0.72
28:V:161:A:N3	28:V:2237:C:O2'	2.20	0.72
28:V:1843:G:OP2	28:V:1844:A:O2'	2.06	0.72
17:K:88:ARG:O	17:K:88:ARG:HG3	1.88	0.72
10:D:153:ARG:NH1	28:V:2054:C:OP1	2.22	0.72
33:a:1077:A:N1	33:a:1118:G:O2'	2.20	0.72
42:j:55:VAL:O	46:n:41:ARG:NH1	2.23	0.72
46:n:31:HIS:O	46:n:32:SER:OG	2.05	0.72
3:2:34:ARG:NH2	28:V:513:A:OP1	2.23	0.72
33:a:436:G:O2'	36:d:29:ARG:NH1	2.22	0.71
14:H:22:G:N7	14:H:46:G:N2	2.33	0.71
27:U:80:ARG:NH1	28:V:343:A:OP2	2.22	0.71
36:d:147:ASN:O	36:d:152:LYS:NZ	2.19	0.71
28:V:1765:G:N2	28:V:1768:A:OP2	2.23	0.71
28:V:2841:C:O2	28:V:2908:A:O2'	2.06	0.71
4:3:13:ARG:NH2	28:V:253:G:OP1	2.22	0.71
28:V:1525:G:O2'	28:V:1526:G:OP1	2.07	0.71
33:a:591:C:OP2	33:a:767:G:N1	2.23	0.71
25:S:8:ARG:O	25:S:9:THR:OG1	2.06	0.71
28:V:2143:A:N3	28:V:2196:U:O2'	2.19	0.71
33:a:775:A:OP2	33:a:821:G:N2	2.23	0.71
18:L:55:MET:O	18:L:60:ARG:NH2	2.24	0.71
9:C:260:ARG:NH1	28:V:1828:G:OP1	2.22	0.70
13:G:3:ARG:NH1	28:V:2778:A:OP1	2.24	0.70
24:R:68:ALA:O	24:R:89:ARG:NE	2.23	0.70
28:V:1171:G:OP2	28:V:1172:A:O2'	2.08	0.70
28:V:2159:U:O2'	28:V:2187:A:N1	2.22	0.70
13:G:96:ARG:NH1	13:G:98:SER:OG	2.25	0.70
28:V:560:A:N3	28:V:625:C:O2'	2.21	0.70
33:a:1324:U:O2'	33:a:1369:A:N3	2.24	0.70
33:a:22:U:O2'	33:a:582:A:N6	2.24	0.70
48:p:8:LYS:NZ	48:p:30:ASP:OD1	2.23	0.70
28:V:2135:G:N2	28:V:2212:C:C2	2.59	0.70
28:V:1783:C:N4	28:V:2746:G:O4'	2.25	0.70
8:B:47:C:N4	8:B:48:G:O6	2.25	0.70
10:D:145:SER:OG	28:V:2541:C:O2	2.09	0.70
6:6:14:VAL:N	6:6:22:PHE:O	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:409:C:O2'	33:a:630:A:N3	2.24	0.70
33:a:598:U:O2'	40:h:57:GLN:OE1	2.09	0.70
33:a:1036:C:N4	33:a:1046:G:O6	2.25	0.69
33:a:1087:G:N2	33:a:1090:A:OP2	2.25	0.69
24:R:67:ARG:NH2	24:R:89:ARG:O	2.25	0.69
33:a:754:U:OP1	33:a:861:U:O2'	2.09	0.69
33:a:184:G:O6	33:a:206:A:N6	2.25	0.69
52:t:48:LYS:O	52:t:52:THR:HG23	1.92	0.69
28:V:1715:C:O2	28:V:2022:U:O2'	2.09	0.69
4:3:57:ARG:NH2	18:L:51:GLU:OE1	2.25	0.69
28:V:482:C:O2'	28:V:483:C:O5'	2.09	0.69
49:q:22:THR:HG21	49:q:73:LYS:NZ	2.08	0.69
33:a:136:U:OP1	48:p:65:LYS:NZ	2.22	0.69
28:V:229:A:O2'	28:V:231:A:N1	2.26	0.69
29:W:41:GLY:N	29:W:72:ASP:OD1	2.26	0.69
33:a:1005:C:N3	33:a:1056:A:O2'	2.25	0.69
28:V:2105:U:OP2	28:V:2267:G:N2	2.25	0.69
28:V:162:A:OP2	28:V:163:U:O2'	2.10	0.68
33:a:159:A:N6	33:a:354:G:O6	2.25	0.68
33:a:466:G:O6	33:a:484:U:O2	2.11	0.68
54:v:135:ASP:O	54:v:139:CYS:HB2	1.93	0.68
28:V:1263:G:N2	28:V:1266:A:OP2	2.24	0.68
28:V:1453:A:N1	28:V:1635:G:C6	2.61	0.68
28:V:2127:U:O2'	28:V:2128:U:OP1	2.09	0.68
33:a:1016:A:O2'	33:a:1017:A:OP1	2.10	0.68
33:a:1160:A:H5''	42:j:44:THR:HG23	1.76	0.68
35:c:119:ILE:HG12	35:c:136:GLN:HG3	1.73	0.68
10:D:73:GLU:O	10:D:74:THR:HG23	1.94	0.68
28:V:528:G:O2'	28:V:553:A:N6	2.26	0.68
28:V:689:A:O2'	28:V:690:A:OP1	2.12	0.68
35:c:146:GLN:NE2	35:c:203:ARG:O	2.26	0.68
33:a:283:G:O5'	49:q:18:LYS:NZ	2.26	0.68
33:a:886:A:H1'	40:h:12:THR:HG21	1.76	0.68
8:B:53:U:O2'	8:B:54:U:O4'	2.11	0.68
28:V:2772:U:OP2	28:V:2784:C:N4	2.27	0.68
33:a:1066:U:OP1	35:c:162:ALA:N	2.27	0.68
40:h:14:ILE:O	40:h:18:ASN:ND2	2.26	0.68
33:a:475:A:O2'	33:a:476:U:O5'	2.11	0.68
33:a:1249:U:OP1	39:g:119:ARG:NH1	2.27	0.68
28:V:2818:C:O2'	28:V:2917:G:N2	2.27	0.67
14:H:55:U:O2'	14:H:56:C:OP1	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:e:36:LEU:HD21	37:e:134:ILE:HG12	1.75	0.67
17:K:28:SER:HG	28:V:2592:U:HO2'	1.40	0.67
28:V:1122:C:O2'	28:V:1123:A:N7	2.27	0.67
28:V:2404:G:N2	28:V:2407:A:OP2	2.27	0.67
33:a:1073:C:OP2	33:a:1074:G:O2'	2.10	0.67
33:a:1330:U:H4'	33:a:1331:C:OP2	1.95	0.67
28:V:2149:G:O2'	28:V:2150:G:O4'	2.09	0.67
16:J:78:HIS:ND1	16:J:79:THR:O	2.27	0.67
20:N:49:THR:HG21	28:V:2865:U:H5''	1.77	0.66
28:V:1845:A:O2'	28:V:1846:G:OP1	2.12	0.66
28:V:1972:U:O2'	28:V:1973:U:OP2	2.13	0.66
17:K:22:ILE:HG22	17:K:23:LYS:H	1.59	0.66
8:B:12:U:OP2	8:B:68:C:O2'	2.13	0.66
25:S:78:GLU:OE1	28:V:24:G:N2	2.28	0.66
33:a:455:G:O2'	33:a:456:A:O5'	2.11	0.66
33:a:968:A:O2'	33:a:995:C:O2'	2.00	0.66
33:a:1059:U:OP1	46:n:2:ALA:N	2.29	0.66
36:d:191:GLU:OE1	36:d:191:GLU:N	2.29	0.66
42:j:98:ILE:H	42:j:98:ILE:HD12	1.60	0.66
28:V:722:A:N3	28:V:2472:C:O2'	2.29	0.66
8:B:16:G:O6	8:B:17:A:N6	2.29	0.66
16:J:63:ILE:O	16:J:94:ARG:NH1	2.28	0.66
28:V:2200:A:O2'	28:V:2201:U:OP2	2.14	0.66
33:a:129:A:O2'	33:a:130:C:O5'	2.14	0.66
14:H:18:G:O2'	14:H:57:G:N2	2.29	0.65
33:a:1456:A:OP1	33:a:1457:C:N4	2.23	0.65
38:f:11:ARG:NH2	38:f:13:ASN:O	2.29	0.65
19:M:77:LYS:HE3	28:V:1002:G:H5''	1.78	0.65
25:S:15:ARG:NH2	28:V:1306:G:OP1	2.30	0.65
28:V:2009:G:O2'	28:V:2010:A:OP1	2.12	0.65
40:h:54:ASP:OD1	40:h:58:GLY:N	2.28	0.65
27:U:86:GLU:N	27:U:86:GLU:OE1	2.29	0.65
33:a:855:G:O2'	33:a:856:C:OP1	2.14	0.65
33:a:1264:G:O2'	33:a:1267:G:N3	2.27	0.65
1:O:11:MET:SD	28:V:16:G:O2'	2.54	0.65
33:a:1170:C:N3	33:a:1184:G:N1	2.45	0.65
50:r:42:GLY:O	50:r:68:ARG:NH2	2.29	0.65
44:l:59:ASN:OD1	44:l:60:SER:N	2.30	0.65
24:R:57:THR:O	24:R:101:ASN:ND2	2.29	0.65
26:T:35:ASN:OD1	26:T:36:LYS:N	2.30	0.65
9:C:13:ARG:NH1	9:C:16:MET:SD	2.71	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:2072:C:OP1	28:V:2806:G:O2'	2.15	0.64
28:V:2825:C:N3	28:V:2826:A:N6	2.45	0.64
33:a:518:A:O2'	33:a:519:A:O4'	2.08	0.64
28:V:2244:G:HO2'	28:V:2245:G:P	2.19	0.64
49:q:13:ARG:NH1	49:q:14:VAL:O	2.30	0.64
28:V:226:A:O2'	28:V:467:C:O2	2.15	0.64
28:V:76:C:O2'	28:V:77:U:OP2	2.14	0.64
28:V:2651:C:O2'	28:V:2850:G:N7	2.30	0.64
24:R:89:ARG:NH2	28:V:1263:G:OP2	2.31	0.64
28:V:688:G:O2'	28:V:2378:G:O2'	2.16	0.64
47:o:5:GLN:O	47:o:9:ASN:OD1	2.14	0.64
28:V:482:C:O2'	28:V:483:C:O4'	2.16	0.64
28:V:2584:U:O2'	28:V:2585:C:O4'	2.15	0.64
28:V:344:G:O2'	28:V:346:G:OP2	2.12	0.63
37:e:132:THR:OG1	37:e:135:ASN:OD1	2.12	0.63
30:X:67:SER:O	30:X:71:THR:HG23	1.98	0.63
32:Z:6:ILE:HG23	32:Z:54:VAL:HG13	1.79	0.63
8:B:30:C:N4	8:B:31:G:O6	2.31	0.63
28:V:1304:G:OP2	28:V:1305:A:O2'	2.14	0.63
28:V:2244:G:O2'	28:V:2245:G:O5'	2.15	0.63
33:a:302:C:OP1	33:a:619:G:O2'	2.08	0.63
17:K:107:ARG:NH2	22:P:34:GLU:OE1	2.31	0.63
28:V:1314:A:N1	28:V:1334:C:O2'	2.30	0.63
33:a:1463:A:O2'	33:a:1464:G:O5'	2.12	0.63
28:V:1310:C:O2'	28:V:1693:C:OP2	2.14	0.63
9:C:69:ARG:O	9:C:189:ARG:NH1	2.32	0.63
17:K:31:LYS:NZ	28:V:2025:C:OP1	2.25	0.63
50:r:37:PHE:HD1	50:r:60:LEU:HD21	1.63	0.63
7:A:44:A:OP1	33:a:1508:U:O2'	2.14	0.63
32:Z:12:VAL:HG22	32:Z:20:ARG:HD2	1.80	0.63
33:a:1313:G:H21	33:a:1342:A:H62	1.45	0.63
50:r:41:ARG:O	50:r:77:SER:OG	2.11	0.63
28:V:177:G:O2'	28:V:178:A:O5'	2.16	0.62
28:V:2847:G:O2'	28:V:2849:U:OP2	2.17	0.62
10:D:124:LYS:NZ	28:V:2028:C:OP1	2.31	0.62
13:G:3:ARG:NH1	28:V:2780:G:OP2	2.32	0.62
28:V:342:A:O2'	28:V:343:A:O4'	2.15	0.62
33:a:1106:C:O2	33:a:1179:A:O2'	2.17	0.62
1:0:6:ARG:NH1	28:V:2048:U:OP2	2.32	0.62
28:V:675:C:O2	28:V:685:U:O2'	2.17	0.62
33:a:1259:A:OP1	41:i:68:HIS:ND1	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:33:LYS:NZ	28:V:2772:U:OP1	2.33	0.62
21:O:30:ARG:NH1	21:O:96:ASP:OD2	2.32	0.62
33:a:587:C:O2'	33:a:737:A:N3	2.31	0.62
33:a:304:U:O2'	33:a:565:C:O2	2.17	0.62
33:a:1088:U:O2'	33:a:1089:G:OP1	2.17	0.62
33:a:530:G:O2'	33:a:545:C:O2'	2.18	0.62
33:a:774:G:H1	33:a:821:G:HO2'	1.48	0.62
44:l:5:ASN:O	44:l:9:ARG:HG2	1.98	0.62
23:Q:92:ARG:O	23:Q:95:LEU:N	2.33	0.61
28:V:2148:A:N6	28:V:2199:G:N7	2.48	0.61
28:V:1103:A:N6	28:V:1133:G:OP2	2.33	0.61
33:a:1065:A:O2'	35:c:159:ALA:O	2.17	0.61
43:k:31:ASN:OD1	43:k:32:THR:N	2.34	0.61
30:X:72:LEU:O	30:X:75:LEU:HD22	2.00	0.61
28:V:1474:C:N4	28:V:1618:A:OP2	2.26	0.61
13:G:20:ASN:OD1	13:G:24:THR:OG1	2.19	0.61
3:2:14:LYS:NZ	28:V:818:G:OP1	2.30	0.61
40:h:8:ALA:O	40:h:12:THR:HG23	2.01	0.61
28:V:1971:C:OP2	28:V:1972:U:O2'	2.09	0.61
28:V:2057:U:H2'	28:V:2058:G:C8	2.35	0.61
8:B:48:G:O2'	8:B:49:G:O5'	2.18	0.61
11:E:57:VAL:HG11	11:E:79:ARG:HB3	1.82	0.61
28:V:1216:C:N3	28:V:1220:G:N1	2.44	0.61
28:V:2169:G:N2	28:V:2181:C:O2	2.33	0.61
28:V:1380:U:OP2	28:V:1433:U:O2'	2.16	0.61
33:a:1455:A:O2'	33:a:1456:A:O4'	2.16	0.61
42:j:44:THR:HG22	42:j:70:HIS:HA	1.82	0.60
8:B:46:A:OP1	21:O:35:ARG:NH1	2.34	0.60
18:L:30:THR:OG1	28:V:1231:G:OP1	2.19	0.60
20:N:19:ASP:OD1	20:N:67:ARG:NH1	2.34	0.60
31:Y:6:ILE:O	31:Y:60:ARG:NH2	2.34	0.60
6:6:34:GLU:OE1	45:m:57:ARG:NE	2.33	0.60
33:a:541:A:N6	33:a:1215:G:O2'	2.35	0.60
33:a:1187:G:N2	33:a:1190:G:OP2	2.34	0.60
2:1:25:ASN:ND2	28:V:2314:C:OP1	2.34	0.60
28:V:2365:A:H61	29:W:51:THR:HG21	1.67	0.60
33:a:224:U:O2'	33:a:477:A:N6	2.35	0.60
5:4:20:LYS:NZ	28:V:2770:A:OP1	2.35	0.60
28:V:1074:A:N3	28:V:2515:G:O2'	2.31	0.60
17:K:3:GLN:NE2	28:V:2024:U:O2	2.35	0.60
28:V:2162:G:O2'	28:V:2187:A:N1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1413:C:O2	33:a:1529:A:O2'	2.19	0.60
53:u:60:GLU:N	53:u:60:GLU:OE1	2.34	0.60
8:B:49:G:HO2'	8:B:50:A:C5'	2.11	0.60
28:V:747:G:O2'	28:V:1677:A:N3	2.28	0.60
28:V:500:A:N3	28:V:504:A:O2'	2.35	0.59
33:a:855:G:OP2	50:r:19:THR:OG1	2.08	0.59
16:J:24:LYS:N	16:J:64:GLU:OE2	2.35	0.59
33:a:332:G:N1	33:a:335:A:OP2	2.34	0.59
33:a:977:C:P	33:a:978:A:HO2'	2.24	0.59
28:V:559:A:O2'	28:V:1257:C:OP1	2.20	0.59
28:V:689:A:N6	28:V:2398:A:O2'	2.26	0.59
48:p:2:ALA:N	48:p:24:ASP:OD1	2.35	0.59
53:u:39:LEU:H	53:u:39:LEU:HD23	1.67	0.59
13:G:108:VAL:HG13	13:G:109:GLY:H	1.68	0.59
18:L:41:ARG:NH2	28:V:854:U:OP2	2.36	0.59
28:V:2685:U:O2	28:V:2694:A:N7	2.35	0.59
22:P:49:LYS:NZ	28:V:2714:G:OP1	2.35	0.59
22:P:92:VAL:HG21	22:P:97:LEU:HD21	1.85	0.59
33:a:387:C:N4	33:a:388:G:O6	2.35	0.59
18:L:18:ARG:NH2	28:V:1290:G:N7	2.50	0.59
28:V:441:C:O2'	28:V:442:C:OP1	2.17	0.59
28:V:2717:G:N1	28:V:2749:U:OP2	2.31	0.59
33:a:181:G:HO2'	33:a:182:U:P	2.22	0.59
33:a:1330:U:OP2	33:a:1331:C:H2'	2.03	0.59
44:l:69:ARG:NH1	44:l:75:GLU:OE1	2.36	0.59
28:V:2806:G:OP1	28:V:2810:A:O2'	2.16	0.58
33:a:1248:A:O2'	39:g:114:LYS:O	2.21	0.58
36:d:19:LEU:N	36:d:25:GLU:OE2	2.35	0.58
28:V:1473:A:N6	28:V:1619:A:OP2	2.32	0.58
40:h:93:GLU:N	40:h:93:GLU:OE1	2.36	0.58
33:a:641:G:O2'	33:a:642:U:O5'	2.18	0.58
41:i:70:GLY:O	41:i:75:GLN:OE1	2.21	0.58
27:U:51:ASN:O	27:U:53:GLN:N	2.35	0.58
28:V:88:G:O2'	28:V:89:U:OP1	2.21	0.58
28:V:1109:G:O2'	28:V:1110:C:O5'	2.20	0.58
4:3:32:LEU:HD12	28:V:2421:A:OP1	2.04	0.58
8:B:34:C:N4	8:B:47:C:O2	2.35	0.58
28:V:2535:U:OP2	28:V:2605:G:N1	2.35	0.58
9:C:150:LYS:NZ	28:V:1830:G:OP2	2.36	0.58
20:N:49:THR:HG21	28:V:2865:U:C5'	2.34	0.58
12:F:135:GLN:O	12:F:141:ILE:HG21	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:2605:G:O2'	28:V:2608:C:OP2	2.14	0.58
12:F:161:ASN:N	12:F:165:GLU:OE2	2.37	0.58
28:V:1469:G:HO2'	28:V:1545:C:HO2'	1.46	0.58
33:a:1186:G:OP1	41:i:99:LYS:NZ	2.35	0.58
22:P:51:ARG:NH1	28:V:2713:U:OP2	2.36	0.58
33:a:789:G:N1	33:a:810:U:OP2	2.37	0.57
38:f:51:GLU:OE1	38:f:51:GLU:N	2.36	0.57
28:V:248:G:O2'	28:V:431:A:N1	2.37	0.57
28:V:1867:C:N4	28:V:1928:A:O4'	2.38	0.57
28:V:2517:A:N6	28:V:2518:G:O6	2.36	0.57
33:a:492:C:OP2	33:a:493:G:O2'	2.11	0.57
24:R:31:GLU:N	24:R:31:GLU:OE1	2.38	0.57
47:o:74:ASP:OD2	47:o:74:ASP:N	2.38	0.57
53:u:33:LEU:HD12	53:u:33:LEU:O	2.03	0.57
33:a:993:A:H2	33:a:1231:G:H22	1.53	0.57
35:c:11:ARG:NH2	35:c:176:THR:O	2.37	0.57
11:E:127:GLU:N	11:E:127:GLU:OE1	2.37	0.57
28:V:573:C:N4	28:V:2808:U:OP2	2.37	0.57
28:V:275:A:H62	28:V:296:G:N2	2.03	0.57
28:V:1265:A:C6	28:V:1266:A:N1	2.73	0.57
24:R:84:LYS:NZ	28:V:862:U:OP1	2.37	0.57
33:a:596:G:O2'	33:a:597:G:OP2	2.19	0.57
8:B:41:C:O2'	8:B:43:A:N7	2.35	0.57
37:e:164:LEU:O	40:h:116:LYS:NZ	2.21	0.57
28:V:1158:G:O2'	28:V:1159:U:O5'	2.22	0.56
33:a:37:G:O2'	44:l:128:SER:O	2.17	0.56
33:a:1088:U:HO2'	33:a:1089:G:P	2.27	0.56
14:H:7:G:O2'	14:H:49:G:O4'	2.22	0.56
28:V:971:A:O2'	28:V:972:U:O4'	2.22	0.56
24:R:81:ASN:ND2	28:V:610:U:OP1	2.37	0.56
28:V:648:G:O2'	28:V:649:G:OP2	2.20	0.56
28:V:1065:U:OP1	28:V:1081:U:O2'	2.22	0.56
28:V:1159:U:O2'	28:V:1160:G:OP2	2.20	0.56
31:Y:13:GLU:N	31:Y:13:GLU:OE1	2.37	0.56
33:a:473:G:N2	33:a:476:U:OP2	2.38	0.56
33:a:569:A:C6	37:e:128:LEU:HD13	2.40	0.56
33:a:790:A:OP2	33:a:809:G:N1	2.36	0.56
50:r:14:LYS:NZ	50:r:48:ARG:O	2.35	0.56
40:h:53:GLU:N	40:h:53:GLU:OE1	2.39	0.56
7:A:47:G:O6	33:a:1503:A:N6	2.38	0.56
9:C:182:ARG:NH1	28:V:1829:C:OP1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:563:U:O2'	33:a:564:C:OP1	2.23	0.56
36:d:14:ARG:HA	36:d:32:ALA:HB1	1.87	0.56
5:4:19:ARG:NE	28:V:2785:U:OP2	2.36	0.56
9:C:108:LYS:N	9:C:194:GLN:O	2.36	0.56
28:V:840:A:OP2	28:V:2100:A:O2'	2.23	0.56
33:a:422:A:H62	33:a:439:A:H1'	1.71	0.56
33:a:1526:G:N2	33:a:1529:A:OP2	2.27	0.56
28:V:1425:C:O2'	28:V:1426:A:OP2	2.21	0.56
28:V:2534:G:O2'	28:V:2535:U:O5'	2.23	0.56
34:b:2:SER:HG	34:b:22:SER:CB	2.17	0.56
12:F:73:SER:OG	14:H:56:C:O4'	2.21	0.56
17:K:8:LEU:HD13	17:K:84:CYS:SG	2.46	0.56
8:B:31:G:O2'	8:B:32:U:OP1	2.23	0.56
8:B:49:G:HO2'	8:B:50:A:P	2.29	0.56
16:J:40:LYS:NZ	28:V:1055:A:OP2	2.28	0.56
28:V:85:G:O2'	28:V:86:C:OP2	2.20	0.56
28:V:529:C:O2'	28:V:543:A:N1	2.37	0.56
28:V:1898:G:N2	28:V:1901:A:OP2	2.31	0.56
33:a:261:U:O4'	33:a:283:G:N2	2.30	0.55
4:3:8:ARG:NH1	28:V:247:A:OP2	2.39	0.55
33:a:330:C:N3	33:a:340:G:N2	2.52	0.55
37:e:36:LEU:HD21	37:e:134:ILE:CG1	2.35	0.55
26:T:31:ASP:OD1	26:T:32:VAL:N	2.40	0.55
28:V:252:C:OP2	28:V:2423:C:O2'	2.20	0.55
28:V:976:U:O2'	32:Z:25:THR:O	2.20	0.55
33:a:1168:U:O4'	33:a:1191:G:N2	2.39	0.55
54:w:238:GLN:HA	54:w:241:LYS:HD2	1.87	0.55
4:3:57:ARG:NH1	28:V:880:C:O2'	2.38	0.55
28:V:1116:A:HO2'	28:V:1117:G:P	2.28	0.55
28:V:1244:A:O2'	28:V:1245:G:OP1	2.23	0.55
28:V:290:U:O2'	28:V:291:C:O5'	2.22	0.55
33:a:329:A:O2'	33:a:330:C:O4'	2.16	0.55
9:C:44:ASN:ND2	28:V:1835:C:O2	2.40	0.55
38:f:52:ILE:HG22	38:f:53:ASN:H	1.71	0.55
51:s:58:VAL:HG13	51:s:58:VAL:O	2.07	0.55
28:V:421:A:C8	28:V:422:C:C6	2.95	0.55
28:V:1828:G:N2	28:V:1848:A:OP2	2.36	0.55
54:w:75:LEU:HD11	54:w:263:THR:HA	1.88	0.55
33:a:701:U:OP2	43:k:30:ASN:ND2	2.39	0.55
19:M:42:ILE:HD12	19:M:97:VAL:HG21	1.89	0.55
28:V:1713:A:O2'	28:V:1719:G:N7	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:2320:U:O2'	28:V:2403:C:O2	2.24	0.55
28:V:2593:A:O2'	28:V:2594:A:O4'	2.21	0.55
50:r:26:ILE:HD11	50:r:60:LEU:HD12	1.89	0.55
8:B:48:G:O2'	8:B:49:G:P	2.65	0.55
28:V:18:C:O2'	28:V:598:U:OP1	2.25	0.55
28:V:2119:A:N6	28:V:2259:G:O6	2.40	0.55
25:S:77:ASP:OD2	25:S:78:GLU:N	2.40	0.54
33:a:986:G:N2	33:a:1372:A:OP2	2.40	0.54
13:G:108:VAL:HG13	13:G:109:GLY:N	2.22	0.54
28:V:217:G:O2'	28:V:218:G:O5'	2.24	0.54
28:V:1068:G:N2	28:V:1069:U:O4	2.30	0.54
33:a:445:U:O4	33:a:504:A:N7	2.40	0.54
33:a:848:G:O2'	33:a:849:G:P	2.65	0.54
33:a:1018:U:O2'	33:a:1019:C:P	2.65	0.54
41:i:93:GLU:OE1	41:i:93:GLU:N	2.38	0.54
4:3:18:GLY:O	4:3:19:SER:OG	2.20	0.54
28:V:309:U:H3'	28:V:310:C:H5''	1.88	0.54
28:V:2163:A:N3	28:V:2188:G:O2'	2.39	0.54
54:w:116:ILE:HB	54:w:119:ILE:HB	1.89	0.54
21:O:90:ILE:O	21:O:91:SER:OG	2.17	0.54
28:V:524:A:N6	28:V:547:A:OP1	2.41	0.54
28:V:1126:A:O2'	28:V:1127:U:OP2	2.23	0.54
33:a:351:U:O2'	33:a:354:G:O6	2.22	0.54
33:a:1298:A:N1	33:a:1380:G:O2'	2.37	0.54
33:a:1356:G:N7	41:i:107:ASP:CG	2.64	0.54
28:V:688:G:N2	28:V:691:U:OP2	2.28	0.54
28:V:859:C:O2'	28:V:1266:A:O2'	2.24	0.54
21:O:19:ARG:NH1	21:O:47:ASP:OD2	2.41	0.54
33:a:70:G:H22	33:a:99:A:H62	1.54	0.54
7:A:31:A:C6	7:A:32:U:C4	2.94	0.54
33:a:665:G:O2'	47:o:28:GLN:NE2	2.41	0.54
9:C:243:ARG:NH1	28:V:2268:G:OP1	2.41	0.54
28:V:689:A:HO2'	28:V:690:A:P	2.29	0.54
28:V:1139:G:O2'	28:V:1140:U:O5'	2.25	0.54
34:b:2:SER:OG	34:b:22:SER:OG	2.03	0.54
10:D:9:LYS:HB2	10:D:200:ILE:HD13	1.90	0.54
28:V:1525:G:O2'	28:V:1526:G:P	2.66	0.54
28:V:1530:G:O2'	28:V:1531:G:OP1	2.24	0.54
28:V:2182:G:H2'	28:V:2183:G:O4'	2.08	0.54
36:d:13:ARG:NE	36:d:32:ALA:O	2.41	0.54
37:e:94:ILE:HD11	37:e:136:MET:SD	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:168:GLU:N	9:C:168:GLU:OE1	2.41	0.53
16:J:38:ARG:HH12	28:V:1053:C:H5'	1.72	0.53
28:V:1158:G:HO2'	28:V:1159:U:C5'	2.20	0.53
28:V:2135:G:C2	28:V:2212:C:O2	2.61	0.53
33:a:1499:G:O2'	33:a:1500:U:P	2.66	0.53
37:e:95:LEU:HD23	37:e:128:LEU:HD11	1.90	0.53
9:C:243:ARG:NH2	28:V:2104:U:OP1	2.39	0.53
28:V:285:U:H1'	30:X:46:ALA:HB2	1.90	0.53
47:o:71:ARG:NH2	47:o:78:TYR:OH	2.39	0.53
8:B:31:G:O2'	8:B:32:U:P	2.66	0.53
28:V:446:G:OP2	53:u:55:LYS:NZ	2.38	0.53
28:V:1269:A:O2'	28:V:1270:C:OP1	2.26	0.53
28:V:2022:U:C2'	28:V:2023:C:OP1	2.57	0.53
38:f:42:ASP:OD1	38:f:61:GLN:OE1	2.25	0.53
18:L:16:ARG:NH2	28:V:633:U:OP2	2.39	0.53
21:O:38:LYS:O	21:O:68:THR:HG22	2.09	0.53
28:V:775:G:H3'	28:V:776:G:H5'	1.89	0.53
30:X:35:LEU:HD23	30:X:35:LEU:O	2.08	0.53
28:V:27:G:N2	28:V:559:A:OP2	2.23	0.53
28:V:1339:A:H4'	28:V:1340:A:H5'	1.88	0.53
28:V:2043:A:O2'	28:V:2044:A:O4'	2.21	0.53
12:F:67:VAL:O	12:F:67:VAL:HG13	2.08	0.53
15:I:87:UNK:HA	15:I:88:UNK:C	2.38	0.53
28:V:1605:C:OP2	28:V:1606:A:O2'	2.16	0.53
33:a:1330:U:O4	51:s:36:ARG:NH2	2.34	0.53
33:a:1462:U:O2'	33:a:1463:A:OP1	2.26	0.53
35:c:47:SER:O	35:c:121:ARG:NH2	2.42	0.53
54:w:56:ILE:HA	54:w:109:MET:HE1	1.90	0.53
4:3:46:LYS:NZ	28:V:2379:C:OP1	2.37	0.53
28:V:510:G:N2	28:V:513:A:OP2	2.39	0.53
33:a:563:U:O2'	33:a:564:C:P	2.67	0.53
33:a:757:A:HO2'	33:a:758:A:P	2.31	0.53
16:J:32:GLU:OE2	16:J:32:GLU:N	2.42	0.53
28:V:2135:G:C2	28:V:2212:C:C2	2.97	0.53
28:V:2166:C:H2'	28:V:2167:C:C1'	2.39	0.53
28:V:2308:G:N7	29:W:22:ARG:NH2	2.56	0.53
33:a:1025:G:O2'	33:a:1026:A:O4'	2.24	0.53
28:V:25:U:C2'	28:V:26:G:O5'	2.57	0.53
28:V:84:A:N1	28:V:98:U:O2'	2.42	0.53
28:V:1542:A:O2'	28:V:1543:U:OP2	2.25	0.53
33:a:1032:C:O2'	33:a:1033:G:OP1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:v:26:LEU:HB3	54:v:274:GLN:HG3	1.91	0.52
28:V:1820:A:N6	28:V:1857:G:O2'	2.40	0.52
33:a:113:G:H4'	33:a:114:A:O5'	2.09	0.52
33:a:699:G:OP2	43:k:31:ASN:ND2	2.40	0.52
33:a:1246:C:O2'	33:a:1309:G:N2	2.38	0.52
48:p:24:ASP:OD1	48:p:25:SER:N	2.43	0.52
33:a:855:G:HO2'	33:a:856:C:P	2.32	0.52
33:a:1330:U:H2'	33:a:1331:C:C5	2.45	0.52
28:V:874:U:O2'	28:V:2097:U:N3	2.42	0.52
49:q:22:THR:HG22	49:q:49:HIS:HA	1.91	0.52
50:r:27:ASP:O	50:r:29:LYS:N	2.43	0.52
28:V:2228:A:C8	28:V:2229:C:C5	2.97	0.52
33:a:1269:G:O2'	33:a:1284:A:N6	2.43	0.52
33:a:1315:A:N6	33:a:1340:G:O2'	2.42	0.52
8:B:31:G:HO2'	8:B:32:U:P	2.33	0.52
16:J:38:ARG:NH1	28:V:1053:C:C5'	2.73	0.52
28:V:136:C:N4	28:V:137:G:O6	2.43	0.52
28:V:187:C:N3	28:V:216:A:N6	2.58	0.52
28:V:421:A:C2	28:V:448:A:C4	2.97	0.52
28:V:1530:G:O2'	28:V:1531:G:P	2.68	0.52
17:K:22:ILE:HD11	17:K:42:THR:HG23	1.91	0.52
28:V:905:G:O2'	28:V:2297:A:O2'	2.27	0.52
28:V:2079:C:H2'	28:V:2080:A:O4'	2.09	0.52
28:V:2254:A:H1'	28:V:2255:C:OP2	2.10	0.52
33:a:1499:G:O2'	33:a:1500:U:OP1	2.27	0.52
54:w:370:ALA:HB3	54:w:372:PHE:CE2	2.45	0.52
8:B:6:U:OP1	21:O:11:ARG:NH1	2.42	0.52
8:B:49:G:H4'	8:B:50:A:OP1	2.10	0.52
18:L:131:SER:OG	28:V:683:A:OP1	2.21	0.52
20:N:22:THR:HG22	20:N:66:ILE:HG23	1.91	0.52
27:U:72:ASP:OD2	27:U:97:SER:OG	2.24	0.52
28:V:200:A:N6	28:V:2459:A:O2'	2.40	0.52
28:V:746:A:N3	28:V:1678:G:O2'	2.38	0.52
29:W:80:PHE:N	29:W:84:ARG:O	2.36	0.52
33:a:1406:C:OP2	37:e:29:ARG:NH2	2.43	0.52
49:q:22:THR:HG21	49:q:73:LYS:CE	2.39	0.52
11:E:53:ASN:ND2	28:V:848:G:O6	2.41	0.52
28:V:557:U:O2'	28:V:1255:G:N2	2.43	0.52
28:V:1882:A:O2'	28:V:1883:A:P	2.68	0.52
33:a:855:G:O2'	33:a:856:C:P	2.68	0.52
33:a:1013:G:N2	33:a:1014:A:O2'	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:c:23:TYR:O	35:c:58:ARG:NH2	2.44	0.52
33:a:487:C:O2'	33:a:488:U:OP1	2.25	0.51
39:g:74:GLU:O	39:g:89:VAL:N	2.43	0.51
24:R:27:ALA:O	24:R:65:GLN:NE2	2.44	0.51
28:V:2092:C:N4	28:V:2530:C:O2	2.42	0.51
35:c:148:VAL:HG12	35:c:201:ILE:HG23	1.91	0.51
28:V:1565:U:HO2'	28:V:1566:G:P	2.33	0.51
28:V:2021:G:N2	28:V:2025:C:O2'	2.44	0.51
28:V:2754:A:O2'	28:V:2755:U:OP2	2.23	0.51
43:k:38:ASP:OD1	43:k:42:ASN:N	2.43	0.51
28:V:966:U:C2	28:V:967:G:C8	2.99	0.51
28:V:2278:U:N3	28:V:2282:G:OP2	2.42	0.51
28:V:2606:A:O4'	28:V:2641:C:N4	2.43	0.51
33:a:739:G:O2'	33:a:775:A:O4'	2.26	0.51
33:a:939:G:O6	33:a:1398:C:N4	2.43	0.51
54:v:71:ILE:HG12	54:v:95:LEU:HD22	1.92	0.51
7:A:35:A:C5	7:A:36:U:C5	2.99	0.51
28:V:1177:G:O2'	28:V:2054:C:O2'	2.27	0.51
33:a:37:G:H21	44:l:128:SER:HB2	1.75	0.51
33:a:372:A:H4'	33:a:373:U:OP1	2.11	0.51
33:a:1187:G:O2'	33:a:1189:A:N7	2.38	0.51
39:g:131:THR:O	39:g:131:THR:HG23	2.11	0.51
7:A:35:A:C4	7:A:36:U:C6	2.99	0.51
15:I:87:UNK:N	28:V:2091:A:N1	2.58	0.51
17:K:50:GLY:O	17:K:53:LYS:NZ	2.41	0.51
28:V:1017:C:O2'	28:V:1029:A:N3	2.41	0.51
28:V:1757:G:O2'	28:V:1758:U:O5'	2.24	0.51
49:q:71:ALA:O	49:q:72:THR:OG1	2.25	0.51
6:6:57:ASP:OD1	6:6:58:ARG:N	2.44	0.51
25:S:98:LYS:NZ	28:V:1362:G:OP1	2.44	0.51
28:V:1371:G:N7	28:V:1654:A:O2'	2.37	0.51
30:X:111:ASP:OD1	30:X:112:LYS:N	2.44	0.51
16:J:13:GLU:N	16:J:13:GLU:OE2	2.44	0.51
28:V:1565:U:O2'	28:V:1566:G:P	2.68	0.51
30:X:97:GLN:OE1	30:X:97:GLN:N	2.42	0.51
33:a:965:U:O2'	33:a:966:U:P	2.68	0.51
45:m:87:ARG:O	45:m:91:HIS:ND1	2.39	0.51
28:V:1529:G:O2'	28:V:1530:G:P	2.69	0.51
33:a:896:G:O6	33:a:922:C:N4	2.44	0.51
33:a:1148:G:H4'	33:a:1149:U:O5'	2.11	0.51
10:D:163:ARG:NH2	28:V:2850:G:O6	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:J:79:THR:OG1	16:J:80:GLN:N	2.42	0.51
28:V:140:A:HO2'	28:V:1447:C:HO2'	1.59	0.51
28:V:1914:A:O2'	28:V:1915:U:OP1	2.26	0.51
28:V:2823:C:H2'	28:V:2824:G:H8	1.76	0.51
54:v:391:THR:HG22	54:v:395:HIS:CD2	2.46	0.51
19:M:77:LYS:HE3	28:V:1002:G:C5'	2.42	0.50
28:V:39:C:O2'	28:V:659:A:N1	2.41	0.50
28:V:343:A:O2'	28:V:362:C:O2	2.24	0.50
33:a:662:U:O4	40:h:57:GLN:NE2	2.40	0.50
28:V:393:U:O2	28:V:394:U:C5	2.64	0.50
28:V:1524:A:N6	28:V:1561:G:O2'	2.43	0.50
33:a:757:A:O2'	33:a:758:A:O5'	2.25	0.50
48:p:47:ALA:O	48:p:48:GLU:HG2	2.12	0.50
33:a:584:G:O2'	33:a:830:G:OP2	2.20	0.50
52:t:62:VAL:HG22	52:t:67:VAL:O	2.10	0.50
12:F:112:ARG:NH2	12:F:134:GLU:OE2	2.44	0.50
28:V:987:A:N3	28:V:1231:G:O2'	2.44	0.50
28:V:1027:A:O2'	28:V:2065:C:O2'	2.25	0.50
28:V:2824:G:H22	28:V:2826:A:H3'	1.76	0.50
23:Q:98:LEU:HD21	24:R:13:LYS:CE	2.42	0.50
28:V:1002:G:N2	28:V:1006:A:OP2	2.44	0.50
4:3:12:LYS:NZ	28:V:252:C:O2	2.44	0.50
9:C:123:ASP:O	9:C:128:ASN:ND2	2.42	0.50
28:V:1929:A:O2'	28:V:1930:A:OP1	2.25	0.50
28:V:2229:C:O2'	28:V:2256:A:N1	2.44	0.50
31:Y:28:LEU:HD13	31:Y:37:LEU:HD11	1.94	0.50
33:a:946:C:O2'	33:a:1391:C:N3	2.44	0.50
28:V:88:G:O2'	28:V:89:U:P	2.69	0.50
33:a:41:G:N3	33:a:412:G:N2	2.58	0.50
54:v:144:GLY:HA2	54:v:147:LEU:HD12	1.94	0.50
54:v:234:ASN:HA	54:v:237:LEU:HD12	1.93	0.50
8:B:37:A:C2	8:B:42:G:C2	3.00	0.50
34:b:19:PHE:O	34:b:23:VAL:HG13	2.12	0.50
2:1:29:ARG:NH1	2:1:48:THR:O	2.44	0.50
27:U:33:VAL:CG2	27:U:65:VAL:HG22	2.41	0.50
28:V:588:C:N4	28:V:596:G:O6	2.45	0.50
33:a:790:A:O2'	33:a:1532:U:O2	2.30	0.50
33:a:843:U:O4	33:a:844:A:N6	2.45	0.50
2:1:5:ILE:N	2:1:19:SER:O	2.42	0.49
22:P:75:PRO:HB2	22:P:78:THR:HG23	1.94	0.49
28:V:30:G:O2'	28:V:1254:A:N3	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1148:G:H1'	33:a:1149:U:OP2	2.12	0.49
7:A:50:C:N4	33:a:1406:C:C2'	2.75	0.49
28:V:545:U:H2'	28:V:546:G:O4'	2.12	0.49
30:X:64:GLN:O	30:X:68:LEU:HD23	2.11	0.49
32:Z:52:HIS:ND1	32:Z:53:LEU:HD12	2.27	0.49
33:a:207:U:HO2'	33:a:208:A:P	2.31	0.49
19:M:28:HIS:O	19:M:134:ARG:NH2	2.43	0.49
28:V:644:G:N2	28:V:649:G:O3'	2.46	0.49
33:a:39:U:O2'	33:a:556:A:N1	2.44	0.49
33:a:270:A:O2'	52:t:70:ASN:OD1	2.18	0.49
43:k:28:THR:OG1	43:k:31:ASN:O	2.24	0.49
23:Q:48:ARG:NH2	28:V:604:C:O2	2.46	0.49
28:V:2882:G:N2	28:V:2885:A:OP2	2.40	0.49
5:4:35:LYS:NZ	28:V:2771:G:OP1	2.36	0.49
13:G:59:GLN:OE1	13:G:61:GLU:N	2.45	0.49
33:a:848:G:HO2'	33:a:849:G:P	2.35	0.49
1:0:27:MET:HE1	25:S:35:ILE:HG13	1.93	0.49
13:G:78:GLU:OE1	13:G:82:LYS:NZ	2.44	0.49
15:I:84:UNK:O	15:I:85:UNK:C	2.61	0.49
20:N:13:ARG:NH1	28:V:2719:A:OP2	2.45	0.49
28:V:285:U:C2	28:V:289:C:H1'	2.46	0.49
28:V:2125:U:H2'	28:V:2126:G:O4'	2.13	0.49
33:a:358:G:O2'	33:a:359:G:O4'	2.24	0.49
46:n:46:GLU:OE2	46:n:46:GLU:HA	2.11	0.49
22:P:14:ARG:NH1	22:P:78:THR:O	2.43	0.49
28:V:282:G:O2'	28:V:283:G:O5'	2.31	0.49
28:V:902:G:N1	28:V:970:A:C2	2.80	0.49
28:V:2385:C:H2'	28:V:2386:U:O4'	2.13	0.49
28:V:2716:U:H2'	28:V:2717:G:O4'	2.13	0.49
39:g:75:VAL:O	39:g:75:VAL:HG13	2.12	0.49
19:M:45:ARG:NH2	28:V:2513:G:OP1	2.41	0.49
28:V:432:C:O2'	28:V:435:G:N2	2.46	0.49
30:X:53:LYS:HE3	30:X:57:GLU:OE2	2.13	0.49
33:a:259:G:N2	33:a:261:U:O4	2.46	0.49
33:a:455:G:O2'	33:a:456:A:P	2.70	0.49
33:a:820:C:O2'	33:a:911:A:N1	2.46	0.49
7:A:33:A:C5	34:b:13:GLU:HB3	2.48	0.49
9:C:264:ASN:OD1	9:C:265:LYS:N	2.46	0.49
14:H:54:U:O4	14:H:58:A:N7	2.46	0.49
28:V:482:C:O2'	28:V:483:C:C5'	2.61	0.49
28:V:2398:A:N6	28:V:2399:G:O6	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:885:C:O2'	40:h:15:ARG:NH1	2.45	0.49
33:a:1450:G:O2'	33:a:1470:A:N6	2.42	0.49
38:f:48:LEU:HD13	38:f:52:ILE:HD11	1.94	0.49
39:g:12:VAL:HG13	39:g:12:VAL:O	2.12	0.49
28:V:1713:A:N3	28:V:1715:C:N4	2.60	0.49
28:V:2170:A:H61	28:V:2179:U:H3	1.61	0.49
38:f:48:LEU:HD13	38:f:52:ILE:CD1	2.43	0.49
54:w:99:VAL:HG13	54:w:126:LEU:HD22	1.95	0.49
27:U:56:ILE:O	27:U:56:ILE:HG22	2.13	0.48
28:V:1876:A:O2'	28:V:1877:A:N7	2.45	0.48
28:V:2331:U:H5'	54:w:203:GLN:H	1.78	0.48
12:F:49:ALA:O	12:F:52:SER:OG	2.26	0.48
23:Q:10:THR:OG1	28:V:1291:A:OP1	2.26	0.48
28:V:76:C:OP1	31:Y:48:LYS:NZ	2.45	0.48
28:V:772:G:O3'	28:V:773:G:O4'	2.31	0.48
28:V:2122:G:O6	28:V:2254:A:C8	2.65	0.48
33:a:508:A:N1	33:a:555:A:O2'	2.40	0.48
33:a:1249:U:H5	39:g:116:MET:HE3	1.78	0.48
40:h:20:VAL:HG12	40:h:20:VAL:O	2.13	0.48
28:V:445:C:OP1	53:u:32:ASN:ND2	2.45	0.48
28:V:508:C:H2'	28:V:509:C:O4'	2.13	0.48
33:a:1149:U:H2'	33:a:1149:U:O2	2.12	0.48
33:a:1188:A:O2'	41:i:106:ARG:NH2	2.45	0.48
7:A:31:A:C5	7:A:32:U:C5	3.01	0.48
7:A:45:C:O2'	7:A:46:A:O5'	2.16	0.48
28:V:195:C:N4	28:V:206:A:O2'	2.46	0.48
28:V:688:G:H21	28:V:692:A:H62	1.59	0.48
28:V:1243:A:H61	28:V:1284:A:N6	2.11	0.48
28:V:1819:C:OP2	28:V:1857:G:N1	2.44	0.48
28:V:2159:U:O2'	28:V:2162:G:O2'	2.31	0.48
39:g:102:ARG:O	39:g:106:ASN:ND2	2.46	0.48
47:o:24:SER:O	47:o:27:VAL:N	2.46	0.48
24:R:50:ASN:O	24:R:51:PRO:C	2.56	0.48
33:a:267:G:OP1	52:t:78:ARG:NH1	2.47	0.48
33:a:1499:G:HO2'	33:a:1500:U:P	2.35	0.48
48:p:48:GLU:CG	48:p:48:GLU:O	2.61	0.48
12:F:141:ILE:HG22	12:F:141:ILE:O	2.13	0.48
13:G:47:GLU:N	13:G:47:GLU:OE2	2.47	0.48
18:L:21:ARG:NH2	28:V:631:G:OP1	2.45	0.48
33:a:445:U:H3	33:a:504:A:H62	1.61	0.48
54:w:56:ILE:HD11	54:w:119:ILE:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:J:23:GLY:N	16:J:64:GLU:OE1	2.42	0.48
33:a:205:C:N4	33:a:206:A:H62	2.11	0.48
45:m:42:ASP:O	45:m:43:THR:HG23	2.14	0.48
33:a:631:A:OP2	33:a:632:C:N4	2.39	0.48
33:a:1210:A:H1'	33:a:1211:U:OP2	2.13	0.48
33:a:1322:U:OP1	51:s:5:LEU:HD13	2.13	0.48
13:G:87:GLY:N	13:G:166:GLU:OE2	2.46	0.48
13:G:123:GLU:OE2	13:G:123:GLU:N	2.44	0.48
28:V:224:A:O4'	28:V:236:A:O2'	2.30	0.48
28:V:1441:U:O2'	28:V:1517:A:N1	2.37	0.48
32:Z:47:ILE:HD12	32:Z:54:VAL:HG11	1.96	0.48
33:a:890:C:C5'	44:l:9:ARG:NH1	2.64	0.48
8:B:34:C:N3	8:B:47:C:O2'	2.42	0.48
28:V:242:U:HO2'	28:V:668:G:HO2'	1.61	0.48
28:V:1966:A:O2'	28:V:1968:U:OP2	2.27	0.48
30:X:21:VAL:HG23	30:X:26:ALA:HB2	1.94	0.48
31:Y:15:GLU:OE1	31:Y:16:GLN:NE2	2.44	0.48
33:a:746:C:C2	33:a:747:U:C5	3.02	0.48
33:a:1046:G:O2'	33:a:1047:C:O4'	2.32	0.48
33:a:1136:U:O2'	33:a:1289:A:H2'	2.13	0.48
54:v:235:ASN:ND2	54:v:238:GLN:OE1	2.47	0.48
28:V:505:G:O2'	28:V:516:G:O6	2.28	0.47
28:V:546:G:N1	28:V:549:A:OP2	2.39	0.47
28:V:1529:G:O2'	28:V:1530:G:O5'	2.30	0.47
33:a:1091:G:OP2	37:e:32:ARG:NH1	2.47	0.47
13:G:125:GLU:N	13:G:125:GLU:OE1	2.47	0.47
28:V:1135:G:N2	28:V:1136:U:O4	2.47	0.47
33:a:180:G:C2	33:a:209:A:C2	3.02	0.47
33:a:473:G:H21	33:a:477:A:H2	1.62	0.47
33:a:1463:A:O2'	33:a:1464:G:P	2.72	0.47
8:B:40:C:N4	8:B:41:C:H41	2.12	0.47
13:G:115:GLU:OE2	13:G:115:GLU:N	2.47	0.47
28:V:2580:C:N4	28:V:2581:U:O4	2.47	0.47
33:a:371:A:OP1	44:l:44:ARG:N	2.41	0.47
36:d:163:GLU:N	36:d:184:GLU:OE2	2.46	0.47
7:A:45:C:HO2'	7:A:46:A:P	2.33	0.47
28:V:2335:U:H2'	28:V:2336:G:C8	2.49	0.47
41:i:50:GLN:OE1	41:i:80:ARG:NH2	2.47	0.47
52:t:45:ASP:OD1	52:t:46:LYS:N	2.47	0.47
13:G:22:ASN:OD1	13:G:23:ASN:N	2.47	0.47
28:V:2830:A:O2'	28:V:2831:A:OP2	2.23	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:h:97:VAL:HG12	40:h:98:LEU:HG	1.95	0.47
28:V:88:G:HO2'	28:V:89:U:P	2.36	0.47
28:V:2139:G:O2'	28:V:2149:G:OP1	2.33	0.47
28:V:2536:C:O2	28:V:2612:G:N2	2.47	0.47
33:a:269:U:N3	33:a:272:C:OP2	2.42	0.47
33:a:527:C:O2'	44:l:60:SER:OG	2.03	0.47
33:a:613:G:O6	33:a:644:A:N6	2.47	0.47
33:a:1018:U:O2'	33:a:1019:C:O5'	2.32	0.47
13:G:65:LEU:O	13:G:69:THR:HG23	2.14	0.47
16:J:20:ASP:OD1	16:J:59:ASN:ND2	2.44	0.47
28:V:585:G:O6	28:V:599:G:N2	2.48	0.47
28:V:775:G:H3'	28:V:776:G:C5'	2.44	0.47
28:V:1093:G:O2'	28:V:1094:A:O5'	2.32	0.47
28:V:1380:U:OP1	28:V:1436:U:N3	2.44	0.47
28:V:2330:A:H2'	28:V:2331:U:C6	2.49	0.47
33:a:908:G:N2	33:a:911:A:OP2	2.48	0.47
33:a:1078:G:N2	33:a:1200:A:N3	2.59	0.47
33:a:1463:A:HO2'	33:a:1464:G:P	2.36	0.47
38:f:7:MET:HE2	50:r:29:LYS:HZ2	1.80	0.47
40:h:52:VAL:N	40:h:59:ILE:O	2.40	0.47
47:o:34:ASP:OD1	47:o:34:ASP:C	2.57	0.47
9:C:157:SER:O	9:C:195:VAL:HG21	2.14	0.47
28:V:1417:A:O2'	28:V:1419:G:N7	2.26	0.47
28:V:2487:U:O2'	28:V:2489:U:O4	2.32	0.47
33:a:886:A:C1'	40:h:12:THR:HG21	2.45	0.47
10:D:138:ARG:NH2	28:V:791:C:OP2	2.47	0.47
19:M:84:GLY:O	19:M:85:SER:OG	2.23	0.47
20:N:45:GLU:O	20:N:49:THR:HG23	2.15	0.47
22:P:23:GLY:N	22:P:47:VAL:O	2.44	0.47
28:V:677:A:N3	28:V:2444:G:O2'	2.47	0.47
28:V:1015:G:N2	28:V:1031:C:OP1	2.39	0.47
28:V:1322:G:N2	28:V:1325:A:OP2	2.46	0.47
28:V:2616:A:N6	28:V:2637:G:O2'	2.47	0.47
28:V:2799:C:H2'	28:V:2799:C:O2	2.15	0.47
33:a:113:G:H1'	33:a:114:A:OP2	2.15	0.47
33:a:261:U:C1'	33:a:283:G:H21	2.27	0.47
39:g:109:ARG:CB	39:g:116:MET:HE1	2.44	0.47
42:j:29:ALA:HB1	42:j:36:VAL:HG21	1.97	0.47
8:B:37:A:H4'	8:B:38:U:OP1	2.14	0.47
20:N:35:THR:HG21	28:V:1696:G:H3'	1.96	0.47
20:N:93:GLU:OE1	20:N:93:GLU:N	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:784:G:N2	33:a:813:U:O4	2.47	0.47
39:g:13:LEU:N	39:g:14:PRO:HD2	2.30	0.47
40:h:5:ASP:N	40:h:5:ASP:OD1	2.46	0.47
47:o:63:ARG:HD2	47:o:87:LEU:HD11	1.97	0.47
54:w:171:ARG:NH2	54:w:174:SER:OG	2.48	0.47
8:B:70:G:H21	8:B:102:A:H62	1.62	0.46
10:D:168:GLN:NE2	28:V:2802:U:OP1	2.44	0.46
12:F:106:VAL:HG12	12:F:110:ARG:HG3	1.97	0.46
28:V:2732:C:C2	28:V:2733:C:C5	3.04	0.46
39:g:116:MET:HE2	39:g:119:ARG:HH11	1.81	0.46
41:i:44:LEU:O	41:i:48:ILE:HG13	2.15	0.46
48:p:20:ILE:N	48:p:38:GLY:O	2.45	0.46
19:M:30:GLY:O	19:M:134:ARG:NH2	2.47	0.46
28:V:497:G:N1	28:V:501:A:OP2	2.43	0.46
30:X:116:GLU:OE1	30:X:116:GLU:N	2.48	0.46
33:a:766:U:H2'	33:a:767:G:O4'	2.15	0.46
33:a:890:C:OP1	44:l:9:ARG:NH1	2.48	0.46
33:a:1186:G:H2'	33:a:1187:G:O4'	2.14	0.46
28:V:648:G:O2'	28:V:649:G:P	2.74	0.46
28:V:1027:A:HO2'	28:V:2065:C:HO2'	1.59	0.46
28:V:2036:U:C2	28:V:2037:C:C5	3.04	0.46
28:V:2295:A:H4'	28:V:2296:A:OP2	2.15	0.46
28:V:2897:G:O2'	28:V:2898:A:O4'	2.27	0.46
33:a:342:C:O2'	33:a:1443:A:O2'	2.31	0.46
33:a:590:G:N2	33:a:768:A:OP2	2.45	0.46
33:a:1162:G:OP1	42:j:16:ARG:NH2	2.45	0.46
33:a:1462:U:O2'	33:a:1463:A:P	2.73	0.46
9:C:260:ARG:NH2	9:C:266:SER:OG	2.45	0.46
13:G:20:ASN:OD1	13:G:21:ASP:N	2.49	0.46
28:V:1450:C:C4	28:V:1451:U:C5	3.03	0.46
28:V:1475:G:HO2'	28:V:1476:C:H6	1.60	0.46
28:V:1692:U:O3'	28:V:1693:C:H4'	2.16	0.46
28:V:2534:G:HO2'	28:V:2535:U:P	2.37	0.46
33:a:848:G:O2'	33:a:849:G:O5'	2.32	0.46
33:a:1313:G:O3'	33:a:1314:G:O4'	2.32	0.46
50:r:64:ILE:CD1	50:r:73:LEU:HD13	2.45	0.46
54:v:99:VAL:HG13	54:v:126:LEU:HD22	1.98	0.46
12:F:158:THR:O	21:O:1:MET:N	2.47	0.46
28:V:1315:G:OP2	28:V:1690:G:O2'	2.33	0.46
28:V:2525:C:O2'	28:V:2526:A:O5'	2.25	0.46
33:a:474:A:HO2'	33:a:475:A:C5'	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:589:C:H2'	33:a:590:G:O4'	2.16	0.46
9:C:27:ASP:OD1	9:C:27:ASP:N	2.42	0.46
9:C:170:LYS:NZ	28:V:2252:A:OP1	2.40	0.46
31:Y:24:GLU:O	31:Y:28:LEU:HD23	2.16	0.46
47:o:78:TYR:CZ	47:o:82:ILE:HD11	2.51	0.46
48:p:68:ASP:O	48:p:72:ASN:ND2	2.48	0.46
50:r:37:PHE:CD1	50:r:60:LEU:HD21	2.47	0.46
51:s:30:VAL:HG22	51:s:48:THR:HG23	1.98	0.46
3:2:39:ARG:NH2	28:V:515:G:N7	2.63	0.46
23:Q:49:ASP:OD2	28:V:580:U:O2'	2.34	0.46
28:V:1818:A:H2'	28:V:1819:C:O4'	2.15	0.46
33:a:641:G:O2'	33:a:642:U:P	2.74	0.46
8:B:30:C:C2	8:B:49:G:N2	2.84	0.46
25:S:77:ASP:OD1	28:V:24:G:O2'	2.26	0.46
28:V:1403:G:N2	28:V:1406:A:OP2	2.49	0.46
28:V:1525:G:HO2'	28:V:1526:G:P	2.35	0.46
28:V:2162:G:N2	28:V:2187:A:OP2	2.42	0.46
13:G:75:ASN:ND2	28:V:2776:G:OP1	2.46	0.46
14:H:47:U:H1'	14:H:48:C:OP2	2.16	0.46
19:M:35:GLN:HB2	19:M:132:VAL:HG21	1.98	0.46
28:V:1450:C:C2	28:V:1451:U:C6	3.03	0.46
28:V:2122:G:H4'	30:X:25:TYR:HB3	1.96	0.46
54:v:139:CYS:HB3	54:v:255:LEU:HD11	1.97	0.46
9:C:154:LEU:HD13	9:C:176:LEU:HD21	1.97	0.46
33:a:381:A:N3	33:a:491:A:N6	2.64	0.46
33:a:1318:G:H5''	45:m:91:HIS:NE2	2.31	0.46
36:d:32:ALA:HB3	36:d:33:PRO:CD	2.39	0.46
36:d:79:ALA:O	36:d:85:ASN:ND2	2.46	0.46
28:V:139:A:C2	28:V:1449:C:C5	3.03	0.45
35:c:130:ARG:NH1	35:c:167:TYR:OH	2.48	0.45
39:g:111:ARG:NH2	39:g:126:ASP:OD2	2.50	0.45
54:v:252:LEU:HD23	54:v:255:LEU:HD12	1.98	0.45
9:C:208:ALA:HB2	28:V:1819:C:O2'	2.15	0.45
20:N:32:THR:OG1	20:N:33:THR:N	2.48	0.45
33:a:965:U:O2'	33:a:966:U:O5'	2.32	0.45
33:a:1441:G:N2	33:a:1478:A:OP2	2.42	0.45
40:h:97:VAL:HG11	40:h:131:VAL:O	2.16	0.45
28:V:175:G:N1	28:V:177:G:O6	2.49	0.45
31:Y:17:LYS:HB3	31:Y:53:MET:HE3	1.99	0.45
7:A:35:A:C6	7:A:36:U:C2	3.04	0.45
9:C:245:SER:O	9:C:245:SER:OG	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:84:ARG:NH2	28:V:518:A:OP1	2.41	0.45
28:V:340:U:H2'	28:V:341:G:O4'	2.17	0.45
28:V:514:G:H2'	28:V:515:G:C8	2.52	0.45
28:V:1527:C:C2'	28:V:1528:U:OP1	2.64	0.45
33:a:158:G:N2	33:a:161:A:OP2	2.36	0.45
33:a:547:U:OP1	44:l:124:ALA:N	2.43	0.45
33:a:1165:G:HO2'	33:a:1189:A:N6	2.14	0.45
33:a:1366:A:OP1	33:a:1368:C:N4	2.48	0.45
47:o:30:ALA:O	47:o:33:THR:OG1	2.32	0.45
49:q:21:LYS:O	49:q:50:ASP:N	2.50	0.45
13:G:120:GLU:HB2	13:G:122:ILE:HD11	1.99	0.45
23:Q:22:LYS:NZ	28:V:1259:G:OP1	2.41	0.45
28:V:25:U:H2'	28:V:26:G:O5'	2.17	0.45
28:V:2220:A:H2'	28:V:2221:C:C6	2.51	0.45
28:V:2731:G:C2	28:V:2732:C:C6	3.05	0.45
33:a:1326:C:HO2'	51:s:10:PHE:HZ	1.63	0.45
42:j:26:VAL:HG21	42:j:39:PRO:HD3	1.98	0.45
9:C:54:GLN:NE2	28:V:1852:G:OP1	2.49	0.45
26:T:5:ARG:NH2	31:Y:23:GLU:OE2	2.50	0.45
28:V:632:U:H2'	28:V:633:U:C6	2.51	0.45
28:V:1392:A:OP2	28:V:1416:G:N1	2.41	0.45
28:V:1559:C:H3'	28:V:1560:U:H5''	1.99	0.45
28:V:2228:A:N7	28:V:2229:C:C4	2.84	0.45
33:a:420:U:O2'	33:a:421:G:O5'	2.28	0.45
33:a:668:C:N4	33:a:669:A:N6	2.65	0.45
54:v:78:ALA:HB2	54:v:84:LEU:HD11	1.98	0.45
19:M:87:LYS:NZ	28:V:1001:U:OP1	2.35	0.45
28:V:1116:A:O2'	28:V:1118:C:N4	2.43	0.45
28:V:1631:A:C4'	28:V:1632:G:OP1	2.64	0.45
28:V:2695:C:O2	28:V:2695:C:O4'	2.35	0.45
33:a:757:A:O2'	33:a:758:A:P	2.73	0.45
35:c:104:GLU:N	35:c:104:GLU:OE2	2.50	0.45
47:o:17:THR:OG1	47:o:21:ASP:OD2	2.34	0.45
54:v:53:ALA:HA	54:v:56:ILE:HD12	1.98	0.45
54:w:78:ALA:HB2	54:w:84:LEU:HD11	1.98	0.45
10:D:12:MET:HE1	10:D:191:ASN:OD1	2.16	0.45
16:J:89:THR:HG23	16:J:92:GLU:H	1.81	0.45
28:V:1018:G:OP2	28:V:1019:A:O2'	2.27	0.45
28:V:2121:U:N3	28:V:2255:C:OP2	2.50	0.45
28:V:2228:A:N7	28:V:2229:C:C5	2.85	0.45
28:V:2295:A:C3'	28:V:2296:A:H5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:g:56:ASN:OD1	39:g:57:ASP:N	2.50	0.45
44:l:127:ARG:O	44:l:132:THR:OG1	2.28	0.45
7:A:39:U:O2	7:A:39:U:O4'	2.34	0.45
28:V:75:G:O5'	31:Y:44:ARG:NH2	2.50	0.45
28:V:275:A:N6	28:V:296:G:N2	2.65	0.45
28:V:441:C:C2'	28:V:442:C:OP1	2.64	0.45
28:V:494:A:N1	28:V:501:A:O2'	2.40	0.45
33:a:993:A:N3	33:a:993:A:H2'	2.31	0.45
38:f:7:MET:HE2	50:r:29:LYS:NZ	2.32	0.45
5:4:17:ILE:O	5:4:24:MET:N	2.44	0.44
28:V:115:C:H2'	28:V:116:G:O4'	2.16	0.44
28:V:689:A:H61	28:V:2398:A:C2'	2.27	0.44
28:V:1471:G:N2	28:V:1621:G:N7	2.65	0.44
28:V:2022:U:O2'	28:V:2023:C:OP1	2.35	0.44
28:V:2420:G:O2'	28:V:2458:G:N2	2.50	0.44
33:a:74:A:C2	33:a:96:G:O6	2.69	0.44
36:d:62:GLY:O	36:d:111:ARG:NH2	2.43	0.44
36:d:125:ARG:NH2	36:d:127:ASP:OD2	2.44	0.44
45:m:58:ASP:OD1	45:m:59:ILE:N	2.50	0.44
11:E:78:ILE:HG23	11:E:79:ARG:HG2	2.00	0.44
22:P:75:PRO:HD2	22:P:78:THR:HG21	2.00	0.44
28:V:1957:A:H2'	28:V:1958:G:O4'	2.17	0.44
28:V:2182:G:H2'	28:V:2183:G:C8	2.52	0.44
33:a:528:C:H2'	33:a:529:A:O4'	2.16	0.44
33:a:1336:G:H2'	33:a:1337:C:O4'	2.17	0.44
10:D:28:ILE:HD12	10:D:188:ILE:HD13	1.99	0.44
24:R:63:GLU:N	24:R:63:GLU:OE2	2.51	0.44
28:V:1877:A:N7	33:a:711:A:N6	2.61	0.44
28:V:2467:U:O3'	28:V:2468:A:H3'	2.16	0.44
33:a:207:U:H4'	33:a:208:A:OP1	2.18	0.44
33:a:676:G:OP1	33:a:741:C:O2'	2.31	0.44
33:a:1165:G:O2'	33:a:1189:A:N6	2.50	0.44
3:2:25:LYS:NZ	28:V:213:C:OP1	2.47	0.44
7:A:31:A:C4	7:A:32:U:C6	3.05	0.44
13:G:11:ILE:O	13:G:49:ASN:ND2	2.49	0.44
28:V:432:C:O2'	28:V:433:G:OP2	2.35	0.44
28:V:2615:C:OP2	28:V:2637:G:N1	2.44	0.44
37:e:99:ALA:HB1	37:e:103:THR:HG21	1.99	0.44
52:t:20:HIS:O	52:t:23:THR:OG1	2.30	0.44
54:w:391:THR:HG22	54:w:395:HIS:CD2	2.52	0.44
13:G:88:LEU:N	13:G:132:VAL:O	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:K:80:ASP:OD2	22:P:62:ARG:NH2	2.43	0.44
28:V:492:C:H2'	28:V:493:G:O4'	2.17	0.44
28:V:1494:G:O2'	28:V:1592:A:N3	2.41	0.44
28:V:1697:A:H2'	28:V:1698:G:O4'	2.17	0.44
28:V:2819:A:O2'	28:V:2917:G:O2'	2.35	0.44
42:j:25:ILE:HD13	42:j:90:LEU:HD13	2.00	0.44
44:l:115:LEU:C	44:l:117:THR:N	2.76	0.44
54:v:23:ALA:HB2	54:v:284:ARG:HH22	1.83	0.44
54:w:549:LYS:HE2	54:w:553:GLU:OE1	2.18	0.44
28:V:475:A:C2'	28:V:476:A:O5'	2.66	0.44
28:V:790:A:N6	28:V:802:G:O6	2.51	0.44
28:V:1479:G:H2'	28:V:1480:A:O4'	2.17	0.44
33:a:286:G:H4'	33:a:287:A:OP1	2.18	0.44
33:a:405:A:N7	33:a:556:A:O2'	2.51	0.44
4:3:32:LEU:HD13	28:V:2420:G:OP2	2.18	0.44
16:J:38:ARG:HH12	28:V:1053:C:C5'	2.29	0.44
17:K:97:ARG:HE	33:a:347:C:P	2.41	0.44
28:V:1243:A:H2'	28:V:1244:A:N3	2.33	0.44
30:X:17:GLU:O	30:X:19:LYS:HG3	2.18	0.44
45:m:33:VAL:HG13	45:m:59:ILE:HG21	1.99	0.44
48:p:48:GLU:O	48:p:48:GLU:HG3	2.18	0.44
54:v:172:LEU:HD12	54:v:172:LEU:HA	1.89	0.44
10:D:114:SER:HB3	10:D:169:ILE:HD12	1.99	0.44
17:K:71:ARG:NH1	17:K:77:ILE:HG22	2.32	0.44
28:V:347:G:O2'	28:V:348:U:OP1	2.31	0.44
28:V:993:A:O2'	28:V:1030:G:N2	2.46	0.44
28:V:1451:U:H2'	28:V:1452:C:C6	2.52	0.44
33:a:1496:G:H2'	33:a:1497:G:O4'	2.18	0.44
37:e:25:VAL:HG12	37:e:26:LYS:N	2.32	0.44
54:v:24:SER:OG	54:v:25:SER:N	2.49	0.44
54:v:154:LEU:HB2	54:v:247:GLU:HG2	1.99	0.44
23:Q:92:ARG:O	23:Q:93:LYS:C	2.60	0.44
27:U:40:MET:HE1	27:U:60:GLU:HG3	1.99	0.44
28:V:78:U:C2	28:V:79:C:C5	3.06	0.44
28:V:181:G:O2'	28:V:182:C:O5'	2.36	0.44
33:a:1184:G:H2'	33:a:1185:A:C8	2.52	0.44
7:A:30:A:C2	7:A:31:A:H1'	2.53	0.43
28:V:419:G:N2	28:V:448:A:OP2	2.51	0.43
28:V:1451:U:C2	28:V:1637:G:N1	2.86	0.43
28:V:2307:A:OP2	29:W:20:ASN:ND2	2.51	0.43
28:V:2803:C:H2'	28:V:2804:A:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:275:A:N6	28:V:296:G:H21	2.16	0.43
28:V:2324:C:H2'	28:V:2325:U:C6	2.53	0.43
28:V:2446:C:C2	28:V:2447:A:C8	3.06	0.43
28:V:2486:U:H2'	28:V:2487:U:O4'	2.18	0.43
8:B:37:A:N1	8:B:42:G:C6	2.86	0.43
33:a:755:G:H2'	33:a:756:U:C4'	2.48	0.43
33:a:998:G:H1'	33:a:1025:G:H22	1.83	0.43
33:a:1087:G:O2'	33:a:1089:G:O6	2.35	0.43
33:a:1122:C:O2'	35:c:178:ARG:NH2	2.41	0.43
33:a:1141:G:H3'	33:a:1142:C:C5'	2.48	0.43
41:i:28:ILE:HD13	41:i:35:ILE:HD11	2.00	0.43
48:p:10:MET:N	48:p:17:PHE:O	2.49	0.43
50:r:24:THR:O	50:r:25:HIS:C	2.60	0.43
54:w:57:ILE:HD13	54:w:284:ARG:HG3	2.00	0.43
13:G:87:GLY:C	13:G:88:LEU:HD22	2.43	0.43
28:V:657:G:N2	28:V:661:A:OP2	2.46	0.43
28:V:1785:G:H4'	28:V:1787:G:O4'	2.19	0.43
28:V:2196:U:O3'	28:V:2197:G:O4'	2.35	0.43
33:a:1196:G:N3	46:n:60:SER:OG	2.42	0.43
33:a:1441:G:O2'	33:a:1477:G:O6	2.34	0.43
10:D:55:ASP:OD2	10:D:77:LYS:NZ	2.39	0.43
18:L:86:ALA:O	18:L:89:THR:HG22	2.18	0.43
28:V:1882:A:O2'	28:V:1883:A:OP1	2.37	0.43
33:a:1462:U:O2'	33:a:1463:A:O4'	2.33	0.43
23:Q:15:LYS:NZ	28:V:1257:C:OP2	2.43	0.43
25:S:21:MET:HA	25:S:24:ILE:HD12	2.01	0.43
28:V:140:A:O2'	28:V:1447:C:O2'	2.28	0.43
28:V:514:G:H2'	28:V:515:G:O4'	2.19	0.43
28:V:1463:C:H2'	28:V:1464:A:O4'	2.19	0.43
28:V:2378:G:H3'	28:V:2379:C:H5''	1.98	0.43
33:a:442:C:C2	33:a:443:U:C5	3.06	0.43
33:a:613:G:H2'	33:a:614:U:O4'	2.18	0.43
33:a:891:G:H2'	33:a:892:C:O4'	2.19	0.43
36:d:81:LYS:NZ	37:e:101:GLU:O	2.49	0.43
24:R:50:ASN:O	24:R:52:THR:N	2.52	0.43
28:V:1243:A:O2'	28:V:1244:A:P	2.76	0.43
47:o:74:ASP:OD1	47:o:77:ARG:NE	2.52	0.43
49:q:66:THR:HG22	49:q:67:ARG:N	2.33	0.43
54:w:60:ARG:HG3	54:w:109:MET:HG3	2.00	0.43
7:A:44:A:C2'	7:A:45:C:H5'	2.48	0.43
22:P:14:ARG:NH2	22:P:78:THR:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:2295:A:N6	28:V:2302:A:OP2	2.52	0.43
33:a:736:G:N2	33:a:739:G:OP2	2.45	0.43
33:a:1048:A:H2'	33:a:1049:G:O4'	2.19	0.43
28:V:371:G:N2	28:V:380:C:N3	2.67	0.43
28:V:554:U:C4'	28:V:555:C:OP2	2.66	0.43
28:V:1565:U:O2'	28:V:1566:G:OP1	2.27	0.43
28:V:1569:A:H5'	28:V:1571:G:C4	2.53	0.43
33:a:86:G:H2'	33:a:87:C:O4'	2.18	0.43
33:a:209:A:HO2'	33:a:210:A:C1'	2.20	0.43
33:a:928:A:H2'	33:a:929:A:O4'	2.19	0.43
33:a:939:G:N1	33:a:1398:C:N3	2.66	0.43
48:p:47:ALA:O	48:p:48:GLU:CG	2.67	0.43
18:L:38:GLN:OE1	28:V:878:G:O2'	2.31	0.43
28:V:461:C:O3'	28:V:1907:G:N2	2.52	0.43
28:V:508:C:H2'	28:V:509:C:C6	2.54	0.43
28:V:1420:G:O6	28:V:1421:A:N6	2.52	0.43
28:V:2534:G:O2'	28:V:2535:U:P	2.77	0.43
33:a:420:U:HO2'	33:a:421:G:P	2.41	0.43
33:a:1155:A:H2'	33:a:1155:A:N3	2.34	0.43
44:l:120:VAL:HG22	44:l:121:GLU:N	2.34	0.43
54:v:239:GLN:HA	54:v:242:VAL:HG12	2.01	0.43
54:w:473:GLU:HA	54:w:497:ARG:NH1	2.33	0.43
9:C:124:ILE:O	9:C:124:ILE:HG23	2.18	0.42
10:D:154:VAL:HG21	28:V:2647:G:H21	1.84	0.42
27:U:58:ASN:OD1	27:U:59:GLN:N	2.51	0.42
28:V:242:U:O2'	28:V:668:G:O2'	2.36	0.42
28:V:1520:A:N6	28:V:1566:G:O6	2.52	0.42
28:V:1696:G:O2'	28:V:1697:A:OP2	2.30	0.42
30:X:62:LEU:HD22	30:X:134:HIS:NE2	2.33	0.42
33:a:331:U:H2'	33:a:332:G:O4'	2.19	0.42
33:a:1058:G:OP1	46:n:3:LYS:N	2.52	0.42
33:a:1188:A:H2'	33:a:1189:A:O4'	2.19	0.42
41:i:12:ARG:O	41:i:15:SER:OG	2.35	0.42
20:N:2:SER:OG	20:N:3:TYR:N	2.43	0.42
28:V:419:G:H22	28:V:447:G:H3'	1.84	0.42
28:V:2279:G:OP1	28:V:2304:C:O2'	2.34	0.42
28:V:2333:G:H22	28:V:2341:U:H3	1.67	0.42
33:a:263:G:O6	33:a:274:G:O6	2.37	0.42
36:d:15:LEU:HD13	36:d:56:LYS:HA	2.01	0.42
39:g:90:GLU:OE2	39:g:90:GLU:HA	2.19	0.42
28:V:1759:U:O2'	28:V:1760:A:O5'	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:1870:U:C2	28:V:1871:G:C8	3.06	0.42
28:V:2295:A:H3'	28:V:2296:A:H5'	2.00	0.42
45:m:85:SER:O	45:m:86:TYR:C	2.62	0.42
25:S:24:ILE:HD11	25:S:36:LEU:HD21	2.01	0.42
28:V:349:C:N4	28:V:357:G:O6	2.52	0.42
28:V:655:C:N4	28:V:656:A:H62	2.17	0.42
28:V:1273:G:C2	28:V:1274:U:C4	3.08	0.42
28:V:1757:G:HO2'	28:V:1758:U:P	2.42	0.42
28:V:2036:U:N3	28:V:2037:C:C5	2.87	0.42
28:V:2076:C:O2'	28:V:2848:A:N1	2.46	0.42
33:a:23:G:H2'	33:a:24:G:C8	2.55	0.42
50:r:26:ILE:CD1	50:r:60:LEU:HD12	2.49	0.42
51:s:30:VAL:HG13	51:s:48:THR:O	2.18	0.42
52:t:58:ILE:O	52:t:62:VAL:HG23	2.19	0.42
7:A:31:A:C2	7:A:32:U:C2	3.07	0.42
9:C:177:ASN:O	9:C:178:SER:OG	2.32	0.42
9:C:265:LYS:NZ	28:V:2255:C:O2	2.41	0.42
28:V:421:A:N7	28:V:422:C:C6	2.88	0.42
28:V:2037:C:O2	28:V:2038:G:C8	2.72	0.42
28:V:2524:G:C2'	28:V:2525:C:H5'	2.50	0.42
28:V:2777:A:H2'	28:V:2778:A:O4'	2.19	0.42
30:X:120:GLY:O	30:X:121:ILE:C	2.63	0.42
32:Z:18:ASP:O	32:Z:22:THR:HG23	2.19	0.42
28:V:285:U:C1'	30:X:46:ALA:HB2	2.48	0.42
28:V:1275:G:H4'	28:V:1276:G:OP1	2.19	0.42
28:V:1801:G:N2	28:V:1803:C:H5''	2.35	0.42
33:a:1225:A:C2	33:a:1226:C:C5	3.08	0.42
51:s:30:VAL:HG11	51:s:50:ALA:HB2	2.01	0.42
54:v:116:ILE:H	54:v:116:ILE:HG12	1.70	0.42
54:w:382:GLU:HG2	54:w:391:THR:HG21	2.01	0.42
33:a:360:C:O2	33:a:363:C:N4	2.51	0.42
37:e:82:PRO:O	40:h:99:ASN:ND2	2.48	0.42
45:m:65:VAL:HG12	45:m:66:GLU:N	2.35	0.42
53:u:20:HIS:O	53:u:21:ALA:HB3	2.19	0.42
9:C:245:SER:O	9:C:246:PRO:C	2.62	0.42
18:L:125:ALA:O	18:L:146:ILE:N	2.46	0.42
23:Q:102:ASP:O	23:Q:104:THR:N	2.53	0.42
27:U:67:ASN:ND2	28:V:373:A:OP2	2.52	0.42
28:V:85:G:O2'	28:V:86:C:H5'	2.20	0.42
28:V:1244:A:C2'	28:V:1245:G:OP1	2.67	0.42
28:V:1265:A:C2	28:V:1266:A:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:1305:A:H4'	28:V:1306:G:O5'	2.20	0.42
28:V:1452:C:N3	28:V:1636:A:N1	2.67	0.42
28:V:2205:A:H4'	28:V:2206:C:OP1	2.20	0.42
33:a:1323:C:N4	33:a:1333:A:N1	2.67	0.42
33:a:1483:G:H2'	33:a:1484:G:C8	2.54	0.42
35:c:46:LEU:HD13	35:c:51:VAL:HG21	2.02	0.42
37:e:12:GLU:O	37:e:13:GLU:C	2.62	0.42
39:g:91:VAL:O	39:g:96:ARG:NE	2.52	0.42
13:G:122:ILE:HD12	13:G:122:ILE:N	2.34	0.42
20:N:29:ARG:NH2	20:N:118:GLU:OE2	2.53	0.42
28:V:1942:A:N3	28:V:1942:A:H2'	2.35	0.42
28:V:1968:U:O4'	28:V:2620:C:O2'	2.27	0.42
28:V:2459:A:N3	28:V:2459:A:H2'	2.35	0.42
33:a:877:G:O2'	33:a:883:A:N1	2.42	0.42
33:a:990:C:C5	33:a:991:U:C4	3.08	0.42
36:d:191:GLU:O	36:d:192:ALA:HB3	2.20	0.42
37:e:107:ALA:HB2	37:e:125:SER:OG	2.20	0.42
43:k:84:LEU:HD23	43:k:84:LEU:H	1.83	0.42
54:w:60:ARG:HA	54:w:60:ARG:HD3	1.83	0.42
8:B:31:G:O6	8:B:48:G:O6	2.37	0.42
12:F:106:VAL:HG11	12:F:139:PRO:HD3	2.00	0.42
28:V:1843:G:OP2	28:V:1844:A:C2'	2.67	0.42
28:V:2134:A:N6	28:V:2135:G:O6	2.53	0.42
28:V:2135:G:N1	28:V:2212:C:C2	2.87	0.42
28:V:2140:U:OP2	28:V:2174:C:N4	2.49	0.42
33:a:248:C:HO2'	33:a:249:G:H8	1.66	0.42
33:a:440:A:C5	33:a:441:G:C8	3.08	0.42
45:m:34:LEU:HD22	45:m:39:VAL:HG21	2.02	0.42
7:A:32:U:H2'	7:A:33:A:C8	2.55	0.41
10:D:6:LEU:N	10:D:6:LEU:HD23	2.35	0.41
28:V:760:G:H2'	28:V:761:U:C6	2.54	0.41
28:V:1305:A:H1'	28:V:1306:G:OP2	2.20	0.41
28:V:2022:U:O2'	28:V:2023:C:P	2.78	0.41
33:a:369:G:H2'	33:a:370:G:O4'	2.20	0.41
33:a:1020:C:C2	33:a:1021:U:C5	3.08	0.41
36:d:84:GLU:OE2	36:d:182:ARG:NE	2.53	0.41
49:q:30:TYR:HB3	49:q:41:LYS:HA	2.02	0.41
9:C:167:LYS:O	9:C:169:GLY:N	2.53	0.41
28:V:81:G:H2'	28:V:82:G:O4'	2.20	0.41
28:V:2445:C:N3	28:V:2446:C:C5	2.88	0.41
33:a:305:G:N2	33:a:308:A:OP2	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1499:G:H2'	33:a:1500:U:C6	2.55	0.41
40:h:3:MET:O	40:h:4:THR:OG1	2.35	0.41
28:V:153:C:H2'	28:V:154:A:H8	1.85	0.41
28:V:797:A:OP1	28:V:1660:C:N4	2.52	0.41
28:V:1478:G:H2'	28:V:1479:G:C8	2.55	0.41
28:V:2365:A:H61	29:W:51:THR:CG2	2.32	0.41
33:a:328:G:H2'	33:a:329:A:C8	2.55	0.41
33:a:459:A:H4'	33:a:460:A:O5'	2.20	0.41
33:a:641:G:H4'	33:a:642:U:OP1	2.21	0.41
33:a:1318:G:O6	33:a:1338:G:O6	2.38	0.41
33:a:1339:U:H2'	33:a:1340:G:O4'	2.20	0.41
43:k:84:LEU:HD23	43:k:84:LEU:N	2.35	0.41
47:o:81:LEU:C	47:o:81:LEU:HD23	2.45	0.41
54:v:54:SER:HA	54:v:57:ILE:HG22	2.03	0.41
54:w:271:GLN:HA	54:w:274:GLN:HG2	2.03	0.41
11:E:46:GLN:N	28:V:490:A:OP1	2.54	0.41
14:H:55:U:HO2'	14:H:56:C:P	2.38	0.41
19:M:17:MET:HE3	19:M:41:TRP:CD1	2.56	0.41
23:Q:50:ARG:O	23:Q:54:LYS:NZ	2.52	0.41
24:R:14:VAL:HG13	24:R:97:ILE:HD13	2.01	0.41
28:V:911:G:H2'	28:V:912:C:C6	2.56	0.41
28:V:1087:U:O2	28:V:1160:G:C6	2.72	0.41
28:V:2296:A:OP2	28:V:2296:A:H3'	2.21	0.41
28:V:2459:A:C3'	28:V:2460:U:H5'	2.51	0.41
28:V:2550:C:H2'	28:V:2551:U:O4'	2.20	0.41
36:d:67:GLN:OE1	36:d:67:GLN:N	2.46	0.41
44:l:123:ARG:NE	44:l:125:GLN:O	2.54	0.41
48:p:57:LEU:CD1	48:p:79:ILE:HG23	2.50	0.41
28:V:24:G:C2	28:V:25:U:C5	3.09	0.41
28:V:2624:G:N2	28:V:2627:A:OP2	2.46	0.41
28:V:2874:G:N7	28:V:2892:G:N2	2.60	0.41
37:e:85:ILE:HD11	37:e:146:GLU:HB3	2.02	0.41
52:t:61:ALA:CB	52:t:67:VAL:HG21	2.42	0.41
54:v:549:LYS:HE2	54:v:553:GLU:OE1	2.21	0.41
9:C:254:THR:HG21	28:V:1853:G:O2'	2.20	0.41
10:D:134:SER:OG	10:D:135:HIS:N	2.54	0.41
27:U:47:PRO:O	27:U:52:PRO:HB3	2.21	0.41
28:V:567:U:H2'	28:V:568:G:C8	2.55	0.41
28:V:2178:C:H2'	28:V:2179:U:O4'	2.21	0.41
28:V:2721:C:O2	28:V:2872:U:O2'	2.38	0.41
31:Y:11:THR:OG1	31:Y:12:ALA:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Z:47:ILE:CD1	32:Z:54:VAL:HG11	2.50	0.41
36:d:168:ASP:OD1	36:d:169:ALA:N	2.53	0.41
37:e:46:VAL:HG22	37:e:47:GLY:N	2.35	0.41
41:i:30:VAL:O	41:i:30:VAL:HG23	2.21	0.41
45:m:87:ARG:C	45:m:91:HIS:HD1	2.27	0.41
28:V:2374:G:C5	28:V:2376:C:C5	3.09	0.41
33:a:41:G:C2	33:a:412:G:C2	3.08	0.41
33:a:1169:G:N2	33:a:1185:A:N1	2.68	0.41
33:a:1222:A:O2'	33:a:1224:G:N7	2.42	0.41
2:1:36:CYS:O	2:1:40:LYS:N	2.49	0.41
9:C:123:ASP:OD2	9:C:124:ILE:N	2.54	0.41
17:K:22:ILE:O	17:K:23:LYS:C	2.63	0.41
18:L:114:ASN:OD1	18:L:114:ASN:N	2.52	0.41
20:N:99:THR:O	28:V:2906:U:O2'	2.38	0.41
28:V:932:C:H2'	28:V:933:C:C1'	2.51	0.41
28:V:2316:A:HO2'	28:V:2317:A:C5'	2.33	0.41
33:a:472:C:H3'	33:a:473:G:C8	2.56	0.41
33:a:572:A:H2'	33:a:576:G:C8	2.56	0.41
33:a:608:C:N4	33:a:649:A:H61	2.19	0.41
33:a:1227:C:H2'	33:a:1228:U:C6	2.56	0.41
33:a:1330:U:H2'	33:a:1331:C:C4	2.56	0.41
35:c:42:ILE:HG12	35:c:46:LEU:HD12	2.03	0.41
37:e:105:VAL:HG13	37:e:121:ALA:O	2.20	0.41
45:m:77:ILE:HG22	45:m:81:ILE:HD12	2.02	0.41
7:A:33:A:C5	34:b:13:GLU:CB	3.04	0.41
9:C:154:LEU:O	9:C:155:VAL:C	2.63	0.41
10:D:14:GLN:CG	10:D:22:LEU:HD22	2.51	0.41
10:D:106:GLU:OE1	10:D:106:GLU:N	2.40	0.41
13:G:43:GLU:N	13:G:43:GLU:OE1	2.53	0.41
16:J:30:SER:HB2	16:J:106:ILE:HD13	2.02	0.41
17:K:63:VAL:HG13	17:K:102:VAL:HG13	2.03	0.41
17:K:73:ASP:OD2	17:K:75:SER:OG	2.34	0.41
28:V:523:G:C4	28:V:525:A:OP2	2.74	0.41
28:V:526:A:H4'	28:V:527:A:OP1	2.21	0.41
28:V:762:A:C6	47:o:56:LEU:HD22	2.55	0.41
28:V:789:C:H4'	28:V:1720:C:O2'	2.21	0.41
28:V:1095:C:C2	28:V:1096:A:C8	3.08	0.41
28:V:1227:G:H2'	28:V:1228:G:O4'	2.21	0.41
28:V:1346:A:N7	28:V:1667:A:N6	2.69	0.41
28:V:2468:A:H1'	28:V:2469:C:OP2	2.21	0.41
28:V:2733:C:H2'	28:V:2734:A:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:2874:G:H1'	28:V:2891:G:H21	1.86	0.41
33:a:335:A:O2'	33:a:336:C:O4'	2.32	0.41
33:a:942:C:HO2'	33:a:943:G:H8	1.65	0.41
33:a:962:U:O3'	33:a:974:A:N6	2.46	0.41
33:a:1088:U:O2'	33:a:1089:G:P	2.78	0.41
33:a:1135:U:N3	33:a:1137:G:C8	2.89	0.41
33:a:1476:C:H2'	33:a:1477:G:O4'	2.21	0.41
37:e:25:VAL:HG12	37:e:26:LYS:H	1.86	0.41
39:g:126:ASP:O	39:g:129:ASN:O	2.39	0.41
45:m:15:VAL:HG23	45:m:43:THR:O	2.20	0.41
54:v:155:ARG:O	54:v:159:THR:OG1	2.34	0.41
54:w:102:MET:HE2	54:w:276:LEU:HD13	2.03	0.41
54:w:236:SER:HA	54:w:239:GLN:HE21	1.86	0.41
18:L:21:ARG:HA	28:V:858:U:H2'	2.03	0.41
28:V:310:C:H4'	28:V:310:C:OP1	2.20	0.41
28:V:803:C:H2'	28:V:804:G:O4'	2.21	0.41
28:V:2135:G:H2'	28:V:2136:C:O4'	2.21	0.41
28:V:2234:C:O2	28:V:2234:C:H2'	2.20	0.41
28:V:2333:G:N2	28:V:2341:U:H3	2.18	0.41
33:a:482:G:OP2	48:p:71:ARG:NH1	2.53	0.41
36:d:89:LEU:O	36:d:92:SER:OG	2.34	0.41
47:o:39:LEU:HD22	47:o:56:LEU:HD12	2.03	0.41
54:v:71:ILE:HG13	54:v:270:LEU:HD22	2.03	0.41
8:B:49:G:O2'	8:B:50:A:O4'	2.37	0.40
28:V:178:A:O2'	28:V:179:A:C8	2.73	0.40
28:V:448:A:H2'	28:V:449:A:C8	2.56	0.40
28:V:1447:C:H2'	28:V:1448:U:C6	2.56	0.40
28:V:1755:C:O4'	28:V:2884:G:N2	2.54	0.40
28:V:1891:G:C6	28:V:1910:G:C6	3.08	0.40
28:V:1967:A:O2'	28:V:1968:U:H5''	2.22	0.40
28:V:2122:G:C2	28:V:2123:A:N7	2.89	0.40
28:V:2799:C:N3	28:V:2800:C:C5	2.89	0.40
33:a:195:A:N1	49:q:66:THR:HG23	2.36	0.40
33:a:363:C:C4	33:a:364:A:N7	2.89	0.40
33:a:1133:A:H2'	33:a:1134:G:C8	2.56	0.40
45:m:80:LEU:O	45:m:85:SER:HB3	2.21	0.40
10:D:103:SER:N	10:D:106:GLU:OE2	2.52	0.40
10:D:195:ALA:O	10:D:198:SER:OG	2.35	0.40
17:K:88:ARG:O	17:K:88:ARG:CG	2.64	0.40
18:L:1:MET:SD	18:L:2:LYS:N	2.94	0.40
28:V:216:A:C2'	28:V:217:G:O5'	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:1650:C:H2'	28:V:1651:G:O4'	2.22	0.40
28:V:2261:C:OP2	53:u:27:ARG:NH2	2.54	0.40
28:V:2433:C:H2'	28:V:2434:G:O4'	2.21	0.40
28:V:2574:G:H2'	28:V:2575:U:O4'	2.21	0.40
28:V:2800:C:C2	28:V:2801:C:C5	3.09	0.40
33:a:22:U:H2'	33:a:23:G:O4'	2.21	0.40
33:a:176:G:O2'	33:a:177:G:OP1	2.25	0.40
33:a:672:A:H2'	33:a:673:G:O4'	2.21	0.40
1:0:15:LEU:O	1:0:18:THR:OG1	2.24	0.40
9:C:13:ARG:HE	28:V:775:G:H4'	1.86	0.40
14:H:17(A):G:HO2'	14:H:18:G:P	2.36	0.40
27:U:92:ARG:O	27:U:101:LEU:N	2.48	0.40
28:V:941:U:O3'	28:V:942:U:O4'	2.40	0.40
28:V:967:G:H21	28:V:2298:A:H8	1.68	0.40
28:V:1325:A:N1	28:V:1368:U:O2'	2.46	0.40
28:V:1396:C:H2'	28:V:1397:G:O4'	2.22	0.40
28:V:1790:U:O2'	28:V:1791:A:O5'	2.36	0.40
28:V:2159:U:O2	28:V:2188:G:C6	2.75	0.40
33:a:19:U:H2'	33:a:20:C:C6	2.57	0.40
33:a:207:U:H2'	33:a:208:A:C8	2.55	0.40
33:a:1166:A:H4'	33:a:1167:C:O4'	2.21	0.40
33:a:1201:C:OP1	35:c:4:LYS:NZ	2.49	0.40
34:b:21:ARG:O	34:b:24:SER:OG	2.35	0.40
47:o:24:SER:O	47:o:25:PRO:C	2.64	0.40
54:w:63:ALA:HA	54:w:64:PRO:HD3	1.95	0.40
8:B:31:G:H2'	8:B:32:U:C6	2.55	0.40
18:L:76:VAL:HG13	18:L:112:LEU:CD1	2.51	0.40
28:V:1035:G:C8	32:Z:13:ILE:HD11	2.57	0.40
28:V:1494:G:C6	28:V:1512:G:C6	3.09	0.40
28:V:2257:G:N2	53:u:34:GLN:OE1	2.54	0.40
33:a:530:G:OP2	44:l:64:LYS:NZ	2.39	0.40
33:a:1018:U:O2'	33:a:1019:C:OP1	2.39	0.40
33:a:1088:U:O2	37:e:135:ASN:ND2	2.54	0.40
33:a:1369:A:OP2	46:n:35:ARG:NH2	2.54	0.40
41:i:5:GLN:OE1	41:i:20:ARG:NH1	2.52	0.40
8:B:95:U:H2'	8:B:96:G:O4'	2.20	0.40
9:C:46:GLN:OE1	28:V:1835:C:O2'	2.25	0.40
11:E:202:VAL:HA	11:E:205:VAL:HG12	2.04	0.40
14:H:54:U:H3	14:H:58:A:H62	1.69	0.40
28:V:363:C:H2'	28:V:364:A:O4'	2.22	0.40
28:V:1306:G:OP2	28:V:1306:G:O4'	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:1366:C:H2'	28:V:1367:G:O4'	2.22	0.40
28:V:1507:U:C5'	28:V:1508:C:O5'	2.70	0.40
28:V:1819:C:H2'	28:V:1820:A:C8	2.57	0.40
28:V:2393:C:H2'	28:V:2394:G:O4'	2.21	0.40
28:V:2798:C:H2'	28:V:2799:C:H5'	2.03	0.40
33:a:566:G:H2'	33:a:567:G:O4'	2.20	0.40
33:a:671:A:H2'	33:a:672:A:C8	2.56	0.40
33:a:1087:G:H3'	33:a:1088:U:H5''	2.04	0.40
33:a:1219:C:H2'	33:a:1220:U:O4'	2.21	0.40
40:h:2:VAL:O	40:h:3:MET:HB3	2.22	0.40
54:v:71:ILE:HD12	54:v:75:LEU:HB2	2.04	0.40
54:v:77:ARG:NE	54:v:82:SER:OG	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/59 (88%)	50 (96%)	2 (4%)	0	100	100
2	1	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
3	2	42/44 (96%)	42 (100%)	0	0	100	100
4	3	62/66 (94%)	60 (97%)	2 (3%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	6	61/66 (92%)	60 (98%)	1 (2%)	0	100	100
9	C	270/277 (98%)	260 (96%)	10 (4%)	0	100	100
10	D	204/209 (98%)	193 (95%)	11 (5%)	0	100	100
11	E	203/207 (98%)	193 (95%)	10 (5%)	0	100	100
12	F	174/179 (97%)	161 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	G	173/179 (97%)	165 (95%)	8 (5%)	0	100	100
16	J	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
17	K	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
18	L	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
19	M	133/144 (92%)	132 (99%)	1 (1%)	0	100	100
20	N	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
21	O	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
22	P	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
23	Q	115/119 (97%)	107 (93%)	6 (5%)	2 (2%)	7	34
24	R	99/102 (97%)	88 (89%)	11 (11%)	0	100	100
25	S	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
26	T	88/95 (93%)	87 (99%)	1 (1%)	0	100	100
27	U	99/103 (96%)	92 (93%)	7 (7%)	0	100	100
29	W	80/94 (85%)	76 (95%)	4 (5%)	0	100	100
30	X	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
31	Y	63/66 (96%)	62 (98%)	1 (2%)	0	100	100
32	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
34	b	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
35	c	204/218 (94%)	194 (95%)	10 (5%)	0	100	100
36	d	193/200 (96%)	176 (91%)	17 (9%)	0	100	100
37	e	162/166 (98%)	155 (96%)	7 (4%)	0	100	100
38	f	90/95 (95%)	87 (97%)	3 (3%)	0	100	100
39	g	149/156 (96%)	144 (97%)	5 (3%)	0	100	100
40	h	129/132 (98%)	116 (90%)	13 (10%)	0	100	100
41	i	101/130 (78%)	95 (94%)	6 (6%)	0	100	100
42	j	93/102 (91%)	87 (94%)	6 (6%)	0	100	100
43	k	116/131 (88%)	110 (95%)	6 (5%)	0	100	100
44	l	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
45	m	90/121 (74%)	85 (94%)	5 (6%)	0	100	100
46	n	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	34
47	o	83/89 (93%)	79 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	p	86/90 (96%)	81 (94%)	5 (6%)	0	100	100
49	q	82/87 (94%)	76 (93%)	6 (7%)	0	100	100
50	r	62/79 (78%)	56 (90%)	5 (8%)	1 (2%)	7	36
51	s	75/92 (82%)	69 (92%)	6 (8%)	0	100	100
52	t	81/88 (92%)	79 (98%)	2 (2%)	0	100	100
53	u	56/62 (90%)	54 (96%)	2 (4%)	0	100	100
54	v	544/785 (69%)	527 (97%)	15 (3%)	2 (0%)	30	66
54	w	589/785 (75%)	569 (97%)	16 (3%)	4 (1%)	18	55
All	All	6293/7048 (89%)	5986 (95%)	297 (5%)	10 (0%)	44	77

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	v	384	SER
54	w	384	SER
23	Q	103	LEU
50	r	28	TYR
54	w	382	GLU
54	w	114	VAL
54	w	337	ASN
46	n	32	SER
54	v	114	VAL
23	Q	93	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	48/53 (91%)	46 (96%)	2 (4%)	26	48
2	1	46/47 (98%)	46 (100%)	0	100	100
3	2	39/39 (100%)	39 (100%)	0	100	100
4	3	54/56 (96%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	53/55 (96%)	53 (100%)	0	100	100
9	C	220/225 (98%)	219 (100%)	1 (0%)	81	82
10	D	167/170 (98%)	167 (100%)	0	100	100
11	E	169/170 (99%)	168 (99%)	1 (1%)	78	81
12	F	151/154 (98%)	149 (99%)	2 (1%)	61	73
13	G	148/151 (98%)	148 (100%)	0	100	100
16	J	120/123 (98%)	120 (100%)	0	100	100
17	K	101/101 (100%)	101 (100%)	0	100	100
18	L	110/110 (100%)	110 (100%)	0	100	100
19	M	109/116 (94%)	108 (99%)	1 (1%)	70	77
20	N	99/100 (99%)	98 (99%)	1 (1%)	68	77
21	O	93/93 (100%)	93 (100%)	0	100	100
22	P	100/100 (100%)	100 (100%)	0	100	100
23	Q	96/98 (98%)	96 (100%)	0	100	100
24	R	83/84 (99%)	83 (100%)	0	100	100
25	S	90/93 (97%)	90 (100%)	0	100	100
26	T	81/85 (95%)	81 (100%)	0	100	100
27	U	85/87 (98%)	85 (100%)	0	100	100
29	W	64/74 (86%)	64 (100%)	0	100	100
30	X	124/124 (100%)	121 (98%)	3 (2%)	43	63
31	Y	56/57 (98%)	55 (98%)	1 (2%)	51	67
32	Z	52/53 (98%)	52 (100%)	0	100	100
34	b	51/51 (100%)	51 (100%)	0	100	100
35	c	168/178 (94%)	168 (100%)	0	100	100
36	d	169/173 (98%)	167 (99%)	2 (1%)	63	74
37	e	128/130 (98%)	127 (99%)	1 (1%)	73	78
38	f	81/84 (96%)	78 (96%)	3 (4%)	30	51
39	g	127/132 (96%)	127 (100%)	0	100	100
40	h	111/112 (99%)	111 (100%)	0	100	100
41	i	81/102 (79%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	j	86/92 (94%)	86 (100%)	0	100	100
43	k	90/100 (90%)	90 (100%)	0	100	100
44	l	114/116 (98%)	114 (100%)	0	100	100
45	m	80/104 (77%)	80 (100%)	0	100	100
46	n	53/54 (98%)	53 (100%)	0	100	100
47	o	80/83 (96%)	79 (99%)	1 (1%)	61	73
48	p	74/76 (97%)	74 (100%)	0	100	100
49	q	77/80 (96%)	77 (100%)	0	100	100
50	r	56/64 (88%)	56 (100%)	0	100	100
51	s	69/81 (85%)	68 (99%)	1 (1%)	59	72
52	t	66/70 (94%)	66 (100%)	0	100	100
53	u	47/50 (94%)	47 (100%)	0	100	100
54	v	472/674 (70%)	467 (99%)	5 (1%)	65	75
54	w	513/674 (76%)	509 (99%)	4 (1%)	73	78
All	All	5386/5933 (91%)	5357 (100%)	29 (0%)	78	82

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	11	MET
1	0	28	THR
9	C	197	ASN
11	E	32	VAL
12	F	122	PHE
12	F	164	GLU
19	M	44	ASN
20	N	83	LEU
30	X	30	LEU
30	X	68	LEU
30	X	75	LEU
31	Y	23	GLU
36	d	90	LEU
36	d	94	LEU
37	e	120	VAL
38	f	18	SER
38	f	52	ILE
38	f	89	ILE

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Mol	Chain	Res	Type
47	o	42	HIS
51	s	25	THR
54	v	71	ILE
54	v	116	ILE
54	v	338	THR
54	v	526	LEU
54	v	596	THR
54	w	189	ILE
54	w	205	TYR
54	w	230	ILE
54	w	596	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
2	1	22	ASN
6	6	6	HIS
9	C	53	HIS
9	C	90	ASN
11	E	82	GLN
12	F	63	GLN
18	L	17	ASN
18	L	35	HIS
18	L	70	ASN
20	N	27	ASN
23	Q	38	GLN
25	S	28	GLN
26	T	55	ASN
30	X	43	ASN
35	c	99	HIS
35	c	101	ASN
37	e	45	HIS
38	f	28	ASN
38	f	61	GLN
39	g	153	HIS
42	j	78	ASN
44	l	6	GLN
44	l	86	ASN
48	p	72	ASN
48	p	77	GLN
51	s	29	GLN
54	v	3	GLN

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Mol	Chain	Res	Type
54	v	137	ASN
54	v	143	HIS
54	v	160	GLN
54	v	234	ASN
54	v	235	ASN
54	v	271	GLN
54	v	356	GLN
54	v	374	HIS
54	v	409	ASN
54	v	490	ASN
54	v	517	ASN
54	v	555	GLN
54	v	557	GLN
54	w	46	GLN
54	w	194	ASN
54	w	238	GLN
54	w	239	GLN
54	w	274	GLN
54	w	309	HIS
54	w	316	GLN
54	w	374	HIS
54	w	409	ASN
54	w	555	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	H	76/77 (98%)	14 (18%)	2 (2%)
28	V	2881/2928 (98%)	634 (22%)	64 (2%)
33	a	1532/1533 (99%)	266 (17%)	0
7	A	25/26 (96%)	12 (48%)	5 (20%)
8	B	111/112 (99%)	28 (25%)	4 (3%)
All	All	4625/4676 (98%)	954 (20%)	75 (1%)

All (954) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	33	A
7	A	34	A
7	A	35	A
7	A	37	G

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Mol	Chain	Res	Type
7	A	38	A
7	A	39	U
7	A	40	G
7	A	43	G
7	A	45	C
7	A	46	A
7	A	47	G
7	A	49	A
8	B	10	G
8	B	11	A
8	B	12	U
8	B	22	G
8	B	23	U
8	B	31	G
8	B	32	U
8	B	33	U
8	B	38	U
8	B	39	A
8	B	41	C
8	B	48	G
8	B	49	G
8	B	50	A
8	B	53	U
8	B	54	U
8	B	55	A
8	B	59	U
8	B	60	C
8	B	62	U
8	B	66	C
8	B	86	U
8	B	87	U
8	B	97	A
8	B	101	U
8	B	107	G
8	B	108	C
8	B	110	G
14	H	9	A
14	H	17	U
14	H	18	G
14	H	19	U
14	H	21	A
14	H	36	C

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Mol	Chain	Res	Type
14	H	37	A
14	H	48	C
14	H	55	U
14	H	56	C
14	H	70	A
14	H	72	C
14	H	74	C
14	H	76	A
28	V	8	U
28	V	13	A
28	V	23	G
28	V	26	G
28	V	34	U
28	V	46	C
28	V	51	G
28	V	60	G
28	V	71	A
28	V	74	U
28	V	75	G
28	V	76	C
28	V	77	U
28	V	78	U
28	V	79	C
28	V	85	G
28	V	86	C
28	V	87	U
28	V	89	U
28	V	90	A
28	V	92	G
28	V	93	C
28	V	99	U
28	V	100	U
28	V	101	G
28	V	117	A
28	V	119	U
28	V	124	A
28	V	125	A
28	V	141	U
28	V	145	G
28	V	162	A
28	V	164	U
28	V	175	G

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Mol	Chain	Res	Type
28	V	176	A
28	V	177	G
28	V	178	A
28	V	179	A
28	V	182	C
28	V	184	G
28	V	186	C
28	V	187	C
28	V	188	C
28	V	199	A
28	V	200	A
28	V	202	A
28	V	207	A
28	V	215	G
28	V	216	A
28	V	219	A
28	V	224	A
28	V	225	A
28	V	226	A
28	V	231	A
28	V	232	U
28	V	233	G
28	V	234	C
28	V	242	U
28	V	251	G
28	V	252	C
28	V	253	G
28	V	258	A
28	V	269	G
28	V	283	G
28	V	284	C
28	V	286	U
28	V	287	G
28	V	291	C
28	V	296	G
28	V	297	G
28	V	301	U
28	V	302	A
28	V	307	A
28	V	308	C
28	V	310	C
28	V	329	A

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Mol	Chain	Res	Type
28	V	342	A
28	V	344	G
28	V	345	A
28	V	346	G
28	V	348	U
28	V	352	G
28	V	361	G
28	V	367	G
28	V	373	A
28	V	374	A
28	V	375	C
28	V	382	G
28	V	407	A
28	V	410	G
28	V	411	G
28	V	412	A
28	V	418	A
28	V	419	G
28	V	420	U
28	V	421	A
28	V	432	C
28	V	433	G
28	V	434	U
28	V	442	C
28	V	444	U
28	V	445	C
28	V	458	G
28	V	459	A
28	V	471	G
28	V	476	A
28	V	477	A
28	V	482	C
28	V	483	C
28	V	491	C
28	V	498	U
28	V	502	C
28	V	504	A
28	V	506	U
28	V	512	G
28	V	527	A
28	V	528	G
28	V	530	A

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Mol	Chain	Res	Type
28	V	537	A
28	V	548	A
28	V	550	G
28	V	554	U
28	V	555	C
28	V	556	C
28	V	568	G
28	V	573	C
28	V	575	A
28	V	577	U
28	V	578	A
28	V	579	G
28	V	592	A
28	V	593	A
28	V	595	G
28	V	598	U
28	V	599	G
28	V	607	G
28	V	616	A
28	V	617	G
28	V	619	A
28	V	632	U
28	V	647	A
28	V	648	G
28	V	649	G
28	V	658	A
28	V	659	A
28	V	662	U
28	V	667	A
28	V	673	A
28	V	683	A
28	V	690	A
28	V	691	U
28	V	692	A
28	V	699	A
28	V	700	U
28	V	701	G
28	V	702	A
28	V	718	C
28	V	719	C
28	V	733	U
28	V	764	C

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Mol	Chain	Res	Type
28	V	765	A
28	V	773	G
28	V	777	C
28	V	787	C
28	V	788	G
28	V	790	A
28	V	794	U
28	V	795	G
28	V	810	G
28	V	811	A
28	V	822	G
28	V	823	G
28	V	829	A
28	V	831	U
28	V	832	G
28	V	837	U
28	V	845	G
28	V	852	G
28	V	859	C
28	V	866	A
28	V	874	U
28	V	892	U
28	V	906	G
28	V	908	A
28	V	913	A
28	V	914	C
28	V	929	G
28	V	931	C
28	V	933	C
28	V	934	U
28	V	935	A
28	V	936	C
28	V	937	C
28	V	939	G
28	V	940	G
28	V	941	U
28	V	942	U
28	V	943	A
28	V	944	C
28	V	957	A
28	V	959	C
28	V	961	C

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Mol	Chain	Res	Type
28	V	962	C
28	V	964	A
28	V	973	G
28	V	980	C
28	V	987	A
28	V	991	A
28	V	992	G
28	V	999	A
28	V	1005	A
28	V	1007	G
28	V	1020	A
28	V	1027	A
28	V	1029	A
28	V	1036	A
28	V	1042	A
28	V	1051	C
28	V	1053	C
28	V	1054	A
28	V	1055	A
28	V	1058	U
28	V	1059	A
28	V	1068	G
28	V	1073	A
28	V	1079	U
28	V	1091	U
28	V	1094	A
28	V	1101	G
28	V	1102	G
28	V	1103	A
28	V	1106	U
28	V	1110	C
28	V	1111	U
28	V	1116	A
28	V	1117	G
28	V	1118	C
28	V	1119	A
28	V	1121	C
28	V	1124	C
28	V	1125	C
28	V	1126	A
28	V	1127	U
28	V	1128	U

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Mol	Chain	Res	Type
28	V	1134	A
28	V	1139	G
28	V	1148	C
28	V	1158	G
28	V	1159	U
28	V	1160	G
28	V	1161	A
28	V	1173	A
28	V	1178	U
28	V	1179	A
28	V	1180	C
28	V	1181	C
28	V	1182	G
28	V	1185	G
28	V	1187	U
28	V	1188	A
28	V	1243	A
28	V	1244	A
28	V	1245	G
28	V	1248	C
28	V	1249	U
28	V	1251	U
28	V	1259	G
28	V	1260	A
28	V	1264	G
28	V	1265	A
28	V	1270	C
28	V	1275	G
28	V	1276	G
28	V	1278	G
28	V	1293	A
28	V	1296	G
28	V	1306	G
28	V	1311	G
28	V	1312	A
28	V	1313	A
28	V	1315	G
28	V	1323	A
28	V	1325	A
28	V	1326	A
28	V	1327	U
28	V	1339	A

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Mol	Chain	Res	Type
28	V	1340	A
28	V	1341	U
28	V	1343	C
28	V	1344	C
28	V	1351	U
28	V	1352	U
28	V	1362	G
28	V	1364	C
28	V	1365	U
28	V	1368	U
28	V	1369	C
28	V	1370	C
28	V	1371	G
28	V	1372	C
28	V	1375	A
28	V	1384	C
28	V	1385	G
28	V	1389	C
28	V	1404	A
28	V	1415	C
28	V	1417	A
28	V	1418	U
28	V	1422	C
28	V	1423	A
28	V	1425	C
28	V	1426	A
28	V	1427	G
28	V	1431	G
28	V	1434	A
28	V	1435	U
28	V	1436	U
28	V	1442	A
28	V	1449	C
28	V	1450	C
28	V	1457	U
28	V	1459	U
28	V	1460	G
28	V	1465	A
28	V	1466	U
28	V	1472	G
28	V	1473	A
28	V	1475	G

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Mol	Chain	Res	Type
28	V	1476	C
28	V	1489	U
28	V	1490	A
28	V	1499	A
28	V	1500	U
28	V	1501	U
28	V	1502	G
28	V	1506	A
28	V	1507	U
28	V	1508	C
28	V	1514	C
28	V	1516	A
28	V	1525	G
28	V	1526	G
28	V	1527	C
28	V	1528	U
28	V	1529	G
28	V	1530	G
28	V	1531	G
28	V	1532	A
28	V	1536	A
28	V	1539	C
28	V	1540	A
28	V	1542	A
28	V	1543	U
28	V	1547	U
28	V	1553	A
28	V	1557	G
28	V	1558	G
28	V	1559	C
28	V	1560	U
28	V	1566	G
28	V	1568	G
28	V	1570	U
28	V	1571	G
28	V	1573	C
28	V	1614	A
28	V	1617	A
28	V	1626	U
28	V	1632	G
28	V	1634	U
28	V	1638	A

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Mol	Chain	Res	Type
28	V	1653	A
28	V	1655	A
28	V	1661	A
28	V	1679	A
28	V	1691	A
28	V	1692	U
28	V	1693	C
28	V	1696	G
28	V	1697	A
28	V	1699	A
28	V	1700	A
28	V	1708	U
28	V	1719	G
28	V	1727	A
28	V	1738	U
28	V	1745	A
28	V	1757	G
28	V	1758	U
28	V	1759	U
28	V	1760	A
28	V	1761	G
28	V	1775	G
28	V	1776	A
28	V	1778	A
28	V	1779	G
28	V	1780	C
28	V	1781	C
28	V	1782	G
28	V	1785	G
28	V	1791	A
28	V	1792	G
28	V	1793	G
28	V	1802	A
28	V	1810	G
28	V	1811	C
28	V	1813	A
28	V	1829	C
28	V	1830	G
28	V	1837	U
28	V	1838	A
28	V	1843	G
28	V	1845	A

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Mol	Chain	Res	Type
28	V	1846	G
28	V	1850	A
28	V	1858	A
28	V	1862	C
28	V	1864	G
28	V	1877	A
28	V	1883	A
28	V	1885	A
28	V	1887	G
28	V	1891	G
28	V	1895	A
28	V	1899	U
28	V	1904	G
28	V	1915	U
28	V	1935	G
28	V	1943	C
28	V	1948	A
28	V	1958	G
28	V	1959	G
28	V	1965	A
28	V	1966	A
28	V	1967	A
28	V	1968	U
28	V	1969	U
28	V	1973	U
28	V	1984	U
28	V	1992	C
28	V	1993	G
28	V	1996	C
28	V	1999	A
28	V	2000	A
28	V	2001	G
28	V	2010	A
28	V	2020	U
28	V	2022	U
28	V	2023	C
28	V	2025	C
28	V	2026	A
28	V	2050	G
28	V	2051	U
28	V	2052	A
28	V	2054	C

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Mol	Chain	Res	Type
28	V	2059	A
28	V	2060	A
28	V	2061	G
28	V	2062	A
28	V	2064	G
28	V	2072	C
28	V	2079	C
28	V	2084	C
28	V	2085	G
28	V	2089	A
28	V	2090	G
28	V	2098	G
28	V	2114	C
28	V	2121	U
28	V	2122	G
28	V	2123	A
28	V	2125	U
28	V	2128	U
28	V	2131	U
28	V	2134	A
28	V	2135	G
28	V	2136	C
28	V	2145	G
28	V	2146	A
28	V	2147	U
28	V	2148	A
28	V	2149	G
28	V	2154	G
28	V	2156	G
28	V	2161	G
28	V	2162	G
28	V	2167	C
28	V	2174	C
28	V	2177	G
28	V	2182	G
28	V	2184	U
28	V	2185	G
28	V	2187	A
28	V	2188	G
28	V	2189	G
28	V	2197	G
28	V	2199	G

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Mol	Chain	Res	Type
28	V	2200	A
28	V	2201	U
28	V	2203	C
28	V	2204	U
28	V	2205	A
28	V	2206	C
28	V	2208	C
28	V	2219	G
28	V	2226	U
28	V	2227	A
28	V	2228	A
28	V	2229	C
28	V	2230	C
28	V	2231	C
28	V	2232	A
28	V	2233	C
28	V	2234	C
28	V	2245	G
28	V	2246	G
28	V	2252	A
28	V	2254	A
28	V	2255	C
28	V	2267	G
28	V	2268	G
28	V	2280	G
28	V	2296	A
28	V	2307	A
28	V	2312	C
28	V	2316	A
28	V	2317	A
28	V	2328	G
28	V	2330	A
28	V	2334	U
28	V	2335	U
28	V	2336	G
28	V	2337	G
28	V	2338	A
28	V	2341	U
28	V	2347	G
28	V	2348	C
28	V	2350	G
28	V	2351	A

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Mol	Chain	Res	Type
28	V	2356	A
28	V	2362	A
28	V	2363	C
28	V	2364	A
28	V	2368	G
28	V	2376	C
28	V	2378	G
28	V	2379	C
28	V	2401	G
28	V	2412	G
28	V	2414	C
28	V	2431	U
28	V	2432	C
28	V	2435	C
28	V	2452	U
28	V	2453	C
28	V	2454	A
28	V	2455	A
28	V	2457	G
28	V	2458	G
28	V	2459	A
28	V	2460	U
28	V	2469	C
28	V	2470	C
28	V	2477	A
28	V	2488	A
28	V	2504	C
28	V	2505	A
28	V	2507	A
28	V	2511	A
28	V	2523	G
28	V	2525	C
28	V	2527	C
28	V	2531	G
28	V	2532	A
28	V	2534	G
28	V	2535	U
28	V	2547	A
28	V	2549	C
28	V	2558	G
28	V	2564	G
28	V	2583	U

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Mol	Chain	Res	Type
28	V	2584	U
28	V	2593	A
28	V	2596	G
28	V	2601	A
28	V	2602	C
28	V	2605	G
28	V	2611	G
28	V	2613	U
28	V	2614	U
28	V	2631	A
28	V	2632	G
28	V	2638	U
28	V	2639	C
28	V	2642	U
28	V	2644	U
28	V	2659	G
28	V	2675	C
28	V	2690	G
28	V	2711	G
28	V	2718	U
28	V	2720	C
28	V	2743	G
28	V	2755	U
28	V	2762	A
28	V	2763	C
28	V	2764	G
28	V	2765	G
28	V	2773	G
28	V	2777	A
28	V	2784	C
28	V	2785	U
28	V	2794	A
28	V	2806	G
28	V	2807	A
28	V	2808	U
28	V	2818	C
28	V	2823	C
28	V	2824	G
28	V	2826	A
28	V	2831	A
28	V	2845	A
28	V	2859	G

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Mol	Chain	Res	Type
28	V	2860	A
28	V	2867	U
28	V	2868	G
28	V	2884	G
28	V	2892	G
28	V	2897	G
28	V	2899	C
28	V	2900	A
28	V	2901	G
28	V	2905	C
28	V	2916	A
28	V	2918	G
33	a	10	A
33	a	11	G
33	a	31	A
33	a	32	C
33	a	33	G
33	a	34	A
33	a	41	G
33	a	49	C
33	a	50	C
33	a	53	A
33	a	75	G
33	a	77	U
33	a	78	G
33	a	84	U
33	a	85	U
33	a	86	G
33	a	87	C
33	a	89	C
33	a	90	C
33	a	93	G
33	a	99	A
33	a	114	A
33	a	119	C
33	a	120	A
33	a	128	A
33	a	129	A
33	a	130	C
33	a	136	U
33	a	142	A
33	a	143	C

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Mol	Chain	Res	Type
33	a	153	U
33	a	154	C
33	a	158	G
33	a	162	C
33	a	172	U
33	a	177	G
33	a	181	G
33	a	182	U
33	a	189	A
33	a	197	G
33	a	208	A
33	a	209	A
33	a	211	A
33	a	218	U
33	a	219	U
33	a	221	G
33	a	249	G
33	a	253	U
33	a	255	G
33	a	258	A
33	a	259	G
33	a	274	G
33	a	275	C
33	a	287	A
33	a	297	G
33	a	314	A
33	a	336	C
33	a	337	A
33	a	338	C
33	a	340	G
33	a	352	A
33	a	354	G
33	a	360	C
33	a	362	G
33	a	373	U
33	a	375	U
33	a	380	C
33	a	381	A
33	a	385	G
33	a	392	G
33	a	396	G
33	a	405	A

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Mol	Chain	Res	Type
33	a	414	G
33	a	419	A
33	a	420	U
33	a	421	G
33	a	429	U
33	a	430	C
33	a	435	C
33	a	436	G
33	a	437	U
33	a	448	U
33	a	456	A
33	a	460	A
33	a	461	C
33	a	466	G
33	a	474	A
33	a	475	A
33	a	476	U
33	a	477	A
33	a	478	G
33	a	481	C
33	a	485	A
33	a	487	C
33	a	488	U
33	a	489	U
33	a	490	G
33	a	491	A
33	a	494	G
33	a	502	C
33	a	504	A
33	a	506	A
33	a	508	A
33	a	518	A
33	a	520	C
33	a	526	G
33	a	527	C
33	a	530	G
33	a	536	G
33	a	541	A
33	a	542	A
33	a	556	A
33	a	564	C
33	a	568	A

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Mol	Chain	Res	Type
33	a	571	U
33	a	573	U
33	a	582	A
33	a	585	G
33	a	586	G
33	a	590	G
33	a	597	G
33	a	605	A
33	a	641	G
33	a	642	U
33	a	643	C
33	a	651	A
33	a	662	U
33	a	696	A
33	a	732	U
33	a	733	G
33	a	756	U
33	a	757	A
33	a	758	A
33	a	764	G
33	a	787	G
33	a	802	U
33	a	803	A
33	a	824	A
33	a	826	C
33	a	841	G
33	a	849	G
33	a	853	C
33	a	855	G
33	a	856	C
33	a	882	A
33	a	883	A
33	a	885	C
33	a	924	A
33	a	943	G
33	a	944	C
33	a	945	A
33	a	950	C
33	a	963	G
33	a	964	G
33	a	966	U
33	a	968	A

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Mol	Chain	Res	Type
33	a	969	A
33	a	970	U
33	a	979	A
33	a	981	G
33	a	985	A
33	a	986	G
33	a	987	A
33	a	993	A
33	a	999	U
33	a	1002	U
33	a	1003	G
33	a	1007	U
33	a	1008	C
33	a	1009	C
33	a	1010	U
33	a	1011	C
33	a	1012	U
33	a	1014	A
33	a	1015	C
33	a	1017	A
33	a	1019	C
33	a	1023	G
33	a	1024	A
33	a	1028	A
33	a	1030	G
33	a	1033	G
33	a	1035	C
33	a	1036	C
33	a	1039	U
33	a	1041	C
33	a	1042	G
33	a	1046	G
33	a	1047	C
33	a	1050	A
33	a	1053	G
33	a	1058	G
33	a	1064	C
33	a	1075	U
33	a	1088	U
33	a	1089	G
33	a	1095	U
33	a	1104	G

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Mol	Chain	Res	Type
33	a	1105	U
33	a	1111	A
33	a	1112	A
33	a	1118	G
33	a	1122	C
33	a	1134	G
33	a	1135	U
33	a	1136	U
33	a	1140	A
33	a	1142	C
33	a	1145	U
33	a	1148	G
33	a	1149	U
33	a	1153	G
33	a	1161	A
33	a	1166	A
33	a	1168	U
33	a	1176	A
33	a	1178	A
33	a	1190	G
33	a	1192	U
33	a	1193	G
33	a	1205	A
33	a	1206	A
33	a	1211	U
33	a	1221	U
33	a	1222	A
33	a	1223	U
33	a	1237	C
33	a	1259	A
33	a	1261	A
33	a	1267	G
33	a	1278	A
33	a	1279	G
33	a	1289	A
33	a	1294	A
33	a	1295	C
33	a	1296	A
33	a	1308	A
33	a	1314	G
33	a	1326	C
33	a	1329	C

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Mol	Chain	Res	Type
33	a	1330	U
33	a	1331	C
33	a	1341	A
33	a	1347	G
33	a	1355	A
33	a	1366	A
33	a	1370	G
33	a	1372	A
33	a	1373	U
33	a	1377	G
33	a	1387	C
33	a	1407	A
33	a	1451	A
33	a	1455	A
33	a	1460	U
33	a	1462	U
33	a	1463	A
33	a	1464	G
33	a	1490	A
33	a	1500	U
33	a	1502	A
33	a	1503	A
33	a	1516	U
33	a	1527	G
33	a	1539	G
33	a	1540	G

All (75) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	33	A
7	A	34	A
7	A	38	A
7	A	39	U
7	A	45	C
8	B	31	G
8	B	37	A
8	B	48	G
8	B	49	G
14	H	47	U
14	H	55	U
28	V	88	G

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Mol	Chain	Res	Type
28	V	183	A
28	V	252	C
28	V	347	G
28	V	411	G
28	V	441	C
28	V	444	U
28	V	549	A
28	V	554	U
28	V	689	A
28	V	772	G
28	V	810	G
28	V	905	G
28	V	1093	G
28	V	1172	A
28	V	1243	A
28	V	1244	A
28	V	1250	G
28	V	1264	G
28	V	1269	A
28	V	1275	G
28	V	1305	A
28	V	1351	U
28	V	1435	U
28	V	1448	U
28	V	1507	U
28	V	1525	G
28	V	1527	C
28	V	1529	G
28	V	1530	G
28	V	1535	U
28	V	1565	U
28	V	1567	U
28	V	1570	U
28	V	1631	A
28	V	1726	G
28	V	1757	G
28	V	1784	A
28	V	1828	G
28	V	1882	A
28	V	1914	A
28	V	1972	U
28	V	1991	C

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Mol	Chain	Res	Type
28	V	2009	G
28	V	2022	U
28	V	2127	U
28	V	2155	A
28	V	2205	A
28	V	2254	A
28	V	2316	A
28	V	2335	U
28	V	2336	G
28	V	2349	A
28	V	2364	A
28	V	2452	U
28	V	2454	A
28	V	2468	A
28	V	2510	G
28	V	2534	G
28	V	2631	A
28	V	2710	C
28	V	2805	A
28	V	2883	C
28	V	2904	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

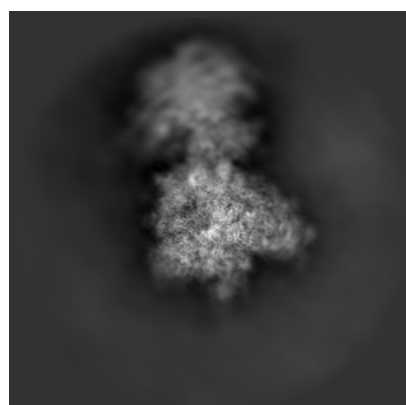
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14159. These allow visual inspection of the internal detail of the map and identification of artifacts.

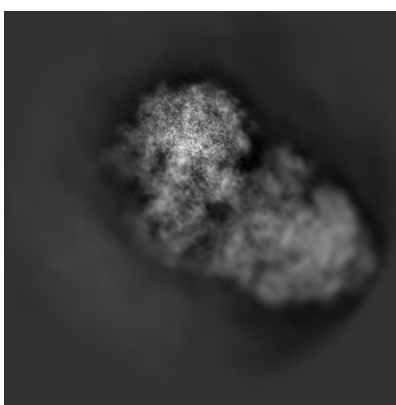
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

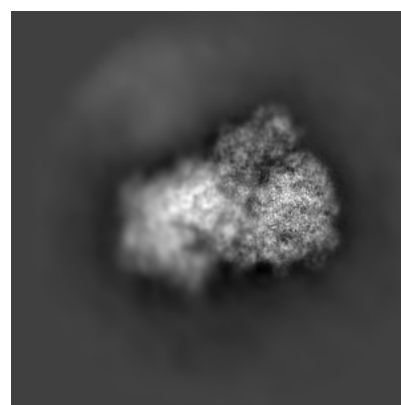
6.1.1 Primary map



X



Y

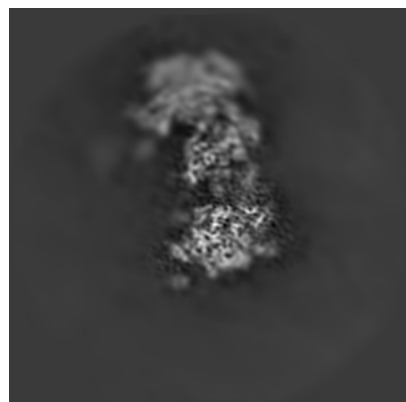


Z

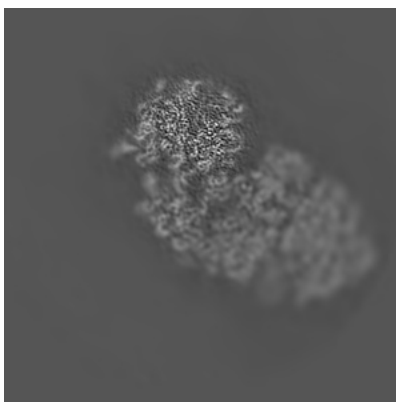
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

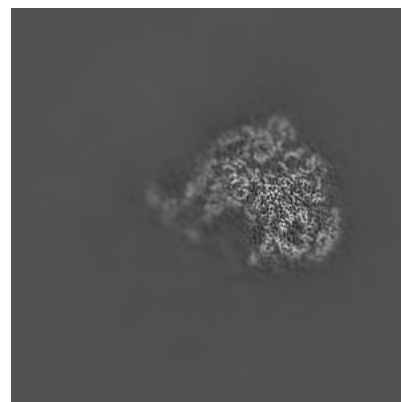
6.2.1 Primary map



X Index: 184



Y Index: 184

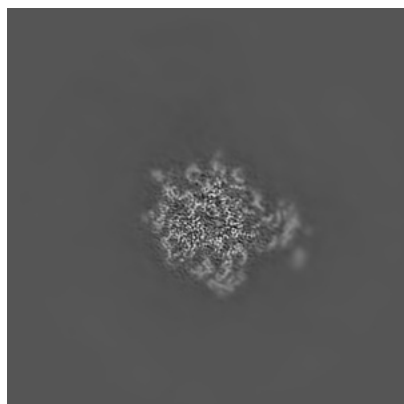


Z Index: 184

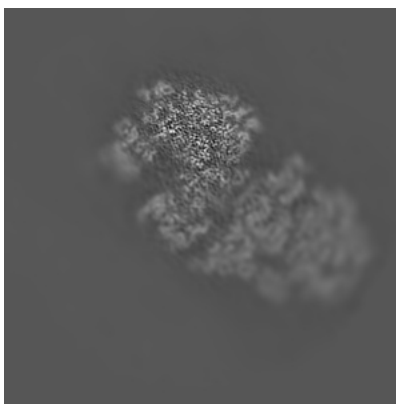
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

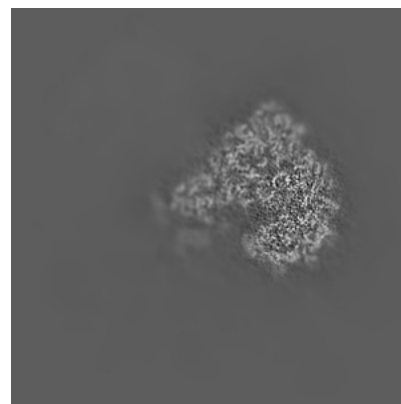
6.3.1 Primary map



X Index: 254



Y Index: 196

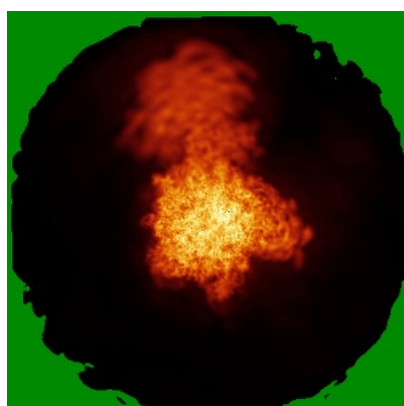


Z Index: 169

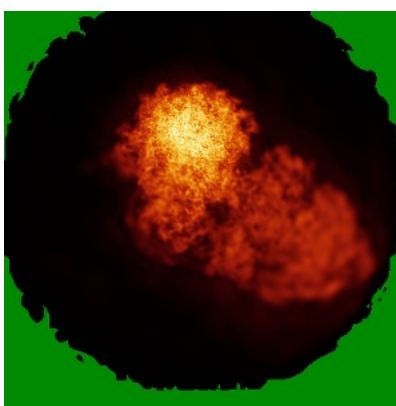
The images above show the largest variance slices of the map in three orthogonal directions.

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

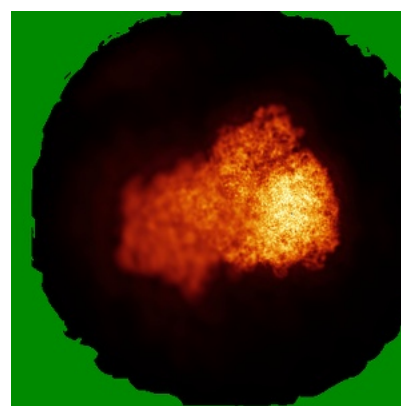
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

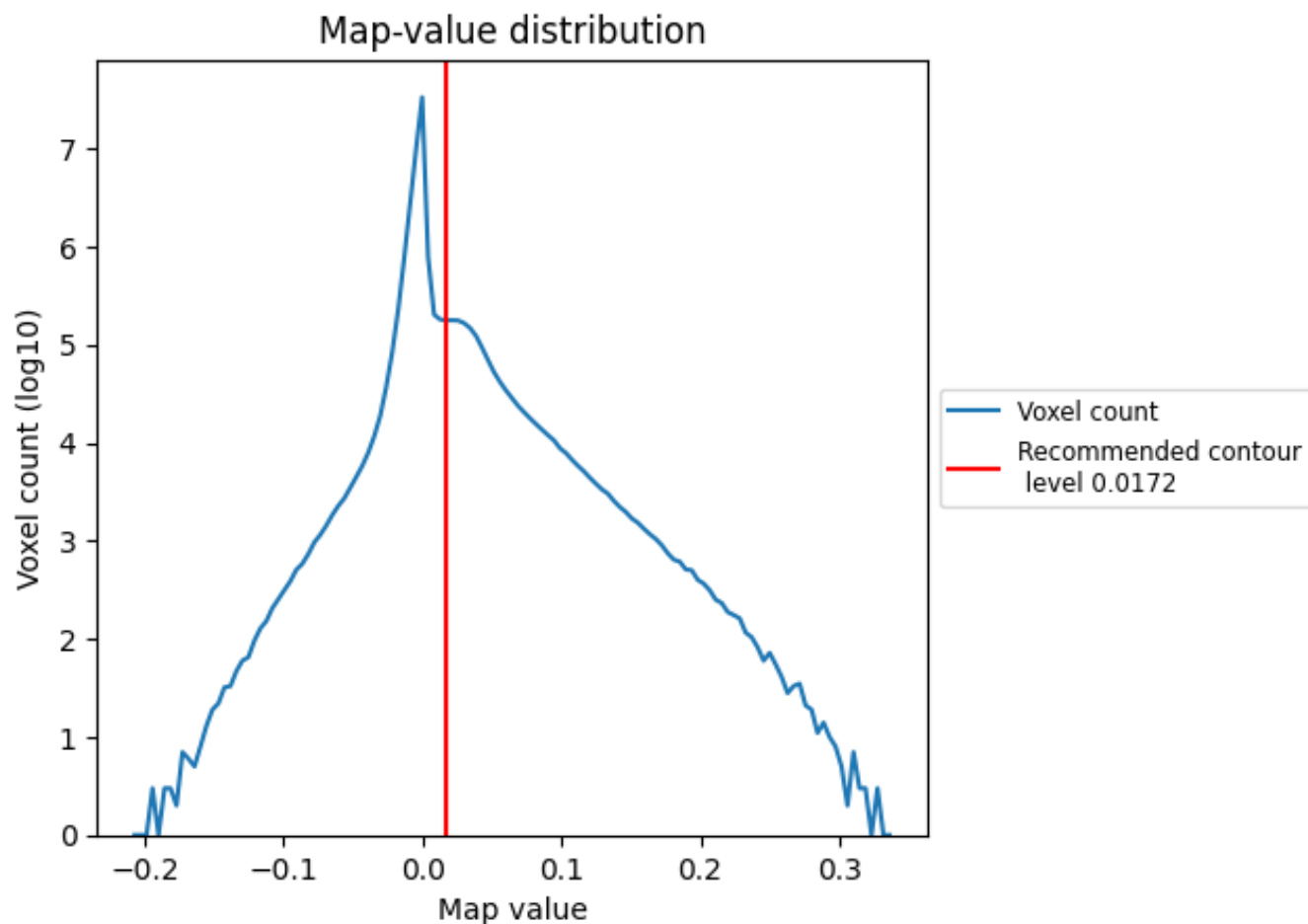
6.6 Mask visualisation

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

7 Map analysis [i](#)

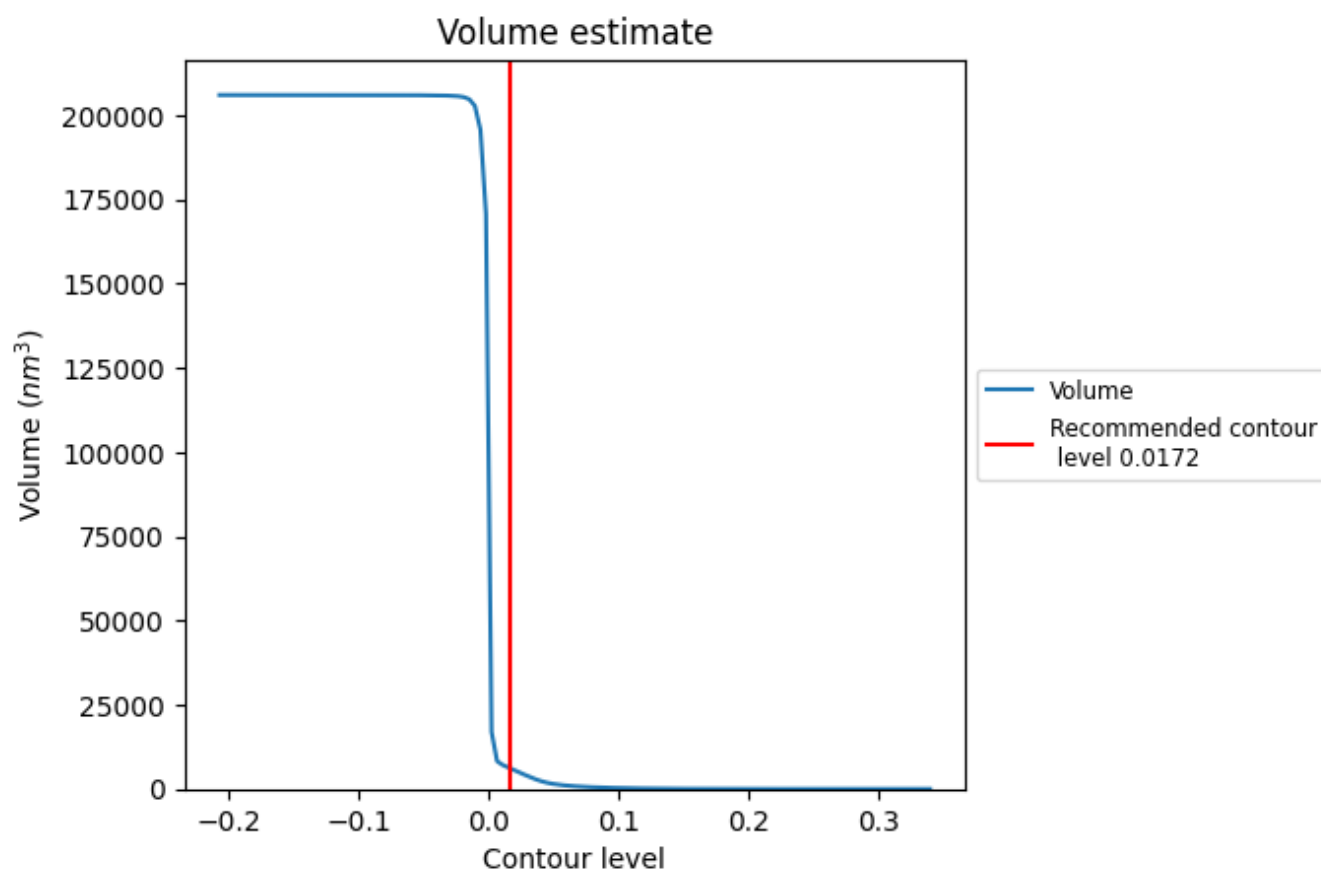
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

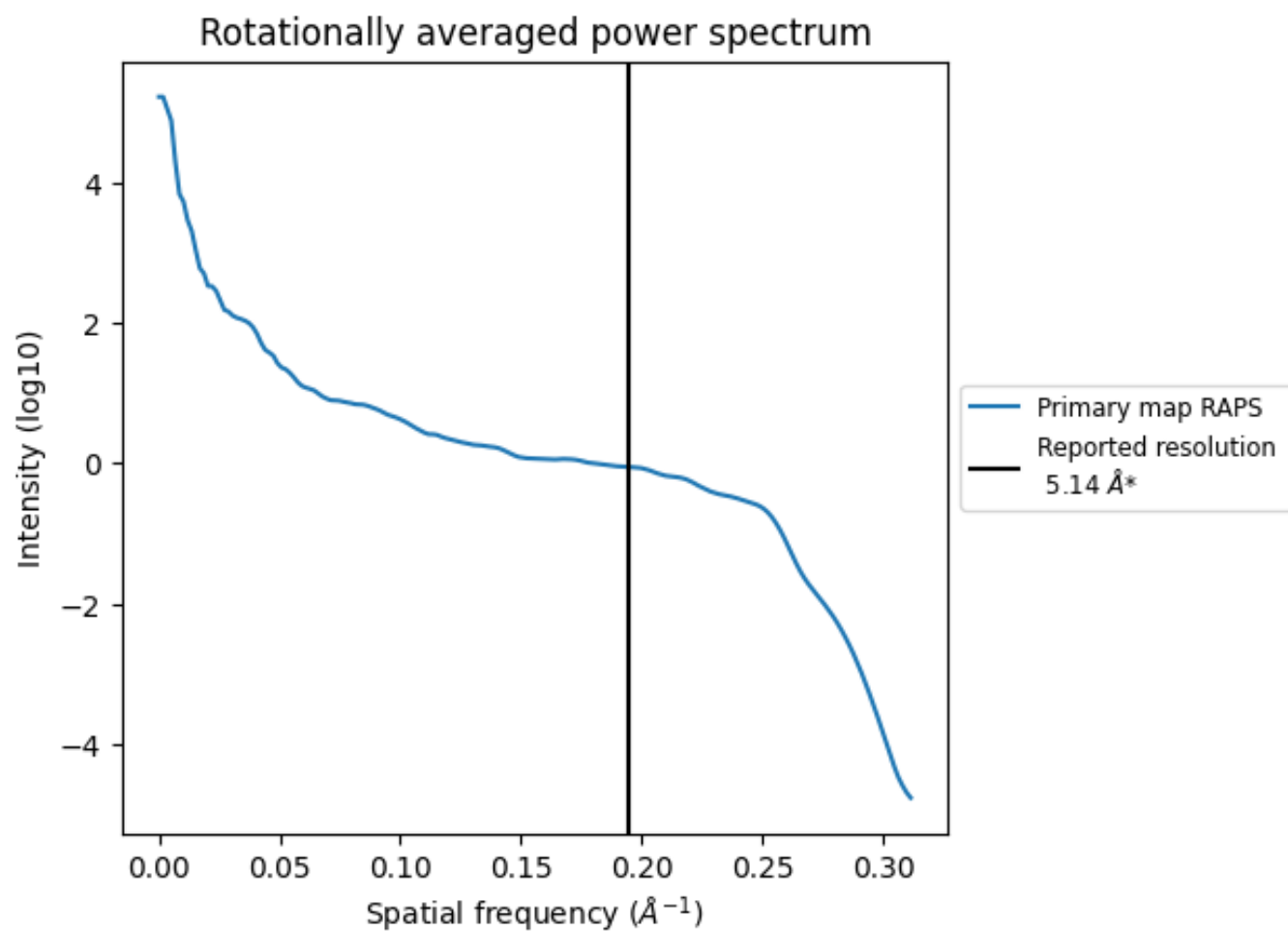
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6043 nm^3 ; this corresponds to an approximate mass of 5459 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 0.195 Å⁻¹

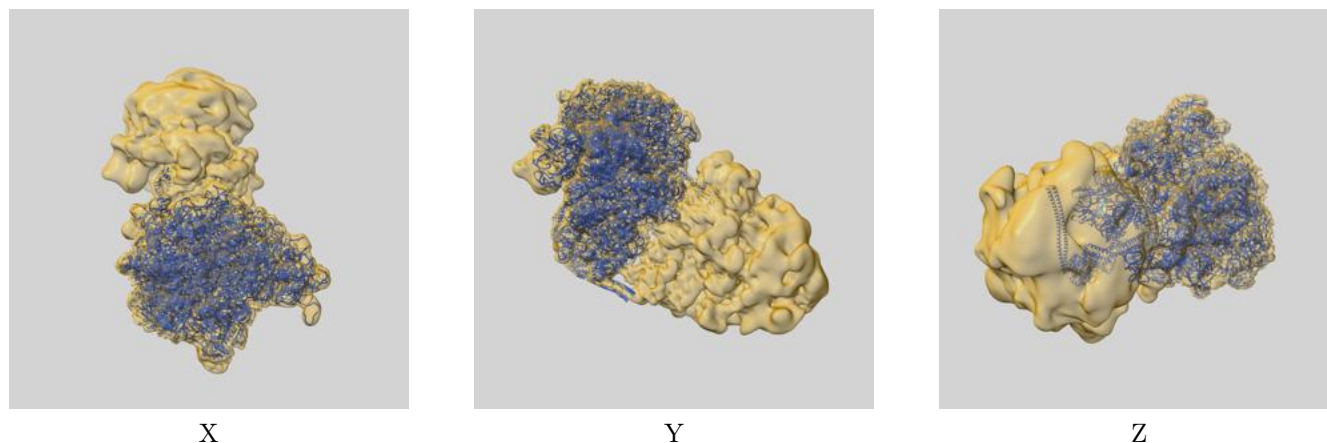
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

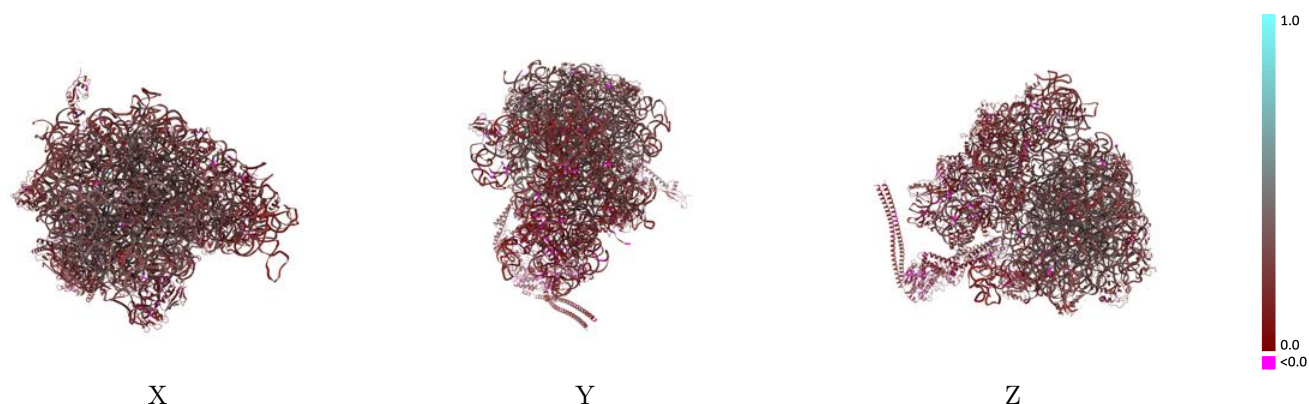
This section contains information regarding the fit between EMDB map EMD-14159 and PDB model 7QV3. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



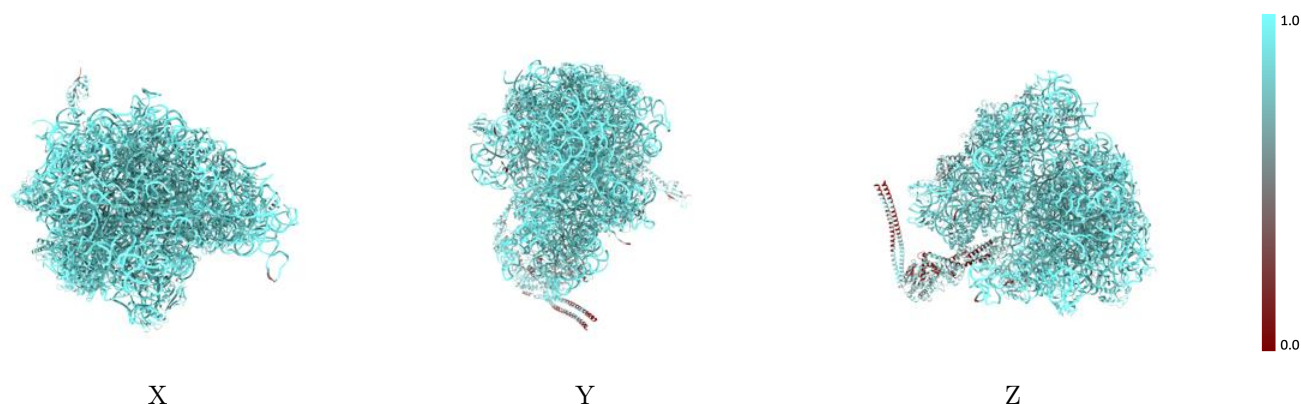
The images above show the 3D surface view of the map at the recommended contour level 0.0172 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



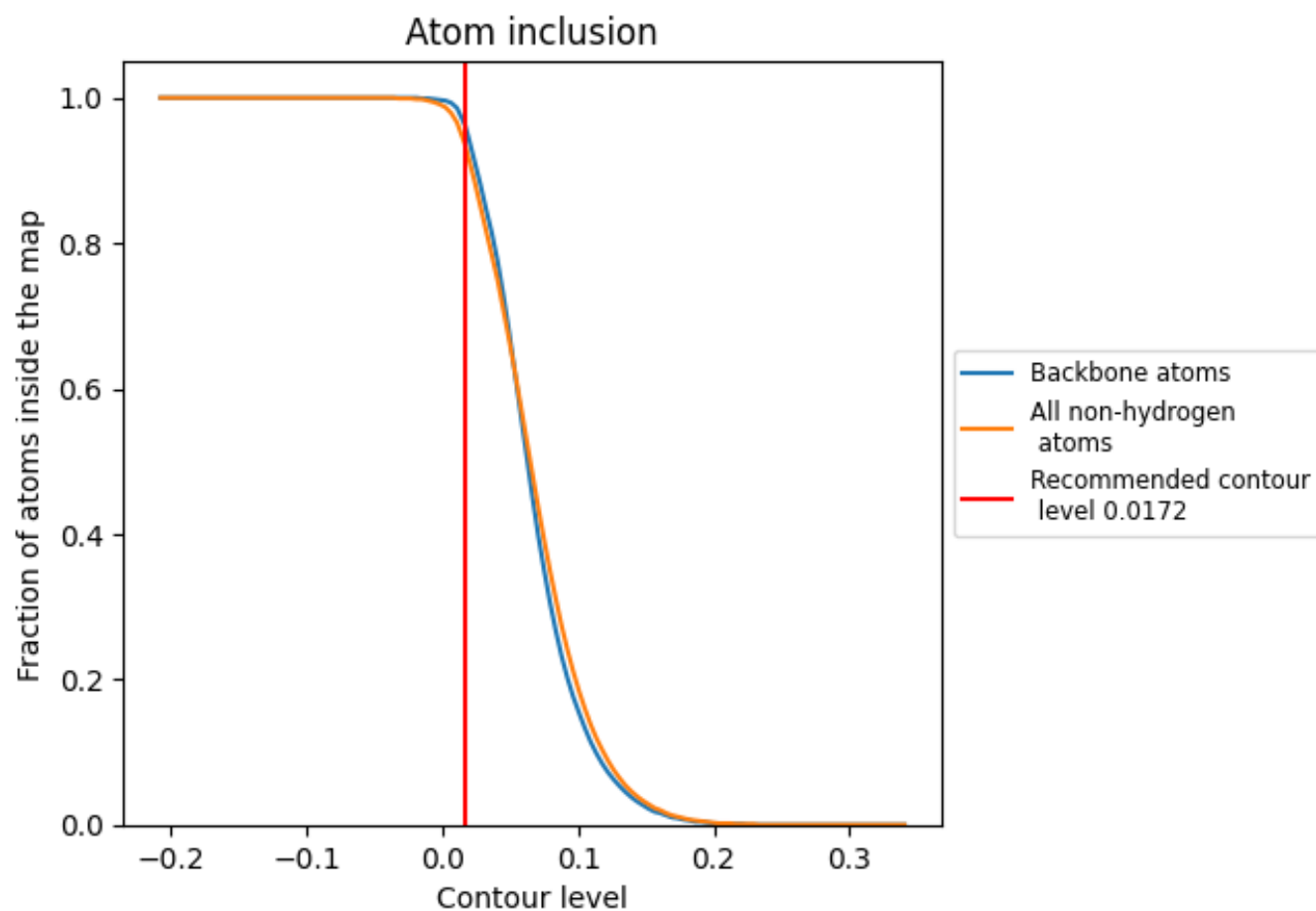
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0172).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0172) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.2480
0	 0.9080	 0.3000
1	 0.9220	 0.2440
2	 0.8960	 0.3180
3	 0.9000	 0.3550
4	 0.8550	 0.2090
6	 0.9300	 0.1610
A	 0.7980	 0.1250
B	 0.9940	 0.2530
C	 0.8930	 0.3170
D	 0.9070	 0.3090
E	 0.9200	 0.2620
F	 0.9030	 0.1500
G	 0.9260	 0.1810
H	 0.9700	 0.2330
I	 0.6500	 0.1160
J	 0.9230	 0.2970
K	 0.8720	 0.3210
L	 0.9260	 0.2840
M	 0.9100	 0.2600
N	 0.9120	 0.2830
O	 0.9260	 0.1790
P	 0.8950	 0.2790
Q	 0.9150	 0.2940
R	 0.9560	 0.2990
S	 0.8960	 0.2950
T	 0.9030	 0.2850
U	 0.9440	 0.2500
V	 0.9780	 0.3050
W	 0.8800	 0.2850
X	 0.7510	 0.1500
Y	 0.9530	 0.1900
Z	 0.9240	 0.2580
a	 0.9880	 0.2230
b	 0.6450	 0.1060



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Chain	Atom inclusion	Q-score
c	 0.6960	 0.1140
d	 0.8750	 0.1380
e	 0.8590	 0.1790
f	 0.8440	 0.1720
g	 0.8630	 0.1620
h	 0.8830	 0.1770
i	 0.9120	 0.1440
j	 0.9070	 0.1250
k	 0.8780	 0.2000
l	 0.8990	 0.1720
m	 0.9100	 0.1630
n	 0.8380	 0.1000
o	 0.8880	 0.1610
p	 0.8790	 0.1400
q	 0.8990	 0.1600
r	 0.8530	 0.1970
s	 0.9610	 0.1090
t	 0.8920	 0.1630
u	 0.8840	 0.2900
v	 0.4980	 0.0920
w	 0.7590	 0.1080