



## Full wwPDB EM Validation Report ⓘ

Jun 30, 2025 – 12:32 PM JST

PDB ID : 9K10 / pdb\_00009k10  
EMDB ID : EMD-61960  
Title : EF-G2 bound 50S ribosome subunit complex of M. smegmatis  
Authors : Sengupta, J.; Baid, P.  
Deposited on : 2024-10-16  
Resolution : 3.60 Å (reported)  
Based on initial model : 7XAM

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

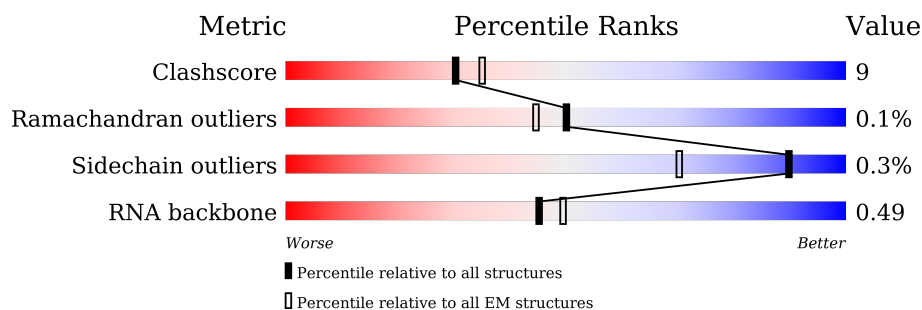
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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.












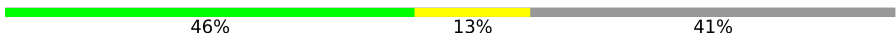















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	3	24	
2	5	709	
2	6	709	
3	B	118	
4	C	278	
5	D	217	
6	E	215	

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Mol	Chain	Length	Quality of chain
7	F	187	
8	G	179	
9	H	151	
10	I	175	
11	J	142	
12	K	147	
13	L	122	
14	M	147	
15	N	138	
16	O	199	
17	P	127	
18	Q	113	
19	R	129	
20	S	103	
21	T	153	
22	U	100	
23	V	105	
24	W	215	
25	X	88	
26	Y	64	
27	Z	77	
28	a	61	
29	b	57	
30	c	55	
31	d	47	

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Mol	Chain	Length	Quality of chain
32	e	64	<div><div></div><div>77%</div><div>22%</div><div></div></div>
33	f	37	<div><div></div><div>78%</div><div>22%</div><div></div></div>
34	g	75	<div><div></div><div>43%</div><div>21%</div><div>36%</div><div></div></div>
35	A	3127	<div><div></div><div>58%</div><div>33%</div><div>7%</div><div></div></div>

## 2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 107523 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 bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a protein called Translation elongation factor EF-G.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	709	Total	C	N	O	S	0	0
			5299	3311	931	1039	18		
2	6	709	Total	C	N	O	S	0	0
			5299	3311	931	1039	18		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 4 is a protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

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

- Molecule 11 is a protein called 50S ribosomal protein L11.

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

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

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

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

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

- Molecule 17 is a protein called 50S ribosomal protein L18.

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

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

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

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 27 is a protein called 50S ribosomal protein L29.



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

- Molecule 28 is a protein called 50S ribosomal protein L30.

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

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

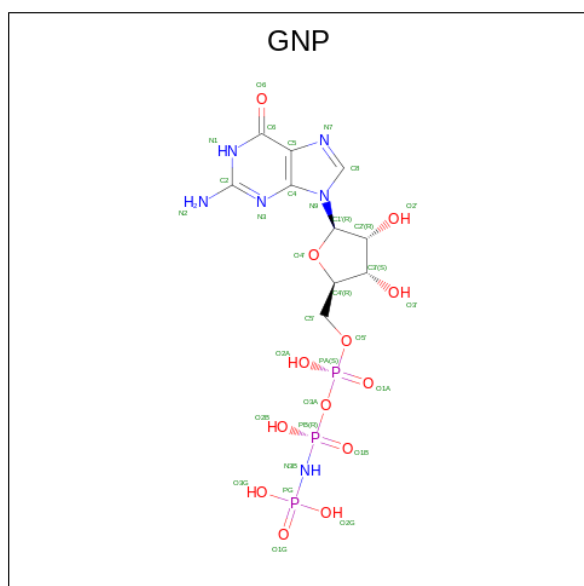
- Molecule 34 is a protein called 50S ribosomal protein L31.

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

- Molecule 35 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	3062	Total	C	N	O	P	0	0
			65763	29311	12094	21296	3062		

- Molecule 36 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula:  $C_{10}H_{17}N_6O_{13}P_3$ ) (labeled as "Ligand of Interest" by depositor).



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Mol	Chain	Residues	Atoms		AltConf
37	F	1	Total 1	Mg 1	0
37	N	1	Total 1	Mg 1	0
37	T	1	Total 1	Mg 1	0
37	X	1	Total 1	Mg 1	0
37	A	388	Total 388	Mg 388	0


- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

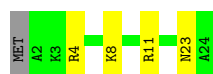
Mol	Chain	Residues	Atoms		AltConf
38	Y	1	Total 1	Zn 1	0
38	c	1	Total 1	Zn 1	0
38	f	1	Total 1	Zn 1	0
38	g	1	Total 1	Zn 1	0

### 3 Residue-property plots

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

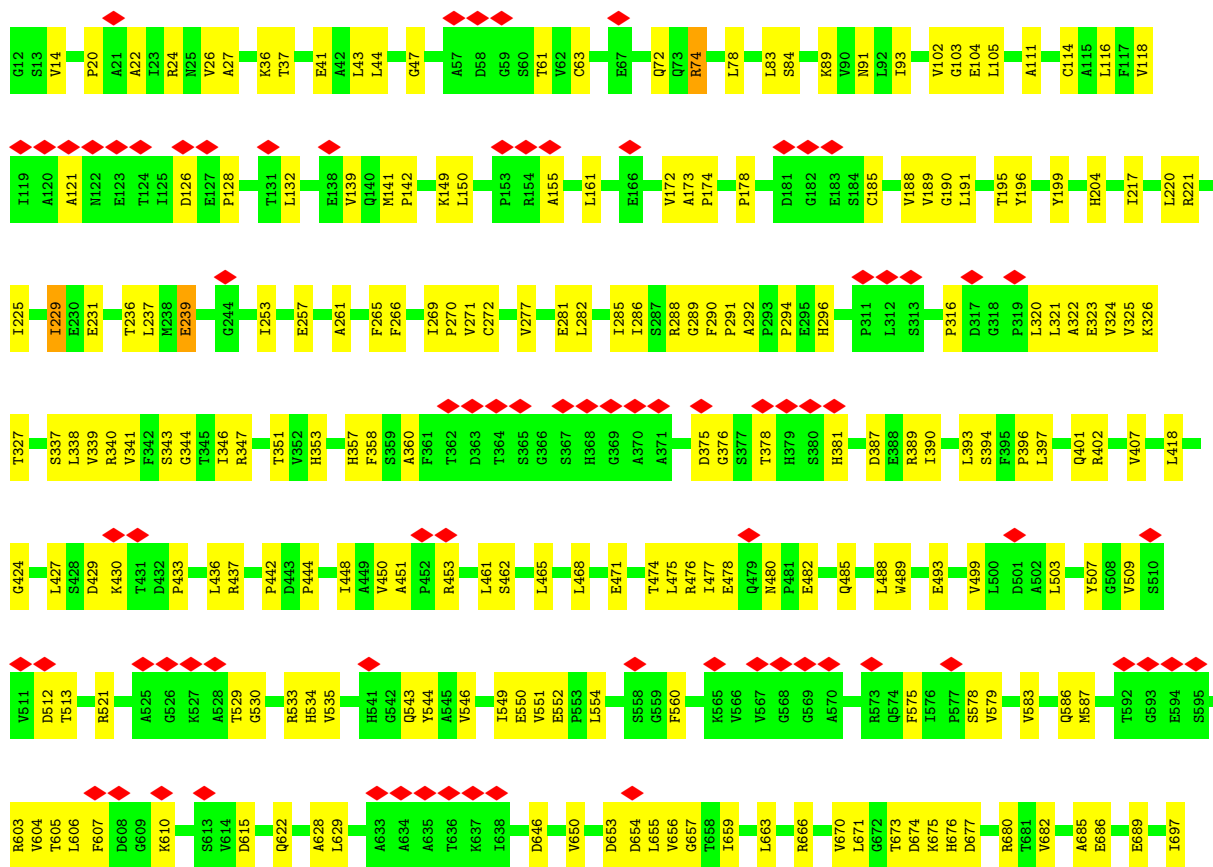
- Molecule 1: 50S ribosomal protein bL37

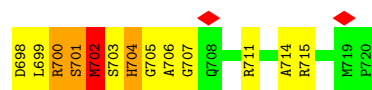
Chain 3: 



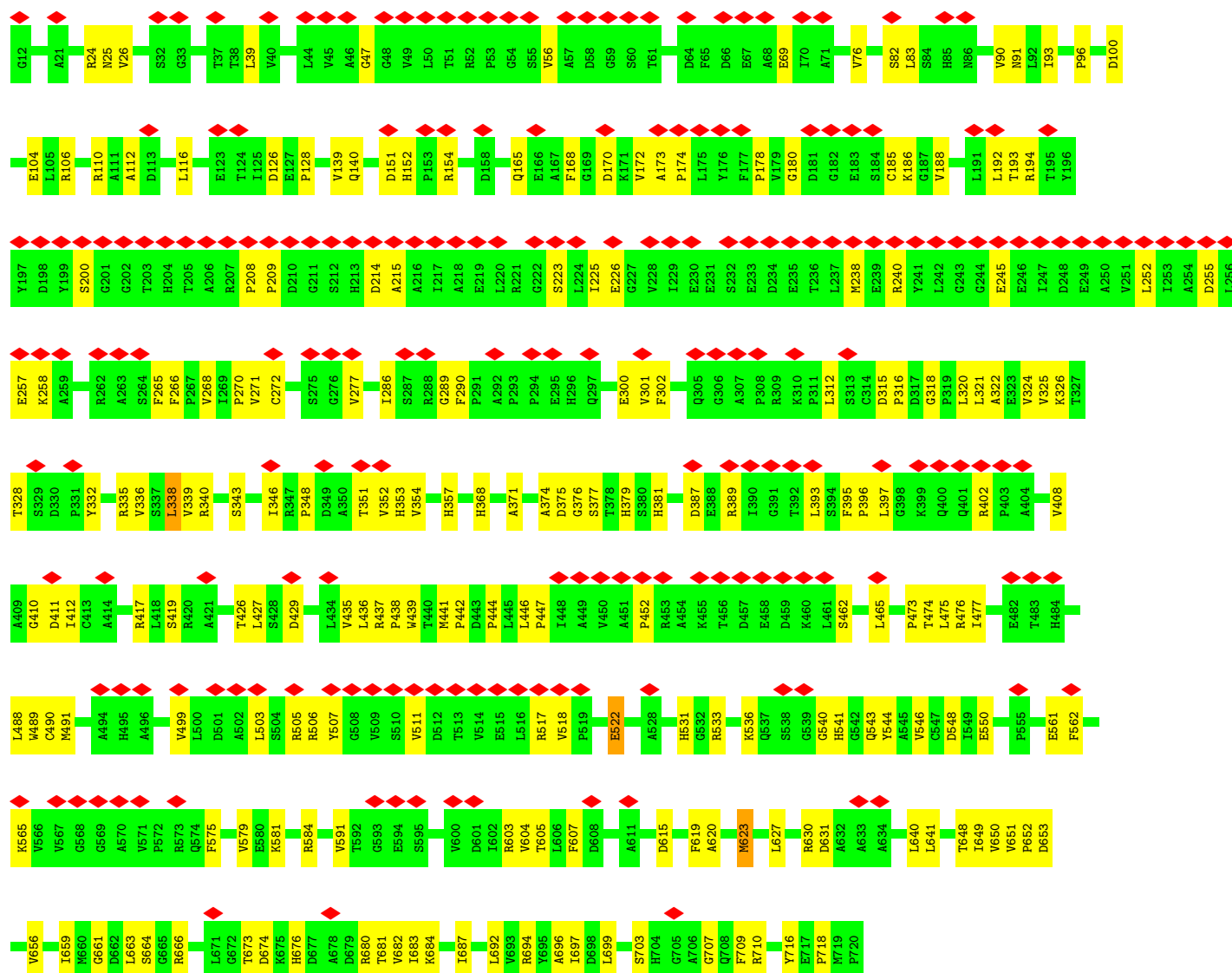
- Molecule 2: Translation elongation factor EF-G

Chain 5: 

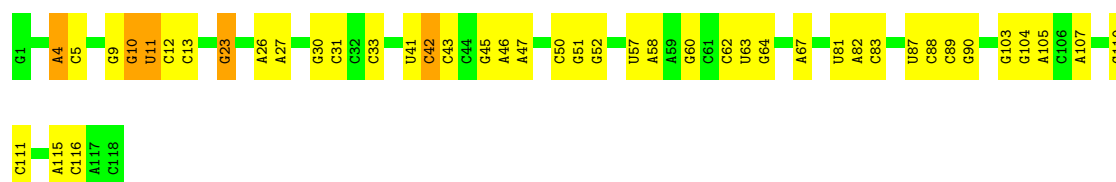




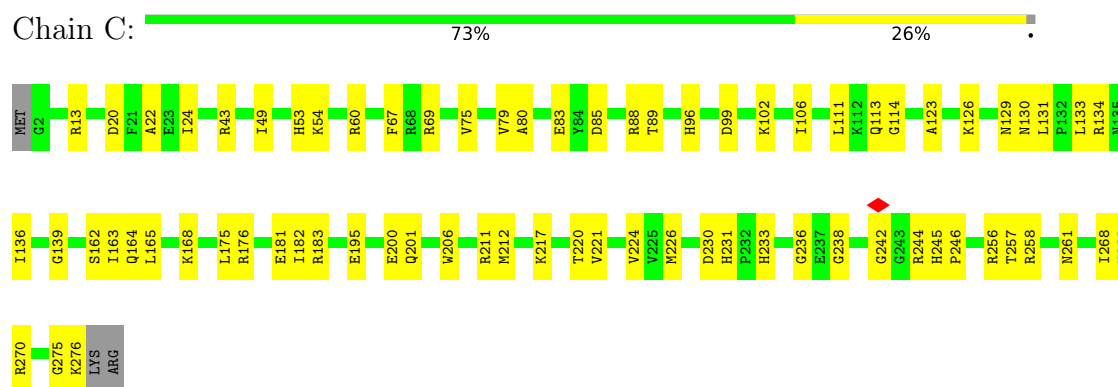
• Molecule 2: Translation elongation factor EF-G



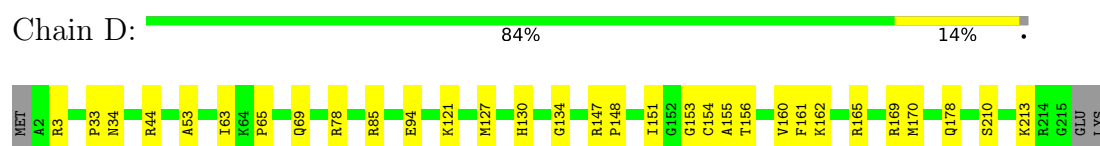
• Molecule 3: 5S ribosomal RNA



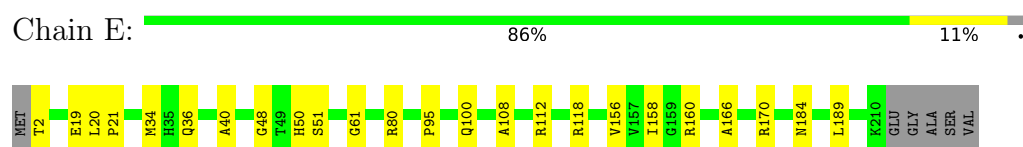
- Molecule 4: 50S ribosomal protein L2



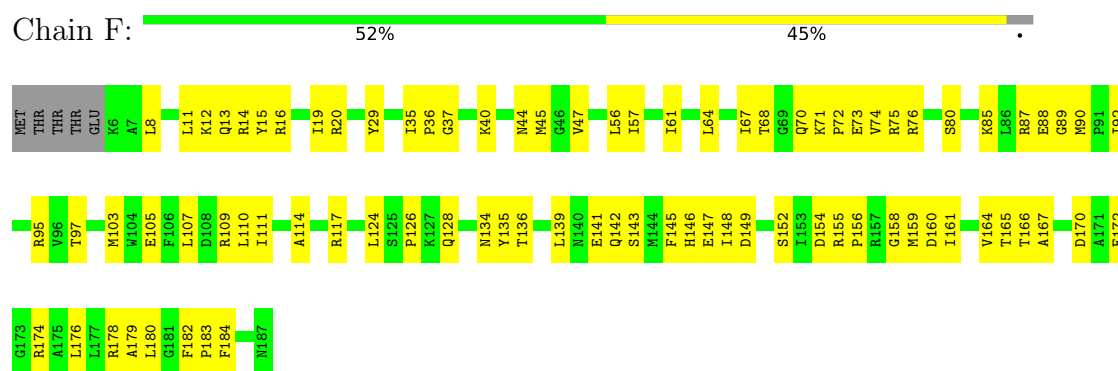
- Molecule 5: 50S ribosomal protein L3



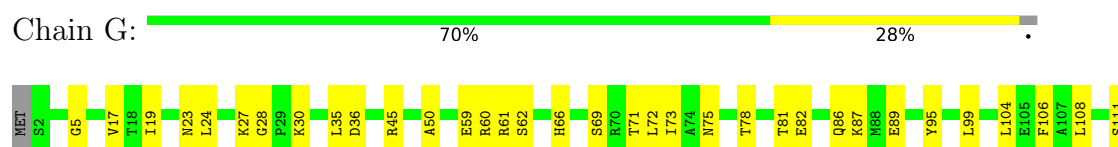
- Molecule 6: 50S ribosomal protein L4



- Molecule 7: 50S ribosomal protein L5



- Molecule 8: 50S ribosomal protein L6





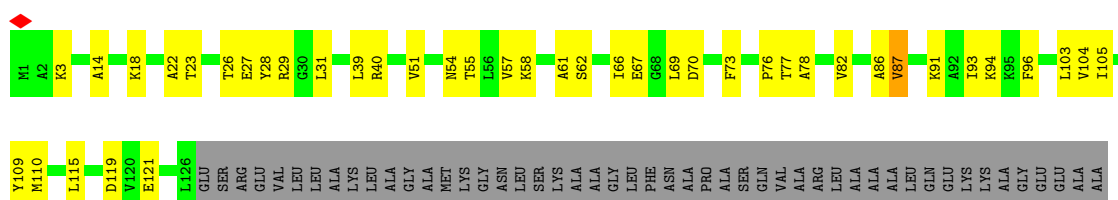
- Molecule 9: 50S ribosomal protein L9

Chain H: 83% 17%



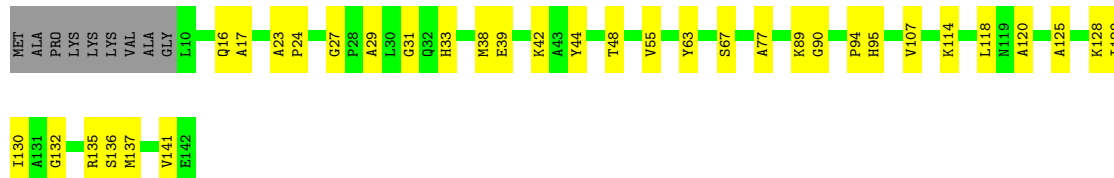
- Molecule 10: 50S ribosomal protein L10

Chain I: 48% 23% 28%



- Molecule 11: 50S ribosomal protein L11

Chain J: 70% 24% 6%



- Molecule 12: 50S ribosomal protein L13

Chain K: 80% 20%



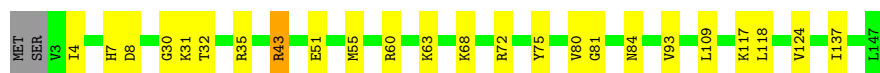
- Molecule 13: 50S ribosomal protein L14

Chain L: 76% 24%



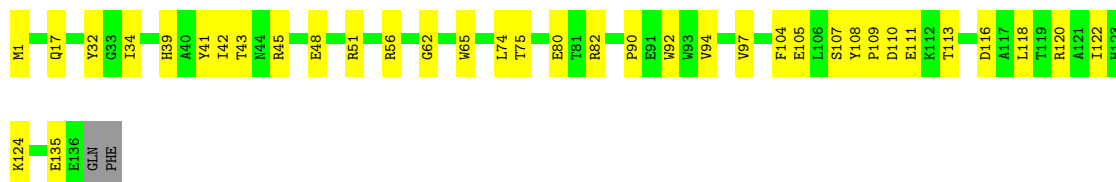
- Molecule 14: 50S ribosomal protein L15

Chain M: 82% 16%



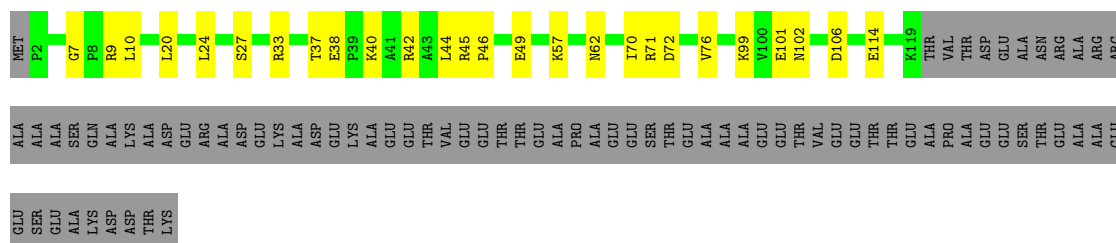
- Molecule 15: 50S ribosomal protein L16

Chain N: 72% 26% .



- Molecule 16: 50S ribosomal protein L17

Chain O: 46% 13% 41%



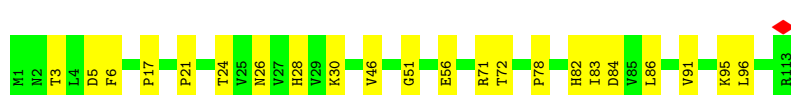
- Molecule 17: 50S ribosomal protein L18

Chain P: 78% 21% .



- Molecule 18: 50S ribosomal protein L19

Chain Q: 81% 19%



- Molecule 19: 50S ribosomal protein L20

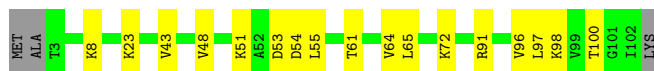
Chain R: 81% 15% .



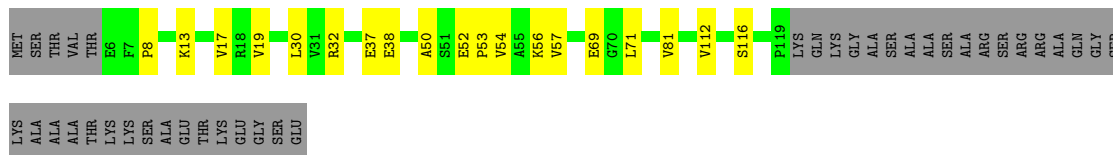
- Molecule 20: 50S ribosomal protein L21

Chain S: 81% 17% .

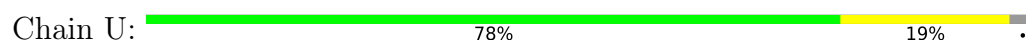




- Molecule 21: 50S ribosomal protein L22



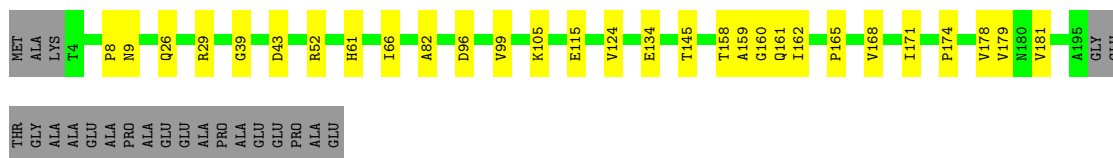
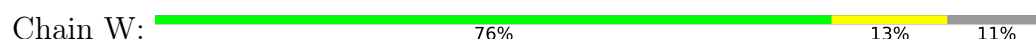
- Molecule 22: 50S ribosomal protein L23



- Molecule 23: Large ribosomal subunit protein uL24



- Molecule 24: 50S ribosomal protein L25



- Molecule 25: 50S ribosomal protein L27



- Molecule 26: 50S ribosomal protein L28



- Molecule 27: 50S ribosomal protein L29

Chain Z:  64% 19% 17%



- Molecule 28: 50S ribosomal protein L30

Chain a:  89% 8% .



- Molecule 29: 50S ribosomal protein L32

Chain b:  75% 19% 5%




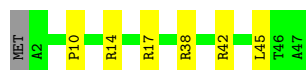
- Molecule 30: 50S ribosomal protein L33 1

Chain c:  67% 22% 11%



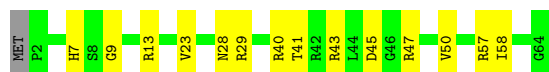
- Molecule 31: 50S ribosomal protein L34

Chain d:  85% 13% .




- Molecule 32: 50S ribosomal protein L35

Chain e:  77% 22% .



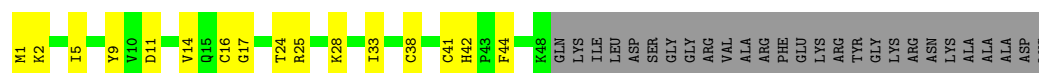
- Molecule 33: 50S ribosomal protein L36

Chain f:  78% 22%



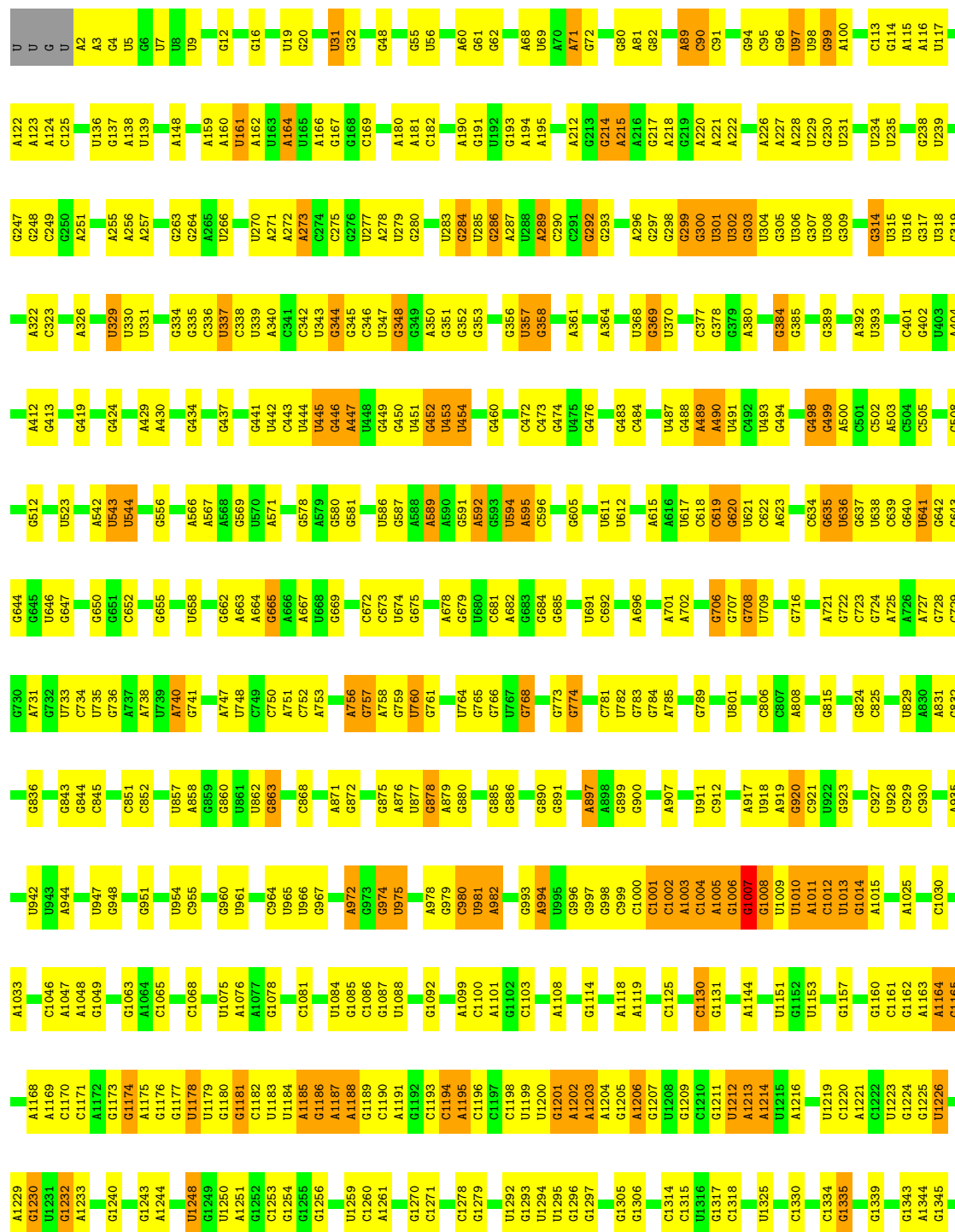
- Molecule 34: 50S ribosomal protein L31

Chain g:  43% 21% 36%



• Molecule 35: 23S ribosomal RNA

Chain A:  58% 33% 7%



A2609	A2522	U2411	A2342	G2251	G2158	U2098	C2025	A1865	U1732	G1629	C	G1479	G1353
C2610	A2523	U2412	G2343	A2254	G2159	G2099	A2026	C1866	C1733	U1630	C	A1480	G1359
U2611	C2524	G2413	U2344	A2255	A2160	A2100	A2026	C1867	C1734	G1631	A	C1485	G1359
A2616	C2525	U2345	U2345	A2256	A2161	A2101	G2033	G1870	U1735	G1632	C	G1486	A1362
C2622	U2526	U2420	G2346	A2257	A2162	G2102	G2034	G1871	G1736	U1633	C	A1493	G1362
A2623	G2527	A2421	G2347	U2261	U2163	C2103	G2040	A1872	A1737	C1634	G	U1494	G1365
C2627	G2528	U2348	G2348	C2262	U2164	G2104	G2040	U1877	A1750	A1635	U	G1507	G1384
C2627	A2529	A2349	A2349	C2263	C2165	G2105	C2043	G1885	C1753	G1639	A	A1499	G1371
A2630	C2530	U2425	G2350	U2264	U2166	A2106	C2043	A1886	G1754	U1641	C	A1500	A1377
G2631	G2531	C2426	C2352	U2265	U2167	G2107	A2046	G1892	A1755	G1645	C	G1501	G1384
A2631	C2532	G2427	C2353	U2266	G2169	A2108	C2047	U1937	U1757	A1648	A	G1507	G1385
G2640	C2533	A2434	U2353	A2266	U2170	A2109	G2048	G1927	G1758	A1649	C	U1508	G1386
G2640	U2435	U2435	U2354	C2267	U2171	U2110	G2049	C1928	A1760	U1650	C	A1510	G1387
G2645	U2436	A2436	U2355	G2276	G2172	U2111	C2050	A1929	G1761	C1651	U	G1513	U1389
G2645	C2437	A2357	U2356	G2277	G2173	U2112	C2051	U1937	C1762	A1656	U	C1514	G1393
U2647	G2440	A2358	A2358	G2278	U2174	A2113	C2052	G1938	G1763	G1657	G	G1522	A1394
C2648	G2441	C2362	A2363	G2279	U2175	G2114	C2053	U1939	A1764	U1665	G	G1523	G1395
A2649	G2447	A2364	C2364	G2280	A2176	G2115	C2054	A1940	G1765	A1666	U	G1524	U1397
A2650	G2448	A2365	A2365	A2284	G2178	C2116	C2055	U1946	U1766	G1670	G	G1528	G1400
A2650	U2449	A2366	A2366	A2285	U2179	C2117	G2059	U1947	A1767	U1678	U	G1529	A1415
A2654	C2450	G2367	G2367	A2286	C2182	C2118	A2064	A1948	U1768	G1676	U	C1531	A1416
U2655	A2451	C2368	C2368	C2287	G2183	C2119	G2066	G1950	U1782	G1677	C	G1532	G1425
A2657	G2462	G2369	G2369	C2288	A2184	G2121	G2067	G1953	G1766	A1679	G	C1534	U1428
A2657	U2463	U2373	U2373	C2289	C2185	U2122	U2068	C1954	G1767	U1680	U	G1535	C1429
A2658	U2464	U2374	U2374	C2290	G2186	A2123	U2069	A1956	G1788	U1681	G	U1537	C1430
A2659	A2465	G2375	G2375	C2291	U2187	A2124	A2070	G1963	A1789	G1687	U	G1538	U1431
C2665	U2466	G2376	G2376	A2294	U2188	A2125	A2071	U1964	A1791	G1687	G	A1539	G1434
C2669	U2467	U2377	U2377	C2295	C2189	C2126	G2072	G1973	U1798	A1690	G	C1435	C1436
A2672	U2468	G2379	G2379	C2296	A2190	G2127	A2073	A1974	G1802	A1691	G	A1542	A1437
A2677	A2470	U2380	U2380	U2297	C2191	G2128	G2074	U1975	G1804	G1703	C	A1543	G1443
G2678	C2471	A2381	A2381	U2298	G2192	C2129	G2075	U1981	A1803	C1705	U	C1545	U1444
G2679	C2472	G2382	G2382	G2315	A2194	A2131	A2076	A1996	G1805	A1706	G	C1548	C1448
U2686	A2490	U2383	U2383	U2316	U2195	U2132	A2077	U1997	C1825	U1713	U	G1549	U1455
U2687	A2491	G2384	G2384	C2320	G2196	G2133	G2077	C1998	A1826	A1714	U	U1551	U1456
C2688	A2492	G2385	G2385	U2321	U2197	U2135	C2078	A2001	U1715	A1716	C	A1552	G1457
C2689	G2495	U2386	U2386	C2322	U2215	A	C2079	G1840	G1716	U1717	U	U1554	G1458
C2690	U2496	G2387	G2387	A2326	G2216	C	G2080	A2008	G1719	A1556	U	C1465	C1466
C2691	A2497	U2388	U2388	C2327	U2217	U	U2081	G2014	G1720	G1622	C	U1467	U1468
C2691	A2498	U2389	U2389	U2328	G2220	A	U2082	G2015	A1850	G1625	A	A1468	A1469
A2692	A2502	G2391	G2391	C2329	A2221	U	A2083	G2017	U1854	G1626	A	A1478	C1478
A2693	U2507	A2393	A2393	U2330	A2227	C	A2084	G2018	A1855	U1729	A	A1488	A1488
A2694	C2508	A2394	A2394	U2331	A2227	C	C2085	G2019	U1854	U1730	A	A1488	A1488
C2698	C2509	U2395	U2395	U2332	A2238	C2145	U2086	G2020	U1854	U1730	A	A1488	A1488
C2699	A2510	G2396	G2396	U2333	A2239	A2146	C2087	G2021	U1854	U1730	A	A1488	A1488
A2700	A2511	U2401	U2401	U2334	A2244	C2147	U2088	G2022	U1854	U1730	A	A1488	A1488
A2701	C2512	C2402	C2402	G2335	A2244	C2148	C2089	G2023	U1854	U1730	A	A1488	A1488
A2702	G2603	U2406	U2406	U2336	U2246	U2150	U2090	G2024	U1854	U1730	A	A1488	A1488
G2705	U2515	U2515	U2515	U2337	A2247	A2151	U2091	G2025	U1854	U1730	A	A1488	A1488
U2715	U2516	C2517	C2517	G2338	A2247	A2152	U2092	G2026	U1854	U1730	A	A1488	A1488
U2716	G2606	G2606	G2606	G2339	C2248	G2153	U2093	G2027	U1854	U1730	A	A1488	A1488
U2717	G2607	U2408	U2408	U2341	G2249	G2154	G2093	G2028	U1854	U1730	A	A1488	A1488
G2608	G2608	A2410	A2410	U2341	A2250	U2155	G2094	G2029	U1854	U1730	A	A1488	A1488

A3081	G2718	U2833	C2950
U3082	G2719	U2837	C2953
C3088	C2720	A2838	U2953
A3089	G2726	U2839	A2957
A3093	A2727	C2853	G2961
U3096	U2728	A2854	A2962
C3101	G2729	G2857	G2968
A3104	U2730	A2858	C2969
C3105	G2731	G2861	U2970
C3106	C2732	G2862	G2971
G3107	U2735	G2865	A2972
A3112	G2738	A2866	A2982
A3113	C2739	A2867	A2982
A3114	A2742	A2868	G2985
A3115	U2743	G2869	A3002
C3116	C2744	C2870	U3009
U3117	G2745	U2871	C3013
U3118	G2749	G2872	A3014
A3119	G2750	U2873	C3015
C3120	G2760	C2874	C3019
A	U2761	G2879	U3020
A	C2762	A2884	A3021
C	G2774	G2885	G3022
A	C2775	G2886	G3023
	U2778	G2887	A3024
	U2779	G2888	A3030
	C2780	C2891	A3031
	G2781	A2902	G3032
	C2782	A2903	G3033
	G2783	U2908	C3034
	C2784	A2912	C3038
	A2785	U2913	C3039
	U2786	A2914	G3040
	U2787	C2915	C3041
	A2788	U2922	A3042
	U2789	C2923	C3046
	A2790	C2924	A3056
	G2791	C2925	C3067
	C2796	A2926	U3068
	C2797	G2933	G3069
	G2800	G2805	G3070
	G2806	C2936	A3071
	U2810	G2937	G3078
	U2810	G2938	U3079
	A2826	G2941	A3080
	G2827	G2942	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39621	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	54	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.118	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.00715	Depositor
Map size (Å)	483.0, 483.0, 483.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	3	0.27	0/191	0.41	0/247
2	5	0.17	0/5405	0.38	1/7360 (0.0%)
2	6	0.20	1/5405 (0.0%)	0.39	0/7360
3	B	0.27	0/2821	0.27	0/4396
4	C	0.36	0/2153	0.45	0/2895
5	D	0.35	0/1609	0.45	0/2165
6	E	0.32	0/1592	0.39	0/2153
7	F	0.21	0/1467	0.42	0/1973
8	G	0.24	0/1369	0.36	0/1848
9	H	0.18	0/1027	0.36	0/1398
10	I	0.16	0/925	0.39	2/1246 (0.2%)
11	J	0.16	0/1006	0.36	0/1364
12	K	0.36	0/1157	0.37	0/1567
13	L	0.33	0/946	0.39	0/1268
14	M	0.31	0/1091	0.49	2/1457 (0.1%)
15	N	0.32	0/1118	0.46	0/1506
16	O	0.36	0/945	0.43	0/1267
17	P	0.27	0/966	0.48	0/1298
18	Q	0.30	0/921	0.41	0/1236
19	R	0.35	0/1000	0.37	0/1341
20	S	0.34	0/764	0.42	0/1030
21	T	0.34	0/887	0.40	0/1204
22	U	0.30	0/766	0.34	0/1030
23	V	0.28	0/738	0.35	0/987
24	W	0.24	0/1443	0.35	0/1970
25	X	0.33	0/595	0.33	0/798
26	Y	0.35	0/478	0.44	0/641
27	Z	0.34	0/534	0.47	0/713
28	a	0.33	0/477	0.30	0/640
29	b	0.34	0/427	0.45	0/572
30	c	0.20	0/413	0.36	0/553
31	d	0.35	0/380	0.45	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	e	0.20	0/507	0.33	0/672
33	f	0.31	0/303	0.37	0/401
34	g	0.14	0/372	0.32	0/503
35	A	0.34	0/73637	0.33	5/114895 (0.0%)
All	All	0.32	1/115835 (0.0%)	0.35	10/172454 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	6	517	ARG	C-N	6.23	1.40	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	1761	G	P-O3'-C3'	20.49	150.93	120.20
35	A	1538	G	P-O3'-C3'	7.56	131.54	120.20
35	A	1007	G	C2'-C3'-O3'	-6.78	103.52	113.70
35	A	1761	G	OP1-P-O3'	6.57	127.71	108.00
14	M	43	ARG	CA-C-N	-6.24	114.04	121.90
14	M	43	ARG	C-N-CA	-6.24	114.04	121.90
35	A	1761	G	OP2-P-O3'	-5.86	90.43	108.00
2	5	700	ARG	N-CA-C	-5.69	105.44	112.38
10	I	87	VAL	N-CA-CB	-5.35	104.48	112.67
10	I	87	VAL	CB-CA-C	5.07	115.72	110.70

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	189	0	205	3	0
2	5	5299	0	5230	167	0
2	6	5299	0	5229	163	0
3	B	2522	0	1285	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	2110	0	2165	65	0
5	D	1587	0	1629	24	0
6	E	1569	0	1607	19	0
7	F	1445	0	1476	69	0
8	G	1348	0	1399	37	0
9	H	1018	0	988	19	0
10	I	918	0	959	32	0
11	J	990	0	1021	43	0
12	K	1130	0	1167	24	0
13	L	938	0	999	28	0
14	M	1078	0	1151	20	0
15	N	1092	0	1128	22	0
16	O	928	0	972	21	0
17	P	956	0	991	20	0
18	Q	907	0	938	13	0
19	R	988	0	1038	15	0
20	S	754	0	802	10	0
21	T	873	0	909	12	0
22	U	756	0	802	12	0
23	V	732	0	782	18	0
24	W	1428	0	1443	18	0
25	X	586	0	601	12	0
26	Y	470	0	480	12	0
27	Z	531	0	541	16	0
28	a	474	0	500	5	0
29	b	423	0	463	11	0
30	c	405	0	407	13	0
31	d	377	0	411	5	0
32	e	502	0	541	13	0
33	f	299	0	321	6	0
34	g	364	0	348	15	0
35	A	65763	0	33080	774	0
36	5	32	0	13	1	0
36	6	32	0	13	2	0
37	A	388	0	0	0	0
37	B	9	0	0	0	0
37	C	5	0	0	0	0
37	D	1	0	0	0	0
37	F	1	0	0	0	0
37	N	1	0	0	0	0
37	T	1	0	0	0	0
37	X	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Y	1	0	0	0	0
38	c	1	0	0	0	0
38	f	1	0	0	0	0
38	g	1	0	0	0	0
All	All	107523	0	74034	1581	0

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

All (1581) 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)
2:6:332:TYR:OH	13:L:47:ILE:HD12	1.68	0.92
35:A:2086:U:H3	35:A:2096:G:H1	1.25	0.84
11:J:89:LYS:HB3	35:A:1182:C:H5''	1.60	0.82
35:A:860:G:HO2'	35:A:863:G:HO2'	1.26	0.81
4:C:261:ASN:HD21	35:A:2451:A:H5''	1.45	0.81
35:A:1002:C:H2'	35:A:1003:A:H5''	1.61	0.81
35:A:1174:G:H4'	35:A:1204:A:H8	1.46	0.81
35:A:337:U:N3	35:A:344:G:N1	2.29	0.81
35:A:1201:G:N2	35:A:1204:A:OP2	2.12	0.81
35:A:1194:C:H2'	35:A:1195:A:C8	2.17	0.79
35:A:1540:U:H3	35:A:1632:G:H1	1.25	0.79
2:6:332:TYR:OH	13:L:47:ILE:CD1	2.30	0.79
11:J:94:PRO:HD2	35:A:1194:C:H1'	1.63	0.79
31:d:17:ARG:NH1	35:A:886:G:OP1	2.15	0.79
35:A:747:A:N6	35:A:768:G:O2'	2.16	0.79
27:Z:36:MET:HE3	27:Z:41:LEU:HD23	1.65	0.79
12:K:116:ARG:HH12	35:A:615:A:H2	1.32	0.78
14:M:43:ARG:NH2	35:A:923:G:N7	2.33	0.77
16:O:38:GLU:OE1	29:b:42:ARG:NH2	2.17	0.77
5:D:3:ARG:NH1	5:D:210:SER:O	2.15	0.77
2:5:393:LEU:HD13	2:5:407:VAL:HG23	1.67	0.77
19:R:25:ARG:NH1	35:A:2245:C:OP1	2.18	0.77
35:A:1198:C:H2'	35:A:1199:U:C6	2.20	0.76
15:N:32:TYR:OH	15:N:111:GLU:OE1	2.03	0.76
27:Z:22:LEU:HD11	27:Z:58:TYR:CE1	2.21	0.76
2:6:110:ARG:HG2	2:6:439:TRP:HE3	1.50	0.76
16:O:33:ARG:HG2	16:O:114:GLU:HG3	1.68	0.75
11:J:114:LYS:O	11:J:118:LEU:N	2.17	0.75
35:A:451:U:H2'	35:A:452:G:C8	2.22	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:279:U:H3	35:A:307:G:H1	1.35	0.75
7:F:143:SER:HA	7:F:148:ILE:HD11	1.69	0.75
10:I:28:TYR:HD2	10:I:78:ALA:HB2	1.52	0.74
19:R:58:ARG:O	19:R:62:ILE:HG13	1.87	0.74
35:A:1198:C:H2'	35:A:1199:U:H6	1.51	0.74
11:J:128:LYS:HE2	35:A:1198:C:H5''	1.69	0.74
35:A:1194:C:H2'	35:A:1195:A:H8	1.52	0.74
35:A:1541:G:N1	35:A:1631:A:N6	2.35	0.74
8:G:106:PHE:HB3	8:G:108:LEU:HD23	1.68	0.74
35:A:2174:G:H1	35:A:2178:G:HO2'	1.25	0.74
7:F:20:ARG:HE	7:F:35:ILE:HG21	1.51	0.73
35:A:994:A:N6	35:A:1014:G:O2'	2.20	0.73
35:A:3013:C:H5'	35:A:3014:A:H5'	1.69	0.73
2:5:236:THR:HA	2:5:239:GLU:HG3	1.70	0.73
35:A:2048:G:H1	35:A:2198:C:H42	1.35	0.73
2:5:675:LYS:HE3	11:J:27:GLY:O	1.88	0.73
34:g:11:ASP:HA	34:g:25:ARG:HG3	1.70	0.73
35:A:2157:G:H2'	35:A:2158:C:H2'	1.70	0.73
17:P:98:GLU:OE2	17:P:126:LYS:NZ	2.18	0.72
35:A:337:U:O2	35:A:344:G:N2	2.22	0.72
26:Y:41:ARG:HG2	26:Y:43:GLY:H	1.52	0.72
35:A:1188:A:N7	35:A:1214:A:O2'	2.23	0.72
2:5:257:GLU:HG2	2:5:289:GLY:HA2	1.69	0.72
35:A:1758:G:H2'	35:A:1759:A:H8	1.53	0.72
35:A:2726:G:H5''	35:A:2727:A:H5''	1.70	0.72
11:J:118:LEU:HD21	35:A:1177:G:O4'	1.89	0.72
14:M:84:ASN:ND2	14:M:117:LYS:O	2.21	0.72
35:A:1754:G:H22	35:A:1759:A:H61	1.37	0.72
35:A:1541:G:C6	35:A:1631:A:N6	2.58	0.71
35:A:1005:A:H3'	35:A:1006:G:H8	1.55	0.71
4:C:43:ARG:HE	4:C:49:ILE:HG12	1.55	0.71
35:A:2155:U:O2'	35:A:2157:G:N2	2.23	0.71
19:R:73:ASP:O	19:R:114:ARG:NH2	2.23	0.71
34:g:24:THR:HG22	34:g:25:ARG:H	1.56	0.71
2:5:673:THR:O	11:J:23:ALA:HB1	1.91	0.71
9:H:124:ILE:HG22	9:H:125:LYS:H	1.55	0.71
35:A:2102:G:H2'	35:A:2103:C:C2	2.26	0.71
13:L:7:ARG:NH1	13:L:18:GLU:OE2	2.22	0.70
35:A:160:A:H3'	35:A:161:U:H5''	1.71	0.70
27:Z:22:LEU:HD11	27:Z:58:TYR:HE1	1.55	0.70
7:F:29:TYR:OH	7:F:172:GLU:OE1	2.09	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:1627:U:H2'	35:A:1628:A:H8	1.57	0.70
35:A:1229:A:H8	35:A:1230:G:H1'	1.55	0.69
7:F:178:ARG:NH2	7:F:182:PHE:O	2.25	0.69
8:G:150:ARG:NH1	8:G:163:VAL:O	2.24	0.69
6:E:2:THR:HG22	6:E:21:PRO:HA	1.75	0.69
8:G:78:THR:HA	8:G:81:THR:HG22	1.73	0.69
2:6:100:ASP:HA	2:6:491:MET:HG2	1.73	0.69
34:g:2:LYS:HD2	34:g:5:ILE:HD11	1.72	0.69
2:5:461:LEU:HD13	2:5:509:VAL:HG11	1.74	0.69
35:A:2902:A:H2'	35:A:2903:A:C8	2.28	0.69
35:A:256:A:H2'	35:A:257:A:H8	1.58	0.69
35:A:1195:A:H3'	35:A:1196:C:C6	2.28	0.69
35:A:2323:G:H1	35:A:2412:U:H3	1.40	0.69
35:A:1187:A:H4'	35:A:1188:A:H5''	1.75	0.68
2:5:178:PRO:HD3	2:5:270:PRO:HG3	1.75	0.68
35:A:996:G:H2'	35:A:997:G:H8	1.56	0.68
35:A:2122:U:O2'	35:A:2125:A:N6	2.25	0.68
22:U:19:LYS:NZ	35:A:1455:U:OP1	2.25	0.68
25:X:64:PRO:HB3	35:A:759:G:H1	1.59	0.68
2:5:444:PRO:O	2:5:476:ARG:NH2	2.26	0.68
4:C:69:ARG:HB2	4:C:130:ASN:HD22	1.57	0.68
10:I:87:VAL:HG13	10:I:91:LYS:HZ3	1.58	0.68
35:A:981:U:O2'	35:A:982:A:OP2	2.10	0.68
2:6:649:ILE:HB	2:6:683:ILE:HB	1.76	0.67
12:K:98:THR:HG23	12:K:124:VAL:HG13	1.76	0.67
2:6:47:GLY:HA3	2:6:83:LEU:HD11	1.77	0.67
2:6:565:LYS:HE3	2:6:607:PHE:HB3	1.75	0.67
35:A:2255:A:N3	35:A:2679:G:O2'	2.27	0.67
35:A:2356:G:H2'	35:A:2380:G:H1	1.60	0.67
4:C:245:HIS:HB2	4:C:246:PRO:HD3	1.77	0.67
33:f:2:LYS:HB2	33:f:34:GLN:HB3	1.75	0.67
22:U:34:HIS:ND1	22:U:36:ASP:OD1	2.27	0.67
15:N:17:GLN:OE1	15:N:39:HIS:HB3	1.95	0.67
35:A:1550:G:O6	35:A:1620:U:O4	2.13	0.67
35:A:289:A:H62	35:A:299:G:H22	1.42	0.67
35:A:2101:A:H2'	35:A:2102:G:C8	2.29	0.67
35:A:2329:G:H1	35:A:2406:U:H3	1.43	0.66
35:A:2552:A:H2'	35:A:2553:G:C8	2.30	0.66
31:d:38:ARG:HG3	31:d:45:LEU:HD21	1.78	0.66
10:I:40:ARG:NH2	35:A:1201:G:O3'	2.28	0.66
15:N:118:LEU:O	15:N:122:ILE:HD12	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Z:14:THR:N	27:Z:17:GLU:OE2	2.25	0.66
35:A:137:G:H21	35:A:1524:G:H1'	1.59	0.66
2:5:320:LEU:HA	2:5:344:GLY:HA3	1.75	0.66
2:5:324:VAL:HG22	2:5:339:VAL:HG22	1.76	0.66
4:C:236:GLY:O	4:C:244:ARG:NE	2.28	0.66
9:H:27:ARG:NH2	35:A:2315:U:OP2	2.23	0.66
23:V:46:ALA:HB2	35:A:571:A:H4'	1.76	0.66
2:6:676:HIS:HB2	2:6:682:VAL:HG23	1.78	0.66
11:J:94:PRO:HB2	35:A:1195:A:H1'	1.77	0.66
35:A:2351:A:N3	35:A:2396:A:O2'	2.29	0.66
2:5:674:ASP:O	2:5:682:VAL:N	2.29	0.66
2:5:327:THR:HB	2:5:471:GLU:HA	1.76	0.66
35:A:1001:C:C2	35:A:1002:C:H1'	2.31	0.66
17:P:70:VAL:HG12	17:P:83:ARG:HG3	1.78	0.66
35:A:543:U:H3'	35:A:544:U:H5''	1.78	0.65
33:f:31:ARG:NH1	35:A:2702:A:OP1	2.30	0.65
35:A:298:G:H2'	35:A:299:G:C8	2.32	0.65
4:C:43:ARG:HH12	35:A:806:C:H1'	1.61	0.65
35:A:1556:A:N1	35:A:1615:G:O6	2.29	0.65
2:6:352:VAL:HG21	2:6:427:LEU:HD13	1.78	0.65
16:O:57:LYS:O	16:O:62:ASN:ND2	2.30	0.65
35:A:301:U:H5'	35:A:302:U:O5'	1.96	0.65
35:A:273:A:H61	35:A:314:G:H1'	1.62	0.65
35:A:1754:G:H22	35:A:1759:A:N6	1.94	0.65
35:A:2096:G:H2'	35:A:2097:G:C8	2.31	0.65
2:6:39:LEU:HD13	2:6:271:VAL:HG11	1.78	0.65
35:A:1177:G:H2'	35:A:1178:U:C5	2.31	0.65
35:A:3014:A:O2'	35:A:3015:C:H5''	1.97	0.65
4:C:67:PHE:HE1	4:C:106:ILE:HD11	1.60	0.64
11:J:114:LYS:HG3	11:J:130:ILE:HD11	1.77	0.64
35:A:1541:G:N1	35:A:1631:A:C6	2.65	0.64
2:5:229:ILE:CG2	2:5:237:LEU:HB3	2.28	0.64
2:6:687:ILE:HB	2:6:692:LEU:HD21	1.80	0.64
2:5:671:LEU:HG	2:5:685:ALA:HA	1.80	0.64
11:J:129:ILE:HG12	35:A:1198:C:H1'	1.80	0.64
2:6:674:ASP:O	2:6:682:VAL:N	2.30	0.64
2:6:395:PHE:HB2	2:6:402:ARG:HB2	1.79	0.64
2:5:465:LEU:HD13	2:5:477:ILE:HG12	1.79	0.64
7:F:8:LEU:HD21	7:F:13:GLN:HB2	1.80	0.64
35:A:1000:C:H2'	35:A:1001:C:H5''	1.80	0.64
6:E:2:THR:HA	6:E:20:LEU:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:29:TYR:HD2	7:F:35:ILE:HD13	1.61	0.64
35:A:451:U:H2'	35:A:452:G:H8	1.62	0.64
35:A:2160:A:H62	35:A:2194:A:H2'	1.63	0.64
2:5:142:PRO:HG2	2:5:291:PRO:HG3	1.80	0.63
14:M:55:MET:O	14:M:60:ARG:NH1	2.31	0.63
16:O:7:GLY:O	16:O:9:ARG:NH1	2.31	0.63
35:A:2134:G:H2'	35:A:2135:U:H2'	1.80	0.63
2:5:560:PHE:HB2	2:5:587:MET:HE1	1.80	0.63
2:6:257:GLU:HG2	2:6:289:GLY:HA2	1.80	0.63
9:H:126:SER:O	9:H:130:HIS:NE2	2.32	0.63
35:A:1758:G:H2'	35:A:1759:A:C8	2.33	0.63
3:B:81:U:O2'	35:A:1033:A:N3	2.32	0.63
2:5:353:HIS:ND1	2:5:387:ASP:OD1	2.22	0.63
35:A:2425:U:O2'	35:A:2427:G:OP1	2.17	0.63
3:B:4:A:N1	3:B:23:G:O2'	2.26	0.63
24:W:158:THR:HG22	24:W:161:GLN:HG3	1.81	0.63
35:A:1003:A:H1'	35:A:1004:C:H2'	1.79	0.63
35:A:1756:G:H1'	35:A:1758:G:C6	2.34	0.63
13:L:4:GLN:HG3	13:L:5:GLU:HG2	1.81	0.63
35:A:1530:G:H21	35:A:1805:G:H22	1.47	0.63
2:5:325:VAL:HG23	2:5:326:LYS:HG3	1.81	0.63
35:A:1544:U:H3	35:A:1626:G:H1	1.44	0.63
2:5:699:LEU:HA	2:5:702:MET:HE2	1.80	0.63
2:6:301:VAL:HG21	2:6:312:LEU:HG	1.81	0.63
13:L:7:ARG:HE	13:L:20:LEU:HD12	1.64	0.63
35:A:2019:A:H2'	35:A:2020:A:C8	2.34	0.63
2:5:37:THR:HG23	2:5:63:CYS:HB2	1.81	0.62
11:J:136:SER:HB2	35:A:1180:G:N3	2.14	0.62
2:5:172:VAL:HG22	2:5:266:PHE:HB2	1.79	0.62
8:G:99:LEU:HD23	8:G:126:VAL:HG12	1.80	0.62
27:Z:36:MET:HG3	27:Z:47:LEU:HD11	1.80	0.62
35:A:1005:A:H3'	35:A:1006:G:C8	2.34	0.62
2:6:444:PRO:O	2:6:476:ARG:NH2	2.32	0.62
35:A:1202:A:N3	35:A:1223:U:O2'	2.33	0.62
35:A:1754:G:N2	35:A:1759:A:H61	1.97	0.62
2:6:322:ALA:N	2:6:427:LEU:O	2.33	0.62
4:C:238:GLY:HA3	4:C:245:HIS:HA	1.82	0.62
2:5:338:LEU:HD11	2:5:396:PRO:HG3	1.82	0.62
7:F:71:LYS:HZ3	34:g:5:ILE:HB	1.64	0.62
35:A:3079:U:H2'	35:A:3080:A:C8	2.35	0.62
2:6:178:PRO:HA	2:6:188:VAL:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:531:HIS:ND1	2:6:548:ASP:OD1	2.31	0.62
11:J:132:GLY:HA2	11:J:135:ARG:HD2	1.81	0.62
16:O:106:ASP:OD2	35:A:1867:G:O2'	2.16	0.62
34:g:14:VAL:HG22	34:g:33:ILE:HB	1.81	0.62
2:5:44:LEU:HD23	2:5:83:LEU:HD22	1.81	0.62
10:I:40:ARG:CZ	35:A:1201:G:H4'	2.29	0.62
2:6:544:TYR:HB3	2:6:615:ASP:HB3	1.82	0.62
35:A:337:U:O4	35:A:344:G:O6	2.18	0.61
2:5:27:ALA:HA	2:5:93:ILE:HB	1.82	0.61
2:6:82:SER:H	2:6:402:ARG:HH12	1.49	0.61
35:A:2178:G:H21	35:A:2775:C:H5'	1.65	0.61
2:5:670:VAL:HB	35:A:1185:A:C8	2.36	0.61
11:J:114:LYS:HB3	11:J:118:LEU:HD12	1.82	0.61
35:A:1174:G:H4'	35:A:1204:A:C8	2.31	0.61
18:Q:3:THR:HG23	35:A:3096:U:H4'	1.82	0.61
35:A:858:A:O2'	35:A:1877:U:OP1	2.17	0.61
4:C:75:VAL:HG11	4:C:99:ASP:HB2	1.83	0.61
35:A:1002:C:C2'	35:A:1003:A:H5''	2.31	0.61
35:A:1185:A:H2'	35:A:1186:G:C8	2.35	0.61
35:A:993:G:N2	35:A:1015:A:OP2	2.28	0.61
2:6:353:HIS:ND1	2:6:387:ASP:OD1	2.34	0.61
27:Z:36:MET:CE	27:Z:41:LEU:HB3	2.30	0.61
2:5:544:TYR:N	2:5:615:ASP:O	2.34	0.61
2:5:578:SER:HB2	2:5:622:GLN:HG3	1.83	0.61
4:C:164:GLN:HB3	4:C:176:ARG:HG2	1.82	0.61
11:J:90:GLY:HA3	35:A:1181:G:O2'	2.00	0.61
5:D:44:ARG:NH1	35:A:3009:U:OP1	2.30	0.60
35:A:1532:G:O2'	35:A:1803:A:N1	2.30	0.60
35:A:1621:C:H2'	35:A:1622:G:H8	1.65	0.60
35:A:1656:A:H2'	35:A:1657:G:H8	1.65	0.60
35:A:2064:A:H1'	35:A:2065:A:C2	2.36	0.60
2:6:371:ALA:HB1	2:6:441:MET:HG2	1.82	0.60
4:C:231:HIS:CE1	4:C:233:HIS:HD2	2.19	0.60
19:R:83:LEU:HD22	19:R:113:ALA:HB2	1.82	0.60
35:A:2079:C:N4	35:A:2080:G:O6	2.35	0.60
2:5:587:MET:HG3	2:5:629:LEU:HD21	1.83	0.60
35:A:2190:A:OP2	35:A:2191:C:N4	2.33	0.60
21:T:71:LEU:HD23	21:T:116:SER:HB2	1.83	0.60
35:A:1543:A:N1	35:A:1628:A:O2'	2.33	0.60
35:A:1996:U:OP2	35:A:2001:A:N6	2.32	0.60
3:B:83:C:OP1	28:a:16:ARG:NH1	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:1193:C:H2'	35:A:1194:C:C6	2.37	0.60
2:5:586:GLN:HB3	2:5:629:LEU:HD23	1.84	0.60
35:A:2294:A:H2'	35:A:2295:C:C6	2.36	0.60
17:P:46:HIS:ND1	17:P:66:ILE:HD13	2.16	0.60
2:6:641:LEU:HB3	2:6:716:TYR:HB3	1.84	0.60
9:H:62:ILE:O	9:H:66:ASN:N	2.32	0.60
35:A:1550:G:N1	35:A:1620:U:N3	2.50	0.60
16:O:99:LYS:HD2	29:b:42:ARG:HE	1.67	0.59
2:6:475:LEU:HD13	2:6:499:VAL:HG11	1.83	0.59
10:I:3:LYS:HE2	35:A:1163:A:OP1	2.02	0.59
4:C:54:LYS:NZ	35:A:2040:G:OP1	2.35	0.59
35:A:594:U:H5'	35:A:595:A:H5''	1.83	0.59
2:5:217:ILE:O	2:5:221:ARG:HG3	2.02	0.59
2:6:652:PRO:HA	2:6:680:ARG:HA	1.83	0.59
4:C:88:ARG:NH2	35:A:2034:G:OP1	2.35	0.59
10:I:22:ALA:HB2	10:I:110:MET:SD	2.42	0.59
12:K:116:ARG:NH1	35:A:615:A:H2	1.97	0.59
2:5:178:PRO:HA	2:5:188:VAL:HA	1.85	0.59
23:V:75:ASP:OD1	23:V:76:SER:N	2.36	0.59
14:M:32:THR:HG22	14:M:35:ARG:H	1.66	0.59
35:A:346:C:H2'	35:A:347:U:C6	2.37	0.59
16:O:20:LEU:HD21	16:O:40:LYS:HE2	1.85	0.59
2:6:91:ASN:ND2	2:6:411:ASP:OD1	2.35	0.59
4:C:183:ARG:NH2	35:A:2017:C:OP2	2.35	0.59
8:G:111:SER:OG	35:A:2891:C:N3	2.29	0.59
10:I:23:THR:HG22	10:I:109:TYR:HB3	1.85	0.59
12:K:92:LEU:HD11	12:K:99:ARG:HD2	1.84	0.59
8:G:35:LEU:HD11	8:G:72:LEU:HB3	1.83	0.59
20:S:53:ASP:OD1	20:S:54:ASP:N	2.36	0.59
35:A:1885:G:O2'	35:A:2215:U:O4	2.18	0.59
2:6:550:GLU:HB3	2:6:605:THR:HB	1.84	0.59
35:A:621:U:H2'	35:A:622:C:C6	2.38	0.59
35:A:1825:C:N4	35:A:1840:G:OP2	2.27	0.59
2:5:103:GLY:HA3	2:5:474:THR:HG21	1.84	0.58
11:J:29:ALA:O	11:J:33:HIS:ND1	2.34	0.58
11:J:95:HIS:ND1	35:A:1195:A:O3'	2.36	0.58
35:A:429:A:H2'	35:A:430:A:C8	2.38	0.58
7:F:44:ASN:ND2	35:A:2537:C:O4'	2.37	0.58
35:A:2074:G:O2'	35:A:2110:U:O4	2.17	0.58
10:I:40:ARG:NH2	35:A:1201:G:H4'	2.19	0.58
11:J:128:LYS:HD3	35:A:1198:C:H4'	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:339:U:H2'	35:A:340:A:C8	2.37	0.58
35:A:357:U:H4'	35:A:358:G:O5'	2.03	0.58
35:A:3020:U:O2'	35:A:3021:A:O5'	2.20	0.58
2:5:666:ARG:NH2	2:5:698:ASP:OD2	2.35	0.58
35:A:2340:A:N1	35:A:2393:A:N6	2.51	0.58
17:P:42:ARG:HD3	17:P:113:ILE:HD11	1.85	0.58
2:6:83:LEU:HB3	2:6:90:VAL:HB	1.86	0.58
27:Z:36:MET:HE2	27:Z:41:LEU:HB3	1.84	0.58
35:A:2174:G:N1	35:A:2178:G:O2'	2.19	0.58
2:5:229:ILE:HG23	2:5:237:LEU:HB3	1.84	0.58
2:6:505:ARG:HE	2:6:506:ARG:HG3	1.69	0.58
15:N:74:LEU:HD12	15:N:92:TRP:HE1	1.67	0.58
2:5:292:ALA:O	2:5:296:HIS:N	2.34	0.58
2:5:676:HIS:HB2	2:5:682:VAL:HG23	1.86	0.58
7:F:128:GLN:HB3	7:F:135:TYR:CE1	2.39	0.58
8:G:5:GLY:HA3	8:G:66:HIS:CD2	2.39	0.58
26:Y:48:ARG:NH2	35:A:2424:C:OP1	2.33	0.58
35:A:2386:U:OP1	35:A:2393:A:O2'	2.22	0.58
12:K:99:ARG:HA	12:K:102:GLU:HB2	1.84	0.58
35:A:1530:G:H22	35:A:1805:G:H1	1.52	0.58
2:6:540:GLY:N	35:A:3080:A:H5''	2.19	0.58
35:A:998:G:H2'	35:A:999:C:H6	1.69	0.58
2:5:22:ALA:O	2:5:89:LYS:N	2.32	0.57
3:B:10:G:O2'	3:B:11:U:OP1	2.19	0.57
15:N:110:ASP:OD1	15:N:113:THR:OG1	2.21	0.57
20:S:23:LYS:HD3	20:S:96:VAL:HG22	1.86	0.57
32:e:9:GLY:O	32:e:13:ARG:HG2	2.03	0.57
35:A:292:G:N1	35:A:343:U:N3	2.52	0.57
35:A:2095:G:HO2'	35:A:2096:G:H8	1.51	0.57
2:6:676:HIS:H	2:6:681:THR:HA	1.68	0.57
4:C:231:HIS:CE1	4:C:233:HIS:CD2	2.92	0.57
7:F:75:ARG:HH21	7:F:95:ARG:NH2	2.03	0.57
35:A:1001:C:H1'	35:A:1007:G:H22	1.69	0.57
35:A:1185:A:H2'	35:A:1186:G:H8	1.69	0.57
35:A:1186:G:H2'	35:A:1187:A:C5	2.39	0.57
2:5:551:VAL:HG22	2:5:604:VAL:HG22	1.87	0.57
2:6:225:ILE:HG12	2:6:252:LEU:HD22	1.86	0.57
2:6:324:VAL:HA	2:6:339:VAL:HA	1.86	0.57
14:M:51:GLU:OE2	32:e:57:ARG:NH1	2.38	0.57
23:V:4:HIS:NE2	35:A:81:A:OP1	2.36	0.57
35:A:1195:A:H3'	35:A:1196:C:H6	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:1610:C:H2'	35:A:1611:A:H8	1.70	0.57
35:A:2381:A:H4'	35:A:2382:G:O5'	2.04	0.57
4:C:212:MET:HE2	4:C:217:LYS:HE3	1.86	0.57
35:A:284:G:O2'	35:A:286:G:O4'	2.21	0.57
35:A:1542:A:H61	35:A:1628:A:H1'	1.68	0.57
35:A:2761:U:H2'	35:A:2762:C:H6	1.69	0.57
2:6:376:GLY:O	2:6:379:HIS:N	2.33	0.57
10:I:28:TYR:CD2	10:I:78:ALA:HB2	2.35	0.57
22:U:11:ILE:O	27:Z:33:ARG:NH2	2.38	0.57
24:W:158:THR:OG1	24:W:174:PRO:O	2.15	0.57
35:A:303:G:H2'	35:A:304:U:O4'	2.04	0.57
35:A:2169:G:O2'	35:A:2170:U:OP1	2.19	0.57
2:5:448:ILE:N	2:5:488:LEU:O	2.36	0.57
11:J:128:LYS:CD	35:A:1198:C:H4'	2.34	0.57
35:A:1178:U:C2	35:A:1180:G:H5'	2.39	0.57
35:A:2867:A:H2'	35:A:2868:A:H8	1.69	0.57
2:5:78:LEU:HD23	2:5:104:GLU:HB3	1.87	0.57
2:6:302:PHE:N	2:6:435:VAL:O	2.34	0.57
35:A:2761:U:H2'	35:A:2762:C:C6	2.40	0.57
2:6:322:ALA:HB3	2:6:427:LEU:HB2	1.87	0.57
2:6:324:VAL:HG22	2:6:339:VAL:HG22	1.85	0.57
22:U:40:THR:O	22:U:44:ILE:HG13	2.04	0.57
25:X:26:PHE:N	25:X:29:GLN:OE1	2.34	0.57
35:A:2902:A:H2'	35:A:2903:A:H8	1.70	0.57
2:5:357:HIS:CE1	2:5:424:GLY:HA3	2.40	0.57
22:U:12:LEU:HB2	22:U:32:VAL:HG23	1.87	0.57
35:A:1225:G:O2'	35:A:1226:U:H5'	2.05	0.57
35:A:3020:U:H1'	35:A:3022:G:O6	2.04	0.57
30:c:44:ASN:OD1	30:c:45:CYS:N	2.36	0.56
35:A:844:G:H4'	35:A:878:G:H5'	1.87	0.56
2:5:353:HIS:HB2	2:5:430:LYS:HA	1.87	0.56
2:5:468:LEU:HG	2:5:507:TYR:HE2	1.70	0.56
2:5:552:GLU:OE2	2:5:603:ARG:NH1	2.32	0.56
4:C:69:ARG:HB2	4:C:130:ASN:ND2	2.20	0.56
35:A:1530:G:N2	35:A:1805:G:H1	2.03	0.56
2:5:47:GLY:HA3	2:5:83:LEU:HD21	1.87	0.56
2:5:701:SER:C	2:5:703:SER:H	2.13	0.56
2:6:174:PRO:HA	2:6:268:VAL:HB	1.87	0.56
4:C:226:MET:HE2	4:C:230:ASP:HB3	1.87	0.56
8:G:69:SER:O	8:G:73:ILE:HG12	2.06	0.56
18:Q:30:LYS:NZ	18:Q:78:PRO:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:45:TYR:HD1	19:R:48:ARG:HE	1.53	0.56
35:A:292:G:H22	35:A:343:U:H2'	1.70	0.56
35:A:1220:C:H2'	35:A:1221:A:H8	1.70	0.56
35:A:1656:A:H2'	35:A:1657:G:C8	2.40	0.56
24:W:134:GLU:HB2	24:W:171:ILE:HD11	1.87	0.56
10:I:26:THR:HG22	10:I:105:ILE:HA	1.87	0.56
30:c:8:ARG:NH2	35:A:2509:C:OP2	2.38	0.56
4:C:60:ARG:HA	35:A:1788:G:H5'	1.87	0.56
7:F:11:LEU:HD12	7:F:14:ARG:HB3	1.87	0.56
9:H:8:GLU:HG2	9:H:14:ALA:HA	1.88	0.56
35:A:334:G:H2'	35:A:335:G:C8	2.40	0.56
35:A:337:U:C2	35:A:344:G:N1	2.73	0.56
35:A:1174:G:C4'	35:A:1204:A:H8	2.18	0.56
2:5:323:GLU:N	2:5:340:ARG:O	2.39	0.56
7:F:19:ILE:HD12	7:F:179:ALA:HB1	1.87	0.56
15:N:43:THR:HG22	15:N:94:VAL:HG12	1.86	0.56
35:A:1963:G:H2'	35:A:1964:U:C6	2.41	0.56
35:A:2178:G:N2	35:A:2774:G:O3'	2.39	0.56
2:6:106:ARG:HD2	2:6:442:PRO:HD3	1.88	0.56
2:6:332:TYR:HH	13:L:47:ILE:HD12	1.71	0.56
2:6:452:PRO:HA	2:6:511:VAL:HG12	1.87	0.56
23:V:86:ARG:NH2	23:V:104:ASP:OD2	2.39	0.56
35:A:445:U:H4'	35:A:446:G:O5'	2.06	0.56
2:6:321:LEU:HD11	2:6:436:LEU:HG	1.88	0.56
7:F:11:LEU:HD21	7:F:180:LEU:HD12	1.87	0.56
24:W:9:ASN:HD21	24:W:61:HIS:CE1	2.23	0.56
35:A:329:U:O2	35:A:447:A:N6	2.39	0.56
35:A:1164:A:H2'	35:A:1164:A:OP1	2.05	0.56
35:A:1791:A:H2'	35:A:1792:A:C8	2.41	0.56
35:A:2329:G:O6	35:A:2406:U:O4	2.22	0.56
35:A:2862:G:O2'	35:A:3002:A:N6	2.39	0.56
2:5:550:GLU:O	2:5:605:THR:N	2.35	0.55
7:F:107:LEU:HA	7:F:110:LEU:HG	1.89	0.55
24:W:52:ARG:NH2	35:A:1157:G:H4'	2.21	0.55
31:d:14:ARG:NH2	35:A:885:G:OP2	2.39	0.55
13:L:2:ILE:HG13	13:L:8:LEU:HD21	1.88	0.55
24:W:39:GLY:HA3	24:W:99:VAL:HB	1.87	0.55
34:g:16:CYS:SG	34:g:17:GLY:N	2.79	0.55
35:A:2168:U:O4	35:A:2187:U:O2'	2.24	0.55
2:5:43:LEU:HD21	2:5:282:LEU:HD23	1.86	0.55
2:5:84:SER:HA	2:5:89:LYS:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:477:ILE:HD13	2:5:488:LEU:HD23	1.88	0.55
2:6:25:ASN:ND2	2:6:112:ALA:HA	2.21	0.55
35:A:218:A:N3	35:A:234:U:O2'	2.33	0.55
35:A:1118:A:H2'	35:A:1119:A:C8	2.41	0.55
35:A:1554:U:O4	35:A:1617:C:N3	2.39	0.55
35:A:1705:C:H2'	35:A:1706:A:H8	1.72	0.55
13:L:66:VAL:O	13:L:78:LYS:HE2	2.07	0.55
35:A:2120:A:H2'	35:A:2121:G:H8	1.72	0.55
35:A:2358:A:HO2'	35:A:2382:G:HO2'	1.53	0.55
2:5:575:PHE:O	2:5:578:SER:OG	2.17	0.55
35:A:2127:G:H3'	35:A:2128:G:H8	1.70	0.55
10:I:57:VAL:O	10:I:61:ALA:N	2.39	0.55
13:L:76:TYR:O	18:Q:71:ARG:HD2	2.06	0.55
21:T:32:ARG:NH1	21:T:81:VAL:O	2.39	0.55
35:A:190:A:H2'	35:A:191:G:N3	2.22	0.55
2:6:351:THR:HA	2:6:389:ARG:HA	1.89	0.55
16:O:71:ARG:HH22	35:A:2933:G:H5'	1.71	0.55
2:6:338:LEU:HD11	2:6:396:PRO:HG3	1.89	0.55
10:I:82:VAL:HG21	10:I:86:ALA:HA	1.89	0.55
35:A:1165:G:H8	35:A:1165:G:OP2	1.89	0.55
2:5:20:PRO:HD3	2:5:316:PRO:HD3	1.89	0.55
2:5:675:LYS:NZ	11:J:31:GLY:HA3	2.21	0.55
3:B:50:C:O3'	17:P:78:LYS:NZ	2.40	0.55
35:A:453:U:H2'	35:A:454:U:C6	2.41	0.55
35:A:1628:A:N3	35:A:1630:U:N3	2.54	0.55
35:A:2261:U:H2'	35:A:2262:C:C6	2.42	0.55
2:6:536:LYS:HD2	35:A:1929:A:OP1	2.06	0.54
12:K:56:VAL:HB	12:K:124:VAL:HG23	1.88	0.54
16:O:33:ARG:NH1	16:O:114:GLU:OE2	2.40	0.54
21:T:13:LYS:HB2	35:A:581:G:H4'	1.89	0.54
2:6:374:ALA:HA	2:6:473:PRO:HA	1.89	0.54
2:6:377:SER:H	2:6:476:ARG:HG3	1.72	0.54
8:G:86:GLN:NE2	8:G:87:LYS:O	2.40	0.54
9:H:62:ILE:H	9:H:65:ALA:HB3	1.72	0.54
18:Q:24:THR:HG23	18:Q:86:LEU:HB2	1.88	0.54
22:U:69:THR:HG23	22:U:72:GLY:H	1.72	0.54
4:C:257:THR:OG1	35:A:2014:G:O2'	2.25	0.54
8:G:158:TYR:O	8:G:172:ARG:NH2	2.29	0.54
33:f:25:VAL:HB	33:f:34:GLN:HG3	1.89	0.54
35:A:1886:A:O2'	35:A:1892:G:N7	2.31	0.54
35:A:2190:A:H2'	35:A:2191:C:C2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:378:THR:OG1	2:5:462:SER:OG	2.25	0.54
3:B:5:C:OP1	3:B:62:C:O2'	2.25	0.54
7:F:117:ARG:NH1	7:F:145:PHE:O	2.40	0.54
15:N:108:TYR:CD1	15:N:109:PRO:HD2	2.43	0.54
35:A:1690:A:H2'	35:A:1691:A:C8	2.42	0.54
35:A:2730:U:OP2	35:A:2800:G:N1	2.37	0.54
2:5:657:GLY:HA3	35:A:1213:A:OP2	2.07	0.54
2:6:338:LEU:HD12	2:6:412:ILE:HG22	1.90	0.54
15:N:42:ILE:HD12	15:N:97:VAL:HG21	1.89	0.54
30:c:6:ASP:O	30:c:8:ARG:N	2.36	0.54
35:A:1012:C:H2'	35:A:1012:C:O2	2.06	0.54
35:A:2105:G:N2	35:A:2106:A:N7	2.53	0.54
35:A:2160:A:N6	35:A:2194:A:H2'	2.22	0.54
35:A:2510:A:H4'	35:A:2511:A:O4'	2.07	0.54
35:A:2745:C:O2'	35:A:2788:A:N3	2.40	0.54
2:6:674:ASP:N	2:6:682:VAL:O	2.41	0.54
4:C:43:ARG:NH1	35:A:806:C:H1'	2.22	0.54
5:D:169:ARG:HH22	35:A:3046:C:H41	1.54	0.54
7:F:61:ILE:HG23	7:F:72:PRO:HD2	1.90	0.54
11:J:16:GLN:O	11:J:44:TYR:OH	2.26	0.54
11:J:128:LYS:CE	35:A:1198:C:H5''	2.35	0.54
12:K:65:SER:OG	35:A:1259:U:OP2	2.25	0.54
24:W:165:PRO:HD2	24:W:168:VAL:HG21	1.90	0.54
35:A:1928:C:H4'	35:A:3079:U:O2	2.07	0.54
35:A:2351:A:H2'	35:A:2352:C:C6	2.42	0.54
35:A:337:U:N3	35:A:344:G:C6	2.75	0.54
2:5:24:ARG:O	2:5:91:ASN:N	2.35	0.54
10:I:54:ASN:ND2	10:I:73:PHE:O	2.41	0.54
2:5:139:VAL:HG13	2:5:141:MET:HB2	1.91	0.53
2:6:126:ASP:HB2	2:6:128:PRO:HD2	1.90	0.53
35:A:998:G:H2'	35:A:999:C:C6	2.42	0.53
2:5:546:VAL:HB	2:5:610:LYS:HB2	1.89	0.53
4:C:176:ARG:HH22	35:A:2062:G:H5''	1.73	0.53
14:M:124:VAL:HG21	14:M:137:ILE:HD13	1.90	0.53
20:S:43:VAL:HG22	20:S:48:VAL:HG12	1.91	0.53
35:A:2569:G:N3	35:A:2605:C:H2'	2.24	0.53
17:P:73:ILE:HG22	17:P:75:GLY:H	1.72	0.53
24:W:26:GLN:OE1	24:W:29:ARG:NH2	2.33	0.53
35:A:256:A:H2'	35:A:257:A:C8	2.41	0.53
7:F:64:LEU:HA	7:F:67:ILE:HG22	1.91	0.53
17:P:127:PHE:O	35:A:2601:A:O2'	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:40:LYS:NZ	35:A:2571:C:OP1	2.42	0.53
35:A:1099:A:OP2	35:A:1100:C:N4	2.33	0.53
35:A:1553:C:H5''	35:A:1554:U:H5	1.73	0.53
35:A:2256:G:OP1	35:A:2678:G:O2'	2.19	0.53
2:6:328:THR:HG22	2:6:336:VAL:HB	1.90	0.53
24:W:8:PRO:HA	24:W:66:ILE:HG23	1.89	0.53
35:A:3023:G:H2'	35:A:3024:A:O4'	2.08	0.53
2:5:271:VAL:HG21	2:5:282:LEU:HD22	1.91	0.53
2:5:701:SER:HA	35:A:2884:A:N7	2.23	0.53
2:6:69:GLU:HG3	2:6:76:VAL:HG22	1.89	0.53
2:6:151:ASP:OD2	36:6:801:GNP:N2	2.33	0.53
4:C:79:VAL:HG23	4:C:114:GLY:H	1.73	0.53
17:P:66:ILE:O	17:P:71:ARG:NH2	2.40	0.53
2:5:191:LEU:HD13	2:5:220:LEU:HB3	1.91	0.53
2:5:550:GLU:HB3	2:5:605:THR:HB	1.89	0.53
6:E:34:MET:HE2	6:E:189:LEU:HD11	1.89	0.53
1:3:8:LYS:HG2	1:3:11:ARG:HH12	1.72	0.53
2:5:14:VAL:HG13	2:5:402:ARG:HD2	1.90	0.53
7:F:73:GLU:OE2	7:F:75:ARG:NE	2.42	0.53
11:J:95:HIS:HB2	35:A:1195:A:H4'	1.91	0.53
2:6:543:GLN:HB3	2:6:620:ALA:HB2	1.91	0.53
4:C:67:PHE:CE1	4:C:106:ILE:HD11	2.41	0.53
35:A:1196:C:H1'	35:A:1206:A:H2'	1.91	0.53
35:A:2805:G:OP2	35:A:2805:G:N2	2.41	0.53
4:C:206:TRP:O	4:C:211:ARG:HD3	2.09	0.52
16:O:42:ARG:NH2	35:A:3038:C:OP1	2.35	0.52
24:W:178:VAL:HG12	24:W:179:VAL:HG23	1.91	0.52
35:A:81:A:N1	35:A:96:G:O2'	2.35	0.52
35:A:2872:G:H2'	35:A:2873:U:C6	2.44	0.52
2:6:24:ARG:O	2:6:91:ASN:N	2.35	0.52
35:A:2128:G:O2'	35:A:2150:U:O2	2.27	0.52
2:5:189:VAL:HG22	2:5:196:TYR:HB2	1.92	0.52
2:5:269:ILE:HG12	2:5:285:ILE:HD13	1.92	0.52
2:5:397:LEU:HD22	2:5:402:ARG:HD3	1.91	0.52
4:C:226:MET:HE3	35:A:897:A:C2	2.44	0.52
11:J:94:PRO:HD2	35:A:1194:C:C1'	2.37	0.52
32:e:29:ARG:CZ	32:e:45:ASP:HB3	2.39	0.52
35:A:473:C:O2'	35:A:476:G:N2	2.42	0.52
12:K:125:TYR:HH	12:K:132:HIS:HE2	1.58	0.52
15:N:75:THR:HA	15:N:90:PRO:HA	1.89	0.52
32:e:43:ARG:NH2	35:A:2587:U:OP2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:2322:C:H2'	35:A:2323:G:H8	1.73	0.52
2:6:663:LEU:HA	2:6:666:ARG:HB2	1.91	0.52
10:I:14:ALA:O	10:I:18:LYS:HG2	2.10	0.52
12:K:93:LEU:HD12	12:K:97:PRO:HB3	1.90	0.52
30:c:6:ASP:C	30:c:8:ARG:H	2.15	0.52
35:A:353:G:H1	35:A:442:U:H3	1.58	0.52
35:A:1001:C:N3	35:A:1002:C:H1'	2.25	0.52
2:6:69:GLU:HG2	2:6:76:VAL:H	1.73	0.52
7:F:117:ARG:HD2	7:F:146:HIS:CE1	2.45	0.52
15:N:1:MET:HE1	15:N:45:ARG:HA	1.91	0.52
22:U:91:LYS:HD3	22:U:92:PRO:HD2	1.92	0.52
25:X:11:ARG:O	25:X:14:ARG:NH2	2.35	0.52
35:A:857:U:H2'	35:A:858:A:C8	2.45	0.52
35:A:2347:G:O6	35:A:2348:G:N2	2.43	0.52
2:6:436:LEU:O	2:6:438:PRO:HD3	2.10	0.52
6:E:160:ARG:HH12	35:A:706:G:HO2'	1.54	0.52
30:c:8:ARG:HH21	35:A:2508:C:H3'	1.74	0.52
35:A:137:G:H2'	35:A:138:A:C8	2.45	0.52
35:A:429:A:H2'	35:A:430:A:H8	1.74	0.52
35:A:3071:A:N7	35:A:3089:A:O2'	2.31	0.52
4:C:182:ILE:HB	4:C:269:VAL:HB	1.91	0.52
19:R:31:LEU:HD21	35:A:672:C:H4'	1.92	0.52
21:T:69:GLU:OE2	21:T:69:GLU:N	2.43	0.52
35:A:2:A:H2'	35:A:3:A:C8	2.45	0.52
35:A:2922:U:H2'	35:A:2923:C:C6	2.45	0.52
2:5:554:LEU:HD11	2:5:603:ARG:HB2	1.90	0.52
2:6:353:HIS:O	2:6:427:LEU:HA	2.10	0.52
10:I:87:VAL:HG13	10:I:91:LYS:NZ	2.23	0.52
35:A:672:C:H2'	35:A:673:C:C6	2.45	0.52
35:A:1627:U:H2'	35:A:1628:A:C8	2.40	0.52
35:A:1963:G:H2'	35:A:1964:U:H6	1.75	0.52
35:A:2061:U:H2'	35:A:2062:G:C8	2.44	0.52
2:5:702:MET:HG3	8:G:176:LYS:HD3	1.91	0.52
7:F:95:ARG:NH1	35:A:2538:A:OP1	2.43	0.52
7:F:170:ASP:OD1	7:F:174:ARG:NH2	2.41	0.52
35:A:1005:A:H2'	35:A:1006:G:O4'	2.10	0.52
2:5:534:HIS:NE2	2:5:543:GLN:OE1	2.43	0.51
2:5:704:HIS:HB3	35:A:2884:A:H5'	1.92	0.51
2:6:83:LEU:N	2:6:90:VAL:O	2.36	0.51
3:B:42:C:N4	7:F:74:VAL:O	2.37	0.51
9:H:41:ARG:O	9:H:45:ARG:N	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:1715:A:H2'	35:A:1716:A:C8	2.46	0.51
7:F:134:ASN:OD1	7:F:164:VAL:HG23	2.10	0.51
18:Q:28:HIS:CD2	18:Q:82:HIS:HB2	2.46	0.51
35:A:292:G:N2	35:A:343:U:O2	2.43	0.51
2:5:173:ALA:HB3	2:5:265:PHE:HZ	1.76	0.51
9:H:98:ALA:HB2	9:H:114:LYS:HD3	1.91	0.51
26:Y:53:THR:HA	26:Y:56:ILE:HD12	1.90	0.51
35:A:729:C:O2'	35:A:733:U:OP1	2.27	0.51
35:A:1548:C:N4	35:A:1549:G:O6	2.43	0.51
2:6:180:GLY:HA3	2:6:185:CYS:HA	1.92	0.51
2:6:591:VAL:HA	2:6:630:ARG:HH22	1.76	0.51
4:C:181:GLU:HB2	4:C:270:ARG:O	2.10	0.51
29:b:27:LEU:HD23	29:b:38:LYS:HB3	1.92	0.51
35:A:502:C:H2'	35:A:503:A:C8	2.45	0.51
35:A:1179:U:C4	35:A:1188:A:C2	2.99	0.51
2:5:321:LEU:HD11	2:5:436:LEU:HG	1.91	0.51
35:A:279:U:H2'	35:A:280:G:H8	1.75	0.51
35:A:1001:C:H4'	35:A:1001:C:OP1	2.09	0.51
35:A:1211:G:H21	35:A:1216:A:H62	1.58	0.51
2:5:72:GLN:HB3	2:5:74:ARG:NE	2.25	0.51
2:6:650:VAL:HG22	2:6:682:VAL:HG22	1.93	0.51
7:F:15:TYR:OH	7:F:36:PRO:O	2.29	0.51
11:J:94:PRO:HB2	35:A:1195:A:C1'	2.41	0.51
11:J:136:SER:O	35:A:1180:G:N2	2.32	0.51
2:5:654:ASP:OD1	2:5:655:LEU:HG	2.11	0.51
19:R:11:GLN:OE1	19:R:14:ARG:NH1	2.43	0.51
35:A:1314:C:H2'	35:A:1315:C:H6	1.76	0.51
35:A:1541:G:C2	35:A:1631:A:N1	2.78	0.51
35:A:217:G:H22	35:A:235:U:H4'	1.75	0.51
35:A:3019:C:H2'	35:A:3020:U:O4'	2.11	0.51
35:A:337:U:C4	35:A:344:G:O6	2.64	0.51
35:A:1012:C:H3'	35:A:1013:U:C6	2.45	0.51
35:A:1162:G:O3'	35:A:1165:G:H5'	2.11	0.51
35:A:2471:A:H2'	35:A:2472:C:H6	1.76	0.51
6:E:156:VAL:HG12	6:E:158:ILE:HG12	1.92	0.51
7:F:178:ARG:NH1	7:F:184:PHE:HB2	2.26	0.51
35:A:277:U:H2'	35:A:278:A:C8	2.46	0.51
35:A:911:U:H2'	35:A:912:C:C6	2.46	0.51
35:A:928:U:H2'	35:A:929:C:C6	2.46	0.51
35:A:1927:C:O2'	35:A:3080:A:H1'	2.11	0.51
35:A:3030:A:H2'	35:A:3031:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:565:LYS:HE2	2:6:605:THR:HG22	1.93	0.50
4:C:162:SER:HB3	4:C:195:GLU:HG2	1.92	0.50
7:F:80:SER:OG	7:F:88:GLU:N	2.44	0.50
11:J:137:MET:HE1	35:A:1181:G:O5'	2.11	0.50
17:P:83:ARG:HH11	17:P:86:GLN:HE21	1.58	0.50
18:Q:91:VAL:HG11	18:Q:96:LEU:HD21	1.92	0.50
35:A:1634:C:H2'	35:A:1635:A:C8	2.45	0.50
35:A:2350:G:H2'	35:A:2351:A:C8	2.46	0.50
2:5:674:ASP:HA	11:J:23:ALA:HB1	1.94	0.50
13:L:17:LYS:HZ1	13:L:47:ILE:HD13	1.76	0.50
16:O:10:LEU:HD21	16:O:40:LYS:HA	1.93	0.50
32:e:47:ARG:HH22	35:A:725:A:P	2.34	0.50
4:C:224:VAL:HG13	35:A:2043:C:OP1	2.11	0.50
5:D:53:ALA:HB1	5:D:78:ARG:HB2	1.92	0.50
12:K:112:ASN:ND2	35:A:650:G:H5''	2.26	0.50
14:M:84:ASN:HD21	14:M:118:LEU:HA	1.75	0.50
16:O:70:ILE:HD11	16:O:76:VAL:HG22	1.92	0.50
19:R:48:ARG:NH1	35:A:652:C:O2'	2.45	0.50
34:g:16:CYS:SG	34:g:38:CYS:HB3	2.51	0.50
35:A:929:C:H1'	35:A:1339:G:H21	1.75	0.50
35:A:1195:A:H3'	35:A:1196:C:C5	2.47	0.50
35:A:1425:G:N2	35:A:1428:U:C4	2.79	0.50
35:A:2182:C:H2'	35:A:2183:G:C8	2.46	0.50
35:A:1180:G:C6	35:A:1195:A:N1	2.80	0.50
2:6:116:LEU:HD21	2:6:290:PHE:HZ	1.77	0.50
2:6:325:VAL:HG23	2:6:326:LYS:HG3	1.94	0.50
8:G:95:TYR:HD1	8:G:108:LEU:HA	1.76	0.50
19:R:28:ARG:NH1	19:R:38:GLN:OE1	2.45	0.50
35:A:589:A:O2'	35:A:592:A:OP1	2.24	0.50
35:A:750:C:H2'	35:A:751:A:H8	1.75	0.50
35:A:829:U:O2'	35:A:831:A:N7	2.34	0.50
35:A:1679:A:H4'	35:A:1679:A:OP1	2.12	0.50
10:I:51:VAL:HB	35:A:1202:A:N7	2.26	0.50
12:K:125:TYR:OH	12:K:132:HIS:NE2	2.38	0.50
23:V:88:ASP:O	23:V:92:GLY:N	2.45	0.50
32:e:7:HIS:NE2	35:A:251:A:OP1	2.38	0.50
35:A:1610:C:H2'	35:A:1611:A:C8	2.46	0.50
35:A:1732:U:H2'	35:A:1733:C:C6	2.47	0.50
35:A:2076:A:H2'	35:A:2077:C:O4'	2.11	0.50
2:5:322:ALA:HB3	2:5:427:LEU:HB2	1.94	0.50
6:E:160:ARG:NH1	35:A:706:G:O2'	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:141:GLU:CD	7:F:143:SER:H	2.19	0.50
16:O:45:ARG:O	16:O:49:GLU:HG3	2.12	0.50
5:D:130:HIS:CD2	5:D:165:ARG:HB3	2.46	0.50
35:A:2190:A:H5'	35:A:2191:C:C4	2.47	0.50
2:5:161:LEU:HD21	2:5:174:PRO:HG3	1.94	0.50
7:F:149:ASP:O	7:F:152:SER:OG	2.28	0.50
35:A:356:G:H4'	35:A:358:G:C6	2.47	0.50
35:A:2238:A:H2'	35:A:2239:A:C8	2.47	0.50
35:A:2515:U:H2'	35:A:2516:U:C6	2.47	0.50
2:6:417:ARG:CD	13:L:97:ARG:HD3	2.40	0.49
9:H:78:VAL:HB	9:H:146:LEU:HD23	1.93	0.49
11:J:137:MET:HE1	35:A:1181:G:C4'	2.42	0.49
12:K:112:ASN:OD1	12:K:112:ASN:N	2.43	0.49
27:Z:5:THR:OG1	27:Z:9:GLU:OE2	2.24	0.49
35:A:56:U:O2'	35:A:71:A:OP2	2.29	0.49
2:6:332:TYR:HA	13:L:13:ASN:HD22	1.77	0.49
13:L:47:ILE:HG22	13:L:49:GLY:H	1.77	0.49
18:Q:95:LYS:NZ	35:A:3068:U:OP1	2.40	0.49
35:A:1550:G:O6	35:A:1620:U:C4	2.65	0.49
35:A:1621:C:H2'	35:A:1622:G:C8	2.47	0.49
35:A:2465:A:H2'	35:A:2466:G:C8	2.47	0.49
2:5:292:ALA:HB1	2:5:294:PRO:HD2	1.93	0.49
2:5:346:ILE:HB	2:5:407:VAL:HB	1.93	0.49
3:B:63:U:H2'	3:B:64:G:H8	1.77	0.49
4:C:24:ILE:HG23	4:C:83:GLU:HA	1.94	0.49
7:F:147:GLU:HA	34:g:28:LYS:HE3	1.94	0.49
7:F:154:ASP:OD1	7:F:155:ARG:N	2.45	0.49
11:J:128:LYS:HE2	35:A:1198:C:C5'	2.41	0.49
35:A:368:U:O2'	35:A:369:G:H5'	2.12	0.49
2:5:272:CYS:HB2	2:5:277:VAL:HB	1.94	0.49
2:5:353:HIS:CD2	2:5:433:PRO:HB3	2.47	0.49
2:6:550:GLU:O	2:6:605:THR:N	2.44	0.49
3:B:60:G:H4'	17:P:12:GLU:HB2	1.94	0.49
4:C:257:THR:HG1	35:A:2014:G:HO2'	1.56	0.49
5:D:147:ARG:CG	5:D:148:PRO:HD2	2.42	0.49
29:b:3:VAL:HG12	35:A:2239:A:C2	2.47	0.49
35:A:966:U:H2'	35:A:967:G:H8	1.78	0.49
35:A:999:C:H2'	35:A:1000:C:H6	1.78	0.49
2:5:24:ARG:N	2:5:89:LYS:O	2.43	0.49
2:6:357:HIS:HB3	2:6:438:PRO:HG2	1.95	0.49
3:B:10:G:O2'	3:B:11:U:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:118:ARG:NH2	14:M:4:ILE:O	2.45	0.49
9:H:88:THR:HG22	9:H:90:LYS:HG3	1.94	0.49
14:M:63:LYS:HA	32:e:13:ARG:HD3	1.94	0.49
23:V:84:GLY:C	23:V:97:ILE:HG22	2.38	0.49
35:A:2085:C:O2'	35:A:2086:U:OP1	2.29	0.49
35:A:2165:C:H3'	35:A:2166:C:H5'	1.95	0.49
35:A:2530:C:H5''	35:A:2531:G:H2'	1.94	0.49
35:A:2879:G:O2'	35:A:2888:G:O6	2.28	0.49
35:A:3117:U:H2'	35:A:3118:U:C6	2.48	0.49
2:6:376:GLY:H	2:6:476:ARG:HA	1.77	0.49
2:6:533:ARG:H	2:6:627:LEU:HD23	1.78	0.49
15:N:48:GLU:OE1	15:N:51:ARG:NH1	2.46	0.49
16:O:72:ASP:O	16:O:76:VAL:HG23	2.13	0.49
35:A:2248:C:H2'	35:A:2249:G:H8	1.76	0.49
2:6:186:LYS:HB2	2:6:200:SER:HB3	1.95	0.49
10:I:66:ILE:HG22	10:I:109:TYR:CZ	2.47	0.49
13:L:86:ILE:HG22	13:L:94:ARG:HG3	1.93	0.49
19:R:89:GLU:OE1	20:S:8:LYS:NZ	2.38	0.49
35:A:2622:C:H2'	35:A:2623:A:H8	1.77	0.49
5:D:63:ILE:HD11	35:A:3032:G:H5''	1.94	0.49
25:X:35:GLU:HG2	35:A:2578:A:H4'	1.94	0.49
35:A:1756:G:H1'	35:A:1758:G:N1	2.26	0.49
2:6:661:GLY:O	2:6:664:SER:OG	2.26	0.49
28:a:16:ARG:O	28:a:20:ARG:HG3	2.13	0.49
35:A:2:A:H2'	35:A:3:A:H8	1.78	0.49
35:A:2288:C:H2'	35:A:2289:C:C6	2.47	0.49
2:6:376:GLY:HA2	2:6:477:ILE:H	1.77	0.49
3:B:115:A:H2'	3:B:116:C:C6	2.48	0.49
4:C:89:THR:CG2	4:C:201:GLN:HG2	2.43	0.49
6:E:36:GLN:OE1	35:A:774:G:N2	2.34	0.49
8:G:59:GLU:OE2	8:G:62:SER:N	2.39	0.49
11:J:94:PRO:HD2	35:A:1194:C:O2'	2.13	0.49
14:M:80:VAL:CG1	14:M:118:LEU:HB2	2.43	0.49
35:A:297:G:H2'	35:A:298:G:C8	2.47	0.49
13:L:89:ASN:OD1	13:L:90:ASP:N	2.46	0.48
25:X:75:ARG:NH2	35:A:2557:A:OP1	2.46	0.48
35:A:673:C:H2'	35:A:674:U:C6	2.48	0.48
35:A:1400:G:N2	35:A:1443:G:H5''	2.28	0.48
35:A:2867:A:H2'	35:A:2868:A:C8	2.47	0.48
2:5:322:ALA:HA	2:5:341:VAL:HA	1.95	0.48
2:6:561:GLU:HB3	2:6:603:ARG:HH21	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:46:A:C4	3:B:47:A:C8	3.02	0.48
23:V:96:ARG:HE	23:V:105:ILE:HG23	1.78	0.48
25:X:48:GLY:HA3	25:X:79:ASN:OD1	2.13	0.48
35:A:138:A:H2'	35:A:139:U:O2	2.13	0.48
35:A:289:A:N6	35:A:299:G:H1	2.11	0.48
35:A:752:C:H2'	35:A:753:A:H8	1.77	0.48
35:A:1705:C:H2'	35:A:1706:A:C8	2.48	0.48
2:6:368:HIS:HB2	2:6:710:ARG:HB3	1.95	0.48
12:K:102:GLU:O	12:K:106:ILE:HG12	2.13	0.48
13:L:35:ILE:O	13:L:69:ARG:NH1	2.39	0.48
18:Q:51:GLY:HA2	18:Q:56:GLU:HG3	1.96	0.48
25:X:41:ARG:NH1	35:A:2610:C:O2'	2.46	0.48
35:A:339:U:H2'	35:A:340:A:H8	1.76	0.48
35:A:929:C:H1'	35:A:1339:G:N2	2.28	0.48
35:A:2342:A:N6	35:A:2390:U:O2'	2.47	0.48
2:6:165:GLN:HA	2:6:172:VAL:HB	1.94	0.48
5:D:148:PRO:O	35:A:2735:U:O2'	2.29	0.48
23:V:46:ALA:HA	23:V:57:GLY:HA3	1.95	0.48
35:A:32:G:H1'	35:A:542:A:C4	2.49	0.48
35:A:389:G:N1	35:A:392:A:OP2	2.41	0.48
35:A:2019:A:H2'	35:A:2020:A:H8	1.78	0.48
35:A:2551:A:H2'	35:A:2552:A:C8	2.48	0.48
2:5:697:ILE:HD11	35:A:2885:G:H21	1.78	0.48
2:6:172:VAL:HG22	2:6:266:PHE:HB2	1.96	0.48
18:Q:26:ASN:OD1	18:Q:84:ASP:HB2	2.13	0.48
35:A:489:A:H2'	35:A:490:A:C8	2.49	0.48
35:A:2095:G:O2'	35:A:2096:G:H8	1.96	0.48
35:A:2297:U:H2'	35:A:2298:U:C6	2.48	0.48
35:A:2339:G:O6	35:A:2394:A:N6	2.46	0.48
35:A:2420:U:H1'	35:A:2421:A:C8	2.48	0.48
2:5:225:ILE:O	2:5:229:ILE:HG13	2.13	0.48
35:A:980:C:O2'	35:A:981:U:O5'	2.27	0.48
35:A:999:C:H2'	35:A:1000:C:C6	2.48	0.48
4:C:276:LYS:HD3	35:A:2125:A:H62	1.78	0.48
24:W:52:ARG:HH22	35:A:1157:G:H4'	1.77	0.48
32:e:23:VAL:CG1	32:e:47:ARG:HB3	2.43	0.48
35:A:979:G:H2'	35:A:980:C:C6	2.49	0.48
35:A:1529:U:H3'	35:A:1530:G:C8	2.49	0.48
35:A:2096:G:H2'	35:A:2097:G:H8	1.76	0.48
35:A:3022:G:H2'	35:A:3023:G:C8	2.49	0.48
35:A:3030:A:H2'	35:A:3031:A:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:261:ALA:HA	2:5:291:PRO:HB3	1.96	0.48
2:6:25:ASN:HB2	2:6:93:ILE:HD11	1.95	0.48
8:G:60:ARG:HH11	35:A:1153:U:H5'	1.78	0.48
16:O:101:GLU:HG3	16:O:102:ASN:N	2.28	0.48
35:A:2070:A:H2'	35:A:2071:A:C4	2.49	0.48
2:5:451:ALA:N	2:5:512:ASP:O	2.41	0.48
5:D:160:VAL:HG12	5:D:160:VAL:O	2.14	0.48
12:K:55:ILE:HA	12:K:123:LYS:O	2.14	0.48
14:M:93:VAL:HB	14:M:124:VAL:HG12	1.95	0.48
35:A:1468:A:H2'	35:A:1469:A:C8	2.49	0.48
35:A:1940:A:N6	35:A:1954:C:O2'	2.46	0.48
2:5:26:VAL:HG13	2:5:114:CYS:HB3	1.95	0.48
2:5:450:VAL:HG12	2:5:513:THR:HA	1.95	0.48
2:5:583:VAL:HG13	2:5:629:LEU:HD22	1.96	0.48
2:6:475:LEU:HD21	2:6:488:LEU:HD11	1.96	0.48
5:D:154:CYS:C	5:D:156:THR:H	2.21	0.48
7:F:105:GLU:HG3	7:F:109:ARG:HH12	1.79	0.48
10:I:40:ARG:HG2	35:A:1200:U:O3'	2.13	0.48
27:Z:14:THR:OG1	27:Z:17:GLU:OE1	2.31	0.48
27:Z:36:MET:CE	27:Z:41:LEU:HD23	2.41	0.48
35:A:502:C:H2'	35:A:503:A:H8	1.78	0.48
35:A:277:U:H2'	35:A:278:A:H8	1.79	0.47
35:A:2195:U:H1'	35:A:2196:G:C5	2.49	0.47
35:A:2686:U:H2'	35:A:2687:U:C6	2.48	0.47
2:5:41:GLU:HG3	2:5:61:THR:HG22	1.95	0.47
2:5:699:LEU:HG	2:5:707:GLY:HA3	1.95	0.47
2:5:714:ALA:HB1	2:5:715:ARG:NH1	2.29	0.47
4:C:165:LEU:HA	4:C:175:LEU:HD23	1.96	0.47
5:D:121:LYS:HB2	5:D:170:MET:HG3	1.97	0.47
15:N:80:GLU:OE2	35:A:2717:U:O2'	2.21	0.47
35:A:292:G:H2'	35:A:293:G:C8	2.49	0.47
35:A:441:G:H2'	35:A:442:U:C6	2.49	0.47
35:A:543:U:H3'	35:A:544:U:C5'	2.43	0.47
35:A:1087:G:H2'	35:A:1088:U:C6	2.49	0.47
35:A:1732:U:H2'	35:A:1733:C:H6	1.79	0.47
35:A:1939:U:H3	35:A:1955:A:H62	1.61	0.47
4:C:126:LYS:HB2	4:C:129:ASN:HD21	1.79	0.47
4:C:245:HIS:HB2	4:C:246:PRO:CD	2.44	0.47
8:G:71:THR:HG21	35:A:2971:G:H5'	1.96	0.47
15:N:65:TRP:HB2	15:N:105:GLU:HB2	1.96	0.47
26:Y:39:VAL:HG11	26:Y:64:ALA:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:38:ILE:HG22	30:c:39:LYS:N	2.29	0.47
35:A:1314:C:H2'	35:A:1315:C:C6	2.49	0.47
2:5:189:VAL:HA	2:5:196:TYR:HA	1.95	0.47
8:G:108:LEU:O	8:G:153:ARG:NH2	2.33	0.47
14:M:72:ARG:HH12	35:A:724:G:H1	1.62	0.47
35:A:4:G:H2'	35:A:5:U:H6	1.79	0.47
35:A:284:G:C8	35:A:303:G:C5	3.02	0.47
35:A:635:G:O2'	35:A:636:U:O4'	2.32	0.47
35:A:877:U:H4'	35:A:878:G:O5'	2.13	0.47
2:5:322:ALA:N	2:5:427:LEU:O	2.39	0.47
3:B:26:A:H2'	3:B:27:A:C8	2.50	0.47
4:C:270:ARG:NH2	35:A:2062:G:OP1	2.48	0.47
17:P:86:GLN:O	17:P:90:GLU:OE1	2.31	0.47
27:Z:16:ASP:N	27:Z:16:ASP:OD1	2.46	0.47
30:c:38:ILE:HG22	30:c:39:LYS:H	1.79	0.47
35:A:1614:G:H2'	35:A:1615:G:H8	1.79	0.47
35:A:2073:A:N6	35:A:2074:G:N3	2.62	0.47
35:A:2411:U:H2'	35:A:2412:U:C6	2.50	0.47
2:5:190:GLY:N	2:5:195:THR:O	2.34	0.47
2:6:396:PRO:O	2:6:402:ARG:NH2	2.45	0.47
2:6:651:VAL:O	2:6:681:THR:N	2.47	0.47
7:F:29:TYR:CD2	7:F:35:ILE:HD13	2.46	0.47
8:G:95:TYR:CD1	8:G:108:LEU:HD13	2.49	0.47
11:J:23:ALA:HB3	11:J:24:PRO:HD3	1.96	0.47
11:J:90:GLY:N	35:A:1182:C:H5'	2.29	0.47
35:A:138:A:N3	35:A:1523:U:O2'	2.41	0.47
35:A:287:A:N6	35:A:299:G:O2'	2.48	0.47
35:A:1953:C:H2'	35:A:1954:C:O4'	2.15	0.47
35:A:2169:G:H2'	35:A:2170:U:C6	2.49	0.47
2:5:321:LEU:N	2:5:343:SER:O	2.42	0.47
2:5:703:SER:O	2:5:704:HIS:C	2.57	0.47
2:6:320:LEU:HB3	2:6:429:ASP:HB2	1.97	0.47
2:6:446:LEU:HB3	2:6:490:CYS:O	2.14	0.47
4:C:275:GLY:O	4:C:276:LYS:C	2.58	0.47
10:I:66:ILE:HB	10:I:69:LEU:HD12	1.97	0.47
13:L:68:GLU:OE1	35:A:2908:U:O2'	2.28	0.47
17:P:21:ARG:HA	17:P:24:ARG:HG2	1.96	0.47
19:R:48:ARG:NH2	35:A:652:C:O2	2.40	0.47
23:V:44:HIS:CD2	23:V:59:ILE:HD12	2.50	0.47
35:A:247:G:OP2	35:A:249:C:N4	2.48	0.47
35:A:947:U:H2'	35:A:948:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:994:A:H8	35:A:1014:G:H21	1.63	0.47
35:A:1434:G:O2'	35:A:1435:C:H5'	2.15	0.47
35:A:2358:A:N6	35:A:2379:G:O2'	2.47	0.47
35:A:2365:A:H2'	35:A:2366:C:C6	2.49	0.47
35:A:2380:G:N2	35:A:2381:A:N1	2.62	0.47
7:F:107:LEU:O	7:F:111:ILE:HG12	2.15	0.47
14:M:68:LYS:HE3	14:M:68:LYS:HA	1.97	0.47
15:N:74:LEU:HD12	15:N:92:TRP:NE1	2.30	0.47
16:O:71:ARG:NH2	35:A:2933:G:H5'	2.29	0.47
34:g:24:THR:HG22	34:g:25:ARG:N	2.26	0.47
35:A:829:U:H1'	35:A:832:G:N7	2.30	0.47
35:A:1001:C:H1'	35:A:1007:G:N2	2.29	0.47
35:A:2961:G:H2'	35:A:2962:A:C8	2.49	0.47
2:6:332:TYR:CE1	13:L:47:ILE:HG13	2.50	0.47
7:F:67:ILE:HG23	7:F:68:THR:HG23	1.95	0.47
8:G:86:GLN:NE2	8:G:165:TYR:HD1	2.12	0.47
9:H:124:ILE:HG22	9:H:125:LYS:N	2.27	0.47
10:I:26:THR:HG21	10:I:93:ILE:HG21	1.96	0.47
15:N:62:GLY:HA2	15:N:107:SER:O	2.15	0.47
15:N:124:LYS:NZ	35:A:2691:C:O2	2.48	0.47
25:X:38:VAL:HG12	25:X:59:LEU:HB2	1.97	0.47
35:A:580:G:H2'	35:A:581:G:O4'	2.14	0.47
3:B:81:U:H2'	3:B:82:A:C8	2.50	0.47
4:C:139:GLY:O	4:C:164:GLN:NE2	2.42	0.47
8:G:23:ASN:OD1	8:G:24:LEU:N	2.48	0.47
12:K:96:HIS:CD2	12:K:99:ARG:NE	2.83	0.47
17:P:69:ASP:N	17:P:69:ASP:OD1	2.46	0.47
32:e:50:VAL:HG11	32:e:58:ILE:HD12	1.97	0.47
35:A:1478:C:O2'	35:A:2026:A:N3	2.46	0.47
35:A:1633:U:H2'	35:A:1634:C:H6	1.80	0.47
2:6:170:ASP:N	2:6:170:ASP:OD1	2.48	0.46
6:E:160:ARG:NH2	35:A:706:G:O3'	2.43	0.46
11:J:129:ILE:HG12	35:A:1198:C:O2	2.13	0.46
16:O:24:LEU:HB3	16:O:44:LEU:HD22	1.97	0.46
29:b:8:MET:HE3	29:b:12:ASN:HB3	1.98	0.46
35:A:672:C:H2'	35:A:673:C:H6	1.80	0.46
35:A:996:G:H2'	35:A:997:G:C8	2.45	0.46
35:A:1010:U:H4'	35:A:1011:A:OP1	2.14	0.46
7:F:45:MET:SD	7:F:159:MET:HB3	2.55	0.46
7:F:76:ARG:HB3	7:F:89:GLY:HA2	1.97	0.46
16:O:27:SER:OG	35:A:1393:C:O2'	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:41:ARG:NH1	35:A:2611:U:O4'	2.48	0.46
35:A:978:A:H2'	35:A:979:G:C8	2.49	0.46
35:A:2076:A:HO2'	35:A:2133:G:HO2'	1.62	0.46
35:A:3078:G:N2	35:A:3081:A:OP2	2.36	0.46
2:5:659:ILE:CD1	2:5:702:MET:HB3	2.45	0.46
2:6:178:PRO:HD3	2:6:270:PRO:HG3	1.98	0.46
2:6:623:MET:HE3	2:6:623:MET:HB3	1.65	0.46
35:A:2108:A:N6	35:A:2109:A:H62	2.13	0.46
35:A:2329:G:O6	35:A:2407:C:N4	2.48	0.46
35:A:2470:A:H2'	35:A:2471:A:C8	2.50	0.46
2:6:152:HIS:HE1	2:6:154:ARG:HE	1.63	0.46
2:6:651:VAL:HG11	2:6:659:ILE:HG13	1.96	0.46
4:C:258:ARG:NH1	35:A:2016:G:OP1	2.43	0.46
6:E:40:ALA:HB2	6:E:100:GLN:HE21	1.79	0.46
35:A:1532:G:N2	35:A:1804:G:C4	2.84	0.46
35:A:1854:U:H2'	35:A:1855:A:H8	1.81	0.46
35:A:1937:U:H2'	35:A:1938:G:O4'	2.16	0.46
35:A:2515:U:OP1	35:A:2604:U:O2'	2.32	0.46
2:5:461:LEU:HD11	2:5:503:LEU:HD21	1.96	0.46
14:M:84:ASN:ND2	14:M:118:LEU:HA	2.31	0.46
35:A:663:A:N3	35:A:663:A:H2'	2.30	0.46
35:A:1001:C:H3'	35:A:1002:C:O4'	2.14	0.46
35:A:1183:U:H6	35:A:1183:U:O5'	1.98	0.46
35:A:1633:U:H2'	35:A:1634:C:C6	2.51	0.46
35:A:2101:A:H2'	35:A:2102:G:H8	1.78	0.46
2:6:240:ARG:NE	2:6:245:GLU:OE2	2.49	0.46
4:C:123:ALA:HB3	4:C:131:LEU:HD21	1.97	0.46
15:N:17:GLN:NE2	15:N:41:TYR:CE1	2.84	0.46
21:T:54:VAL:O	21:T:57:VAL:HG12	2.16	0.46
22:U:62:ARG:HG2	22:U:62:ARG:HH11	1.80	0.46
35:A:384:G:H2'	35:A:385:G:H8	1.81	0.46
35:A:1750:A:N6	35:A:1763:G:O2'	2.48	0.46
35:A:2884:A:H2'	35:A:2885:G:O4'	2.16	0.46
2:5:482:GLU:OE1	2:5:521:ARG:NH1	2.49	0.46
2:6:417:ARG:CD	13:L:97:ARG:CD	2.86	0.46
7:F:8:LEU:CD2	7:F:13:GLN:HB2	2.44	0.46
12:K:36:LEU:HD11	12:K:122:LEU:HB2	1.96	0.46
13:L:58:VAL:HG22	13:L:59:LYS:H	1.79	0.46
20:S:23:LYS:HE3	35:A:641:U:H1'	1.97	0.46
25:X:18:ALA:HB1	35:A:2495:G:OP1	2.16	0.46
35:A:287:A:C6	35:A:300:G:C6	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:681:C:H2'	35:A:682:A:H8	1.80	0.46
35:A:740:A:O2'	35:A:741:G:OP2	2.28	0.46
35:A:1457:A:O2'	35:A:1459:U:OP2	2.32	0.46
35:A:1513:C:H2'	35:A:1514:C:H6	1.79	0.46
35:A:2162:A:N3	35:A:2162:A:H2'	2.31	0.46
35:A:2321:U:H2'	35:A:2322:C:C6	2.51	0.46
7:F:136:THR:HG21	35:A:2527:G:H21	1.80	0.46
8:G:150:ARG:NH2	8:G:168:GLU:OE1	2.48	0.46
10:I:62:SER:HA	10:I:67:GLU:HG2	1.98	0.46
12:K:21:SER:HA	12:K:61:LYS:HB2	1.98	0.46
35:A:4:G:H2'	35:A:5:U:C6	2.50	0.46
35:A:222:A:O2'	35:A:508:G:N3	2.45	0.46
35:A:442:U:H2'	35:A:443:C:C6	2.51	0.46
35:A:2552:A:H2'	35:A:2553:G:H8	1.77	0.46
2:6:321:LEU:N	2:6:343:SER:O	2.48	0.46
2:6:673:THR:HG22	2:6:683:ILE:HG12	1.98	0.46
7:F:142:GLN:HE22	7:F:156:PRO:HA	1.81	0.46
14:M:31:LYS:HE3	35:A:658:U:H5'	1.98	0.46
31:d:10:PRO:HG3	35:A:1830:C:H5'	1.98	0.46
35:A:611:U:H2'	35:A:612:U:C6	2.51	0.46
35:A:974:G:O2'	35:A:975:U:P	2.73	0.46
35:A:1001:C:C4	35:A:1002:C:H1'	2.51	0.46
35:A:2395:U:H4'	35:A:2396:A:H5'	1.98	0.46
35:A:3033:G:H2'	35:A:3034:C:H6	1.81	0.46
1:3:4:ARG:NH1	35:A:2679:G:O3'	2.49	0.46
2:5:697:ILE:HD11	35:A:2885:G:N2	2.31	0.46
2:6:286:ILE:HA	2:6:290:PHE:CG	2.51	0.46
8:G:30:LYS:HE3	8:G:82:GLU:O	2.16	0.46
13:L:76:TYR:HB2	18:Q:72:THR:HB	1.98	0.46
23:V:72:MET:SD	23:V:80:PRO:HB2	2.56	0.46
27:Z:58:TYR:HD2	35:A:69:U:C6	2.34	0.46
35:A:681:C:H2'	35:A:682:A:C8	2.51	0.46
2:5:36:LYS:HG2	2:5:118:VAL:HB	1.98	0.45
2:5:493:GLU:OE2	35:A:2885:G:O2'	2.18	0.45
9:H:9:VAL:HG23	9:H:12:LEU:HB2	1.98	0.45
9:H:124:ILE:O	9:H:125:LYS:HB2	2.16	0.45
24:W:158:THR:HG23	24:W:160:GLY:H	1.81	0.45
35:A:980:C:HO2'	35:A:981:U:P	2.39	0.45
35:A:1008:G:H2'	35:A:1009:U:O4'	2.17	0.45
35:A:2069:U:H2'	35:A:2113:A:H61	1.80	0.45
35:A:2189:C:H6	35:A:2190:A:H5''	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:2194:A:H1'	35:A:2195:U:O2	2.16	0.45
35:A:2497:A:H2'	35:A:2498:A:C8	2.51	0.45
2:5:347:ARG:O	2:5:390:ILE:HD11	2.16	0.45
9:H:109:GLY:N	9:H:110:PRO:HD2	2.31	0.45
15:N:34:ILE:HD12	15:N:104:PHE:HD2	1.81	0.45
35:A:292:G:N1	35:A:343:U:C2	2.84	0.45
35:A:2247:A:H2'	35:A:2248:C:C6	2.52	0.45
35:A:2345:U:OP2	35:A:2392:A:O2'	2.35	0.45
2:6:649:ILE:O	2:6:683:ILE:N	2.43	0.45
26:Y:22:HIS:HE1	26:Y:24:ARG:HD3	1.81	0.45
26:Y:41:ARG:HH12	35:A:164:A:H4'	1.81	0.45
31:d:42:ARG:NH2	35:A:556:G:N7	2.52	0.45
35:A:751:A:H2'	35:A:752:C:C6	2.51	0.45
35:A:1528:G:H2'	35:A:1529:U:C6	2.52	0.45
35:A:1690:A:H2'	35:A:1691:A:H8	1.81	0.45
2:6:286:ILE:O	2:6:290:PHE:HB2	2.16	0.45
2:6:533:ARG:HH21	2:6:546:VAL:HG21	1.82	0.45
2:6:541:HIS:HB3	35:A:3079:U:H5''	1.99	0.45
2:6:648:THR:HG23	2:6:682:VAL:HG13	1.99	0.45
3:B:43:C:C5	7:F:73:GLU:HG2	2.52	0.45
12:K:144:GLN:HB3	35:A:1130:C:C5	2.51	0.45
17:P:73:ILE:HB	17:P:80:HIS:CE1	2.51	0.45
35:A:263:G:H2'	35:A:264:G:O4'	2.16	0.45
35:A:1755:A:H2'	35:A:1758:G:H1	1.81	0.45
35:A:2553:G:H2'	35:A:2554:U:C6	2.51	0.45
2:5:530:GLY:HA3	2:5:628:ALA:O	2.16	0.45
4:C:163:ILE:HB	4:C:176:ARG:O	2.17	0.45
7:F:12:LYS:HE3	7:F:16:ARG:HH21	1.81	0.45
14:M:81:GLY:HA2	14:M:84:ASN:HD22	1.82	0.45
25:X:69:PHE:CD2	35:A:972:A:H5''	2.51	0.45
35:A:97:U:H5''	35:A:99:G:O4'	2.17	0.45
35:A:380:A:N3	35:A:401:C:O2'	2.45	0.45
2:6:447:PRO:HB3	2:6:489:TRP:CE2	2.52	0.45
4:C:96:HIS:CD2	4:C:102:LYS:HD3	2.51	0.45
5:D:85:ARG:NH1	35:A:2861:U:H5''	2.32	0.45
5:D:94:GLU:CD	5:D:94:GLU:H	2.24	0.45
7:F:44:ASN:OD1	7:F:160:ASP:HB3	2.17	0.45
7:F:47:VAL:HG13	7:F:56:LEU:HD22	1.98	0.45
7:F:126:PRO:HB2	7:F:174:ARG:NH1	2.32	0.45
12:K:41:LYS:NZ	12:K:50:GLY:O	2.42	0.45
21:T:30:LEU:HD22	29:b:24:ALA:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:13:ALA:O	22:U:32:VAL:HG22	2.17	0.45
35:A:214:G:H4'	35:A:215:A:H4'	1.97	0.45
35:A:619:C:H4'	35:A:620:G:C8	2.51	0.45
35:A:2153:G:H1'	35:A:2155:U:C6	2.52	0.45
35:A:2857:A:H2'	35:A:2858:G:H8	1.81	0.45
35:A:3033:G:H2'	35:A:3034:C:C6	2.52	0.45
26:Y:19:SER:OG	26:Y:20:HIS:N	2.50	0.45
30:c:10:LYS:NZ	35:A:2645:G:OP2	2.50	0.45
35:A:181:A:H2'	35:A:182:C:H6	1.82	0.45
35:A:1081:C:O2'	35:A:2497:A:N3	2.41	0.45
35:A:1719:C:C2	35:A:1720:G:C8	3.05	0.45
35:A:2872:G:H2'	35:A:2873:U:H6	1.81	0.45
2:6:214:ASP:OD1	2:6:215:ALA:N	2.50	0.45
2:6:340:ARG:HA	2:6:412:ILE:HA	1.98	0.45
4:C:221:VAL:HG21	35:A:897:A:N7	2.31	0.45
11:J:120:ALA:HB1	11:J:125:ALA:HB3	1.98	0.45
15:N:116:ASP:O	15:N:120:ARG:HG2	2.17	0.45
30:c:6:ASP:OD1	30:c:6:ASP:N	2.50	0.45
35:A:81:A:C2	35:A:100:A:C5	3.04	0.45
35:A:402:G:H4'	35:A:404:A:N7	2.32	0.45
35:A:747:A:H2'	35:A:748:U:O4'	2.16	0.45
35:A:1012:C:H3'	35:A:1013:U:C5	2.52	0.45
35:A:1729:A:H2'	35:A:1731:A:C8	2.51	0.45
35:A:2343:G:H2'	35:A:2344:G:C8	2.52	0.45
2:6:168:PHE:HB2	2:6:172:VAL:HG21	1.99	0.45
4:C:133:LEU:HD23	4:C:136:ILE:HD12	1.99	0.45
10:I:31:LEU:HD11	10:I:103:LEU:HG	1.97	0.45
17:P:121:ARG:NH2	35:A:2600:A:N3	2.58	0.45
35:A:733:U:H2'	35:A:734:C:C6	2.52	0.45
35:A:1232:G:O6	35:A:1233:A:N6	2.50	0.45
35:A:2108:A:H61	35:A:2109:A:H62	1.63	0.45
35:A:3070:G:H4'	35:A:3071:A:H5'	1.98	0.45
2:5:321:LEU:HB3	2:5:343:SER:HB3	1.98	0.45
2:5:478:GLU:HB3	2:5:489:TRP:HE1	1.82	0.45
2:5:700:ARG:HB2	35:A:2884:A:C2	2.51	0.45
11:J:38:MET:SD	11:J:39:GLU:N	2.90	0.45
11:J:94:PRO:CD	35:A:1194:C:H1'	2.40	0.45
12:K:25:LEU:HA	12:K:62:ILE:HD11	1.98	0.45
12:K:123:LYS:HG2	12:K:132:HIS:HE2	1.81	0.45
23:V:81:THR:HG23	23:V:100:THR:HG23	1.99	0.45
24:W:159:ALA:O	24:W:162:ILE:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:159:A:H2'	35:A:160:A:C8	2.52	0.45
35:A:289:A:H62	35:A:299:G:H1	1.63	0.45
35:A:735:U:H2'	35:A:736:G:O4'	2.17	0.45
35:A:1213:A:H2'	35:A:1213:A:N3	2.32	0.45
35:A:1545:C:N4	35:A:1626:G:O6	2.49	0.45
5:D:151:ILE:HG22	35:A:2276:G:OP1	2.17	0.44
12:K:108:MET:HE2	35:A:1256:G:N2	2.32	0.44
18:Q:17:PRO:HG3	18:Q:83:ILE:O	2.17	0.44
33:f:32:HIS:O	33:f:34:GLN:HG2	2.18	0.44
34:g:42:HIS:HD2	34:g:44:PHE:HB3	1.81	0.44
35:A:31:U:O2'	35:A:32:G:H5'	2.18	0.44
35:A:289:A:H5''	35:A:289:A:N3	2.32	0.44
35:A:844:G:O2'	35:A:878:G:H4'	2.16	0.44
35:A:2256:G:N2	35:A:2796:A:OP2	2.51	0.44
2:5:450:VAL:HA	2:5:513:THR:HA	1.97	0.44
2:5:476:ARG:HG2	2:5:489:TRP:CD1	2.52	0.44
2:6:339:VAL:HG11	2:6:427:LEU:HD12	1.99	0.44
8:G:152:LEU:HD23	8:G:152:LEU:HA	1.81	0.44
35:A:193:G:H2'	35:A:194:A:O4'	2.17	0.44
35:A:498:G:H8	35:A:498:G:H5''	1.82	0.44
35:A:728:G:H2'	35:A:729:C:C6	2.53	0.44
35:A:1223:U:H2'	35:A:1224:G:C8	2.51	0.44
1:3:23:ASN:ND2	35:A:1065:C:H4'	2.32	0.44
2:5:351:THR:HA	2:5:389:ARG:HA	2.00	0.44
2:6:26:VAL:HG11	2:6:116:LEU:HG	1.99	0.44
4:C:20:ASP:O	4:C:22:ALA:N	2.48	0.44
8:G:24:LEU:HD23	8:G:73:ILE:HD12	1.99	0.44
10:I:115:LEU:HD12	10:I:119:ASP:HB3	2.00	0.44
22:U:42:ILE:O	22:U:46:ILE:HG12	2.17	0.44
23:V:75:ASP:OD2	23:V:101:ASN:HB2	2.17	0.44
26:Y:8:CYS:SG	26:Y:10:LYS:HB2	2.58	0.44
35:A:90:C:H2'	35:A:91:C:C6	2.52	0.44
35:A:1479:G:H4'	35:A:2025:C:H5	1.82	0.44
2:5:703:SER:OG	2:5:707:GLY:N	2.50	0.44
8:G:19:ILE:HG13	8:G:24:LEU:HD13	1.99	0.44
9:H:32:PRO:HB3	26:Y:64:ALA:HA	1.98	0.44
20:S:72:LYS:HD2	20:S:91:ARG:HG3	2.00	0.44
35:A:621:U:H2'	35:A:622:C:H6	1.83	0.44
35:A:722:G:H2'	35:A:723:C:C6	2.52	0.44
35:A:1011:A:C6	35:A:1012:C:H1'	2.52	0.44
35:A:1544:U:H2'	35:A:1545:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:2622:C:H2'	35:A:2623:A:C8	2.52	0.44
2:6:536:LYS:HZ3	35:A:1929:A:P	2.41	0.44
2:6:653:ASP:HA	2:6:656:VAL:HG23	1.98	0.44
4:C:134:ARG:O	4:C:168:LYS:NZ	2.51	0.44
6:E:51:SER:HB2	6:E:95:PRO:HD3	1.99	0.44
7:F:71:LYS:HZ3	34:g:5:ILE:CB	2.27	0.44
9:H:41:ARG:HG2	35:A:306:U:H5''	2.00	0.44
10:I:94:LYS:HE2	10:I:121:GLU:HA	2.00	0.44
21:T:8:PRO:HB2	21:T:71:LEU:HD21	2.00	0.44
23:V:81:THR:HG22	23:V:82:ARG:O	2.18	0.44
35:A:2738:U:H2'	35:A:2739:C:C6	2.53	0.44
2:6:540:GLY:HA3	35:A:3080:A:OP1	2.17	0.44
7:F:57:ILE:HD12	7:F:57:ILE:H	1.83	0.44
7:F:139:LEU:O	7:F:158:GLY:HA3	2.18	0.44
8:G:95:TYR:CD1	8:G:108:LEU:HA	2.51	0.44
11:J:77:ALA:HB2	11:J:114:LYS:HE3	2.00	0.44
35:A:2440:G:H2'	35:A:2441:G:H8	1.83	0.44
35:A:2557:A:H5''	35:A:2559:A:N3	2.33	0.44
35:A:2781:G:H2'	35:A:2782:C:C6	2.53	0.44
2:5:453:ARG:NH2	2:5:512:ASP:OD2	2.51	0.44
7:F:105:GLU:O	7:F:109:ARG:HG3	2.18	0.44
20:S:61:THR:HG23	20:S:100:THR:OG1	2.18	0.44
20:S:65:LEU:HD11	20:S:98:LYS:HB2	1.99	0.44
35:A:586:U:H2'	35:A:587:G:O4'	2.18	0.44
35:A:1248:U:N3	35:A:2249:G:OP1	2.46	0.44
35:A:2289:C:H2'	35:A:2290:C:H6	1.83	0.44
3:B:43:C:O2	7:F:97:THR:HG22	2.18	0.44
19:R:15:ARG:NH2	35:A:1330:C:OP1	2.46	0.44
20:S:64:VAL:HA	20:S:97:LEU:HD23	1.99	0.44
35:A:964:C:H2'	35:A:965:U:C6	2.52	0.44
35:A:1296:G:H2'	35:A:1297:G:C8	2.53	0.44
35:A:1754:G:N3	35:A:1754:G:H2'	2.33	0.44
35:A:3079:U:O5'	35:A:3079:U:H6	2.00	0.44
2:5:116:LEU:HD23	2:5:116:LEU:HA	1.87	0.43
2:5:286:ILE:O	2:5:290:PHE:HB2	2.18	0.43
2:5:444:PRO:HG2	2:5:476:ARG:HB3	1.99	0.43
2:6:116:LEU:HD23	2:6:116:LEU:HA	1.84	0.43
7:F:40:LYS:HA	7:F:103:MET:SD	2.58	0.43
10:I:27:GLU:HG3	10:I:76:PRO:HG2	1.99	0.43
35:A:815:G:O2'	35:A:1850:A:N3	2.46	0.43
35:A:1013:U:H2'	35:A:1014:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:1665:U:C4	35:A:1687:G:C2	3.06	0.43
35:A:1854:U:H2'	35:A:1855:A:C8	2.53	0.43
35:A:2545:G:H5'	35:A:2546:A:OP2	2.18	0.43
2:5:475:LEU:HD13	2:5:499:VAL:HG21	2.00	0.43
2:5:689:GLU:OE2	2:5:711:ARG:NH2	2.47	0.43
2:5:699:LEU:C	2:5:701:SER:N	2.73	0.43
2:6:696:ALA:HB2	2:6:709:PHE:HE1	1.83	0.43
13:L:13:ASN:OD1	13:L:97:ARG:N	2.49	0.43
35:A:181:A:H2'	35:A:182:C:C6	2.53	0.43
35:A:750:C:H2'	35:A:751:A:C8	2.53	0.43
35:A:1485:C:H2'	35:A:1486:G:O4'	2.18	0.43
35:A:1650:G:H2'	35:A:1651:C:C6	2.53	0.43
2:6:110:ARG:O	2:6:110:ARG:NH1	2.49	0.43
2:6:699:LEU:HG	2:6:707:GLY:HA3	2.00	0.43
7:F:70:GLN:NE2	34:g:1:MET:SD	2.91	0.43
17:P:113:ILE:HD12	17:P:113:ILE:H	1.82	0.43
27:Z:38:THR:OG1	27:Z:40:GLN:HG3	2.18	0.43
30:c:12:THR:HG21	30:c:21:ARG:HD3	2.00	0.43
35:A:736:G:H1'	35:A:740:A:N6	2.34	0.43
35:A:964:C:H2'	35:A:965:U:H6	1.83	0.43
35:A:1334:C:H2'	35:A:1335:G:O4'	2.17	0.43
35:A:1529:U:H3'	35:A:1530:G:H8	1.84	0.43
35:A:1675:U:O2'	35:A:1676:G:N7	2.51	0.43
35:A:2289:C:H2'	35:A:2290:C:C6	2.53	0.43
2:5:199:TYR:CE2	2:5:204:HIS:HB2	2.53	0.43
2:6:223:SER:O	2:6:226:GLU:HG2	2.19	0.43
2:6:543:GLN:OE1	2:6:619:PHE:HB3	2.19	0.43
4:C:53:HIS:ND1	4:C:220:THR:HG22	2.33	0.43
23:V:4:HIS:CD2	35:A:81:A:H5''	2.54	0.43
32:e:29:ARG:HH12	32:e:41:THR:HG22	1.83	0.43
34:g:38:CYS:H	34:g:41:CYS:HB2	1.83	0.43
35:A:137:G:H8	35:A:137:G:OP1	2.01	0.43
35:A:444:U:H5'	35:A:446:G:O5'	2.18	0.43
35:A:1530:G:H21	35:A:1805:G:N2	2.15	0.43
2:6:536:LYS:NZ	35:A:1929:A:P	2.92	0.43
2:6:550:GLU:HB2	2:6:607:PHE:HE2	1.84	0.43
2:6:684:LYS:HD3	2:6:684:LYS:HA	1.74	0.43
4:C:256:ARG:HH11	4:C:256:ARG:HG3	1.82	0.43
6:E:166:ALA:O	6:E:170:ARG:HG3	2.18	0.43
7:F:87:ARG:HB2	7:F:90:MET:SD	2.59	0.43
7:F:105:GLU:OE1	34:g:25:ARG:NE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:147:ALA:O	8:G:151:ARG:HG2	2.19	0.43
22:U:20:SER:O	22:U:24:ILE:HG13	2.18	0.43
25:X:53:ARG:NH2	25:X:57:ASP:OD1	2.51	0.43
35:A:337:U:O2	35:A:344:G:C2	2.71	0.43
35:A:756:A:H3'	35:A:757:G:N2	2.33	0.43
35:A:1614:G:H2'	35:A:1615:G:C8	2.53	0.43
35:A:2077:C:H4'	35:A:2133:G:H4'	2.01	0.43
2:5:37:THR:O	2:5:41:GLU:HG2	2.19	0.43
2:5:551:VAL:HA	2:5:603:ARG:O	2.19	0.43
3:B:50:C:H2'	3:B:51:G:C8	2.53	0.43
5:D:147:ARG:HG2	5:D:148:PRO:HD2	2.00	0.43
7:F:15:TYR:HE1	7:F:176:LEU:HD11	1.83	0.43
12:K:39:LYS:NZ	35:A:1125:C:OP1	2.50	0.43
16:O:101:GLU:HG3	16:O:102:ASN:H	1.83	0.43
27:Z:6:THR:OG1	27:Z:9:GLU:OE1	2.31	0.43
28:a:46:LEU:HD23	28:a:46:LEU:HA	1.82	0.43
35:A:307:G:H2'	35:A:308:U:C6	2.54	0.43
35:A:377:C:H2'	35:A:378:G:H8	1.83	0.43
35:A:443:C:H2'	35:A:444:U:O4'	2.18	0.43
35:A:733:U:H2'	35:A:734:C:H6	1.84	0.43
35:A:929:C:H2'	35:A:930:C:H6	1.84	0.43
35:A:1613:G:H2'	35:A:1614:G:C8	2.54	0.43
35:A:1640:A:O2'	35:A:1641:U:OP1	2.34	0.43
2:5:126:ASP:HB2	2:5:128:PRO:HD2	2.01	0.43
2:6:316:PRO:HB3	2:6:408:VAL:HB	2.00	0.43
3:B:41:U:N3	3:B:45:G:OP2	2.36	0.43
35:A:113:C:H2'	35:A:114:G:O4'	2.18	0.43
35:A:292:G:C2	35:A:343:U:O2	2.72	0.43
35:A:851:C:H2'	35:A:852:C:C6	2.53	0.43
35:A:2873:U:H2'	35:A:2874:C:C6	2.53	0.43
2:5:677:ASP:OD1	2:5:680:ARG:N	2.51	0.43
11:J:63:TYR:HD2	11:J:67:SER:HB3	1.84	0.43
35:A:334:G:H2'	35:A:335:G:H8	1.84	0.43
35:A:483:G:H2'	35:A:484:C:C6	2.54	0.43
35:A:664:A:H5''	35:A:665:G:OP2	2.19	0.43
35:A:1211:G:N2	35:A:1216:A:H62	2.17	0.43
35:A:1730:U:O2'	35:A:1731:A:OP2	2.29	0.43
35:A:2326:A:N6	35:A:2410:A:N6	2.67	0.43
35:A:2467:U:H2'	35:A:2468:U:C6	2.54	0.43
2:5:149:LYS:HG2	36:5:801:GNP:C6	2.48	0.43
2:5:663:LEU:HA	2:5:666:ARG:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:321:LEU:HB3	2:6:343:SER:HB3	2.01	0.43
2:6:531:HIS:H	2:6:631:ASP:HB3	1.83	0.43
2:6:640:LEU:O	2:6:718:PRO:HA	2.18	0.43
8:G:45:ARG:HH12	8:G:50:ALA:N	2.16	0.43
10:I:55:THR:HA	10:I:58:LYS:HB2	2.01	0.43
17:P:98:GLU:OE1	17:P:99:THR:HG23	2.18	0.43
23:V:97:ILE:HD11	23:V:102:GLY:O	2.17	0.43
24:W:115:GLU:OE1	24:W:145:THR:OG1	2.36	0.43
2:5:437:ARG:CZ	2:5:437:ARG:HB3	2.49	0.43
6:E:61:GLY:HA3	6:E:80:ARG:HG2	2.00	0.43
11:J:39:GLU:O	11:J:42:LYS:HG3	2.17	0.43
35:A:61:G:H2'	35:A:62:G:H8	1.84	0.43
35:A:993:G:O2'	35:A:994:A:O4'	2.31	0.43
35:A:1186:G:H2'	35:A:1187:A:N7	2.34	0.43
35:A:1212:U:H3'	35:A:1213:A:C5'	2.49	0.43
35:A:1243:G:OP2	35:A:1244:A:O2'	2.29	0.43
35:A:1552:A:H2'	35:A:1617:C:N4	2.34	0.43
35:A:1735:U:H2'	35:A:1736:G:O4'	2.19	0.43
35:A:2065:A:N3	35:A:2065:A:H3'	2.34	0.43
35:A:2170:U:H2'	35:A:2171:C:O4'	2.19	0.43
2:5:26:VAL:HG21	2:5:290:PHE:HD2	1.84	0.42
2:6:193:THR:O	2:6:194:ARG:HG2	2.18	0.42
2:6:397:LEU:HB2	2:6:402:ARG:NE	2.33	0.42
3:B:110:G:H2'	3:B:111:C:C6	2.53	0.42
4:C:200:GLU:OE2	4:C:200:GLU:N	2.47	0.42
8:G:75:ASN:HA	8:G:78:THR:HG22	2.01	0.42
10:I:29:ARG:NH2	35:A:1171:C:O2	2.52	0.42
35:A:239:U:O2'	35:A:716:G:O2'	2.34	0.42
35:A:1203:A:C8	35:A:1204:A:C6	3.07	0.42
35:A:2885:G:H2'	35:A:2886:A:C8	2.54	0.42
2:5:653:ASP:HA	2:5:656:VAL:HG23	2.00	0.42
2:6:575:PHE:O	2:6:579:VAL:HG23	2.19	0.42
2:6:653:ASP:OD1	2:6:681:THR:OG1	2.26	0.42
4:C:226:MET:HE3	35:A:897:A:N1	2.34	0.42
5:D:94:GLU:OE2	5:D:94:GLU:N	2.48	0.42
6:E:48:GLY:O	6:E:95:PRO:HA	2.19	0.42
13:L:93:PRO:HG3	13:L:114:ILE:HG13	2.00	0.42
17:P:18:ARG:HD2	17:P:107:TYR:CZ	2.54	0.42
18:Q:5:ASP:OD1	18:Q:6:PHE:N	2.52	0.42
29:b:8:MET:HE3	29:b:12:ASN:CB	2.49	0.42
35:A:1648:A:H4'	35:A:1649:C:O5'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:1665:U:H2'	35:A:1666:A:H8	1.84	0.42
4:C:89:THR:HG23	4:C:201:GLN:HG2	2.01	0.42
4:C:256:ARG:HG3	4:C:256:ARG:NH1	2.34	0.42
5:D:151:ILE:HG22	35:A:2276:G:P	2.59	0.42
7:F:165:THR:HG23	7:F:167:ALA:H	1.84	0.42
14:M:30:GLY:O	14:M:32:THR:N	2.52	0.42
15:N:135:GLU:OE2	15:N:135:GLU:N	2.47	0.42
35:A:289:A:H62	35:A:299:G:N2	2.14	0.42
35:A:298:G:O2'	35:A:299:G:H5'	2.19	0.42
35:A:499:G:OP2	35:A:2630:A:O2'	2.30	0.42
35:A:1270:G:H2'	35:A:1271:C:O4'	2.20	0.42
35:A:1755:A:C2'	35:A:1758:G:H22	2.32	0.42
35:A:1781:C:H2'	35:A:1782:U:C6	2.54	0.42
35:A:2120:A:H2'	35:A:2121:G:C8	2.53	0.42
35:A:2327:C:H2'	35:A:2328:G:H8	1.84	0.42
35:A:2491:A:H5''	35:A:2492:A:H5'	2.01	0.42
35:A:2717:U:C4	35:A:2718:G:C8	3.07	0.42
2:5:26:VAL:HG21	2:5:290:PHE:CD2	2.54	0.42
2:5:231:GLU:H	2:5:231:GLU:HG3	1.59	0.42
2:5:650:VAL:HG22	2:5:682:VAL:HG22	2.01	0.42
7:F:128:GLN:HB3	7:F:135:TYR:HE1	1.84	0.42
21:T:37:GLU:HG2	21:T:38:GLU:N	2.34	0.42
23:V:75:ASP:HB2	23:V:81:THR:OG1	2.19	0.42
35:A:993:G:H1'	35:A:1015:A:H62	1.84	0.42
35:A:1169:A:H2'	35:A:1170:C:C6	2.54	0.42
35:A:1530:G:N2	35:A:1805:G:H22	2.13	0.42
35:A:2366:C:H2'	35:A:2367:G:O4'	2.19	0.42
35:A:2529:A:H2'	35:A:2530:C:C6	2.54	0.42
35:A:2941:G:H2'	35:A:2942:G:O4'	2.18	0.42
2:5:111:ALA:HB2	2:5:325:VAL:HG11	2.01	0.42
2:5:699:LEU:O	2:5:700:ARG:C	2.61	0.42
2:6:226:GLU:HA	2:6:238:MET:HE1	2.01	0.42
2:6:315:ASP:OD2	2:6:318:GLY:N	2.53	0.42
3:B:115:A:H2'	3:B:116:C:H6	1.84	0.42
6:E:50:HIS:O	6:E:50:HIS:ND1	2.53	0.42
6:E:108:ALA:O	6:E:112:ARG:HD3	2.20	0.42
8:G:17:VAL:HG13	8:G:24:LEU:HD11	2.01	0.42
9:H:33:ARG:NH2	35:A:2421:A:O5'	2.53	0.42
21:T:81:VAL:HG23	21:T:112:VAL:HG22	2.02	0.42
23:V:2:LYS:HE2	35:A:419:G:OP1	2.19	0.42
30:c:10:LYS:HZ1	35:A:2645:G:P	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:724:G:N2	35:A:727:A:OP2	2.35	0.42
35:A:789:G:H2'	35:A:919:A:H61	1.85	0.42
35:A:996:G:C2	35:A:1013:U:C2	3.08	0.42
35:A:1278:C:C2	35:A:1279:G:C8	3.07	0.42
35:A:1294:U:H2'	35:A:1295:U:C6	2.55	0.42
35:A:1396:G:H2'	35:A:1397:U:C6	2.54	0.42
2:6:703:SER:OG	2:6:707:GLY:N	2.53	0.42
4:C:183:ARG:HG3	4:C:268:ILE:HD13	2.01	0.42
8:G:89:GLU:HG3	8:G:131:LYS:HG2	2.00	0.42
10:I:28:TYR:HE2	10:I:77:THR:O	2.02	0.42
10:I:55:THR:HA	10:I:58:LYS:HD2	2.02	0.42
16:O:45:ARG:HB3	16:O:46:PRO:HD3	2.00	0.42
19:R:79:LEU:O	19:R:83:LEU:HD23	2.20	0.42
28:a:16:ARG:HD3	35:A:1086:C:OP2	2.19	0.42
29:b:9:SER:OG	29:b:12:ASN:OD1	2.36	0.42
32:e:40:ARG:NH2	35:A:2586:G:OP1	2.50	0.42
35:A:1764:A:H2'	35:A:1765:A:C8	2.55	0.42
35:A:2080:G:N7	35:A:2081:U:N3	2.67	0.42
35:A:2265:U:C2	35:A:2266:A:C8	3.08	0.42
35:A:2531:G:H5'	35:A:2532:G:C8	2.54	0.42
2:5:102:VAL:HG13	2:5:442:PRO:HG3	2.01	0.42
2:5:324:VAL:HA	2:5:339:VAL:HA	2.01	0.42
2:5:480:ASN:HB3	2:5:485:GLN:H	1.84	0.42
5:D:33:PRO:C	5:D:34:ASN:HD22	2.27	0.42
7:F:105:GLU:OE2	34:g:9:TYR:OH	2.28	0.42
9:H:91:LEU:HD13	9:H:125:LYS:HA	2.01	0.42
24:W:124:VAL:HG22	24:W:181:VAL:HG22	2.00	0.42
35:A:487:U:H2'	35:A:488:G:O4'	2.20	0.42
35:A:935:A:H4'	35:A:951:G:N2	2.34	0.42
35:A:947:U:H2'	35:A:948:G:H8	1.84	0.42
35:A:1003:A:H2'	35:A:1003:A:OP1	2.19	0.42
35:A:1296:G:H2'	35:A:1297:G:H8	1.85	0.42
35:A:1317:G:C5	35:A:1359:G:C2	3.08	0.42
35:A:1753:C:H3'	35:A:1754:G:H8	1.84	0.42
35:A:2375:G:H2'	35:A:2376:G:H8	1.83	0.42
35:A:2490:A:H4'	35:A:2491:A:N3	2.34	0.42
2:6:116:LEU:HD21	2:6:290:PHE:CZ	2.55	0.42
4:C:43:ARG:HE	4:C:49:ILE:CG1	2.26	0.42
8:G:119:PRO:O	8:G:122:ILE:HG22	2.19	0.42
14:M:4:ILE:HG23	14:M:8:ASP:HB2	2.02	0.42
15:N:82:ARG:HD2	35:A:2720:C:OP2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:82:VAL:O	17:P:86:GLN:OE1	2.37	0.42
35:A:1179:U:C5	35:A:1188:A:C2	3.08	0.42
35:A:1213:A:H3'	35:A:1214:A:H8	1.85	0.42
35:A:2186:C:O2'	35:A:2187:U:O4'	2.37	0.42
2:6:503:LEU:HD12	2:6:507:TYR:CD2	2.55	0.42
4:C:176:ARG:O	4:C:176:ARG:HG3	2.19	0.42
6:E:184:ASN:HD21	35:A:708:G:N2	2.17	0.42
35:A:824:G:H2'	35:A:825:C:C6	2.55	0.42
35:A:1393:C:H2'	35:A:1394:A:H8	1.85	0.42
35:A:2516:U:H2'	35:A:2517:C:C6	2.55	0.42
2:5:199:TYR:CD1	2:5:277:VAL:HG13	2.55	0.42
2:5:575:PHE:O	2:5:579:VAL:HG23	2.19	0.42
2:6:375:ASP:HB3	2:6:376:GLY:H	1.65	0.42
2:6:376:GLY:HA2	2:6:476:ARG:HA	2.01	0.42
2:6:581:LYS:O	2:6:584:ARG:HG2	2.19	0.42
2:6:663:LEU:HA	2:6:663:LEU:HD23	1.92	0.42
4:C:13:ARG:HD2	35:A:843:G:H4'	2.02	0.42
4:C:80:ALA:O	4:C:113:GLN:NE2	2.52	0.42
7:F:92:ILE:HD11	35:A:2535:A:H1'	2.01	0.42
10:I:58:LYS:HG2	10:I:70:ASP:OD1	2.20	0.42
21:T:52:GLU:O	21:T:56:LYS:HG3	2.20	0.42
35:A:1430:C:H2'	35:A:1431:U:C6	2.55	0.42
35:A:2603:G:H2'	35:A:2604:U:C6	2.55	0.42
35:A:2760:G:H2'	35:A:2761:U:C6	2.55	0.42
2:5:121:ALA:HB3	2:5:155:ALA:HB1	2.02	0.41
11:J:17:ALA:HB1	11:J:48:THR:HB	2.01	0.41
11:J:118:LEU:HD23	35:A:1176:G:O2'	2.20	0.41
24:W:82:ALA:HB3	24:W:96:ASP:HB2	2.02	0.41
32:e:40:ARG:HH21	35:A:2586:G:H5''	1.85	0.41
35:A:691:U:H2'	35:A:692:C:C6	2.54	0.41
35:A:751:A:H2'	35:A:752:C:H6	1.85	0.41
35:A:2524:C:H2'	35:A:2525:C:H6	1.84	0.41
35:A:2530:C:OP2	35:A:2531:G:O2'	2.35	0.41
35:A:2936:C:OP1	35:A:2938:G:H4'	2.20	0.41
35:A:3106:C:H6	35:A:3106:C:H2'	1.72	0.41
2:5:105:LEU:HD13	2:5:132:LEU:HD11	2.01	0.41
2:5:533:ARG:HE	2:5:535:VAL:HG21	1.84	0.41
2:5:701:SER:C	2:5:703:SER:N	2.71	0.41
2:6:180:GLY:HA2	2:6:186:LYS:HG2	2.02	0.41
2:6:192:LEU:HD23	2:6:192:LEU:HA	1.92	0.41
2:6:446:LEU:HD22	2:6:697:ILE:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:522:GLU:HG3	2:6:640:LEU:HD23	2.02	0.41
3:B:33:C:C2	3:B:52:G:N2	2.88	0.41
5:D:65:PRO:O	5:D:69:GLN:HG2	2.20	0.41
7:F:11:LEU:HD23	7:F:107:LEU:HD11	2.02	0.41
7:F:20:ARG:HH21	7:F:35:ILE:HG22	1.85	0.41
7:F:110:LEU:HA	7:F:114:ALA:HB3	2.03	0.41
8:G:104:LEU:HD12	8:G:104:LEU:HA	1.86	0.41
28:a:39:ASP:OD1	28:a:44:ARG:HD3	2.20	0.41
35:A:851:C:H2'	35:A:852:C:H6	1.85	0.41
35:A:875:G:H2'	35:A:876:A:O4'	2.20	0.41
35:A:1343:G:H2'	35:A:1345:G:C8	2.56	0.41
35:A:2581:G:H2'	35:A:2583:C:OP2	2.20	0.41
2:5:150:LEU:HD12	2:5:272:CYS:SG	2.60	0.41
4:C:85:ASP:OD2	4:C:88:ARG:NH1	2.38	0.41
7:F:15:TYR:OH	7:F:37:GLY:HA2	2.20	0.41
7:F:85:LYS:O	7:F:87:ARG:NH1	2.53	0.41
22:U:14:PRO:HD3	27:Z:34:PHE:CE1	2.55	0.41
29:b:28:VAL:HG21	29:b:41:ARG:HG3	2.02	0.41
35:A:2216:G:N2	35:A:2220:C:O2'	2.53	0.41
35:A:2400:C:C4	35:A:2401:U:H1'	2.55	0.41
2:5:320:LEU:HD11	2:5:346:ILE:HG12	2.01	0.41
2:6:340:ARG:NH2	2:6:410:GLY:HA2	2.35	0.41
5:D:153:GLY:O	35:A:2276:G:H4'	2.19	0.41
8:G:154:ARG:NH2	35:A:2750:G:OP2	2.54	0.41
18:Q:21:PRO:HA	18:Q:46:VAL:HG12	2.02	0.41
29:b:7:ARG:NH1	35:A:1377:A:N3	2.68	0.41
35:A:89:A:O2'	35:A:90:C:OP1	2.33	0.41
35:A:160:A:C3'	35:A:161:U:H5''	2.46	0.41
35:A:255:A:O2'	35:A:472:C:OP2	2.35	0.41
35:A:2066:G:O2'	35:A:2119:C:H1'	2.20	0.41
35:A:2288:C:H2'	35:A:2289:C:H6	1.85	0.41
35:A:2322:C:H2'	35:A:2323:G:C8	2.53	0.41
2:5:178:PRO:HA	2:5:188:VAL:HG12	2.02	0.41
2:5:320:LEU:HB3	2:5:429:ASP:H	1.86	0.41
2:6:627:LEU:HA	2:6:630:ARG:HG2	2.02	0.41
4:C:242:GLY:HA3	4:C:244:ARG:HH11	1.85	0.41
7:F:147:GLU:N	7:F:147:GLU:OE1	2.53	0.41
8:G:59:GLU:OE1	8:G:61:ARG:N	2.45	0.41
35:A:161:U:H1'	35:A:162:A:C8	2.54	0.41
35:A:279:U:O2	35:A:307:G:N2	2.45	0.41
35:A:662:G:H2'	35:A:2254:A:N7	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:2176:A:N3	35:A:2784:C:O2'	2.46	0.41
35:A:2521:C:C2	35:A:2557:A:N1	2.89	0.41
2:5:583:VAL:HG11	2:5:604:VAL:HG21	2.02	0.41
2:5:702:MET:HE2	2:5:702:MET:HB2	1.80	0.41
2:6:322:ALA:O	2:6:427:LEU:N	2.40	0.41
2:6:335:ARG:HE	2:6:335:ARG:HB2	1.67	0.41
2:6:444:PRO:HD3	2:6:474:THR:O	2.19	0.41
6:E:118:ARG:HA	6:E:118:ARG:HD3	1.91	0.41
7:F:165:THR:OG1	7:F:166:THR:N	2.54	0.41
21:T:50:ALA:O	21:T:53:PRO:HD2	2.21	0.41
26:Y:19:SER:HB3	26:Y:23:ARG:H	1.84	0.41
35:A:2077:C:N4	35:A:2105:G:H22	2.19	0.41
35:A:2101:A:H2'	35:A:2102:G:O4'	2.20	0.41
35:A:2130:G:O2'	35:A:2131:G:O4'	2.37	0.41
35:A:2169:G:HO2'	35:A:2170:U:P	2.43	0.41
35:A:3020:U:OP2	35:A:3020:U:H6	2.04	0.41
35:A:3040:G:H2'	35:A:3042:A:N7	2.35	0.41
35:A:3067:C:H2'	35:A:3068:U:C6	2.55	0.41
2:5:161:LEU:HD11	2:5:174:PRO:HD3	2.02	0.41
2:5:704:HIS:C	2:5:706:ALA:H	2.28	0.41
2:6:272:CYS:SG	2:6:277:VAL:HB	2.60	0.41
2:6:426:THR:HG21	2:6:436:LEU:H	1.85	0.41
7:F:124:LEU:HB3	7:F:135:TYR:OH	2.21	0.41
8:G:35:LEU:HD23	8:G:36:ASP:N	2.35	0.41
13:L:66:VAL:HG23	13:L:82:ASN:OD1	2.20	0.41
14:M:7:HIS:HB3	35:A:1318:C:O2	2.20	0.41
29:b:28:VAL:HG13	35:A:3107:G:O3'	2.21	0.41
35:A:89:A:HO2'	35:A:90:C:P	2.43	0.41
35:A:226:A:C2	35:A:2631:G:H1'	2.55	0.41
35:A:1169:A:C5	35:A:1170:C:C4	3.09	0.41
35:A:2326:A:H2'	35:A:2327:C:H6	1.86	0.41
35:A:2873:U:H2'	35:A:2874:C:H6	1.84	0.41
35:A:2969:C:H2'	35:A:2970:U:C6	2.55	0.41
2:5:358:PHE:O	2:5:360:ALA:N	2.54	0.41
2:6:543:GLN:OE1	35:A:3079:U:H5'	2.20	0.41
2:6:694:ARG:HB2	2:6:697:ILE:HD11	2.03	0.41
5:D:161:PHE:O	5:D:162:LYS:C	2.64	0.41
5:D:178:GLN:OE1	5:D:213:LYS:NZ	2.33	0.41
8:G:27:LYS:HD2	8:G:28:GLY:N	2.36	0.41
10:I:27:GLU:HB3	10:I:104:VAL:HB	2.01	0.41
11:J:16:GLN:HA	11:J:55:VAL:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:68:ALA:O	17:P:72:ALA:N	2.52	0.41
35:A:308:U:H2'	35:A:309:G:H8	1.86	0.41
35:A:920:G:N2	35:A:944:A:OP1	2.54	0.41
35:A:954:U:H2'	35:A:955:C:C6	2.56	0.41
35:A:1201:G:H21	35:A:1203:A:H8	1.67	0.41
35:A:1639:G:H5'	35:A:1640:A:OP1	2.21	0.41
35:A:2194:A:C8	35:A:2196:G:N2	2.88	0.41
35:A:2410:A:C6	35:A:2411:U:C4	3.09	0.41
2:5:394:SER:HB2	2:5:401:GLN:HB3	2.01	0.41
2:6:56:VAL:HG21	36:6:801:GNP:O3A	2.21	0.41
2:6:96:PRO:HG2	2:6:104:GLU:HB2	2.03	0.41
2:6:173:ALA:HB3	2:6:265:PHE:HZ	1.85	0.41
2:6:255:ASP:HA	2:6:258:LYS:HD2	2.03	0.41
5:D:127:MET:HE3	5:D:134:GLY:HA3	2.03	0.41
7:F:182:PHE:HA	7:F:183:PRO:HD3	1.92	0.41
10:I:39:LEU:HD13	10:I:96:PHE:CG	2.56	0.41
13:L:35:ILE:HG22	13:L:105:GLU:HB2	2.03	0.41
14:M:75:TYR:CE1	14:M:109:LEU:HG	2.56	0.41
21:T:17:VAL:HG12	21:T:19:VAL:HG22	2.03	0.41
30:c:42:CYS:HB3	30:c:45:CYS:HB2	2.03	0.41
32:e:28:ASN:HA	35:A:2616:A:H5''	2.02	0.41
33:f:1:MET:HB2	35:A:2750:G:O2'	2.21	0.41
35:A:166:A:H2'	35:A:167:G:O4'	2.20	0.41
35:A:346:C:H2'	35:A:347:U:H6	1.83	0.41
35:A:752:C:H2'	35:A:753:A:C8	2.54	0.41
35:A:808:A:O2'	35:A:1468:A:N3	2.45	0.41
35:A:1174:G:O2'	35:A:1204:A:H1'	2.21	0.41
35:A:1553:C:H5''	35:A:1554:U:C5	2.54	0.41
35:A:1728:U:H4'	35:A:1729:A:O4'	2.20	0.41
35:A:2125:A:H5'	35:A:2127:G:OP2	2.20	0.41
35:A:2148:C:H2'	35:A:2149:C:C6	2.56	0.41
35:A:2327:C:H2'	35:A:2328:G:C8	2.56	0.41
35:A:2861:U:H2'	35:A:2862:G:O4'	2.20	0.41
35:A:3013:C:O2'	35:A:3113:A:N6	2.52	0.41
2:5:185:CYS:HB3	2:5:272:CYS:SG	2.61	0.41
2:5:253:ILE:HG21	2:5:288:ARG:NH2	2.36	0.41
2:5:376:GLY:O	2:5:378:THR:N	2.54	0.41
2:5:705:GLY:C	2:5:707:GLY:H	2.29	0.41
2:6:465:LEU:HD13	2:6:477:ILE:HG21	2.03	0.41
4:C:79:VAL:HG11	4:C:111:LEU:HD21	2.03	0.41
8:G:106:PHE:HB2	8:G:114:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:107:VAL:HG21	11:J:141:VAL:HG13	2.03	0.41
35:A:760:U:H2'	35:A:761:G:H8	1.86	0.41
35:A:781:C:H2'	35:A:782:U:C6	2.56	0.41
35:A:1194:C:C2	35:A:1195:A:C8	3.09	0.41
35:A:1305:G:H2'	35:A:1306:G:H8	1.86	0.41
35:A:1938:G:N2	35:A:1955:A:OP2	2.46	0.41
35:A:2130:G:O2'	35:A:2131:G:O5'	2.37	0.41
2:5:549:ILE:HG22	2:5:606:LEU:HD13	2.03	0.40
2:5:646:ASP:HA	2:5:686:GLU:HA	2.03	0.40
2:6:208:PRO:HA	2:6:209:PRO:HD3	1.98	0.40
3:B:26:A:H2	3:B:115:A:H1'	1.86	0.40
12:K:109:LEU:HD23	12:K:109:LEU:HA	1.93	0.40
13:L:68:GLU:HG2	13:L:78:LYS:HD2	2.03	0.40
16:O:37:THR:OG1	16:O:40:LYS:HD2	2.20	0.40
24:W:43:ASP:OD1	24:W:43:ASP:N	2.54	0.40
24:W:105:LYS:HA	24:W:105:LYS:HD3	1.86	0.40
26:Y:17:SER:HB3	26:Y:27:ARG:HD2	2.03	0.40
35:A:347:U:H2'	35:A:348:G:C8	2.56	0.40
35:A:701:A:H2'	35:A:702:A:C8	2.56	0.40
35:A:857:U:H2'	35:A:858:A:H8	1.84	0.40
35:A:1003:A:H8	35:A:1003:A:P	2.43	0.40
35:A:1804:G:H2'	35:A:1805:G:C8	2.56	0.40
35:A:2857:A:H2'	35:A:2858:G:C8	2.55	0.40
35:A:2925:C:H3'	35:A:2926:A:C5'	2.51	0.40
35:A:3068:U:H2'	35:A:3069:G:O4'	2.22	0.40
2:5:220:LEU:HD23	2:5:220:LEU:HA	1.95	0.40
2:5:550:GLU:HB2	2:5:607:PHE:CE2	2.57	0.40
2:6:139:VAL:O	2:6:140:GLN:HG3	2.21	0.40
2:6:300:GLU:CD	2:6:437:ARG:HD3	2.46	0.40
2:6:335:ARG:NH1	2:6:419:SER:O	2.54	0.40
2:6:348:PRO:HD3	2:6:393:LEU:HD12	2.03	0.40
3:B:104:G:H2'	3:B:105:A:O4'	2.20	0.40
13:L:114:ILE:HD12	13:L:114:ILE:H	1.86	0.40
35:A:123:A:H2'	35:A:124:A:C8	2.56	0.40
35:A:997:G:C4	35:A:998:G:C8	3.10	0.40
35:A:1001:C:H1'	35:A:1007:G:H1	1.87	0.40
35:A:1160:G:H2'	35:A:1161:C:H6	1.86	0.40
35:A:2471:A:H2'	35:A:2472:C:C6	2.54	0.40
2:6:462:SER:O	2:6:465:LEU:HG	2.22	0.40
4:C:106:ILE:HD12	4:C:106:ILE:H	1.87	0.40
7:F:75:ARG:HD3	7:F:75:ARG:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:111:PHE:HB3	13:L:114:ILE:HD13	2.03	0.40
19:R:58:ARG:HA	19:R:61:TRP:CE3	2.56	0.40
20:S:51:LYS:O	20:S:55:LEU:HG	2.21	0.40
23:V:8:THR:HG23	23:V:74:VAL:HG12	2.03	0.40
33:f:4:ASN:O	33:f:36:GLN:HA	2.21	0.40
35:A:220:A:H2	35:A:266:U:H5'	1.87	0.40
35:A:1160:G:H2'	35:A:1161:C:C6	2.55	0.40
35:A:1168:A:C4	35:A:1169:A:C8	3.10	0.40
35:A:1294:U:H2'	35:A:1295:U:H6	1.86	0.40
35:A:2326:A:H2'	35:A:2327:C:C6	2.56	0.40
35:A:2523:A:H2'	35:A:2524:C:C6	2.56	0.40
2:6:562:PHE:CD1	2:6:604:VAL:HG13	2.56	0.40
4:C:244:ARG:H	4:C:244:ARG:HD3	1.87	0.40
7:F:45:MET:CE	7:F:159:MET:HB3	2.51	0.40
9:H:115:ARG:HD3	9:H:115:ARG:HA	1.63	0.40
19:R:62:ILE:HG23	19:R:76:TYR:CZ	2.57	0.40
35:A:271:A:OP2	35:A:314:G:N1	2.29	0.40
35:A:782:U:H2'	35:A:783:G:O4'	2.21	0.40
35:A:1632:G:H8	35:A:1632:G:O5'	2.04	0.40
35:A:2373:G:H2'	35:A:2374:U:C6	2.57	0.40
2:5:337:SER:HB2	2:5:418:LEU:HD12	2.04	0.40
2:5:529:THR:HG22	2:5:550:GLU:HG3	2.04	0.40
2:5:549:ILE:HA	2:5:606:LEU:HA	2.03	0.40
4:C:244:ARG:O	4:C:244:ARG:HG2	2.21	0.40
5:D:155:ALA:H	35:A:2277:G:H5'	1.86	0.40
6:E:2:THR:HB	6:E:19:GLU:HB3	2.03	0.40
15:N:56:ARG:NH1	35:A:2693:A:O2'	2.55	0.40
26:Y:39:VAL:HG12	26:Y:46:LYS:HG2	2.03	0.40
35:A:302:U:O2'	35:A:303:G:N7	2.39	0.40
35:A:1177:G:H2'	35:A:1178:U:C6	2.56	0.40
35:A:1758:G:OP2	35:A:1758:G:H8	2.04	0.40
35:A:2026:A:H8	35:A:2026:A:OP2	2.04	0.40
35:A:2247:A:H2'	35:A:2248:C:H6	1.87	0.40
35:A:2297:U:H2'	35:A:2298:U:H6	1.87	0.40
35:A:2581:G:OP2	35:A:2581:G:H8	2.04	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	3	21/24 (88%)	19 (90%)	2 (10%)	0	100	100
2	5	707/709 (100%)	673 (95%)	31 (4%)	3 (0%)	30	63
2	6	707/709 (100%)	679 (96%)	27 (4%)	1 (0%)	48	79
4	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
5	D	212/217 (98%)	200 (94%)	12 (6%)	0	100	100
6	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
7	F	180/187 (96%)	175 (97%)	5 (3%)	0	100	100
8	G	174/179 (97%)	169 (97%)	5 (3%)	0	100	100
9	H	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
10	I	124/175 (71%)	120 (97%)	4 (3%)	0	100	100
11	J	131/142 (92%)	126 (96%)	5 (4%)	0	100	100
12	K	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
13	L	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
14	M	143/147 (97%)	129 (90%)	14 (10%)	0	100	100
15	N	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
16	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
17	P	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
18	Q	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
19	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
20	S	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
21	T	112/153 (73%)	106 (95%)	6 (5%)	0	100	100
22	U	95/100 (95%)	93 (98%)	2 (2%)	0	100	100
23	V	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
24	W	190/215 (88%)	182 (96%)	8 (4%)	0	100	100
25	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Y	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
27	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
28	a	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	52 (100%)	0	0	100	100
30	c	47/55 (86%)	43 (92%)	3 (6%)	1 (2%)	5	33
31	d	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
32	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
33	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	g	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
All	All	5029/5409 (93%)	4820 (96%)	204 (4%)	5 (0%)	50	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	5	375	ASP
2	6	381	HIS
30	c	7	VAL
2	5	702	MET
2	5	381	HIS

### 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	3	18/19 (95%)	18 (100%)	0	100	100
2	5	564/564 (100%)	557 (99%)	7 (1%)	67	82
2	6	564/564 (100%)	558 (99%)	6 (1%)	70	83
4	C	215/218 (99%)	215 (100%)	0	100	100
5	D	160/163 (98%)	160 (100%)	0	100	100
6	E	169/173 (98%)	169 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	F	151/156 (97%)	150 (99%)	1 (1%)	81	90
8	G	148/150 (99%)	148 (100%)	0	100	100
9	H	90/116 (78%)	90 (100%)	0	100	100
10	I	89/120 (74%)	89 (100%)	0	100	100
11	J	102/108 (94%)	102 (100%)	0	100	100
12	K	119/120 (99%)	119 (100%)	0	100	100
13	L	100/100 (100%)	100 (100%)	0	100	100
14	M	112/114 (98%)	112 (100%)	0	100	100
15	N	114/116 (98%)	114 (100%)	0	100	100
16	O	97/158 (61%)	97 (100%)	0	100	100
17	P	93/94 (99%)	93 (100%)	0	100	100
18	Q	100/100 (100%)	100 (100%)	0	100	100
19	R	97/99 (98%)	97 (100%)	0	100	100
20	S	81/83 (98%)	81 (100%)	0	100	100
21	T	90/117 (77%)	90 (100%)	0	100	100
22	U	83/85 (98%)	83 (100%)	0	100	100
23	V	81/86 (94%)	81 (100%)	0	100	100
24	W	155/168 (92%)	155 (100%)	0	100	100
25	X	58/63 (92%)	58 (100%)	0	100	100
26	Y	50/51 (98%)	50 (100%)	0	100	100
27	Z	58/66 (88%)	58 (100%)	0	100	100
28	a	52/54 (96%)	52 (100%)	0	100	100
29	b	43/46 (94%)	43 (100%)	0	100	100
30	c	47/52 (90%)	47 (100%)	0	100	100
31	d	35/36 (97%)	35 (100%)	0	100	100
32	e	53/54 (98%)	53 (100%)	0	100	100
33	f	35/35 (100%)	35 (100%)	0	100	100
34	g	43/63 (68%)	43 (100%)	0	100	100
All	All	4066/4311 (94%)	4052 (100%)	14 (0%)	90	96

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	5	74	ARG
2	5	229	ILE
2	5	239	GLU
2	5	281	GLU
2	5	701	SER
2	5	702	MET
2	5	704	HIS
2	6	338	LEU
2	6	346	ILE
2	6	354	VAL
2	6	518	VAL
2	6	522	GLU
2	6	623	MET
7	F	161	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	3	23	ASN
2	5	73	GLN
2	5	381	HIS
2	6	73	GLN
2	6	297	GLN
2	6	534	HIS
4	C	135	ASN
4	C	233	HIS
5	D	21	ASN
5	D	130	HIS
6	E	121	ASN
6	E	151	ASN
6	E	208	ASN
7	F	13	GLN
7	F	24	GLN
7	F	62	ASN
7	F	83	GLN
11	J	21	ASN
11	J	32	GLN
11	J	106	GLN
12	K	136	GLN
13	L	4	GLN
14	M	84	ASN
16	O	31	HIS
17	P	53	ASN

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Mol	Chain	Res	Type
19	R	94	ASN
20	S	67	HIS
23	V	31	ASN
24	W	6	ASN
24	W	9	ASN
24	W	64	ASN
24	W	76	GLN
24	W	91	ASN
24	W	143	GLN
25	X	12	ASN
26	Y	47	GLN
27	Z	44	ASN
31	d	9	GLN
32	e	31	HIS
32	e	63	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	B	117/118 (99%)	18 (15%)	1 (0%)
35	A	3059/3127 (97%)	640 (20%)	34 (1%)
All	All	3176/3245 (97%)	658 (20%)	35 (1%)

All (658) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	B	4	A
3	B	9	G
3	B	11	U
3	B	12	C
3	B	13	C
3	B	23	G
3	B	30	G
3	B	31	C
3	B	42	C
3	B	57	U
3	B	58	A
3	B	67	A
3	B	87	U
3	B	88	C
3	B	89	C

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Mol	Chain	Res	Type
3	B	90	G
3	B	103	G
3	B	107	A
35	A	7	U
35	A	9	U
35	A	12	G
35	A	16	G
35	A	19	U
35	A	20	G
35	A	31	U
35	A	48	G
35	A	55	G
35	A	60	A
35	A	68	A
35	A	71	A
35	A	72	G
35	A	80	G
35	A	82	G
35	A	89	A
35	A	90	C
35	A	94	G
35	A	95	C
35	A	98	U
35	A	99	G
35	A	115	A
35	A	116	A
35	A	117	U
35	A	122	A
35	A	125	C
35	A	136	U
35	A	148	A
35	A	161	U
35	A	164	A
35	A	169	C
35	A	180	A
35	A	195	A
35	A	212	A
35	A	214	G
35	A	215	A
35	A	221	A
35	A	227	A
35	A	228	A

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Mol	Chain	Res	Type
35	A	229	U
35	A	230	G
35	A	231	U
35	A	238	G
35	A	248	G
35	A	270	U
35	A	272	A
35	A	273	A
35	A	275	C
35	A	283	U
35	A	285	U
35	A	286	G
35	A	289	A
35	A	290	C
35	A	292	G
35	A	296	A
35	A	299	G
35	A	300	G
35	A	301	U
35	A	302	U
35	A	303	G
35	A	305	G
35	A	314	G
35	A	315	U
35	A	317	G
35	A	318	U
35	A	319	G
35	A	322	A
35	A	323	C
35	A	326	A
35	A	329	U
35	A	330	U
35	A	331	U
35	A	336	C
35	A	337	U
35	A	338	C
35	A	342	C
35	A	344	G
35	A	345	G
35	A	348	G
35	A	350	A
35	A	351	G

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Mol	Chain	Res	Type
35	A	352	G
35	A	357	U
35	A	358	G
35	A	361	A
35	A	364	A
35	A	369	G
35	A	370	U
35	A	384	G
35	A	393	U
35	A	412	A
35	A	413	G
35	A	424	G
35	A	434	G
35	A	437	G
35	A	445	U
35	A	446	G
35	A	447	A
35	A	449	G
35	A	450	G
35	A	452	G
35	A	453	U
35	A	454	U
35	A	460	G
35	A	474	G
35	A	489	A
35	A	490	A
35	A	491	U
35	A	493	U
35	A	494	G
35	A	498	G
35	A	499	G
35	A	500	A
35	A	505	C
35	A	512	G
35	A	523	U
35	A	543	U
35	A	544	U
35	A	566	A
35	A	567	A
35	A	569	G
35	A	578	G
35	A	589	A

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Mol	Chain	Res	Type
35	A	591	G
35	A	592	A
35	A	594	U
35	A	595	A
35	A	596	C
35	A	605	G
35	A	617	U
35	A	618	C
35	A	619	C
35	A	620	G
35	A	623	A
35	A	634	C
35	A	635	G
35	A	636	U
35	A	637	G
35	A	638	U
35	A	639	C
35	A	640	G
35	A	642	G
35	A	644	G
35	A	646	U
35	A	647	G
35	A	655	G
35	A	665	G
35	A	667	A
35	A	669	G
35	A	675	G
35	A	678	A
35	A	679	G
35	A	684	G
35	A	685	G
35	A	696	A
35	A	706	G
35	A	707	G
35	A	708	G
35	A	709	U
35	A	721	A
35	A	731	A
35	A	738	A
35	A	740	A
35	A	756	A
35	A	757	G

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Mol	Chain	Res	Type
35	A	758	A
35	A	760	U
35	A	764	U
35	A	765	G
35	A	766	G
35	A	768	G
35	A	773	G
35	A	774	G
35	A	784	G
35	A	785	A
35	A	801	U
35	A	836	G
35	A	845	C
35	A	862	U
35	A	863	G
35	A	868	C
35	A	871	A
35	A	872	G
35	A	878	G
35	A	879	A
35	A	880	G
35	A	890	G
35	A	891	G
35	A	897	A
35	A	899	G
35	A	900	G
35	A	907	A
35	A	917	A
35	A	918	U
35	A	920	G
35	A	921	C
35	A	927	C
35	A	942	U
35	A	960	G
35	A	961	U
35	A	972	A
35	A	974	G
35	A	975	U
35	A	981	U
35	A	982	A
35	A	994	A
35	A	1001	C

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Mol	Chain	Res	Type
35	A	1002	C
35	A	1003	A
35	A	1004	C
35	A	1005	A
35	A	1006	G
35	A	1007	G
35	A	1008	G
35	A	1010	U
35	A	1011	A
35	A	1012	C
35	A	1013	U
35	A	1014	G
35	A	1025	A
35	A	1030	C
35	A	1046	C
35	A	1047	A
35	A	1048	A
35	A	1049	G
35	A	1063	G
35	A	1068	C
35	A	1075	U
35	A	1076	A
35	A	1078	G
35	A	1085	G
35	A	1092	G
35	A	1101	A
35	A	1103	C
35	A	1108	A
35	A	1114	G
35	A	1130	C
35	A	1131	G
35	A	1144	A
35	A	1151	U
35	A	1164	A
35	A	1165	G
35	A	1173	G
35	A	1174	G
35	A	1175	A
35	A	1178	U
35	A	1181	G
35	A	1184	U
35	A	1185	A

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Mol	Chain	Res	Type
35	A	1186	G
35	A	1187	A
35	A	1188	A
35	A	1189	G
35	A	1190	C
35	A	1191	A
35	A	1194	C
35	A	1195	A
35	A	1201	G
35	A	1202	A
35	A	1203	A
35	A	1205	G
35	A	1206	A
35	A	1207	G
35	A	1209	G
35	A	1212	U
35	A	1213	A
35	A	1214	A
35	A	1219	U
35	A	1226	U
35	A	1230	G
35	A	1232	G
35	A	1240	G
35	A	1248	U
35	A	1250	U
35	A	1251	A
35	A	1253	C
35	A	1254	G
35	A	1260	C
35	A	1261	A
35	A	1292	U
35	A	1293	G
35	A	1325	U
35	A	1335	G
35	A	1344	A
35	A	1353	G
35	A	1362	A
35	A	1365	G
35	A	1371	G
35	A	1384	G
35	A	1386	G
35	A	1387	A

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Mol	Chain	Res	Type
35	A	1389	U
35	A	1415	A
35	A	1416	A
35	A	1428	U
35	A	1435	C
35	A	1436	C
35	A	1437	A
35	A	1444	U
35	A	1448	C
35	A	1456	G
35	A	1465	C
35	A	1467	U
35	A	1480	A
35	A	1493	A
35	A	1494	U
35	A	1499	A
35	A	1501	C
35	A	1507	G
35	A	1508	A
35	A	1510	A
35	A	1522	G
35	A	1529	U
35	A	1531	C
35	A	1532	G
35	A	1533	U
35	A	1534	C
35	A	1536	A
35	A	1540	U
35	A	1549	G
35	A	1550	G
35	A	1551	U
35	A	1552	A
35	A	1553	C
35	A	1625	G
35	A	1629	G
35	A	1630	U
35	A	1632	G
35	A	1633	U
35	A	1639	G
35	A	1640	A
35	A	1641	U
35	A	1645	G

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Mol	Chain	Res	Type
35	A	1648	A
35	A	1649	C
35	A	1670	G
35	A	1676	G
35	A	1678	U
35	A	1679	A
35	A	1680	A
35	A	1681	U
35	A	1703	G
35	A	1713	U
35	A	1714	A
35	A	1715	A
35	A	1716	A
35	A	1717	U
35	A	1720	G
35	A	1724	G
35	A	1728	U
35	A	1731	A
35	A	1737	A
35	A	1754	G
35	A	1756	G
35	A	1757	U
35	A	1767	U
35	A	1769	G
35	A	1786	G
35	A	1789	A
35	A	1798	U
35	A	1802	G
35	A	1826	A
35	A	1844	A
35	A	1864	U
35	A	1866	C
35	A	1867	G
35	A	1870	U
35	A	1871	G
35	A	1872	A
35	A	1892	G
35	A	1946	U
35	A	1947	U
35	A	1949	C
35	A	1950	G
35	A	1973	C

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Mol	Chain	Res	Type
35	A	1975	A
35	A	1981	U
35	A	1990	A
35	A	1998	C
35	A	2008	A
35	A	2017	C
35	A	2018	G
35	A	2026	A
35	A	2033	U
35	A	2046	A
35	A	2050	C
35	A	2053	C
35	A	2055	C
35	A	2059	G
35	A	2065	A
35	A	2066	G
35	A	2067	G
35	A	2068	U
35	A	2069	U
35	A	2071	A
35	A	2075	G
35	A	2076	A
35	A	2078	C
35	A	2081	U
35	A	2082	U
35	A	2083	A
35	A	2085	C
35	A	2086	U
35	A	2089	C
35	A	2091	U
35	A	2092	U
35	A	2093	G
35	A	2094	G
35	A	2095	G
35	A	2096	G
35	A	2099	G
35	A	2100	A
35	A	2103	C
35	A	2104	G
35	A	2107	G
35	A	2108	A
35	A	2110	U

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Mol	Chain	Res	Type
35	A	2111	U
35	A	2112	U
35	A	2113	A
35	A	2114	A
35	A	2116	C
35	A	2117	C
35	A	2120	A
35	A	2123	A
35	A	2124	A
35	A	2125	A
35	A	2126	C
35	A	2127	G
35	A	2128	G
35	A	2129	C
35	A	2130	G
35	A	2131	G
35	A	2133	G
35	A	2147	U
35	A	2149	C
35	A	2150	U
35	A	2151	A
35	A	2153	G
35	A	2154	G
35	A	2155	U
35	A	2156	A
35	A	2157	G
35	A	2159	G
35	A	2160	A
35	A	2161	A
35	A	2162	A
35	A	2163	U
35	A	2164	U
35	A	2166	C
35	A	2167	U
35	A	2168	U
35	A	2169	G
35	A	2170	U
35	A	2171	C
35	A	2172	G
35	A	2179	U
35	A	2183	G
35	A	2184	A

*Continued on next page...*



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Mol	Chain	Res	Type
35	A	2185	C
35	A	2187	U
35	A	2188	G
35	A	2189	C
35	A	2190	A
35	A	2192	G
35	A	2193	A
35	A	2194	A
35	A	2195	U
35	A	2197	G
35	A	2215	U
35	A	2217	U
35	A	2221	A
35	A	2227	A
35	A	2244	A
35	A	2245	C
35	A	2247	A
35	A	2251	G
35	A	2254	A
35	A	2255	A
35	A	2256	G
35	A	2257	A
35	A	2263	G
35	A	2267	C
35	A	2279	C
35	A	2280	G
35	A	2284	A
35	A	2285	G
35	A	2286	A
35	A	2316	G
35	A	2320	C
35	A	2324	A
35	A	2325	U
35	A	2329	G
35	A	2330	U
35	A	2331	U
35	A	2333	G
35	A	2334	U
35	A	2335	G
35	A	2336	U
35	A	2337	A
35	A	2338	G

*Continued on next page...*

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Mol	Chain	Res	Type
35	A	2339	G
35	A	2340	A
35	A	2341	U
35	A	2342	A
35	A	2343	G
35	A	2349	A
35	A	2351	A
35	A	2353	U
35	A	2354	G
35	A	2355	U
35	A	2356	G
35	A	2357	A
35	A	2368	C
35	A	2382	G
35	A	2384	C
35	A	2385	G
35	A	2386	U
35	A	2387	U
35	A	2388	G
35	A	2390	U
35	A	2393	A
35	A	2394	A
35	A	2395	U
35	A	2396	A
35	A	2401	U
35	A	2402	C
35	A	2407	C
35	A	2408	G
35	A	2409	U
35	A	2413	G
35	A	2421	A
35	A	2427	G
35	A	2434	A
35	A	2436	A
35	A	2447	G
35	A	2449	A
35	A	2462	G
35	A	2463	G
35	A	2467	U
35	A	2502	A
35	A	2507	C
35	A	2511	A

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Mol	Chain	Res	Type
35	A	2512	A
35	A	2529	A
35	A	2532	G
35	A	2533	C
35	A	2545	G
35	A	2548	U
35	A	2549	G
35	A	2559	A
35	A	2567	U
35	A	2569	G
35	A	2571	C
35	A	2574	C
35	A	2585	U
35	A	2607	G
35	A	2609	A
35	A	2627	C
35	A	2630	A
35	A	2640	G
35	A	2647	U
35	A	2649	A
35	A	2650	A
35	A	2653	G
35	A	2654	A
35	A	2655	U
35	A	2659	A
35	A	2665	C
35	A	2669	G
35	A	2672	A
35	A	2677	A
35	A	2688	C
35	A	2689	C
35	A	2693	A
35	A	2694	G
35	A	2699	C
35	A	2700	A
35	A	2702	A
35	A	2705	G
35	A	2715	U
35	A	2726	G
35	A	2728	U
35	A	2729	G
35	A	2732	G

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Mol	Chain	Res	Type
35	A	2742	A
35	A	2744	C
35	A	2749	G
35	A	2778	U
35	A	2779	U
35	A	2786	U
35	A	2790	A
35	A	2791	G
35	A	2796	A
35	A	2797	C
35	A	2806	G
35	A	2810	U
35	A	2826	A
35	A	2827	G
35	A	2833	U
35	A	2837	U
35	A	2839	U
35	A	2853	C
35	A	2854	A
35	A	2865	G
35	A	2870	C
35	A	2887	G
35	A	2912	A
35	A	2913	U
35	A	2915	C
35	A	2926	A
35	A	2936	C
35	A	2938	G
35	A	2942	G
35	A	2950	C
35	A	2953	U
35	A	2957	A
35	A	2968	G
35	A	2972	A
35	A	2982	A
35	A	2985	G
35	A	3002	A
35	A	3009	U
35	A	3014	A
35	A	3015	C
35	A	3021	A
35	A	3022	G

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Mol	Chain	Res	Type
35	A	3023	G
35	A	3042	A
35	A	3056	A
35	A	3080	A
35	A	3082	U
35	A	3088	C
35	A	3093	A
35	A	3101	C
35	A	3104	A
35	A	3105	C
35	A	3106	C
35	A	3112	A
35	A	3115	A

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	B	10	G
35	A	89	A
35	A	97	U
35	A	284	G
35	A	299	G
35	A	302	U
35	A	316	U
35	A	357	U
35	A	445	U
35	A	641	U
35	A	643	G
35	A	974	G
35	A	980	C
35	A	981	U
35	A	1007	G
35	A	1010	U
35	A	1012	C
35	A	1084	U
35	A	1164	A
35	A	1185	A
35	A	1186	G
35	A	1253	C
35	A	1436	C
35	A	1730	U
35	A	2085	C

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Mol	Chain	Res	Type
35	A	2088	C
35	A	2094	G
35	A	2130	G
35	A	2163	U
35	A	2168	U
35	A	2169	G
35	A	2342	A
35	A	2350	G
35	A	2381	A
35	A	2698	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 413 ligands modelled in this entry, 411 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
36	GNP	6	801	-	29,34,34	1.60	7 (24%)	33,54,54	2.12	6 (18%)
36	GNP	5	801	-	29,34,34	1.59	7 (24%)	33,54,54	2.14	6 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GNP	6	801	-	-	3/14/38/38	0/3/3/3
36	GNP	5	801	-	-	4/14/38/38	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	6	801	GNP	PB-O3A	4.40	1.64	1.59
36	5	801	GNP	PB-O3A	4.26	1.64	1.59
36	6	801	GNP	C6-N1	3.14	1.38	1.33
36	6	801	GNP	PB-O1B	3.10	1.51	1.46
36	5	801	GNP	C6-N1	3.09	1.38	1.33
36	5	801	GNP	PB-O1B	3.04	1.51	1.46
36	5	801	GNP	PG-N3B	3.01	1.71	1.63
36	6	801	GNP	PG-N3B	2.90	1.70	1.63
36	5	801	GNP	PG-O1G	2.73	1.50	1.46
36	6	801	GNP	PG-O1G	2.67	1.50	1.46
36	5	801	GNP	PB-O2B	-2.22	1.50	1.56
36	6	801	GNP	PB-O2B	-2.16	1.50	1.56
36	6	801	GNP	C5-C6	2.08	1.44	1.41
36	5	801	GNP	C5-C6	2.07	1.44	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	801	GNP	C5-C6-N1	-8.43	111.91	123.43
36	6	801	GNP	C5-C6-N1	-8.42	111.92	123.43
36	5	801	GNP	C2-N1-C6	5.85	125.23	115.93
36	6	801	GNP	C2-N1-C6	5.82	125.17	115.93
36	6	801	GNP	PB-O3A-PA	-2.80	122.76	132.62
36	5	801	GNP	PB-O3A-PA	-2.77	122.86	132.62
36	5	801	GNP	N3-C2-N1	-2.77	123.53	127.22
36	6	801	GNP	N3-C2-N1	-2.76	123.55	127.22
36	5	801	GNP	C4-C5-C6	-2.57	118.35	120.80
36	6	801	GNP	C4-C5-C6	-2.54	118.37	120.80
36	5	801	GNP	C2-N3-C4	-2.17	112.87	115.36
36	6	801	GNP	C2-N3-C4	-2.12	112.93	115.36

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	5	801	GNP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
36	5	801	GNP	C5'-O5'-PA-O1A
36	5	801	GNP	O4'-C4'-C5'-O5'
36	5	801	GNP	C3'-C4'-C5'-O5'
36	6	801	GNP	O4'-C4'-C5'-O5'
36	6	801	GNP	C3'-C4'-C5'-O5'
36	6	801	GNP	C5'-O5'-PA-O1A

There are no ring outliers.

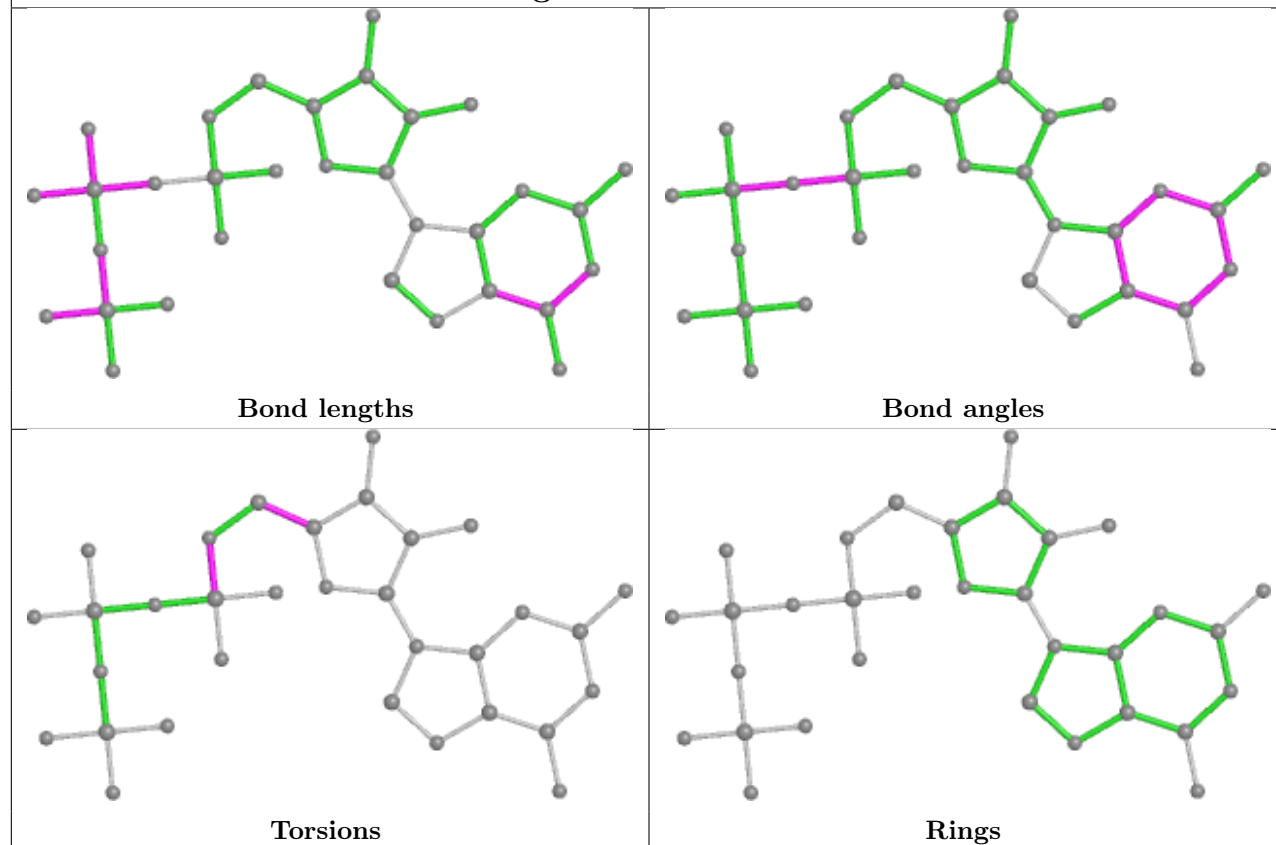
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	6	801	GNP	2	0
36	5	801	GNP	1	0

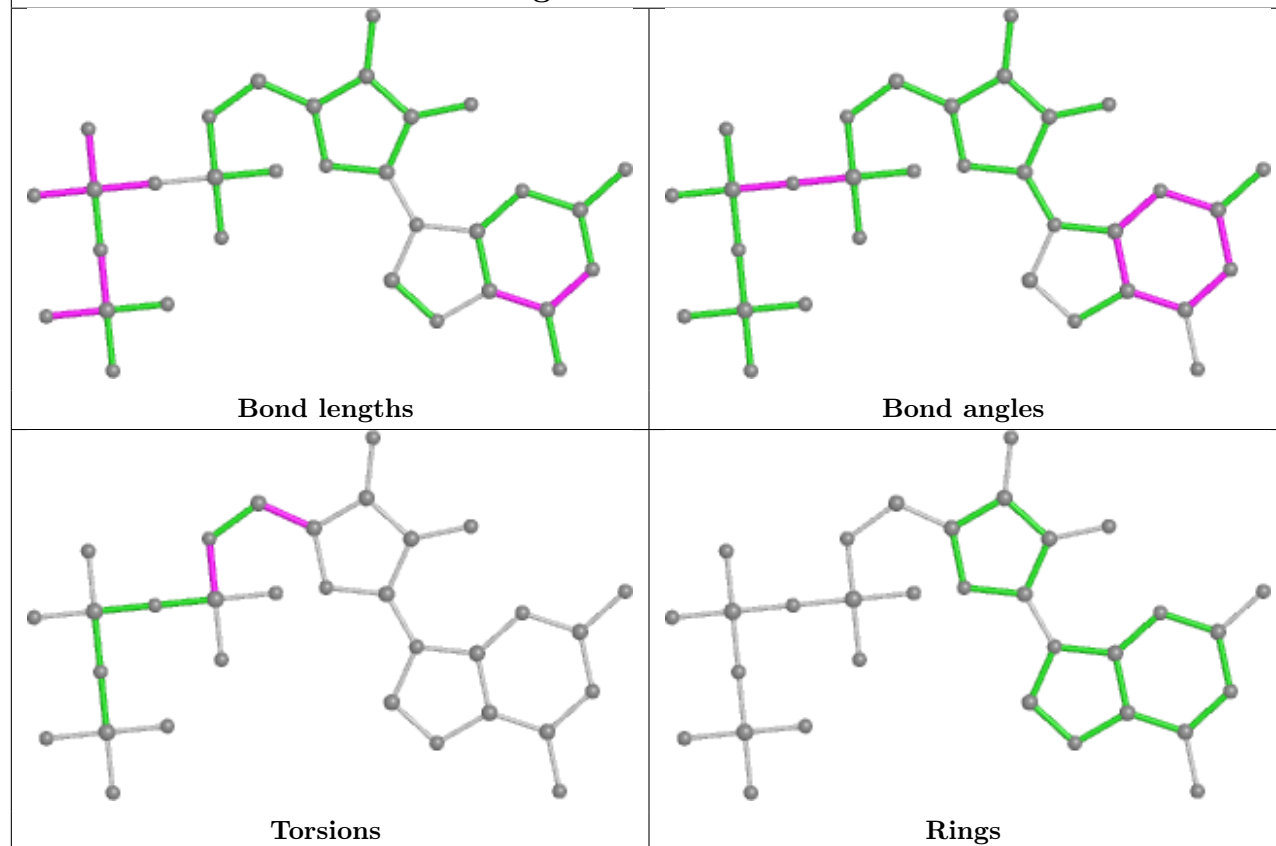
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



## Ligand GNP 6 801



## Ligand GNP 5 801



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

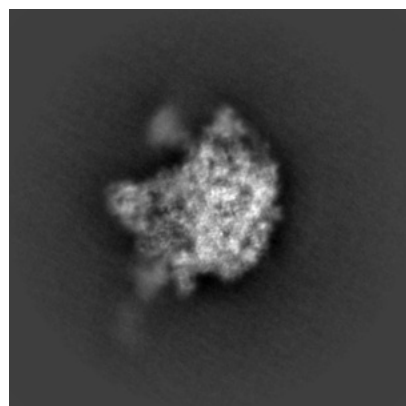
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61960. These allow visual inspection of the internal detail of the map and identification of artifacts.

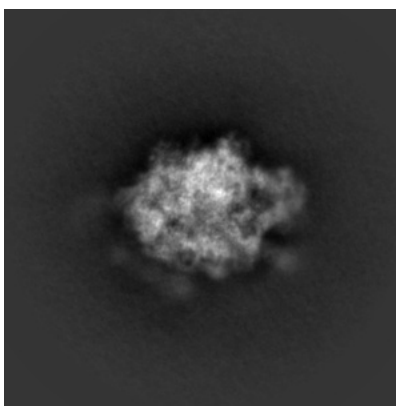
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

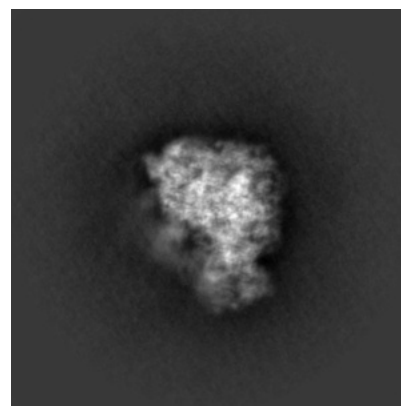
#### 6.1.1 Primary map



X

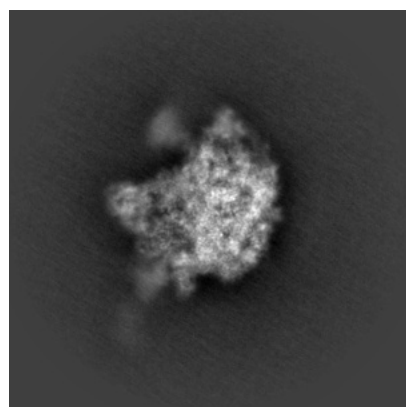


Y

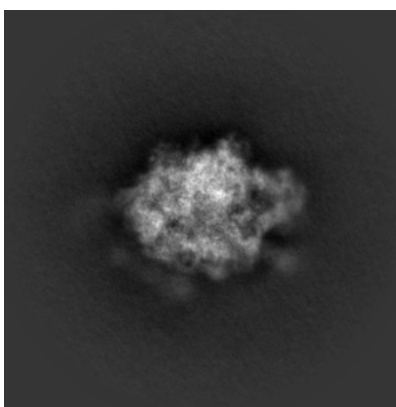


Z

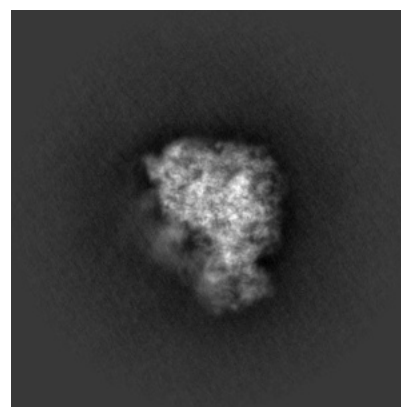
#### 6.1.2 Raw map



X



Y

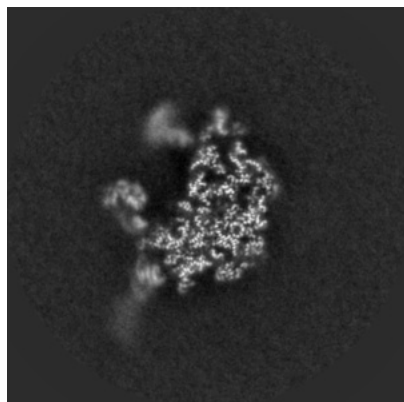


Z

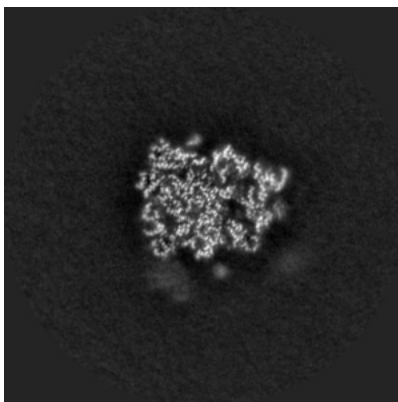
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

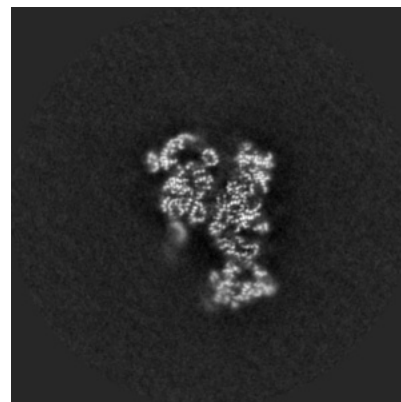
### 6.2.1 Primary map



X Index: 175

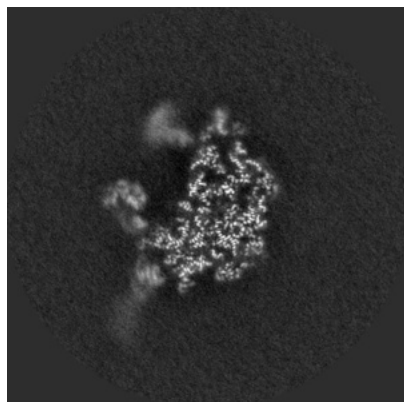


Y Index: 175

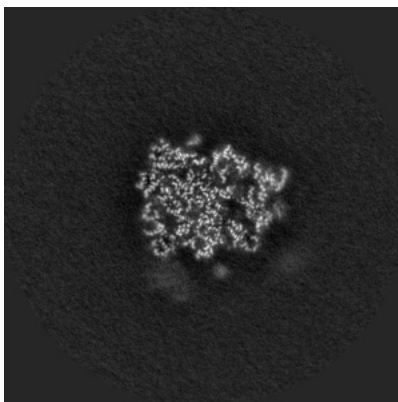


Z Index: 175

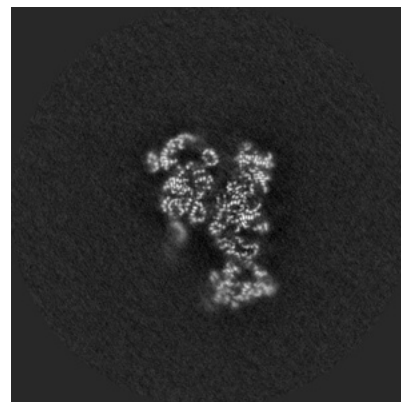
### 6.2.2 Raw map



X Index: 175



Y Index: 175

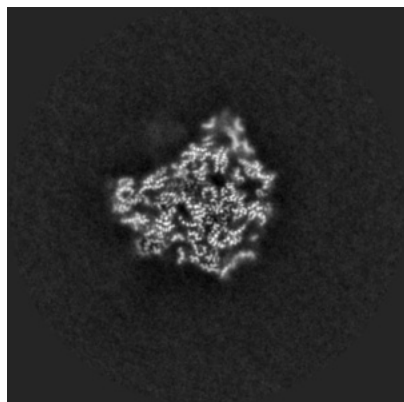


Z Index: 175

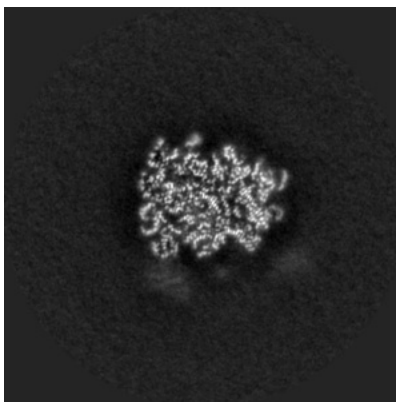
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

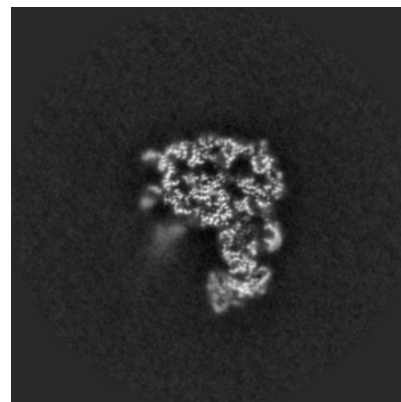
### 6.3.1 Primary map



X Index: 203

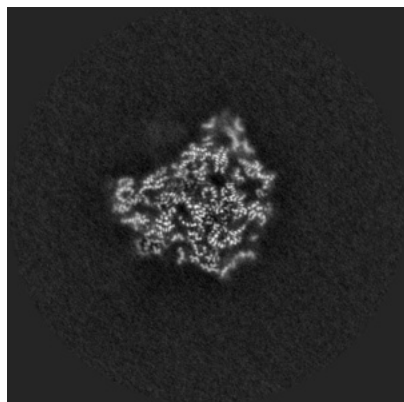


Y Index: 172

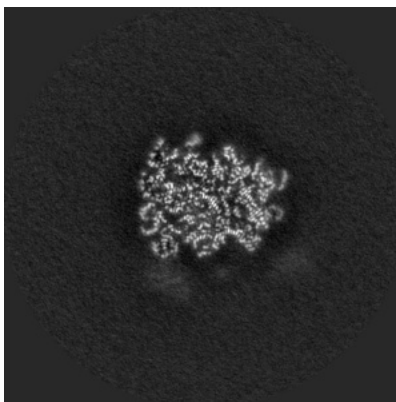


Z Index: 191

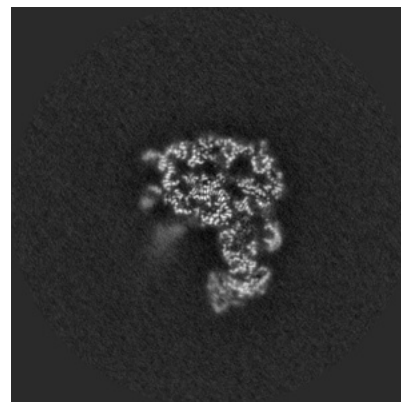
### 6.3.2 Raw map



X Index: 203



Y Index: 172

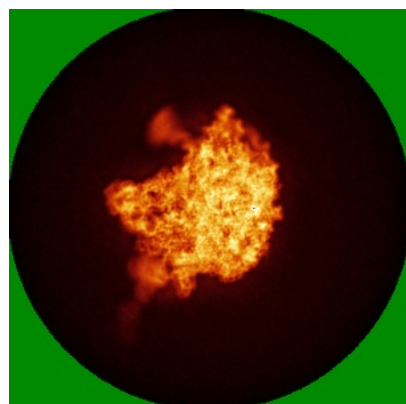


Z Index: 191

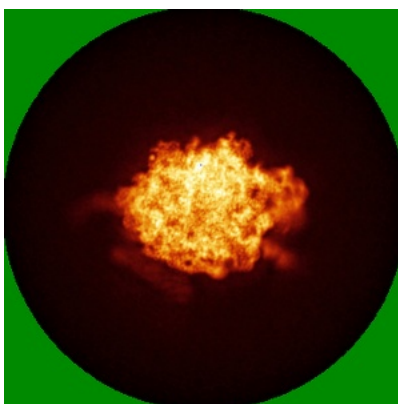
The images above show the largest variance slices of the map in three orthogonal directions.

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

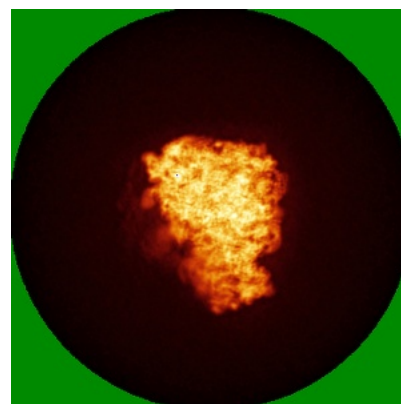
### 6.4.1 Primary map



X

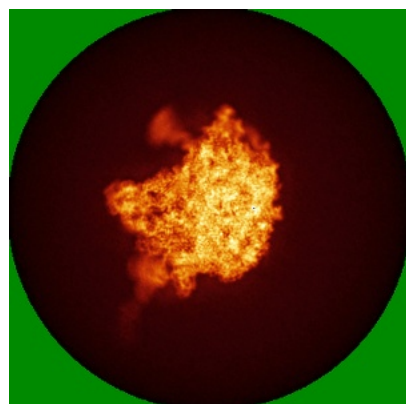


Y

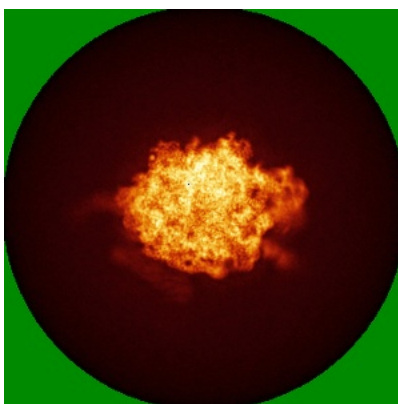


Z

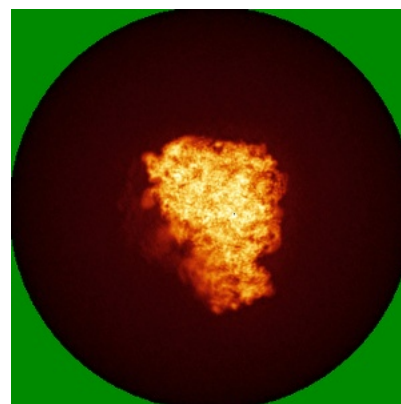
### 6.4.2 Raw map



X



Y



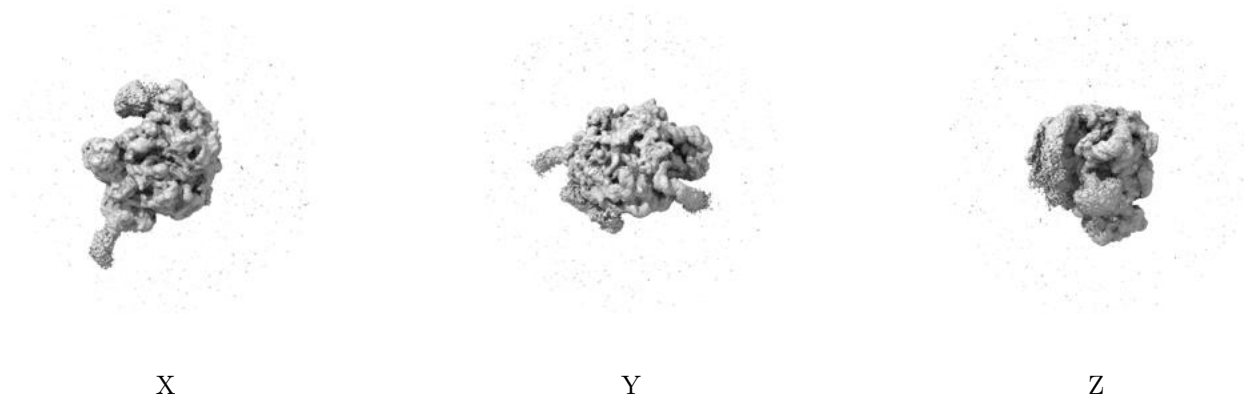
Z

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



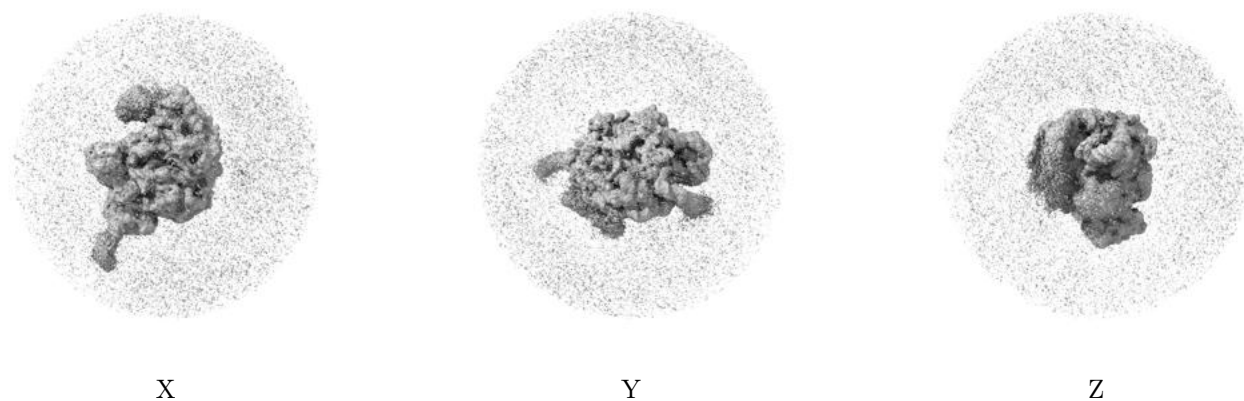
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00715. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

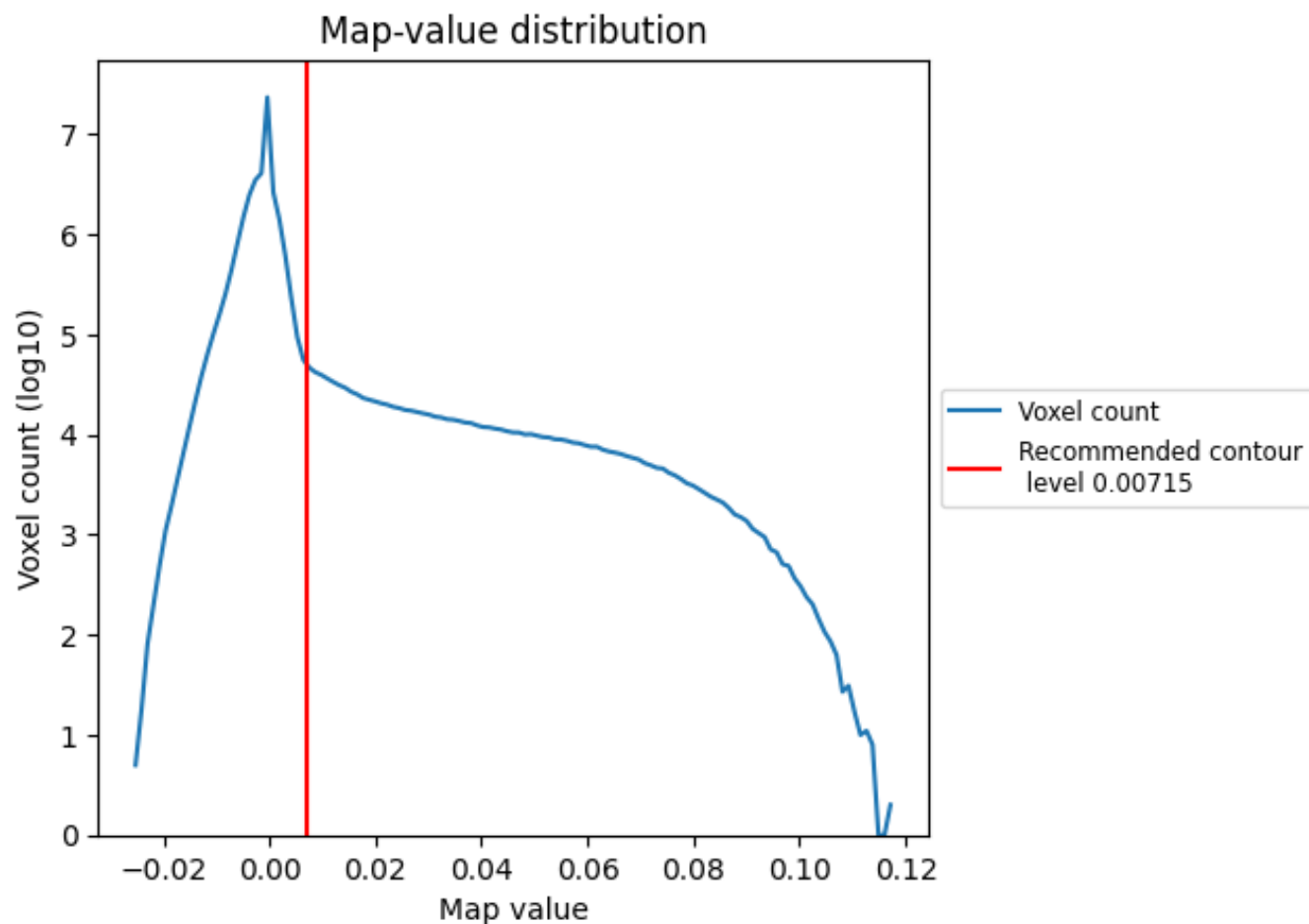
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

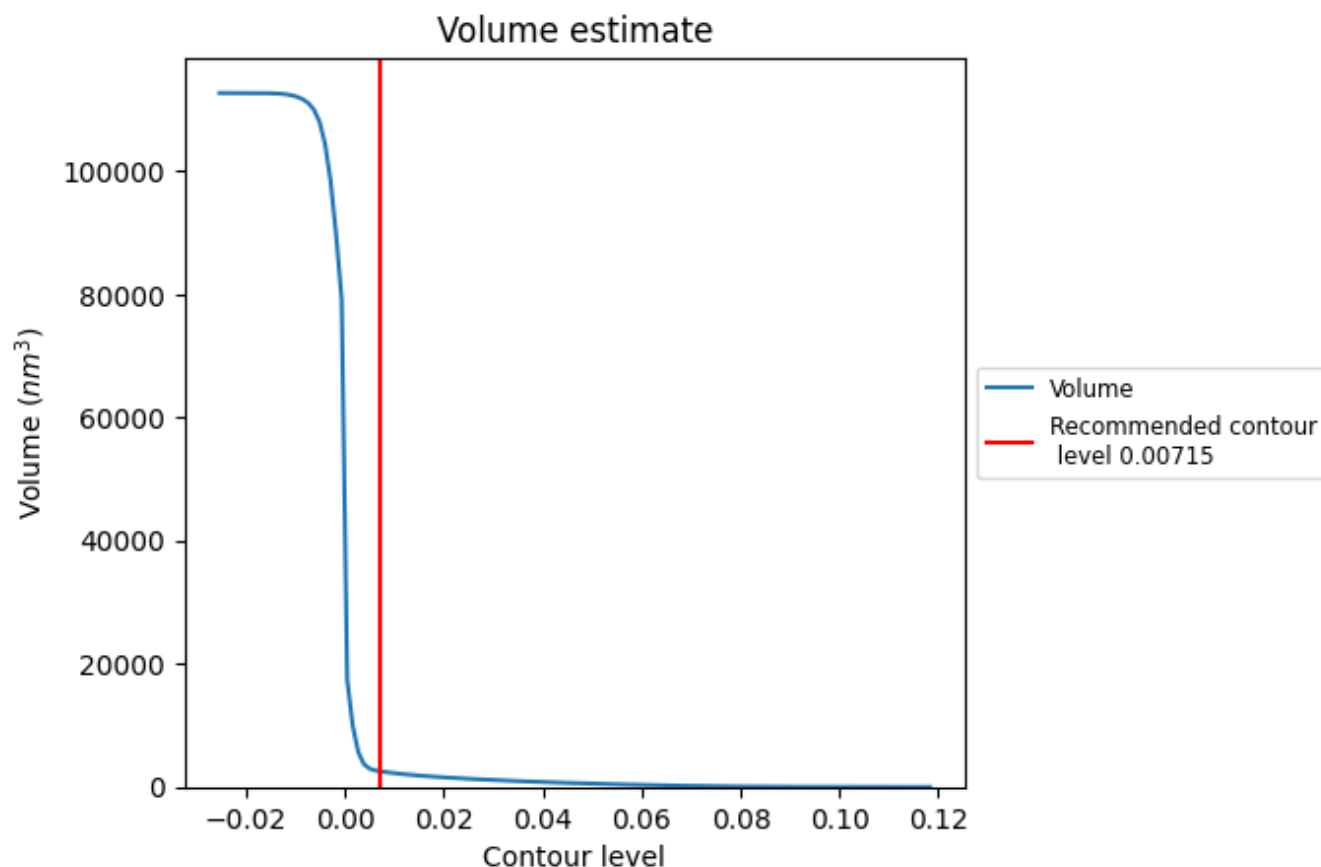
### 7.1 Map-value distribution [i](#)



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



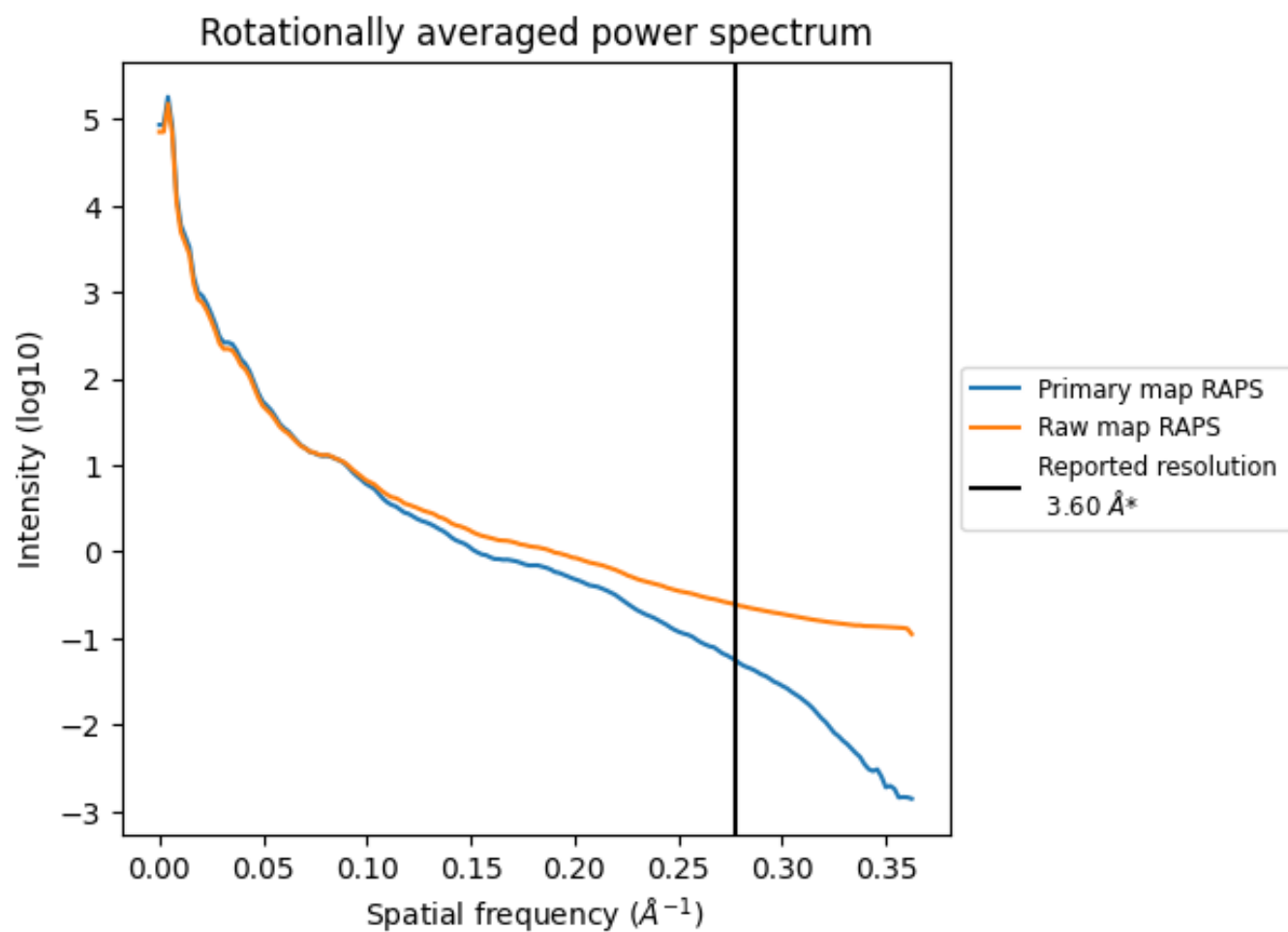
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2544  $\text{nm}^3$ ; this corresponds to an approximate mass of 2298 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 ⓘ

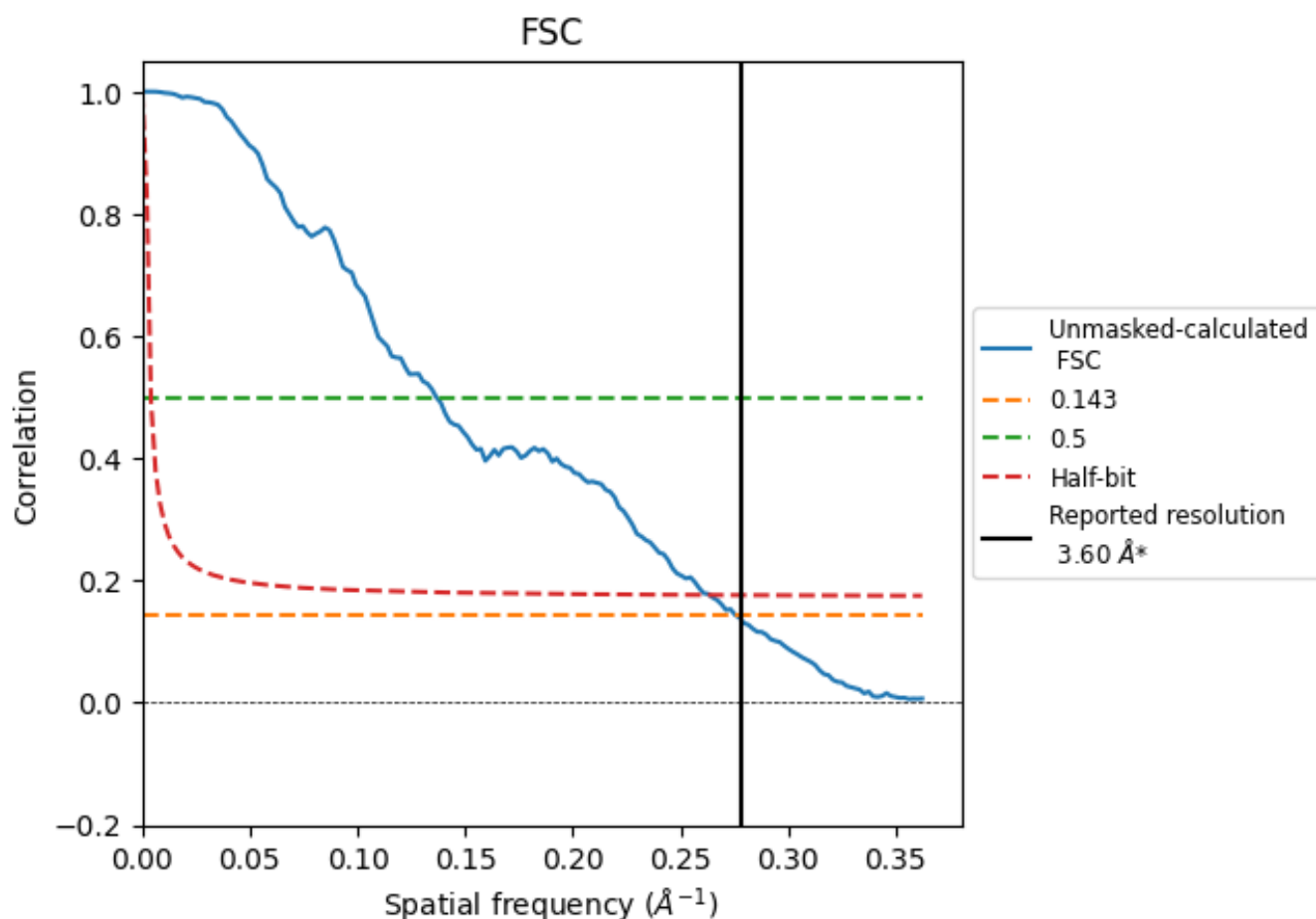


\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.278  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

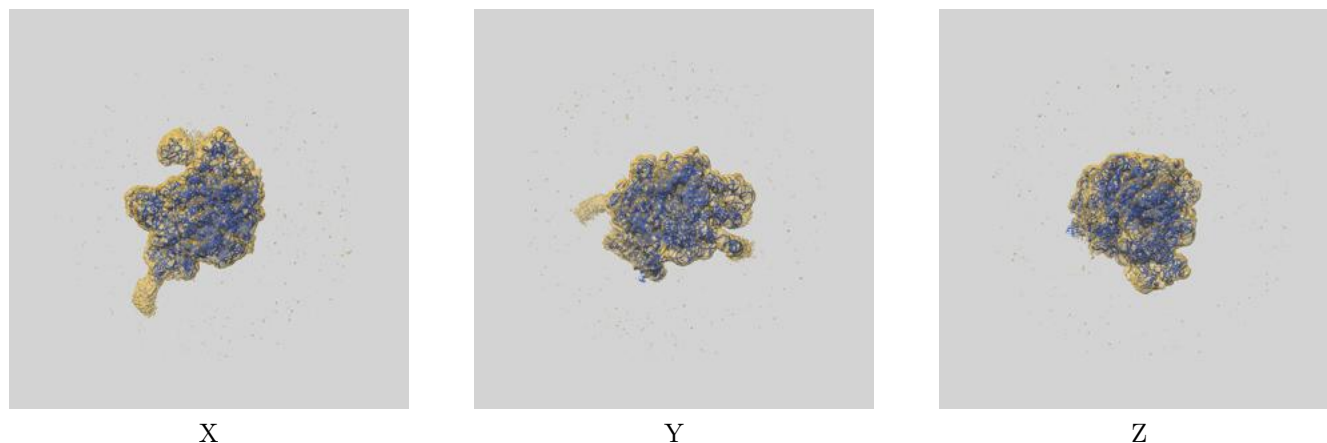
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.63	7.32	3.79

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

## 9 Map-model fit [i](#)

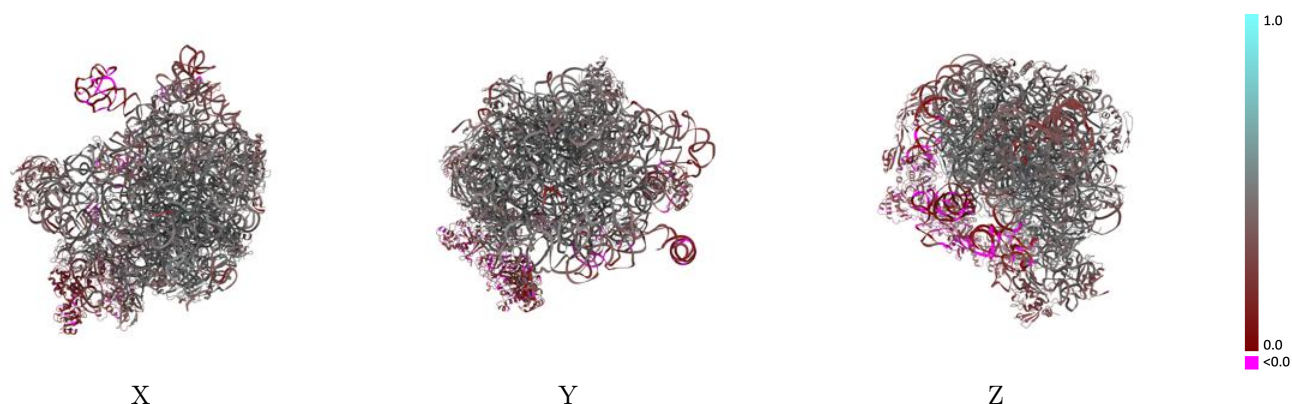
This section contains information regarding the fit between EMDB map EMD-61960 and PDB model 9K10. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

### 9.1 Map-model overlay [i](#)



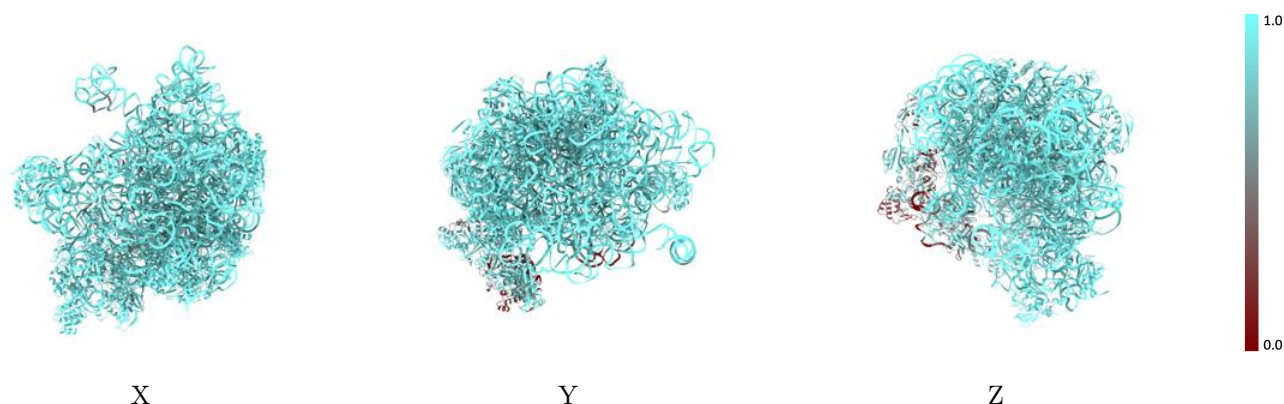
The images above show the 3D surface view of the map at the recommended contour level 0.00715 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



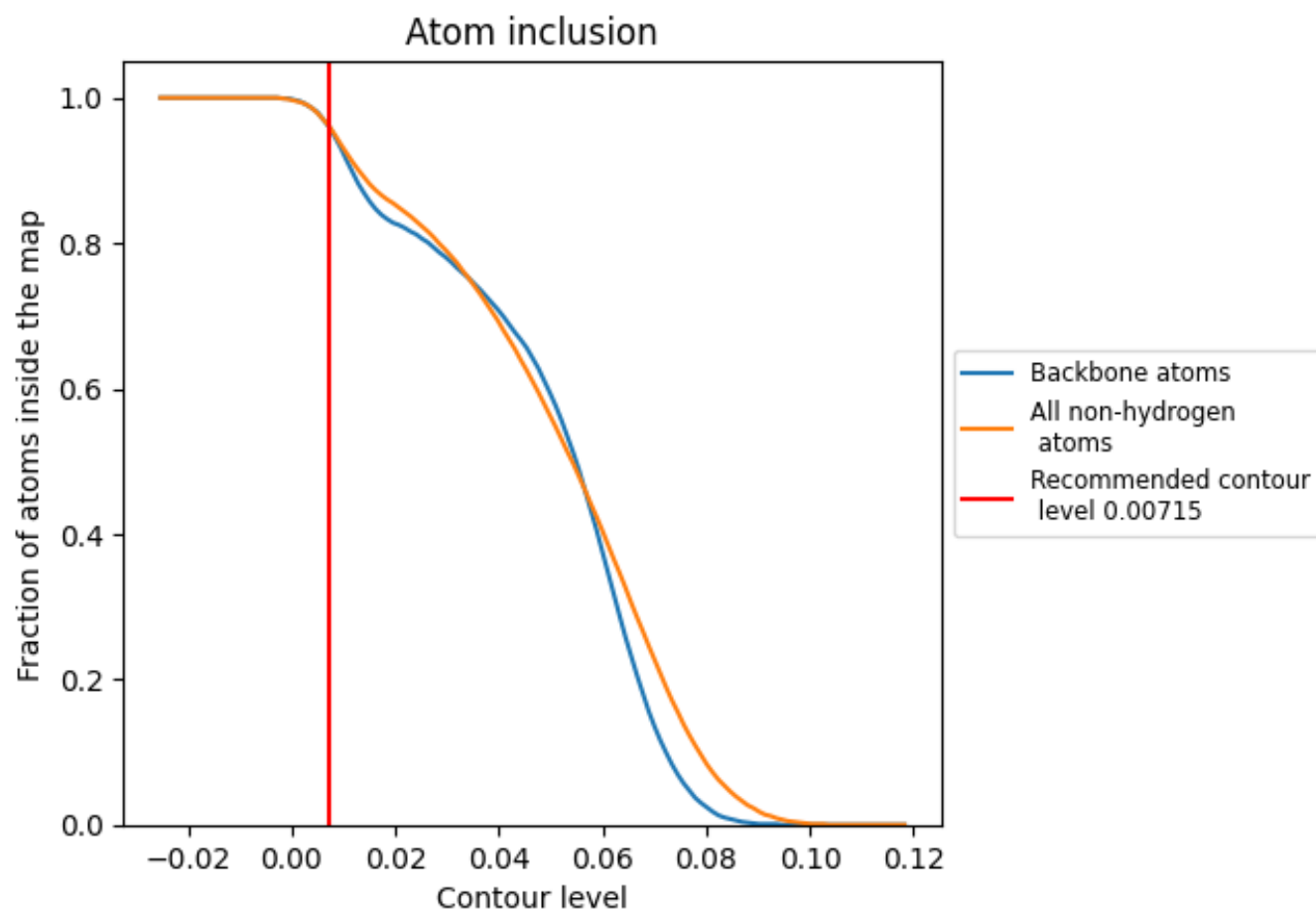
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00715).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.00715) and Q-score for the entire model and for each chain.





Chain	Atom inclusion	Q-score
All	 0.9620	 0.3820
3	 0.9890	 0.4380
5	 0.8110	 0.1370
6	 0.6100	 0.1690
A	 0.9880	 0.4100
B	 0.9980	 0.4130
C	 0.9910	 0.4470
D	 1.0000	 0.4660
E	 0.9940	 0.4420
F	 0.9960	 0.3000
G	 0.9920	 0.3840
H	 0.9680	 0.3500
I	 0.9760	 0.1390
J	 0.9830	 0.1250
K	 0.9940	 0.4520
L	 0.9950	 0.4460
M	 0.9970	 0.4300
N	 0.9960	 0.4480
O	 0.9960	 0.4470
P	 0.9980	 0.3820
Q	 0.9810	 0.4250
R	 0.9970	 0.4460
S	 0.9990	 0.4760
T	 0.9950	 0.4590
U	 0.9910	 0.4310
V	 0.9930	 0.3930
W	 0.9890	 0.3860
X	 1.0000	 0.4690
Y	 0.9960	 0.4550
Z	 0.9980	 0.3900
a	 0.9940	 0.4370
b	 0.9930	 0.4610
c	 0.9870	 0.4290
d	 0.9940	 0.4630
e	 0.9580	 0.4030



*Continued on next page...*



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Chain	Atom inclusion	Q-score
f	 0.9970	 0.4590
g	 0.9890	 0.2600